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Evolution of extreme ontogenetic allometric diversity and heterochrony in pythons, a clade of giant and dwarf snakes

Evolution, 2017; 71(12):2829-2844

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5 September 2018

Evolution of extreme ontogenetic allometric diversity and heterochrony in pythons, a clade of giant and dwarf snakes

Journal:	<i>Evolution</i>
Manuscript ID	17-0274.R1
Manuscript Type:	Original Article
Keywords:	Ontogenetic allometry, heterochrony, Pythonidae, geometric morphometrics

Abstract

Ontogenetic allometry, how species change with size through their lives, and heterochony, a decoupling between shape, size and age, are major contributors to biological diversity. However, macro-evolutionary allometric and heterochronic trends remain poorly understood because previous studies have focused on small groups of closely related species. Here we focus on testing hypotheses about the evolution of allometry and how allometry and heterochrony drive morphological diversification at the level of an entire species-rich and diverse clade. Pythons are a useful system due to their remarkably diverse and well-adapted phenotypes and extreme size disparity. We collected detailed phenotype data on 40 of the 44 species of python from 1,191 specimens. We used a suite of analyses to test for shifts in trajectories that modify morphological diversity. Heterochrony is the main driver of initial divergence within python clades, and shifts in the slopes of allometric trajectories make exploration of novel phenotypes possible later in divergence history. We found that allometric coefficients are highly evolvable and there is an association between ontogenetic allometry and ecology, suggesting that allometry is both labile and adaptive rather than a constraint on possible phenotypes.

Introduction

Allometry, the relationship between biological traits and size (Huxley and Teissier 1936), and its role as both a contributor and constrainer of phenotypic diversity, has been a central focus in evolutionary biology for the last century (Huxley and Teissier 1936; Gould 1966; Mosimann 1970; Klingenberg 1998; 2016).

Ontogenetic allometry, the relationship between biological traits and size through ontogeny (Alberch et al. 1979; Voje et al. 2013) is likely also a major contributor to biological diversity but it is comparatively less well understood. The few studies that have evaluated it among closely related species have concluded that it has played a major role in that clade's phenotypic diversity through ontogeny (Zelditch et al. 2003; Adams and Nistri 2010; Piras et al. 2011). The evolutionary mechanisms that cause ontogenetic allometric trajectories to shift during evolution (see below), thus impacting phenotypic diversity at different developmental stages, remain unclear (Zelditch et al. 2003; Klingenberg 2010; Pélabon et al. 2014). However, extrinsic forces like selective pressures or phenotypic plasticity imposed by ecological factors can affect the intrinsic forces of development (Frankino et al. 2005). Allometry and size-shape relationships have been considered constraints that size and growth impose to the morphologies that organisms can adopt (Simpson 1944; Gould and Lewontin 1979; Maynard Smith et al. 1985). Yet, allometric trajectories themselves can be biological traits under selection and not just constraints (Weber 1990; Frankino et al. 2005; Adams and Nistri 2010; Wilson and Sanchez-Villagra 2010; Klingenberg 2010; Urošević et al. 2013; Porto et al. 2013; Voje et al. 2013; Giannini 2014).

There are several properties of ontogenetic allometric trajectories that can shift the array of phenotypes observed in a clade at any given ontogenetic stage (Zelditch et al. 2012; Sheets and Zelditch 2013). When examined in a statistical regression framework, modifications in the slopes of the allometric regressions, which define the magnitude and direction of shape change with size, can lead to patterns like ontogenetic convergence or divergence. In some European plethodontid salamanders, juveniles start off with very different feet shape but converge onto a similar foot morphology as they grow, which is thought to be an

adaptation to climbing (Adams and Nistri 2010). Conversely, damselfishes show a conserved larval skeletal morphology while they inhabit the homogeneous oceanic environment but diverge into a disparate array of adult morphologies in order to use the more complex and diverse coral reefs as micro-habitat (Frédérich and Vandewalle 2011). Trajectories can shift in their regression intercept, producing parallel trajectories that have the same direction of shape change but never share the same phenotype (Frédérich and Vandewalle 2011; Hipsley and Müller 2017). If trajectories overlap (share an intercept and slope), heterochronic changes, where a decoupling between shape, size and age happens, can induce profound changes in morphological diversity (Gould 1977; Gerber et al. 2008; Bhullar et al. 2012; Foth et al. 2016). Size is the independent variable used in studies of ontogenetic allometry, while time is the independent variable in studies of heterochrony. Without data on the age of the individuals, it is not possible to infer information on rates of change, or establishing heterochronic processes driving evolution {Godfrey:1995gw}. Nevertheless, using size as a proxy of age, it is possible to detect the observable outcomes of heterochrony, like paedomorphosis and peramorphosis, where species become more juvenile or adult looking in respect to the other, respectively (Piras et al. 2011; Gerber and Hopkins 2011). In ontogenetic scaling, a special form of heterochrony, species overlap in size-shape space, where the relationship between size and shape is maintained (i.e. same allometric regression equation), and changes in growth rate will change the juvenile and adult morphologies along the same trajectory (Mitteroecker et al. 2005; Zelditch et al. 2012). Heterochronic changes therefore produce forms that are more peramorphic or paedomorphic in respect to the ancestor (Gould 1977; Alberch et al. 1979; Piras et al. 2011; Gerber and Hopkins 2011). Figure 1 illustrates examples of these patterns, and the workflow used to detect them.

Pythons are a family of Old World constrictor snakes that include 44 species distributed in Africa, Asia, Melanesia and Australia. They exhibit their maximum taxonomic, phenotypic and ecological diversity in the Australasian region (Barker et al. 2015). Several aspects of this family make them an excellent model for the study of morphological diversity, adaptation and allometry. They display one of the most extreme size ranges among any animal family, ranging from the pygmy python (*Antaresia perthensis*) that reach only 65

cm (Esquerré, unpublished data) to the reticulated python (*Malayopython reticulatus*), the longest snake on Earth that can reach almost 9 m in length (Murphy and Henderson 1997) – with difference in mass that spans three orders of magnitude. Their remarkable ecological diversity, particularly in micro-habitat choice, has provided diverging selective pressures driving an equally remarkable head shape diversity (Esquerré and Keogh 2016). This combination of features provides an ideal scenario to test hypotheses on the contributions of allometry to clade diversity and how allometry interacts with ecological factors.

Our study focuses on ontogenetic allometry and observable products of heterochrony in python head and body shape. Here we examine diversity in post-natal ontogenetic allometric trajectories in regard to direction, length (magnitude) and intercept at the family level, and at a genus or clade level, to estimate if closely related species would be more constrained to change shape in the same direction and have similar ontogenetic trajectories. Additionally, we test if among-species morphological disparity increases (indicating ontogenetic divergence) or decreases (indicating ontogenetic convergence) over ontogeny at the whole family level and for each clade separately. In clades where trajectories are overlapping, we explore how the array of phenotypic mega-diversity in pythons is affected by changes along a common ontogenetic trajectory, with the ambition of finding patterns that can be explained by processes of heterochrony. Then, by incorporating ontogenetic allometry into a phylogenetic framework we evaluate how direction and magnitude of shape change with size evolves. This is achieved by mapping those traits on a phylogeny and treating allometry itself as an evolvable trait (Gerber et al. 2008). Finally, we determine if selection on micro-habitat use, which is known to strongly affect adult head morphology (Esquerré and Keogh 2016), impacts the diversity of ontogenetic trajectories directing phenotypic change through growth in pythons.

Material and methods

Sampling

We visited nine major natural history collections (see Table S1) and sampled 1,191 specimens spanning 40

of the 44 recognized species of Pythonidae (Barker et al. 2015), plus *Boa constrictor* from Boidae to have a comparison with this snake family that shows strong convergent evolution with pythons (Esquerré and Keogh 2016). We measured an average of 32.2 specimens per species (range 3-153; see Table S1 for details on sampling). To increase statistical power, we considered some species that are phenotypically and ecologically extremely similar, and have shallow or unassessed genetic divergence, to be a single unit for analyses. This gave us more complete size ranges and did not change our interpretation of the results. Specifically, we grouped *Python breitensteini* with *P. curtus*, *P. natalensis* with *P. sebae*, *Morelia imbricata* with *M. spilota*, *Morelia azurea* with *M. viridis*, all the *Leiopython* species with *L. albertisii*, and *Boa imperator* with *B. constrictor*.

Morphometrics

The head of each specimen was photographed in the dorsal view with a Canon 7D camera with a Canon 100 mm f/2.8 macro lens and a Canon Twin Lite macro flash, mounted on a tripod. We placed a scale-bar next to each specimen to quantify size. On each photograph, we digitized a configuration of 9 landmarks and 26 semilandmarks to characterize head shape (Fig. S1), as described in Esquerré & Keogh (2016). We digitized the landmark and semilandmark coordinates using tpsDig v.2.17 (Rohlf 2015). Semilandmarks were permitted to slide in order to minimize bending energy (Gunz and Mitteroecker 2013) on tpsRelw v.1.54 (Rohlf 2015). To retain only shape variation between the landmark coordinates, the effects of location, scale and orientation were removed with a generalized Procrustes analysis (Rohlf and Slice 1990) taking into account object symmetry (Klingenberg et al. 2002), performed with the function *bilat.symmetry* in the R package *geomorph* 3.0 (Adams et al. 2016). Head size was calculated as centroid size, the square root of the sum of the squared distance of every landmark to the centroid or ‘center’ of the landmark configuration.

For body shape analyses, we measured head length (from the posterior edge of the jaw, marked with a pin on the specimen, to the tip of the snout) and head width (between the posterior edges of the jaw) from the photographs using tpsDig v.2.17 (Rohlf 2015). For each specimen where the body was preserved and in good condition, we measured the snout-vent length (SVL), tail length, mid-body girth (measured at half of

the SVL) and neck girth (measured just posterior to the skull), using a thread that was then measured against a ruler. To avoid overlapping body measurements we subtracted head length from SVL to get a body length measure. To remove the effect of size while maintaining allometric effects, we calculated the log-shape ratios of the body measurements (Mosimann and James 1979; Claude 2013) where, for each individual, we first computed size as the geometric mean of all measurements. Then, each measurement for each specimen was divided by this size estimation to obtain the shape ratios and then log-transformed. These were used as the data for the subsequent analyses. The log-transformed geometric mean was used as size for the analyses of body shape allometry because it uses all of the body measurements as an estimation of size (Mosimann 1970; Claude 2008), rather than just SVL. Before performing the analyses stated below, we tested for the presence of sexual dimorphism with a distance-based ANOVA (Goodall 1991; Anderson 2001) on both head and body shape, and found none. This was performed with the function *procD.lm* in *geomorph*.

Analyses of allometric ontogenetic trajectories

To study allometry at a shallower evolutionary scale and to compare between lineages, we grouped the species in clades which correspond to their genera, except for *Bothrochilus* and *Leiopython* which are sister taxa grouped together here. The following analyses follow the schematic Figure 1, in a step by step procedure where changes in allometry and heterochrony are identified. All the analyses were performed on head shape and body shape variables separately. First, we determined if any species displayed isometric growth (no change in shape with size) by fitting individual regressions for each species of size on shape using *procD.lm* from the R package *geomorph* and assessing the significance with 10,000 iterations. A significant association rejects the null hypothesis of isometry and reveals that there is allometry. A non-significant relationship indicates isometry or lack of sufficient sampling to provide statistical power to detect allometry. We then assessed the relationship of shape and log-transformed size (i.e. allometry) for all species of pythons using two complementary approaches: 1) a homogeneity of slopes test, and 2) a phenotypic trajectory analyses, which are described in detail below. They are both used to establish the patterns of direction and magnitude of shape change with size, by testing for differences in the slope angle and length.

147 The tests differ in that the first considers size as a continuous variable and the second considers size as a
 148 proxy for estimating ontogenetic stage as a categorical variable. It is useful to perform both because together
 149 they provide a robust statistical framework and visualize different aspects of the results, the first being a
 150 size-shape space and the second a morphospace visualization.

151
 152 We performed an homogeneity of slopes (HOS) test, using a distance-based ANCOVA on both head and
 153 body shape including size, species and the interaction of the two terms (Collyer and Adams 2013). The test
 154 performs statistical assessment of the terms in the model using distances among specimens, rather than
 155 explained covariance matrices among variables (Anderson 2001). It quantifies the amount of shape variation
 156 explained by size, computes the allometric slopes for each species, and performs pairwise comparisons for
 157 the slope angles (direction of shape change with size) and slope lengths (amount of shape change with size).
 158 Statistical significance was evaluated with a residual randomization permutation procedure with 10,000
 159 iterations. This was performed using the *advanced.procD.lm* function in *geomorph*. For a simple
 160 visualization of the diverse ontogenetic allometric trajectories among the species, we plotted the first
 161 principal component (PC1) of the matrix of predicted shapes from the multivariate regression (Adams and
 162 Nistri 2010).

163
 164 We performed a phenotypic trajectory analysis (PTA) (Adams and Collyer 2009; Collyer and Adams 2013),
 165 a procedure that quantifies the variation of different attributes of a shape change trajectory between two or
 166 more points. We used species as the groups and juveniles and adults as the trajectory points. First, for each
 167 species we chose the specimens that clearly represented juveniles or adults (sexually mature), leaving out
 168 specimens where sexual maturity was uncertain. We compared the direction and size of the trajectories
 169 between juveniles and adults between all taxa and assessed the significance of these comparisons with
 170 10,000 permutations. This analysis was performed with the function *trajectory.analysis* in *geomorph*. To
 171 visualize the ontogenetic phenotypic trajectories, we plotted the first two PCs of shape variation. To enable
 172 biological interpretation of the PCs from the PTA analysis and the above multivariate regression of head

shape data we used thin plate spline deformation grids (Bookstein 1991). For body shape analyses we examined the PC loadings.

When pairwise species comparisons of slope angle did not reject the null hypothesis of parallel allometric slopes, indicating similar slopes, we performed an additional test to evaluate whether the slopes are overlapping (H_0) or parallel (H_1). This was done by assessing whether there is a shift on the intercept along the Y (shape) axis using pairwise comparisons of the intercepts of the allometric regression of each species. Significance was assessed by comparing the difference to a set of 10,000 permutations, with the *int.test* R function developed by Piras *et al.* (Piras et al. 2011). For species where the null hypothesis of parallel trajectories was rejected, we then investigated the possibility of heterochrony.

It is important to note that due to the limitations of a study using wild-caught rare species, the ontogenetic sampling for all of the species is not complete. This mainly influences the results on magnitude of shape change with size. The broad patterns across the family is clear, but specific comparisons, particularly with *Simalia nauta*, *S. oenpelliensis* and *Liasis fuscus*, where small juveniles could not be measured, should be taken with caution.

Heterochrony

We performed a test to identify patterns of peramorphosis/paedomorphosis with the null hypothesis that two species do not differ in predicted shape at the maximum size of the species being compared using the R function *peram.test* developed by Piras et al. (Piras et al. 2011). A rejection of the null is interpreted as one of them being peramorphic (more ‘adult-like’) or paedomorphic (more ‘juvenile-like’) with respect to the other. Statistical significance was assessed by comparing to a randomly generated distribution of the data with 10,000 permutations.

Finally, we performed two tests developed by (Gerber and Hopkins 2011), and based on (Mitteroecker et al. 2005), to further examine heterochrony by assessing the species trajectories overlap in shape and size-shape space. These tests rely on the fact that heterochrony requires the species shape change trajectories to overlap. They are both based on computing multivariate regressions of shape on size for the species being compared. The first one (Tfh1) is used to identify heterochrony by ontogenetic scaling (maintaining an overlap in size-shape space), which is translated into an extension or truncation of the ontogenetic trajectory. It uses the sum of the squared residuals from the regression as a tests statistic. The second one (Tfh2) is used to identify heterochrony with a size-shape dissociation, and uses the sum of squared distances from each specimen to its nearest point on the regression curve as a test statistic. Statistical significance was assessed with 10,000 permutations for Tfh1 and 500 permutations for Thf2.

The number of pairwise comparisons from the intercept and peramorphosis tests requires that the P -values are corrected with a Benjamini-Hochberg or ‘false discovery rate’ correction (Benjamini and Hochberg 1995). The P -values from the Tfh1 and Tfh2 tests from heterochrony were not corrected since we are interested in accepting the null hypothesis and therefore type II error is a bigger concern than type I error. The P -values from the slope angle and length tests were not corrected since the tests are not independent and do not require correction. For all the tests we considered a P -value below 0.05 (5%) as the threshold for statistical significance.

Ontogenetic convergence and divergence

Slopes that differ in their angular direction, as defined by the HOS test, may be the result of ontogenetic convergence (e.g., Adams and Nistri 2010) or divergence (i.e. allometric repatterning (Webster and Zelditch 2005)). For pythons as a whole, and for each clade where not all species had the same slope, we assessed whether their ontogenetic allometric trajectories display a convergent or divergent pattern, against a null hypothesis of ontogenetic consistency, by comparing the variation among juveniles versus the variation among adults. We calculated and summed the pairwise Euclidean distances between all specimens, using the

first principal component of the predicted morphologies in both ontogenetic stages separately, to calculate the $D = D_{\text{juv}} - D_{\text{adult}}$ statistic. A positive result implies adults are more similar to each other than juveniles are (convergence) and a negative result implies juveniles more similar to each other than adults are (divergence). The significance of the statistic was assessed with 10,000 permutations of the data where depending on the hypothesis of convergence or divergence, a P -value was obtained based on the proportion of iterated D statistics that were below or above the observed D , respectively (Adams and Nistri 2010).

Phylogenetic hypothesis

To examine variation in ontogenetic allometry in an evolutionary context we constructed a time-calibrated ultrametric phylogenetic tree of the pythons. We used the alignment provided for the most recent and complete phylogenetic analysis that included this group (Reynolds et al. 2014). This dataset corresponds to a supermatrix of three mitochondrial and eight nuclear loci of most pythons and boas. Details on how we reconstructed the phylogeny can be found in the Supplementary Information.

Evolution of ontogenetic allometric trajectories

There are currently no methods to perform the preceding statistical analyses for allometric ontogenetic trajectories in a phylogenetic comparative context, taking into account the statistical non-independence of species data when within-species variation is the feature of interest (rather than species averages). Thus, we present a novel approach to visualize the evolution of the parameters of the allometric trajectories in a phylogenetic context. Similarly to what is done in a traditional morphospace visualization, this method is based on plotting the first two principal components of the allometric vector describing the multivariate slopes of the trajectories, similar to what has been called an allometric space (Klingenberg and Froese 1991; Wilson and Sanchez-Villagra 2010). However, in addition to the terminal taxa, we also added the reconstructed ancestral state of each node using a maximum likelihood approach, and the tree topology connecting these, making it analogous to a phylomorphospace (sensu Sidlauskas 2008). We propose this visualization be termed phyloallomspace. This analysis was implemented with the function

plotGMPhyloMorphoSpace of *geomorph*. To reconstruct the evolution of the magnitude of allometric shape change, we used the slope vector length, or magnitude of shape change per unit of size, to perform an ancestral state reconstruction using maximum likelihood. This was performed with the function *contMap* in the R package *phytools* (Revell 2012). We also removed the three species with missing early ontogenetic stages from the evolutionary analysis, to avoid creating any bias in the results.

Ecological influence on ontogenetic allometry

Finally, to test the effect of ecology on ontogenetic allometry, and accounting for phylogenetic relationships, we performed a phylogenetic ANOVA that uses a generalization of phylogenetic generalized least squares (PGLS) for high-dimensional and multivariate data (Adams 2014). This was first performed on the allometric slopes using microhabitat use as the predictor variable, first as coded in Esquerré & Keogh (2016) where *Aspidites melanocephalus* and *A. ramsayi* are considered semi-fossorial and *Liasis mackloti* as semi-aquatic, and second where we lumped the semi-fossorial and semi-aquatic taxa as terrestrial, because these shifts only occur a single time in both cases. This was performed with the *procD.pgls* function in *geomorph* (Adams 2014). To have a visualization of the coupling between the evolution of ecology and allometric coefficients, we performed an ancestral state reconstruction of micro-habitat use by using stochastic character mapping (Huelsenbeck et al. 2003). We ran 10,000 independent stochastic character maps to have an estimate of uncertainty (Revell 2014), using the R package *phytools*.

Results

Ontogenetic allometry

Most of the species displayed allometric growth (i.e. lack of isometry). The species that did display non-significant relationships between size and shape had low samples numbers, so we call caution interpreting results regarding them, namely *Morelia carinata*, *Simalia oenPELLIENSIS*, *S. nauta*, *Python anchietae*, *P. brongersmai* and *L. fuscus* (Table S3). Size, species and the interaction of the two strongly influence python head shape (ANCOVA, size $F_{(1, 1127)} = 320.663$, $P < 0.0001$; species $F_{(31, 1127)} = 47.007$, $P < 0.0001$;

size*species $F_{(31, 1127)} = 4.108$, $P < 0.0001$) and body shape (size $F_{(1, 1040)} = 560.549$, $P < 0.0001$), species $F_{(1, 1040)} = 69.167$, $P < 0.0001$; size*species $F_{(31, 1040)} = 4.096$, $P < 0.0001$). These results indicate that there is clear ontogenetic allometry in both head and body shape and that allometry differs between species in both head and body shape. The pattern is clearly observed on the difference in slopes of trajectories in both head and body shape (Figs. 2 and 3). The raw regression scores, common allometric component (Adams et al. 2013) and raw principal components for all the species and separated by clade can be seen in Figs. S2 and S3.

The head shape changes associated with increasing size, as described by a multivariate regression of shape on log-transformed size (Fig. 2) and by PC1 of the PTA (Fig. 3), involve a broadening of the snout and eyes that become smaller and more dorsally situated. PC2 of the PTA represents a massive enlargement and lateralization of the eyes and a transition to a shorter and more pointed snout. For body shape, PC1 of the PTA represents an elongation of the tail (tail length eigenvector = 0.8) and a slimming of the body (mid-body girth eigenvector = -0.35). PC2 of the PTA mainly represents a thickening of the body (mid-body girth eigenvector = 0.63), an elongation of the body (body length eigenvector = 0.47) and a proportional reduction in head size (head length eigenvector = -0.41; head width eigenvector = -0.43).

Both the HOS test and PTA analyses show equivalent differences of direction and magnitude of shape change in head and body shape, and therefore we only present the results from the first. Head and body shape ontogenetic allometric trajectory diversity is extremely large in pythons. The slope vector lengths and the trajectory path distances, which both translate into the amount of shape change given size, can be seen in Fig S4, but easily interpreted by looking at the steepness of the slopes of shape on size in Fig. 2 and the length of the PTA trajectories on Fig. 3. Pairwise comparison of slope angles and slope vector lengths for head and body shape can be seen in Tables S4-7. Because of the large number of taxa included in these analyses and the great diversity in observed patterns, the results are also summarized on a clade-by-clade

basis in Fig. 4. The main findings supported by the pairwise species comparisons and the visualization of the results can be broken down as follows.

Direction of shape change with size

In general, species within the same genus or clade tended to differ very little in angle of shape change with size, implying parallel or overlapping allometric trajectories within clades (Fig. 4, Tables S4 and S5). The broad pattern is that pythons tend to get broader heads and proportionally smaller and more dorsally situated eyes as they grow. There are a few exceptions, but the most contrasting is *Morelia viridis* which has a significantly different head shape slope orientation from almost all of the species. There are also slope differences in head shape within *Python* and body shape within *Morelia* and *Liasis*.

Magnitude of shape change with size

Similarly to what is observed with the direction of shape change, species within the same clade tend to differ very little in the amount of shape change they go through with size, implying a strong phylogenetic effect on the magnitude of change (Tables S6 and S7). *Simalia clastolepis* has a significantly larger head shape change than most other pythons (Fig. S4 and Table S6). Species in *Simalia* and *Aspidites* tend to show larger amounts of head shape change, whereas other taxa like *Leiopython albertisii*, *Bothrochilus boa* and *Python curtus* display little head shape change with size, getting closer to isometry (Fig. S4 and Table S6), which in multivariate allometry is represented as a flat line parallel to the x-axis (Fig. 4). *Python curtus*, *P. regius* and *P. anchietae* display large amounts of body shape change with size, whereas *Leiopython albertisii*, *Morelia spilota*, *M. bredli* and the two species in the genus *Aspidites* display small amounts of change (Fig. S4 and Table S7).

Intercepts of ontogenetic allometry

Among the species with a similar allometric slope, we did not identify parallel allometric trajectories (different allometric intercepts) within clades for head or body shape, but there were a few cases among

species of different clades (Tables S8 and S9). This indicates that most species with a shared allometric slope have overlapping trajectories.

Heterochrony

Within clades, the most common pattern explaining morphological diversity in pythons is peramorphosis/paedomorphosis (Tables S10 and S11), where slopes and intercepts between species are equivalent but they differ on the maximum size phenotype, one being more “adult-like” or peramorphic than the other. Between clades, both differences in slopes and shifts along the ontogenetic trajectories are responsible for changes in phenotypes. However, within clades many species pairs have equivalent ontogenetic trajectories. The Thf1 and Tfh2 tests found overlapping trajectories in size-shape and shape space mostly within clades. These tests were more conservative in their results, and most species pairs do not display heterochrony according to the test’s definition of heterochrony. However, in both head and body shape, some species pairs within *Python*, *Antaresia*, *Morelia* and *Simalia* display ontogenetic scaling and/or heterochrony via size-shape space dissociation. Furthermore, *Antaresia maculosa* / *A. perthensis* (the largest and smallest species within their clade) and *Simalia boeleni* / *S. clastolepis* display overlap in size-shape space and significantly different maximum size phenotypes in head and body shape respectively, suggesting a strong case of ontogenetic scaling (Tables S12-15).

Ontogenetic convergence and divergence

In the test for ontogenetic convergence/divergence we find convergence in head shape within *Python*, and convergence in body shape within *Morelia* and *Liasis* (Table 1), which is clearly observable from the ontogenetic trajectories (Fig. 4), and from the fact that there is divergence in slopes in those clades (Tables S4 and S5). This means that juveniles of these species are very different to each other but they become very similar as they approach adulthood. More broadly, species with stocky and short-tailed body shapes as juveniles (e.g., *Python curtus*, *P. brongersmai* and *P. regius*) elongate as they grow while species that are

thin and long-tailed as juveniles (e.g. *Simalia*) get stockier and shorter tailed with size, almost converging on body shape with the former.

Phylogenetic hypothesis

Unsurprisingly, the topology recovered by our analysis is identical to the one recovered by (Reynolds et al. 2014). The basal split between the Afro-Asian *Python* genus and the rest of the Pythonidae is dated at the early Oligocene with 33.62 my, with a 95% highest posterior density interval between 26.85 and 40.9 my. Most nodes are supported with a posterior probability higher than 0.95. *Morelia viridis* is not recovered with *Morelia* but with its sister clade *Antaresia* (with low posterior probability). However, preliminary results from a phylogenomic analysis using hundreds of nuclear loci supports the inclusion of this species in *Morelia* (Esquerré et al. *in prep*), therefore it is considered with this clade in the analyses of this paper. For details on the tree topology, divergence times and support see Fig. S5.

Evolution of ontogenetic allometry

The biplot of the inferred evolutionary history of direction of allometric shape change (Fig. 5) highlights the phylogenetic structure found on the grouping of the slopes. For both head and body shape, the genus *Python*, which is sister to all other pythons, displays a distinct set of slopes from the rest, despite being itself very diverse. On both head and body shape, other clades like *Simalia*, *Aspidites* and *Morelia* (except again by *Morelia viridis*) occupy the opposite side of the biplot, while the clades *Antaresia*, *Malayopython*, *Bothrochilus/Leiopython* and most of *Liasis* occupy a middle area of the space.

The ancestral state reconstruction of the magnitude of shape change with size shows a similar pattern of separation in groups of clades as the evolution of direction of shape change. *Simalia*, *Aspidites* and *Morelia* (except *M. viridis*) experience a great amount of head shape change but generally small amounts of body shape change with size. The opposite is true for *Python*, and again, the other clades show intermediate amount of phenotypic change with growth.

378

379 *Ecological influence on allometry*

380 Microhabitat use was found to have a significant effect on the variation of allometric slopes in head shape
 381 with the original micro-habitat codings from Esquerré & Keogh (2016) ($F_{(4, 23)} = 1.736$, $P = \mathbf{0.0062}$) and
 382 considering the semi-fossorial and semi-aquatic species as terrestrial ($F_{(4, 25)} = 2.376$, $P = \mathbf{0.0033}$).

383 Microhabitat use was not found to have significant effect on body shape allometric slopes ($F_{(4, 23)} = 0.759$, P
 384 $= 0.232$) nor when semi-fossorial and semi-aquatic species are coded as terrestrial ($F_{(4, 25)} = 1.087$, $P =$
 385 0.076). The stochastic mapping of micro-habitat predicts terrestriality as the ancestral state of pythons, with
 386 at least three independent origins of semi-arboreality, two of arboreality and one of semi-aquatic and semi-
 387 fossorial micro-habitat preferences (Fig. 5). Comparing the plots representing the evolution of allometry and
 388 ecology in Fig. 5 reveals that there is a tendency of species that have the same ecology to share regions of
 389 allometric space and patterns of magnitude of shape change with size. Fig. S6 displays the ontogenetic
 390 allometric trajectories separated by ecology, showing how there are trends of allometry for each micro-
 391 habitat choice.

392

393

394 **Discussion**

395 Pythons are a morphologically and ecologically mega-diverse group of vertebrates that display phenotypes
 396 that are highly adapted to their ecological lifestyle (Esquerré and Keogh 2016). We have revealed that their
 397 post-natal ontogenetic allometry is evolutionarily labile and they have great diversity in developmental
 398 trajectories. Other published studies of ontogenetic allometric trajectories have focused on variation within
 399 genera or closely related species; as far as we are aware, this is the first study looking into the evolution
 400 ontogenetic allometry at a family level incorporating almost every taxon. Within the Pythonidae we observe
 401 that the shifts in ontogenetic allometric trajectories that change a groups' morphological diversity are not
 402 consistent across all clades. Some clades show ontogenetic convergence, others equivalent trajectories, but
 403 most often the differences observed among phenotypes of a clade are derived from heterochronic processes

(i.e. peramorphosis/paedomorphosis). By the sheer diversity and lability of allometry, and its correlation with ecology in pythons, we suggest that allometry is a highly labile, evolvable and adaptive trait.

Studies within genera normally observe one type of ontogenetic trajectory shift driving the phenotypic diversity: for example ontogenetic convergence in plethodontid salamander foot morphology (Adams and Nistri 2010) or heterochrony in *Podarcis* lizard head shape (Piras et al. 2011). The species-rich and phenotypically conserved old world lacertid lizards also display conserved ontogenetic allometries (Hipsley and Müller 2017). Pythons exhibit these and other patterns too, suggesting that different ontogenetic allometric changes can generate morphological diversity in a relatively short time period. Our data demonstrates that patterns in allometric trajectories in pythons differ within and between clades. Within clades there is a strong pattern of overlapping (similar) trajectories between species, where changes are mostly heterochronic and along the same trajectories. Between clades however, there are discernible shifts in both the direction and magnitude of ontogenetic allometry. This is in agreement with the hypothesis that allometries evolve at million-year time scales and closely related species will tend to show less divergence in their trajectories (Voje et al. 2013). For some clades, like lacertid lizards, phenotypic differences between species are developed pre-natally (observed as shifts in their allometric intercepts), and in others like pythons, differences mostly develop after birth (observed as conserved intercepts but shifts in the extension or slope of the trajectories). In pythons, there is also strong variation in the magnitude of shape change, where some *Python* species experience great body shape transformation as they grow while some *Morelia* and *Aspidites* species experience milder changes.

Heterochronic changes are capable of increasing phenotypic diversity in a short period of time, and induce deep changes in the morphology of lineages (Gould 1977). Birds evolved their unique cranial morphologies by combination of cranial paedomorphosis and beak peramorphosis in relation to theropod dinosaurs (Bhullar et al. 2012; Foth et al. 2016) and heterochrony is a common feature in morphological evolution in squamate reptiles (Piras et al. 2011). Exploring allometric trajectories in size-shape space makes it possible

to infer heterochronic products of processes like paedomorphosis and peramorphosis (Piras et al. 2011) and to distinguish between heterochrony by ontogenetic scaling (with species sharing size-shape space) or by size-shape dissociation (Mitteroecker et al. 2005; Gerber and Hopkins 2011). We identified these two types of heterochrony within four python genera. Most notably, *Antaresia perthensis*, the smallest python in the world, is completely paedomorphic in relation to *Antaresia maculosa*, the largest species within its clade. We identify that the most common form of developmental change fueling initial evolution of pythonid morphologies are heterochronic changes along the trajectories determining the shape at maximum size, where a species changes its phenotype by growing bigger or smaller. Without information on the age of individual specimens though, we can only identify the products and not the processes of heterochronic perturbations (Klingenberg and Spence 1993; Godfrey and Sutherland 1995; Piras et al. 2011), because paedomorphosis or peramorphosis can originate from modifications on age at onset, age at offset and/or growth rate (Reilly et al. 1997). However, snakes generally display indeterminate growth (Andrews 1982; Shine et al. 1998) and size is strongly correlated with age (Gignac and Gregory 2005), which make them a much better model for detecting heterochrony than most animal groups. Our data suggests that heterochrony is the process responsible for morphological evolution at the early stages of diversification, since it is responsible for divergence within clades. It seems that longer evolutionary times are required for allometric slopes to evolve, allowing the ontogenetic allometric trajectories to explore new areas of morphological space (Weston 2003; Wilson and Sánchez-Villagra 2011). Similarly, some closely related dinosaur species tend to have more similar and conserved ontogenies and that these diverge as phylogenetic relatedness decreases (Bhullar et al. 2012; Mallon et al. 2015). Shifts in ontogenetic allometric slopes increases the disparity in a group and aids in finding new phenotypes that better suit the selective pressures.

The analyses of allometric slope, intercept and peramorphosis/paedomorphosis reveal a clear pattern of conserved allometric trajectories and hypermorphosis where differences in the shape attained at maximum size suggest that heterochrony is mostly the cause of morphological evolution at the start of divergence. On the other hand, the Tfh1 and Tfh2 analyses of overlap in size-shape and shape space suggest a much weaker

pattern of heterochrony. Nonetheless, given the strong support of heterochronic patterns found by the previous battery of analyses, and the clear morphological differences in phenotypes between most species of pythons of the same clades, we conclude that the Tfh1 and Tfh2 tests are very conservative in detecting patterns of heterochrony.

Studies of static allometry, where size-phenotype relationships are studied across different organisms at the same developmental stage, have proposed that size imposes strong limitations and constraints on phenotypes (Huxley 1932; Simpson 1944; Gould and Lewontin 1979). What we observe as developmental constraints in studies of ontogenetic allometry and development can be expressions of different processes, like a common development-genetic architecture or limitations in the number of ways development can be produced due to physiological/mechanical limitations (Sanger et al. 2012). Nevertheless, in recent years, studies of ontogenetic allometry (where size-phenotype relationships are studied across developmental stages within a species) have compared the ontogenetic allometric trends between species. Some authors (Wilson and Sanchez-Villagra 2010; Klingenberg 2010; Voje et al. 2013) have concluded that allometry can be an adaptive and evolvable trait that can lead to complex patterns of phenotypic diversity, rather than a constraint on phenotypes imposed by size and ontogeny. Evaluating allometric coefficients in the context of a phylogeny can provide insights into how it evolves and how it is constrained by phylogenetic relatedness (Giannini 2014). Methods do not exist yet that allow for a proper incorporation of phylogenetic information into analyses comparing within-species patterns like ontogenetic allometry, where there are often more individuals than taxa. Nevertheless, examining the evolution of the patterns of allometric trajectories under a phylogenetic framework we observe that the developmental patterns of head and body shape change differ greatly and that there are clade-specific trends that seem to be related to their ecology. For example, the species in the lineage that includes the terrestrial Afro-Asian *Python*, which is sister to all other pythons, display small amounts of head shape change but immense body shape transformation as they grow, including an elongation of the tail and decrease in body girth. The opposite direction and magnitude of allometric shape change is observed in some of the Australo-Papuan clades including the semi-arboreal

482 *Simalia*, *Morelia*, and the semi-fossorial *Aspidites*. These results suggest that allometric coefficients are
 483 more labile than previously thought. More studies at a macro-evolutionary scale are needed to better
 484 understand exactly how evolvable allometry is, and how important it is in shaping the diversity of a group.
 485 The lability of allometry provides evidence that it can be highly evolvable (Pélabon et al. 2014), but a
 486 correlation with ecology suggests it also may be adaptive. In pythons, micro-habitat use drives phenotypic
 487 evolution (Esquerré and Keogh 2016) and our results suggest that it also can have an effect on ontogenetic
 488 allometry. In the Australo-Papuan genus *Morelia* two semi-arboreal species, *Morelia spilota* and *M. bredli*,
 489 show the same ontogenetic allometric trajectory. The closely related *Morelia viridis* on the other hand, is
 490 unique among pythons in most aspects of its ecology and phenotype. It is the only completely arboreal
 491 species in the family and it goes through an extreme ontogenetic color change from bright red or yellow
 492 juveniles to completely green adults. This coloration change has been found to be strongly associated with
 493 changes in head shape allometry and dietary shift from ectothermic to endothermic prey (Natusch and Lyons
 494 2012). This is accompanied by a shift in micro-habitat use, from the edge of rainforest closer to the ground
 495 to the upper and inner rainforest canopy (Wilson et al. 2007). This ontogenetic shift towards arboreality is
 496 the opposite to what is commonly observed on other python species which get increasingly terrestrial with
 497 size and age (Stafford 1986; Luiselli et al. 2007). Since head shape is predicted by micro-habitat, it is
 498 expected under the hypothesis that allometry is a trait under natural selection that the head shape ontogenetic
 499 trajectories of *M. viridis* and the rest of the pythons also go in opposite directions. As additional evidence,
 500 the enigmatic *M. carinata* has been described as ecologically intermediate between *M. viridis* and *M.*
 501 *spilota/M. bredli* (Porter et al. 2012) and it also has an intermediate ontogenetic trajectory between the two.
 502
 503 Phenotypic adaptations to terrestrial and semi-arboreal ecological niches have evolved independently more
 504 than once in pythons, but the remaining ecologies have a single origin. To fully appreciate the role of
 505 ecological factors on the evolution of ontogeny, a comparative study with the boas, a group that has
 506 convergently evolved the same ecomorphological diversity observed in pythons (Esquerré and Keogh 2016),
 507 would shed further light on this topic.

508

509 Data on the ontogeny of ecology in pythons is still anecdotal and incomplete for many species. It is
 510 understood that many pythons, and snakes in general, display a dietary shift from ectothermic to
 511 endothermic prey as they grow (Slip and Shine 1988; Greer 1997; Shine et al. 1998; Luiselli and Angelici
 512 1998; Natusch and Lyons 2012), but detailed studies on habitat use and other ecological factors are
 513 necessary. Several findings of this study need this information to establish the mechanisms behind shifts in
 514 ontogenetic trajectories. For example, the strong ontogenetic convergence in *Python* head shape and *Morelia*
 515 body shape, where juvenile phenotypes are disparate but adults are extremely similar, needs to be
 516 understood in the light of the way their natural history changes with growth, like ontogenetic convergence
 517 driven by adaptation in European plethodontid salamanders {(Adams and Nistri 2010). Nevertheless, our
 518 study adds to a growing body of evidence. Artificial selection on insect allometry has shown that the
 519 direction of change with growth can be shifted by evolution (e.g. Weber 1990; Wilkinson 1993; Emlen
 520 1996; Frankino et al. 2005) and adaptive shifts in the allometries of organisms to match their
 521 ecomorphological needs (Adams and Nistri 2010) demonstrate the possible adaptive properties of allometry.

522

523 Pythons are not only immensely diverse in their shapes and ecologies, but as we have demonstrated here,
 524 also in the way the transform their phenotypes through their lives. Different clades of pythons that display
 525 different ecological attributes also have different ontogenetic allometric trajectories. Some of them display
 526 strong ontogenetic convergence for example, others have very similar trajectories and many evolve their
 527 differences by extending or truncating their trajectories evolving forms that are paedomorphic or
 528 peramorphic. As we compare between clades, the slopes of the trajectories change, suggesting it is more
 529 challenging for biological forms to shift the direction of their change rather than the starting and finishing
 530 points or the rate of change. This enabled pythons to evolve more novel forms as they also shifted in their
 531 ecologies, requiring phenotypes better adapted to their needs. Maybe the remarkably diverse array of
 532 developmental pathways of pythons is not particularly unique. This calls for studies on broader taxonomic
 533 groups on the evolution of ontogenetic allometry and post-natal development. It may be that allometry is

generally more evolvable, and that the constraints it imposes are often adaptations. This would underscore the notion that allometry is often only a static constraint that funnels phenotypic variation in a certain direction, and highlight its role in increasing phenotypic diversity in living organisms. This study provides strong evidence of ontogenetic allometry as a highly evolvable trait and calls to evolutionary biologists, to rethink ‘allometry as a universal constraint on biological traits’ and instead as a trait by itself (Klingenberg 2010).

References

- Adams, D. C. 2014. A method for assessing phylogenetic least squares models for shape and other high-dimensional multivariate data. *Evolution* 68:2675–2688.
- Adams, D. C., and A. Nistri. 2010. Ontogenetic convergence and evolution of foot morphology in European cave salamanders (Family: Plethodontidae). *BMC Evol. Biol.* 10:216.
- Adams, D. C., and M. L. Collyer. 2009. A general framework for the analysis of phenotypic trajectories in evolutionary studies. *Evolution* 63:1143–1154.
- Adams, D. C., F. J. Rohlf, and D. E. Slice. 2013. A field comes of age: geometric morphometrics in the 21st century. *Hystrix* 24:7–14.
- Adams, D. C., M. L. Collyer, A. Kaliontzopoulou, and E. Sherratt. 2016. Geomorph (Version 3.0.2.): Geometric Morphometric Analyses of 2D/3D Landmark Data.
- Alberch, P., S. J. Gould, G. F. Oster, and D. B. Wake. 1979. Size and shape in ontogeny and phylogeny. *Paleobiology* 5:269–317.
- Anderson, M. J. 2001. A new method for non-parametric multivariate analysis of variance. *Austral Ecol.* 26:32–46.
- Andrews, R. M. 1982. Patterns of growth in reptiles. Pp. 273–320 in C. Gans and F. H. Pough, eds. *Biology of the Reptilia Volume 13, Physiology D: Physiological Ecology*.
- Barker, D. G., T. M. Barker, M. A. Davis, and G. W. Schuett. 2015. A review of the systematics and taxonomy of Pythonidae: an ancient serpent lineage. *Zool. J. Linnean Soc.* 175:1–19.
- Benjamini, Y., and Y. Hochberg. 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J R Stat Soc Series B Stat Methodol* 57:289–300. J Royal Statistical Society.
- Bhullar, B.-A. S., J. Marugán-Lobón, F. Racimo, G. S. Bever, T. B. Rowe, M. A. Norell, and A. Abzhanov. 2012. Birds have paedomorphic dinosaur skulls. *Nature* 487:223–226.
- Bookstein, F. L. 1991. *Morphometric tools for landmark data; geometry and biology*. Cambridge University Press, New York.

- 568 Claude, J. 2013. Log-shape ratios, Procrustes superimposition, elliptic Fourier analysis: three worked
569 examples in R. *Hystrix* 24:94–102.
- 570 Claude, J. 2008. *Morphometrics with R*. Springer, New York, USA.
- 571 Collyer, M. L., and D. C. Adams. 2013. Phenotypic trajectory analysis: comparison of shape change patterns
572 in evolution and ecology. *Hystrix* 24:75–83.
- 573 Emlen, D. J. 1996. Artificial selection on horn length-body size allometry in the horned beetle *Onthophagus*
574 *acuminatus* (Coleoptera: Scarabaeidae). *Evolution* 50:1219–1230.
- 575 Esquerré, D., and J. S. Keogh. 2016. Parallel selective pressures drive convergent diversification of
576 phenotypes in pythons and boas. *Ecol. Lett.* 19:800–809.
- 577 Foth, C., B. P. Hedrick, and M. D. Ezcurra. 2016. Cranial ontogenetic variation in early saurischians and the
578 role of heterochrony in the diversification of predatory dinosaurs. *PeerJ* 4:e1589.
- 579 Frankino, W. A., B. J. Zwaan, D. L. Stern, and P. M. Brakefield. 2005. Natural selection and developmental
580 constraints in the evolution of allometries. *Science* 307:718–720.
- 581 Frédérick, B., and P. Vandewalle. 2011. Bipartite life cycle of coral reef fishes promotes increasing shape
582 disparity of the head skeleton during ontogeny: an example from damselfishes (Pomacentridae). *BMC Evol.*
583 *Biol.* 11:1–21.
- 584 Gerber, S., and M. J. Hopkins. 2011. Mosaic heterochrony and evolutionary modularity: the trilobite genus
585 *Zacanthopsis* as a case study. *Evolution* 65:3241–3252.
- 586 Gerber, S., G. J. Eble, and P. Neige. 2008. Allometric space and allometric disparity: a developmental
587 perspective in the macroevolutionary analysis of morphological disparity. *Evolution* 62:1450–1457.
- 588 Giannini, N. P. 2014. Quantitative developmental data in a phylogenetic framework. *J. Exp. Zool. B Mol.*
589 *Dev. Evol.* 322:558–566.
- 590 Gignac, A., and P. T. Gregory. 2005. The effects of body size, age, and food intake during pregnancy on
591 reproductive traits of a viviparous snake, *Thamnophis ordinoides*. *Écoscience* 12:236–243.
- 592 Godfrey, L. R., and M. R. Sutherland. 1995. Flawed inference: why size-based tests of heterochronic
593 processes do not work. *J. Theor. Biol.* 172:43–61.
- 594 Goodall, C. 1991. Procrustes Methods in the Statistical-Analysis of Shape. *J R Stat Soc Series B Stat*
595 *Methodol* 53:285–339.
- 596 Gould, S. J. 1966. Allometry and size in ontogeny and phylogeny. *Biol Rev Camb Philos Soc* 41:587–640.
- 597 Gould, S. J. 1977. *Ontogeny and phylogeny*. Harvard University Press, Cambridge, MA, USA.
- 598 Gould, S. J., and R. C. Lewontin. 1979. The spandrels of San Marco and the Panglossian paradigm: a
599 critique of the adaptationist programme. *Philos Trans R Soc Lond B Biol Sci* 205:581–598.
- 600 Greer, A. E. 1997. *The biology and evolution of Australian snakes*. Surrey Beatty & Sons Pty Limited,
601 Chipping Norton, Australia.
- 602 Gunz, P., and P. Mitteroecker. 2013. Semilandmarks: a method for quantifying curves and surfaces. *Hystrix*
603 24:103–109.

- 604 Hipsley, C. A., and J. Müller. 2017. Developmental dynamics of ecomorphological convergence in a
605 transcontinental lizard radiation. *Evolution* 63:685.
- 606 Huelsenbeck, J. P., R. Nielsen, and J. P. Bollback. 2003. Stochastic mapping of morphological characters.
607 *Syst. Biol.* 52:131–158.
- 608 Huxley, J. S. 1932. Problems of relative growth. L. MacVeagh, New York.
- 609 Huxley, J. S., and G. Teissier. 1936. Terminology of relative growth. *Nature* 137:780–781.
- 610 Klingenberg, C. 2010. There's something afoot in the evolution of ontogenies. *BMC Evol. Biol.* 10:221.
- 611 Klingenberg, C. P. 1998. Heterochrony and allometry: the analysis of evolutionary change in ontogeny. *Biol.*
612 *Rev.* 73:79–123.
- 613 Klingenberg, C. P. 2016. Size, shape, and form: concepts of allometry in geometric morphometrics. *Dev.*
614 *Genes Evol.* 226:1–25.
- 615 Klingenberg, C. P., and J. R. Spence. 1993. Heterochrony and allometry: lessons from the water strider
616 genus *Limnopus*. *Evolution* 47:1834–1853.
- 617 Klingenberg, C. P., and R. Froese. 1991. A multivariate comparison of allometric growth patterns. *Syst.*
618 *Biol.* 40:410–419.
- 619 Klingenberg, C. P., M. Barluenga, and A. Meyer. 2002. Shape analysis of symmetric structures: quantifying
620 variation among individuals and asymmetry. *Evolution* 56:1909–1920.
- 621 Luiselli, L., and F. M. Angelici. 1998. Sexual size dimorphism and natural history traits are correlated with
622 intersexual dietary divergence in royal pythons (*Python regius*) from the rainforests of southeastern Nigeria.
623 *Ital. J. Zool.* 65:183–185.
- 624 Luiselli, L., G. C. Akani, E. A. Eniang, and E. Politano. 2007. Comparative ecology and ecological
625 modeling of sympatric pythons, *Python regius* and *Python sebae*. Pp. 89–100 in R. W. Henderson and R.
626 Powell, eds. *Biology of the boas and pythons*. Eagle Mountain Publishing, Eagle Mountain, Utah, USA.
- 627 Mallon, J. C., M. J. Ryan, and J. A. Campbell. 2015. Skull ontogeny in *Arrhinoceratops brachyops*
628 (Ornithischia: Ceratopsidae) and other horned dinosaurs. *Zool. J. Linnean Soc.* 175:910–929.
- 629 Maynard Smith, J., R. Burian, S. Kauffman, P. Alberch, J. Campbell, B. Goodwin, R. Lande, D. Raup, and
630 L. Wolpert. 1985. Developmental Constraints and Evolution: A Perspective from the Mountain Lake
631 Conference on Development and Evolution. *Q. Rev. Biol.* 60:265–287.
- 632 Mitteroecker, P., P. Gunz, and F. L. Bookstein. 2005. Heterochrony and geometric morphometrics: a
633 comparison of cranial growth in *Pan paniscus* versus *Pan troglodytes*. *Evol. Dev.* 7:244–258.
- 634 Mosimann, J. E. 1970. Size allometry: size and shape variables with characterizations of the lognormal and
635 generalized gamma distributions. *J. Am. Stat. Assoc.* 65:930–945.
- 636 Mosimann, J. E., and F. C. James. 1979. New statistical methods for allometry with application to Florida
637 red-winged blackbirds. *Evolution* 33:444–459.
- 638 Murphy, J. C., and R. W. Henderson. 1997. Tales of giant snakes. Krieger Publishing Company, Malabar,
639 FL, USA.

- 640 Natusch, D. J. D., and J. A. Lyons. 2012. Relationships between ontogenetic changes in prey selection, head
641 shape, sexual maturity, and colour in an Australasian python (*Morelia viridis*). *Biol. J. Linnean Soc.*
642 107:269–276.
- 643 Pélabon, C., C. Firmat, G. H. Bolstad, K. L. Voje, D. Houle, J. Cassara, A. L. Rouzic, and T. F. Hansen.
644 2014. Evolution of morphological allometry. *Ann. N. Y. Acad. Sci.* 1320:58–75.
- 645 Piras, P., D. Salvi, G. Ferrara, L. Maiorino, M. Delfino, L. Pedde, and T. Kotsakis. 2011. The role of post-
646 natal ontogeny in the evolution of phenotypic diversity in *Podarcis* lizards. *J. Evol. Biol.* 24:2705–2720.
- 647 Porter, R., J. Weigel, and R. Shine. 2012. Natural history of the rough-scaled python, *Morelia carinata*
648 (Serpentes: Pythonidae). *Aust. Zool.* 36:137–142.
- 649 Porto, A., L. T. Shirai, F. B. de Oliveira, and G. Marroig. 2013. Size variation, growth strategies, and the
650 evolution of modularity in the mammalian skull. *Evolution* 67:3305–3322.
- 651 Reilly, S. M., E. O. Wiley, and D. J. Meinhardt. 1997. An integrative approach to heterochrony: the
652 distinction between interspecific and intraspecific phenomena. *Biol. J. Linnean Soc.* 60:119–143.
- 653 Revell, L. J. 2014. Graphical methods for visualizing comparative data on phylogenies. Pp. 77–103 in L. Z.
654 Garamszegi, ed. *Modern phylogenetic comparative methods and their application in evolutionary biology.*
655 Springer Berlin Heidelberg, Berlin, Heidelberg.
- 656 Revell, L. J. 2012. phytools: an R package for phylogenetic comparative biology (and other things). *Methods*
657 *Ecol. Evol.* 3:217–223.
- 658 Reynolds, G. R., M. L. Niemiller, and L. J. Revell. 2014. Toward a tree-of-life for the boas and pythons:
659 Multilocus species-level phylogeny with unprecedented taxon sampling. *Mol Phylogenet Evol* 71:201–213.
- 660 Rohlf, F. J. 2015. The tps series of software. *Hystrix* 26:1–4.
- 661 Rohlf, F. J., and D. Slice. 1990. Extensions of the Procrustes method for the optimal superimposition of
662 landmarks. *Syst. Biol.* 39:40–59.
- 663 Sanger, T. J., L. J. Revell, J. J. Gibson-Brown, and J. B. Losos. 2012. Repeated modification of early limb
664 morphogenesis programmes underlies the convergence of relative limb length in *Anolis* lizards. *Proc. R. Soc.*
665 *B* 279:739–748.
- 666 Sheets, H. D., and M. L. Zelditch. 2013. Studying ontogenetic trajectories using resampling methods and
667 landmark data. *Hystrix* 24:67–73.
- 668 Shine, R., P. S. Harlow, J. S. Keogh, and Boeadi. 1998. The influence of sex and body size on food habits of
669 a giant tropical snake, *Python reticulatus*. *Funct. Ecol.* 12:248–258.
- 670 Sidlauskas, B. 2008. Continuous and arrested morphological diversification in sister clades or characiform
671 fishes: a phylomorphospace approach. *Evolution* 62:3135–3156.
- 672 Simpson, G. G. 1944. *Tempo and mode in evolution.* Columbia Univ. Press, New York.
- 673 Slip, D. J., and R. Shine. 1988. Feeding habits of the Diamond Python, *Morelia s. spilota*: ambush predation
674 by a boid snake. *J. Herpetol.* 22:323–330.
- 675 Stafford, P. J. 1986. *Pythons and boas.* T.F.H. Publications, Neptune City, NJ, U.S.A.

- 676 Urošević, A., K. Ljubisavljević, and A. Ivanović. 2013. Patterns of cranial ontogeny in lacertid lizards:
677 morphological and allometric disparity. *J. Evol. Biol.* 26:399–415.
- 678 Voje, K. L., T. F. Hansen, C. K. Egset, G. H. Bolstad, and C. Pélabon. 2013. Allometric constraints and the
679 evolution of allometry. *Evolution* 68:866–885.
- 680 Weber, K. E. 1990. Selection on wing allometry in *Drosophila melanogaster*. *Genetics* 126:975–989.
- 681 Webster, M., and M. L. Zelditch. 2005. Evolutionary modifications of ontogeny: heterochrony and beyond.
682 *Paleobiology* 31:354–372.
- 683 Weston, E. M. 2003. Evolution of ontogeny in the hippopotamus skull: using allometry to dissect
684 developmental change. *Biol. J. Linnean Soc.* 80:625–638.
- 685 Wilkinson, G. S. 1993. Artificial sexual selection alters allometry in the stalk-eyed fly *Cyrtodiopsis*
686 *dalmanni* (Diptera: Diopsidae). *Genet. Res.* 62:213–222.
- 687 Wilson, D., R. Heinsohn, and J. A. Endler. 2007. The adaptive significance of ontogenetic colour change in
688 a tropical python. *Biol. Lett.* 3:40–43.
- 689 Wilson, L. A. B., and M. R. Sanchez-Villagra. 2010. Diversity trends and their ontogenetic basis: an
690 exploration of allometric disparity in rodents. *Proc. R. Soc. B* 277:1227–1234.
- 691 Wilson, L. A. B., and M. R. Sánchez-Villagra. 2011. Evolution and Phylogenetic Signal of Growth
692 Trajectories: The Case of Chelid Turtles. *J. Exp. Zool. B Mol. Dev. Evol.* 316B:50–60.
- 693 Zelditch, M. L., D. L. Swiderski, and H. D. Sheets. 2012. Geometric morphometrics for biologists: a primer.
694 Second Edition. Academic Press, London, UK.
- 695 Zelditch, M. L., H. D. Sheets, and W. L. Fink. 2003. The ontogenetic dynamics of shape disparity.
696 *Paleobiology* 29:139–156.
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Table 1. Test for ontogenetic convergence/divergence in head and body shapes in all pythons (Pythonidae) and each clade that displays allometric slope differences, separately. A positive D statistic means that juveniles are more variable than adults (convergence) and a negative D statistic means that adults are more variable than juveniles (divergence). *P*-values are drawn from the number of times out of 10,000 permutations that the observed D is higher (*P*_{con}, for convergence) and lower (*P*_{div}, for divergence) than the randomized D.

Clade	Head shape			Body shape			Conclusions
	D	<i>P</i> _{con}	<i>P</i> _{div}	D	<i>P</i> _{con}	<i>P</i> _{div}	
Pythonidae	-1.489	0.0001	1	3,594	0.14	0.86	Overall no convergence or divergence
<i>Python</i>	55.66	0.0005	1	-	-	-	Convergence in head shape
<i>Morelia</i>	15.39	0.99	0.008	184.83	0.024	0.98	Convergence on body shape
<i>Simalia</i>	-	-	-	-321.6	0.86	0.14	No convergence or divergence in body shape
<i>Liasis</i>	-	-	-	36.78	0.014	0.99	Divergence on head shape

Figure 1. Schematic of the workflow to identify the different processes and patterns of ontogenetic allometric and heterochronic changes. See Materials and Methods for details on each step and the analyses. Below, a phenotype vs. body size illustration of a hypothetical example of patterns our study seeks to uncover. The gray triangles are a reference trajectory; the green illustrate ontogenetic divergence; the red ontogenetic convergence; the blue parallel ontogenetic trajectories or shifts in the intercept; the ochre heterochrony. The ochre triangles are peramorphic or the gray triangles are paedomorphic, in respect to each other.

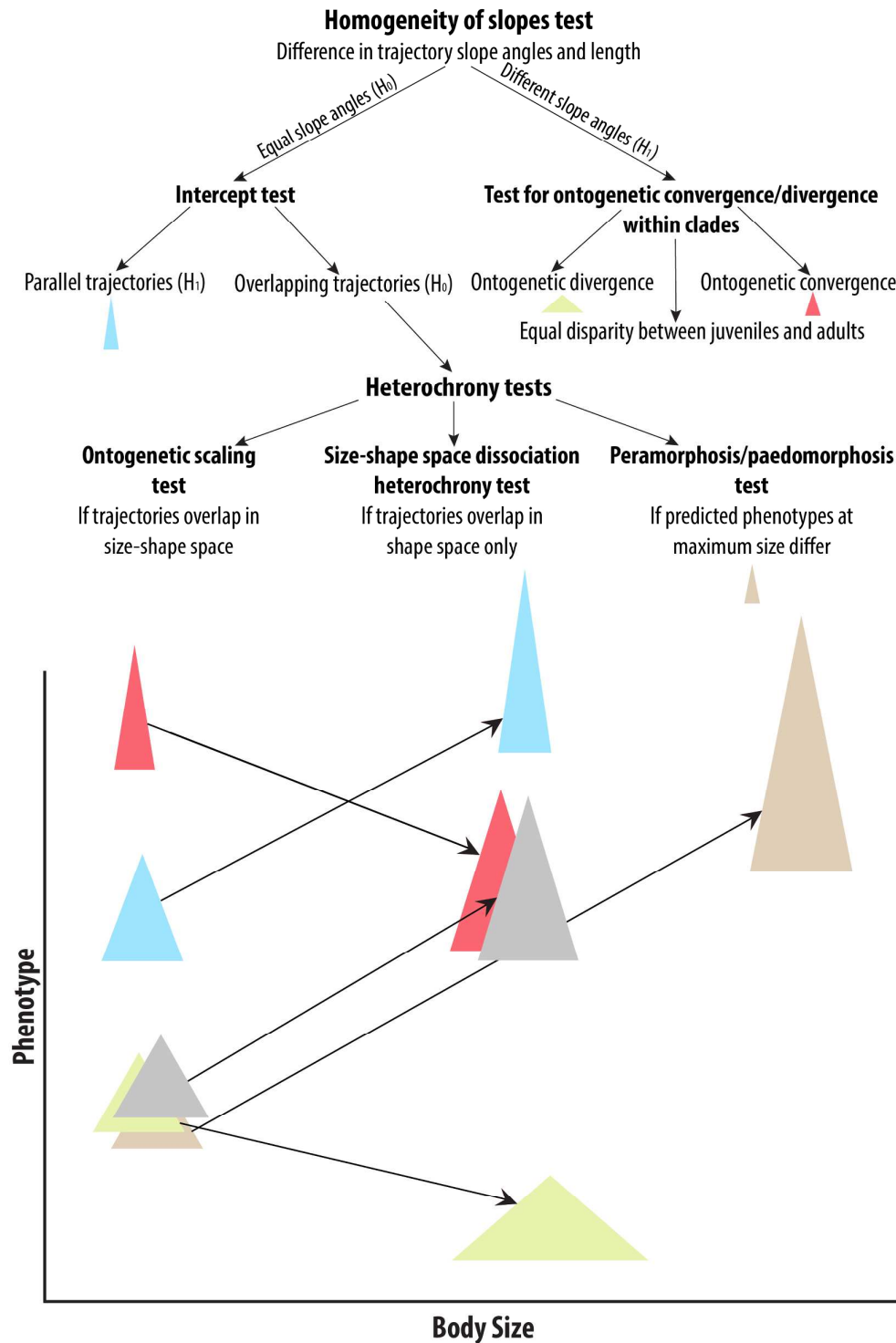


Figure 2. Ontogenetic allometric trajectories derived from the HOS test of head (above) and body (below) shape. The x-axis represents log-transformed centroid size for head and log geometric mean for body. The y-axis on both plots is the first principal component of the predicted values of the multivariate regression of shape on size. Each line of dots represents the predicted allometric trajectory for each species, as per the colored legend between the two plots. The size of the dots for each specimen is proportional to its size. On the head shape plot, thin plate spline deformation grids show the shape change from the mean shape of the dataset to the highest (above) and the lowest (below) specimen on the y-axis. Similarly, on the body shape plot illustrations based on the specimens that are highest and lowest on the y-axis represent the shape difference along the y-axis.

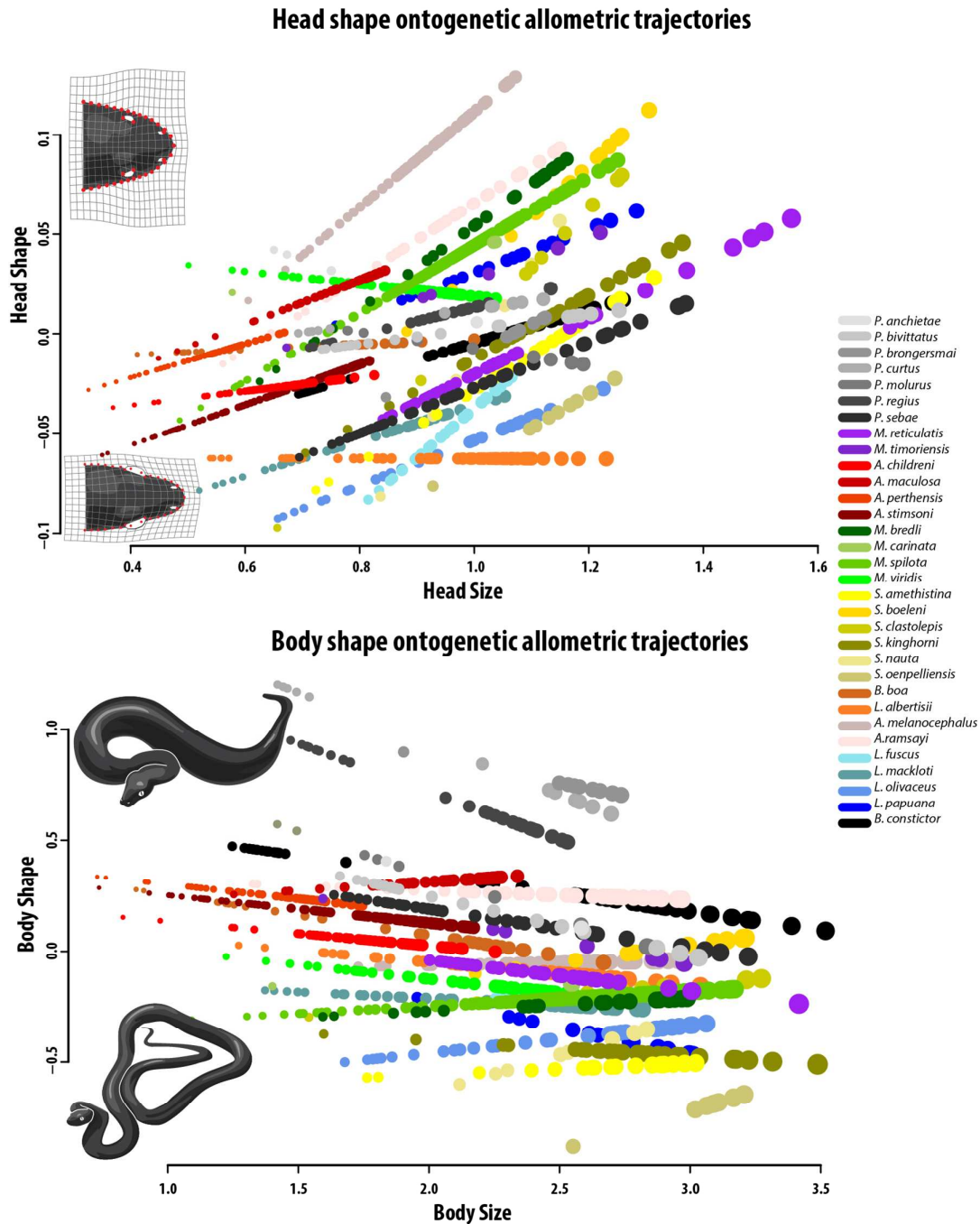


Figure 3. Ontogenetic allometric trajectories derived from the PTA, of head (above) and body (below) shape. The specimens are plotted on a morphospace represented by principal components (PC) 1 and 2 on the x- and y-axes respectively. White dots represent the average shape of juveniles and the black dots the average shape of adults. The lines between them are what we define as trajectories. The color of each line represents the species according to the legend. The gray dots in the background represent the total variation within the sample. The size of the dots for each specimen is proportional to its size. Thin plate spline deformation grids and body shape plot illustrations show the extremes of variation represented by each PC axis.

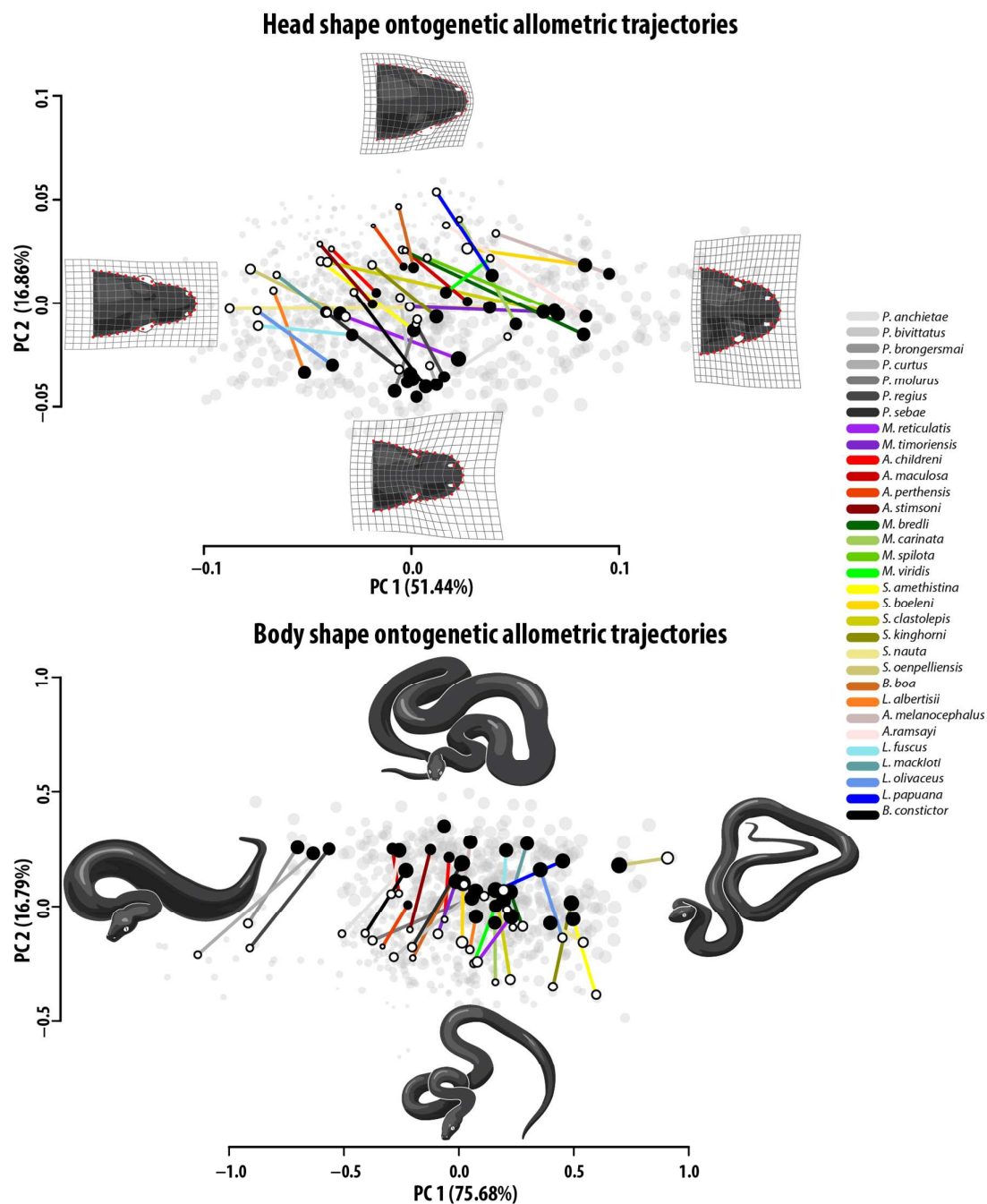


Figure 4. Ontogenetic allometric trajectories derived from the HOS (first and third columns) and PTA (second and fourth columns) tests, of head and body shape of the pythons, separated by clad. The rows of figures at each tip of the tree based on our phylogenetic analysis represent the trajectories of the python species within the clad that is labelled on the right edge of the figure. These are the same trajectories illustrated in Figures 2 and 3 therefore for details on the meaning of the axes and how to interpret them see the respective legends.

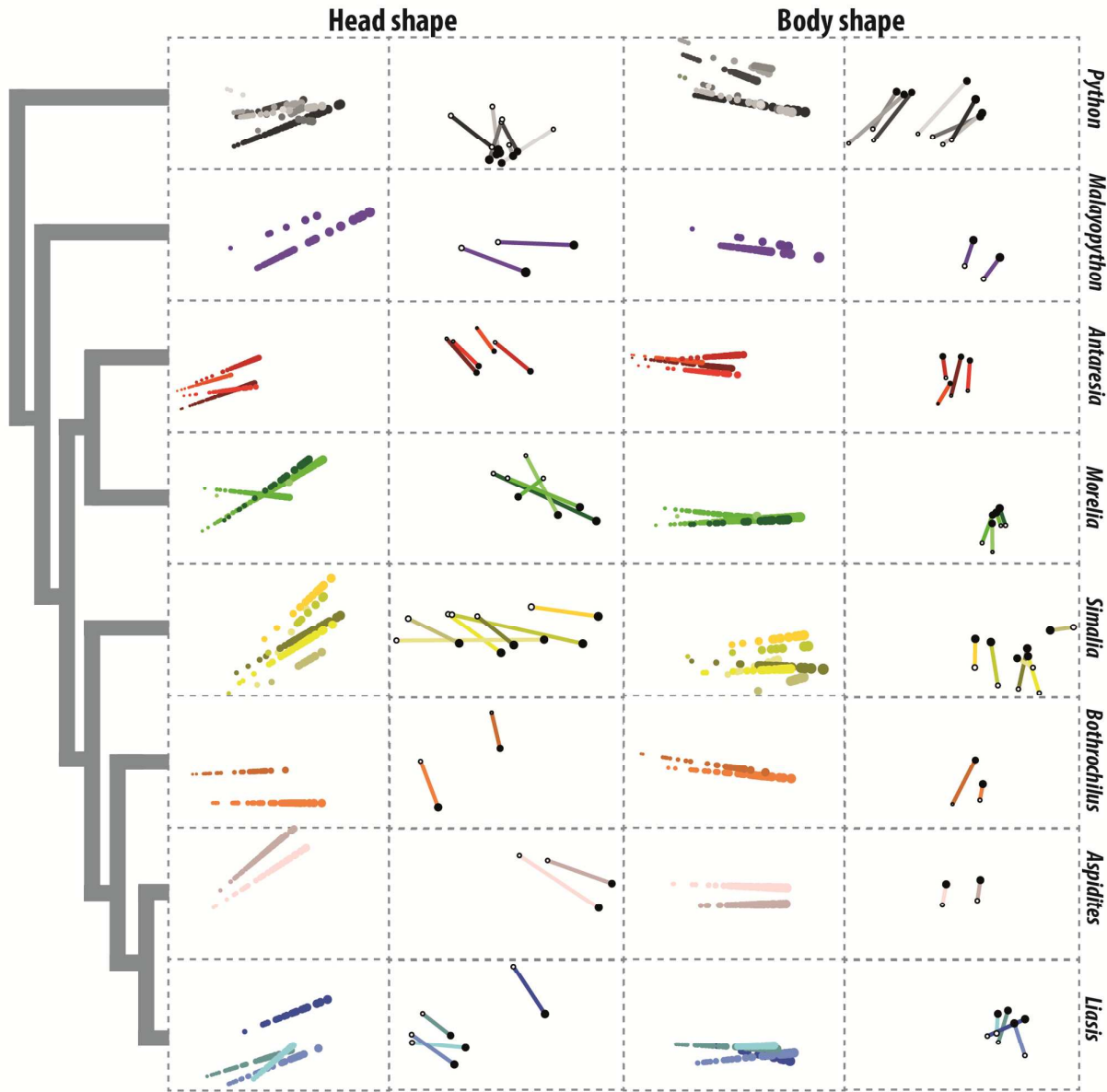
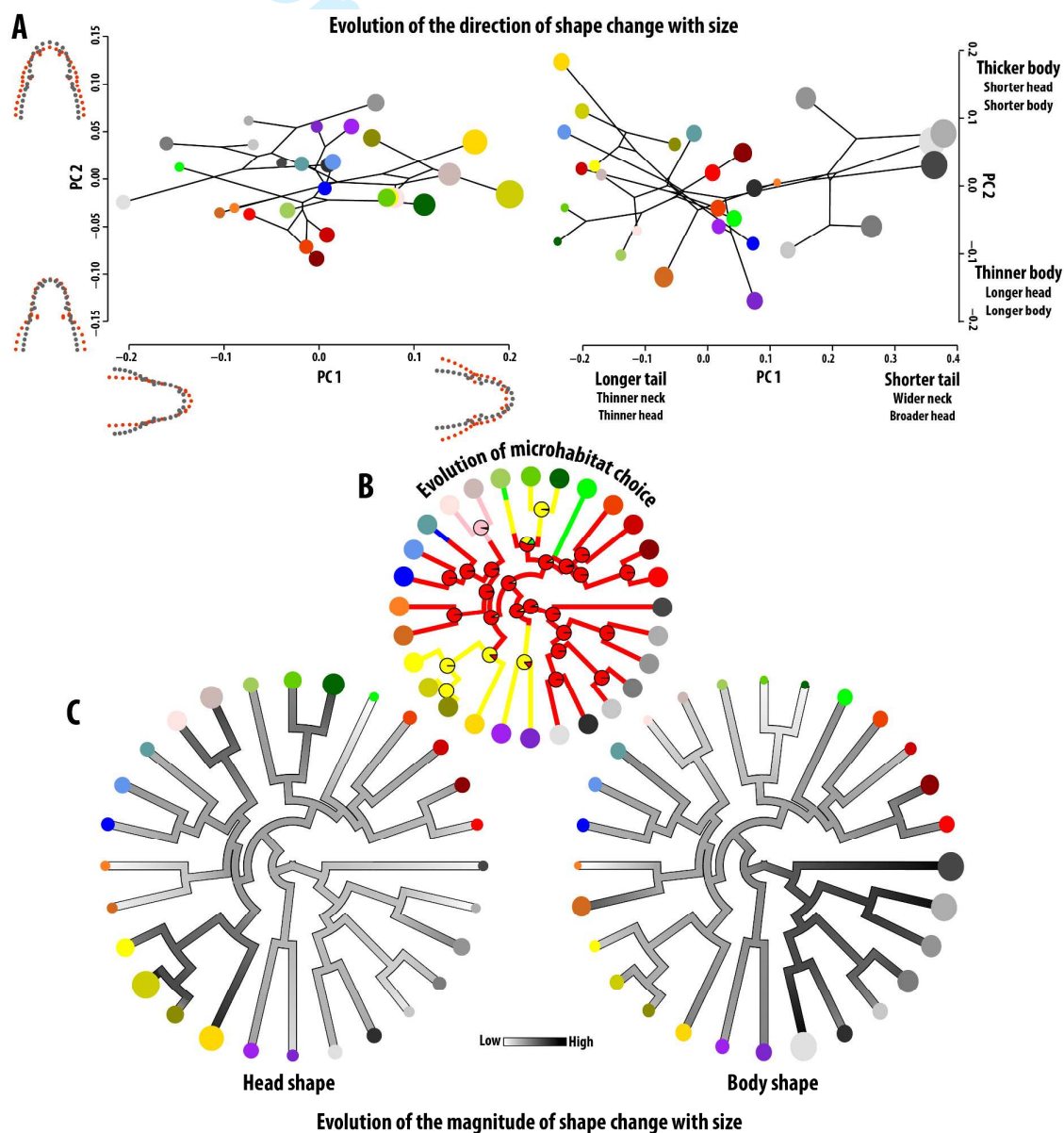


Figure 5. A: Phylomorphospace and ancestral state reconstruction of the slopes of allometric shape change in each python species, left side shows head shape and right side shows body shape. Besides the PC axes for head shape are illustrations describing the shape changes from the mean configuration (gray) to the extremes (red) of each axis. Besides the PC axes for body shape are summaries of the body shape changes occurring with size from the mean shape to the extremes of each axis, with the amount of change approximately proportional to the size of the text. B: Stochastic character mapping of the evolution of ecology in pythons. The base tree is a random of 10,000 replicates and the pie-charts represent the percentage of time each state is reconstructed at that node. Branch and node colors correspond to green: arboreal, yellow: semi-arboreal, red: terrestrial, blue: semi-aquatic and pink: semi-fossorial. C: Ancestral state reconstruction of the slope vector length (magnitude of shape change with size), with black representing high phenotypic change and white representing low. Tips in all figures are colored according to species and clade as in Figures 2 & 3 and on A and C they are sized proportionally to the magnitude of shape change with size.



SUPPORTING INFORMATION

Phylogenetic hypothesis

Using PartitionFinder v.1.1.1 (Lanfear et al. 2012), we found the best partitioning scheme is between mitochondrial and nuclear loci, and that best substitution model for both partitions is GTR+I+G. However, we decided to use GTR+G instead, since the gamma distribution (G) with an alpha parameter can already allow for a proportion of sites with very low rates of evolution, and several problems have been know with using a proportion of invariant sites parameter (I) (Yang 2006).

To estimate the phylogenetic tree and divergence times we used a Bayesian inference with node calibration on BEAST v.2.4.2 (Bouckaert et al. 2014). We used a relaxed lognormal molecular clock for the rate variation in each partition and Yule model of speciation for the branching of the tree. See Table S2 for node calibrations, based on Head (2015). We ran two independent Markov chain Monte Carlo chains for 200 million generations. Details on how we set the parameters can be obtained from the xml file that can be found on the dryad repository. We assessed proper mixing and convergence of the chains using the program Tracer v.1.6.0 (Rambaut et al. 2014) and checked that the effective sample sizes were >200 for every parameter. We also ensured that both runs converged on tree topologies using the R package *rwty* (Warren et al. 2017). We combined the results of both runs on LogCombiner v.2.4.2 and summarized a maximum clade credibility tree keeping the median heights on TreeAnnotator v.2.4.2. Finally, we pruned the tree to include only the taxa present on this study with the R package *ape* (Paradis et al. 2004).

References

Bouckaert, R., J. Heled, D. Kühnert, T. Vaughan, C.-H. Wu, D. Xie, M. A. Suchard, A. Rambaut, and A. J. Drummond. 2014. BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. *PLoS Comp Biol* 10:e1003537.

Head, J.J. 2015. Fossil calibration dates for molecular phylogenetic analysis of snakes 1: Serpentes, Alethinophidia, Boidae, Pythonidae. *Paleontol. Electronica* 18.1.6FC:1-17.

Lanfear, R., B. Calcott, S. Y. W. Ho, and S. Guindon. 2012. Partitionfinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Mol. Biol. Evol.* 29:1695–1701.

Paradis, E., J. Claude, and K. Strimmer. 2004. APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* 20:289–290.

- 802 Rambaut, A., M. A. Suchard, D. Xie, and A. J. Drummond. 2014. Tracer v1.6, Available from
803 <http://beast.bio.ed.ac.uk/Tracer>.
- 804 Warren, D. L., A. J. Geneva, and R. Lanfear. 2017. RWTY (R We There Yet): An R Package for Examining
805 Convergence of Bayesian Phylogenetic Analyses. *Mol. Biol. Evol.* 34:1016–1020.
- 806 Yang, Z. 2006. *Computational Molecular Evolution*. Oxford University Press, Oxford, UK.

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Table S1. Summary of the species used in this study, the sample size for each species, their snout-vent length (SVL) range and head size range. SVL ranges with an asterisk mean that the largest specimen(s) of that species did not have its body preserved. Therefore, for head shape analyses the SVL range is an underrepresentation of the range sampled for that species. All specimens were measured in the following collections: the Queensland Museum, the Museum and Art Gallery of the Northern Territory, the South Australian Museum, the Western Australian Museum, the Australian Museum, the California Academy of Sciences, the University of Texas at Arlington, the American Museum of Natural History and the Museum of Comparative Zoology.

Species	Sample size	SVL range (cm)	Head size range (cm)
<i>Python anchietae</i>	4	72-180	2.15-5.11
<i>Python bivittatus</i>	24	54-274	2.88-8.67
<i>Python brongersmai</i>	10	65-163	3.08-7.06
<i>Python curtus</i>	13	36-151	2.41-6.11
<i>Python molurus</i>	9	51-214*	3.1-8.56
<i>Python regius</i>	31	36-155*	2.43-7.34
<i>Python sebae</i>	48	45-310*	2.49-12.73
<i>Malayopython reticulatus</i>	47	70-718	3.57-19.19
<i>Malayopython timoriensis</i>	7	45-292	2.4-8.41
<i>Antaresia childreni</i>	70	23-131	1.24-3.5
<i>Antaresia maculosa</i>	42	40-132	1.41-4.01
<i>Antaresia perthensis</i>	55	19-67	1.07-2.5
<i>Antaresia stimsoni</i>	88	19-135	1.1-3.37
<i>Morelia bredli</i>	25	52-242	2.17-7.12
<i>Morelia carinata</i>	3	42-156	1.8-5.54
<i>Morelia spilota</i>	153	26-294	1.5-8.62
<i>Morelia viridis</i>	53	33-180	1.53-5.54
<i>Simalia amethystina</i>	29	68-309	2.76-10.5
<i>Simalia boeleni</i>	15	112-306	3.65-9.18
<i>Simalia clastolepis</i>	9	52-344	2.29-9.47
<i>Simalia kinghorni</i>	36	65-469	2.55-12.03
<i>Simalia nauta</i>	8	111-242	3.77-7.26
<i>Simalia oenpelliensis</i>	10	210-406	4.63-9.11
<i>Bothrochilus boa</i>	33	20-185	1.31-5.25
<i>Leiopython albertisii</i>	67	35-283	1.86-9.21
<i>Aspidites melanocephalus</i>	69	68-245	2.15-6.8
<i>Aspidites ramsayi</i>	45	37-258	1.84-7.56
<i>Liasis fuscus</i>	26	116-205	3.18-6.3
<i>Liasis mackloti</i>	44	39-207	1.73-6.15
<i>Liasis olivaceus</i>	37	64-302	2.5-9.26
<i>Liasis papuana</i>	20	93-378	2.83-9.54
<i>Boa constrictor</i>	61	45-269	2.46-9.39

Table S2: Fossil calibrations used for the time-calibrated phylogeny. These calibrations are based on Head (2015). Minimum ages given as millions of years ago (MY).

Taxon	Clade	Minimum age (MY)
<i>Coniophis</i> sp.	Serpentes / (Iguania + Anguimorpha)	98.32
<i>Haasophis terras Sanctus</i>	(Aniliidae + Tropidophiinae) / Macrostromata	93.9
<i>Australophis anilioides</i>	Aniliidae / Tropidophiidae	72.1
<i>Titanoboa cerrejonensis</i>	Boinae / Erycinae	58
<i>Corallus priscus</i>	<i>Corallus</i> / (<i>Chilabothrus</i> +(<i>Epicrates</i> + <i>Eunectes</i>))	50.2
<i>Eunectes stirtoni</i>	<i>Epicrates</i> / <i>Eunectes</i>	12.375
<i>Calamagras weigeli</i>	Ungaliophiinae / Charininae	35.2
Unnamed taxon (UNSM 125562)	<i>Charina</i> / <i>Lichanura</i>	18.7
<i>Ogmophis compactus</i>	Loxocemidae / Pythonidae	35.2
<i>Morelia riversleighensis</i>	Malayopython / Australo-Papuan Pythonidae	12.5

Table S3. Tests statistics from the test for allometry for each species. Isometry is the null hypothesis; *P* values less than 0.05 reject the null hypothesis.

Species	Head shape							Body shape						
	Df	SS	MS	Rsqr	F	Z	P	Df	SS	MS	Rsqr	F	Z	P
<i>Python anchietae</i>	2	0.002	0.002	0.388	1.268	1.102	0.3092	2	0.387	0.387	0.865	12.856	2.087	0.0644
<i>Python bivittatus</i>	22	0.012	0.012	0.243	7.053	4.551	<0.0001	20	0.712	0.712	0.542	23.631	8.385	<0.0001
<i>Python brongersmai</i>	8	0.002	0.002	0.108	0.966	0.771	0.3709	7	0.131	0.131	0.248	2.312	1.548	0.1874
<i>Python curtus</i>	11	0.005	0.005	0.208	2.893	2.071	0.0369	11	1.621	1.621	0.814	47.982	6.413	<0.0001
<i>Python molurus</i>	7	0.006	0.006	0.399	4.640	2.778	0.0003	5	0.393	0.393	0.600	7.511	2.808	0.0024
<i>Python regius</i>	29	0.007	0.007	0.118	3.868	2.908	0.0081	27	1.801	1.801	0.616	43.233	12.507	<0.0001
<i>Python sebae</i>	46	0.055	0.055	0.356	25.377	12.701	<0.0001	36	1.163	1.163	0.422	26.255	12.266	<0.0001
<i>Malayopython reticulatus</i>	45	0.051	0.051	0.362	25.566	12.736	<0.0001	38	0.500	0.500	0.195	9.210	6.063	<0.0001
<i>Malayopython timoriensis</i>	5	0.004	0.004	0.248	1.649	1.254	0.1993	5	0.244	0.244	0.536	5.785	2.509	0.0195
<i>Antaresia childreni</i>	68	0.010	0.010	0.088	6.550	5.075	0.0002	65	0.640	0.640	0.221	18.407	11.588	<0.0001
<i>Antaresia maculosa</i>	40	0.013	0.013	0.133	6.144	4.358	0.0015	40	0.286	0.286	0.107	4.795	3.521	0.0025
<i>Antaresia perthensis</i>	53	0.010	0.010	0.099	5.834	4.492	0.0003	53	0.481	0.481	0.223	15.240	9.653	<0.0001
<i>Antaresia stimsoni</i>	86	0.039	0.039	0.220	24.188	15.192	<0.0001	82	2.366	2.366	0.455	68.495	27.127	<0.0001
<i>Morelia bredli</i>	23	0.047	0.047	0.522	25.130	8.888	<0.0001	22	0.190	0.190	0.224	6.334	4.099	0.0020
<i>Morelia carinata</i>	1	0.005	0.005	0.692	2.252	1.298	0.2460	1	0.065	0.065	0.851	5.724	1.532	0.0813
<i>Morelia spilota</i>	151	0.148	0.148	0.304	65.816	32.371	<0.0001	149	0.998	0.998	0.105	17.502	12.469	<0.0001
<i>Morelia viridis</i>	51	0.011	0.011	0.078	4.303	3.124	0.0101	50	0.955	0.955	0.275	18.924	11.456	<0.0001
<i>Simalia amethystina</i>	27	0.027	0.027	0.320	12.732	7.005	<0.0001	16	0.182	0.182	0.162	3.089	2.150	0.0408
<i>Simalia boeleni</i>	13	0.015	0.015	0.306	5.741	3.234	0.0091	12	0.214	0.214	0.171	2.472	1.915	0.0430
<i>Simalia clastolepis</i>	7	0.030	0.030	0.724	18.353	4.207	<0.0001	6	0.299	0.299	0.568	7.891	3.175	0.0005
<i>Simalia kinghorni</i>	34	0.031	0.031	0.325	16.360	8.827	<0.0001	27	0.447	0.447	0.221	7.670	4.835	0.0004
<i>Simalia nauta</i>	6	0.017	0.017	0.612	9.456	2.956	0.0125	6	0.114	0.114	0.310	2.702	1.825	0.0646
<i>Simalia oenpelliensis</i>	8	0.003	0.003	0.185	1.818	1.468	0.1211	7	0.087	0.087	0.249	2.318	1.669	0.0778
<i>Aspidites melanocephalus</i>	67	0.049	0.049	0.259	23.478	13.012	<0.0001	66	0.390	0.390	0.117	8.759	6.268	<0.0001
<i>Aspidites ramsayi</i>	43	0.052	0.052	0.332	21.358	11.265	<0.0001	42	0.396	0.396	0.147	7.243	5.036	<0.0001
<i>Bothrochilus boa</i>	31	0.014	0.014	0.195	7.524	5.044	0.0002	31	1.851	1.851	0.585	43.610	13.648	<0.0001
<i>Leiopython albertisii</i>	65	0.031	0.031	0.214	17.690	11.131	<0.0001	52	0.330	0.330	0.100	5.760	4.100	0.0016
<i>Liasis fuscus</i>	24	0.012	0.012	0.232	7.264	4.515	0.0008	22	0.127	0.127	0.076	1.798	1.543	0.0905
<i>Liasis mackloti</i>	42	0.025	0.025	0.283	16.543	9.878	<0.0001	41	1.269	1.269	0.423	30.030	13.624	<0.0001
<i>Liasis olivaceus</i>	35	0.032	0.032	0.362	19.854	10.364	<0.0001	33	0.806	0.806	0.408	22.704	10.630	<0.0001
<i>Liasis papuana</i>	18	0.008	0.008	0.223	5.155	3.595	0.0008	12	0.135	0.135	0.266	4.345	2.999	0.0016
<i>Boa constrictor</i>	59	0.041	0.041	0.240	18.665	10.982	<0.0001	54	1.540	1.540	0.300	23.196	12.506	<0.0001

Table S4. Head shape slope angle differences. Pairwise comparisons of the angle between the slopes (direction of allometry) for head shape data in degrees (bottom triangle), and *P*-values of the difference between them computed with 10,000 iterations (upper triangle). Significant values indicating different slope angles are highlighted in green. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.11	0.04	0.10	0.43	0.08	0.03	0.01	0.03	0.18	0.05	0.06	0.06	0.02	0.27	0.01	0.27	0.02	0.00	0.01	0.02	0.00	0.02	0.21	0.30	0.00	0.02	0.01	0.06	0.05	0.04	0.06
<i>Python bivittatus</i>	72.11	-	0.25	0.09	0.14	0.11	0.01	0.01	0.12	0.06	0.03	0.01	0.00	0.01	0.15	0.00	0.00	0.01	0.10	0.02	0.02	0.10	0.37	0.01	0.00	0.00	0.02	0.28	0.02	0.02	0.15	0.01
<i>Python brongersmai</i>	108.28	62.47	-	0.34	0.06	0.34	0.59	0.82	0.82	0.17	0.37	0.30	0.24	0.67	0.45	0.62	0.00	0.59	0.82	0.81	0.78	0.76	0.61	0.17	0.10	0.68	0.49	0.85	0.49	0.70	0.59	0.33
<i>Python curtus</i>	76.90	43.21	57.94	-	0.17	0.15	0.07	0.10	0.38	0.05	0.04	0.01	0.01	0.02	0.14	0.01	0.00	0.03	0.09	0.03	0.07	0.07	0.23	0.02	0.01	0.01	0.02	0.40	0.20	0.11	0.11	0.00
<i>Python molurus</i>	50.82	44.80	94.84	48.76	-	0.05	0.02	0.01	0.03	0.13	0.02	0.01	0.01	0.00	0.06	0.00	0.03	0.00	0.01	0.00	0.01	0.00	0.10	0.07	0.09	0.00	0.00	0.06	0.04	0.02	0.02	0.00
<i>Python regius</i>	79.82	38.99	56.92	41.89	60.06	-	0.08	0.09	0.35	0.11	0.21	0.09	0.04	0.18	0.26	0.07	0.00	0.27	0.33	0.18	0.23	0.18	0.53	0.02	0.02	0.11	0.25	0.45	0.13	0.13	0.46	0.11
<i>Python sebae</i>	90.93	44.99	39.89	41.26	67.49	36.43	-	0.17	0.41	0.04	0.27	0.11	0.01	0.08	0.16	0.02	0.00	0.18	0.23	0.17	0.24	0.24	0.44	0.01	0.00	0.03	0.03	0.49	0.67	0.76	0.70	0.00
<i>Malayopython reticulatus</i>	100.05	47.31	30.47	38.91	74.86	35.43	19.96	-	0.94	0.01	0.07	0.03	0.00	0.12	0.13	0.02	0.00	0.26	0.52	0.32	0.91	0.32	0.59	0.00	0.00	0.11	0.04	0.92	0.15	0.33	0.38	0.00
<i>Malayopython timoriensis</i>	97.20	49.80	34.54	38.67	77.36	38.05	30.40	15.45	-	0.07	0.21	0.10	0.07	0.54	0.32	0.35	0.00	0.56	0.66	0.53	0.88	0.41	0.61	0.04	0.02	0.45	0.34	0.86	0.39	0.56	0.50	0.10
<i>Antaresia childreni</i>	63.55	41.20	72.49	51.76	48.73	41.37	39.37	52.55	57.70	-	0.46	0.32	0.18	0.02	0.23	0.01	0.00	0.04	0.05	0.03	0.02	0.07	0.25	0.61	0.37	0.01	0.02	0.11	0.14	0.07	0.32	0.03
<i>Antaresia maculosa</i>	84.96	49.89	55.13	58.12	72.78	37.73	27.52	38.95	45.93	28.08	-	0.90	0.92	0.35	0.32	0.41	0.00	0.55	0.29	0.34	0.17	0.30	0.48	0.16	0.05	0.17	0.32	0.26	0.27	0.30	0.90	0.32
<i>Antaresia perthensis</i>	83.04	61.60	60.54	68.53	78.42	47.25	36.08	49.11	56.01	32.93	17.04	-	0.79	0.17	0.27	0.15	0.00	0.30	0.17	0.22	0.06	0.25	0.33	0.18	0.06	0.07	0.11	0.13	0.13	0.13	0.51	0.19
<i>Antaresia stimsoni</i>	81.70	55.42	62.23	64.38	76.80	43.73	37.36	48.90	53.78	30.30	13.50	17.26	-	0.07	0.24	0.01	0.00	0.12	0.12	0.13	0.01	0.23	0.29	0.02	0.00	0.02	0.04	0.11	0.01	0.01	0.45	0.06
<i>Morelia bredli</i>	96.71	54.46	38.04	55.64	87.00	34.69	30.52	28.11	29.27	51.10	29.06	37.09	33.34	-	0.38	0.80	0.00	0.84	0.74	0.87	0.32	0.53	0.51	0.00	0.00	0.61	0.63	0.44	0.05	0.16	0.65	0.15
<i>Morelia carinata</i>	66.42	53.23	56.77	59.58	75.47	48.15	50.83	54.25	50.42	49.29	45.22	48.82	44.58	39.07	-	0.21	0.02	0.21	0.22	0.22	0.17	0.22	0.20	0.20	0.21	0.16	0.24	0.19	0.19	0.29	0.37	0.38
<i>Morelia spilota</i>	99.84	53.43	38.12	55.73	84.50	35.53	25.68	25.29	31.46	46.64	22.85	31.86	30.27	12.20	45.07	-	0.00	0.91	0.68	0.85	0.22	0.49	0.57	0.00	0.00	0.36	0.25	0.42	0.02	0.08	0.74	0.00
<i>Morelia viridis</i>	54.43	72.08	119.35	85.64	61.94	73.40	102.80	102.46	96.41	78.33	94.01	96.51	90.47	96.72	83.45	101.42	-	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia amethystina</i>	99.12	54.79	42.52	54.80	83.33	32.03	27.10	24.94	29.87	46.54	24.59	32.73	31.52	15.21	49.45	10.86	95.95	-	0.74	0.87	0.56	0.51	0.69	0.01	0.00	0.67	0.61	0.52	0.12	0.21	0.77	0.12
<i>Simalia boeleni</i>	113.44	55.39	35.02	61.11	92.73	40.77	39.95	29.14	33.02	64.37	43.51	52.15	49.66	24.82	58.28	23.98	99.66	25.36	-	0.98	0.76	0.89	0.93	0.02	0.01	0.98	0.77	0.89	0.14	0.25	0.58	0.26
<i>Simalia clastolepis</i>	110.43	61.84	34.01	64.18	96.87	43.00	36.10	29.88	34.39	60.43	35.71	41.74	40.70	17.48	54.02	15.95	105.09	17.81	15.32	-	0.54	0.86	0.77	0.01	0.00	0.96	0.62	0.63	0.10	0.20	0.56	0.21
<i>Simalia kinghorni</i>	99.00	44.39	33.22	44.87	75.21	31.69	22.87	10.80	19.17	49.95	35.56	45.55	45.86	25.22	52.04	21.50	97.54	20.86	24.11	26.18	-	0.39	0.78	0.00	0.00	0.36	0.24	0.90	0.18	0.42	0.62	0.02
<i>Simalia nauta</i>	131.27	73.85	43.31	82.32	113.11	65.24	56.14	49.69	53.21	80.08	55.60	60.04	57.51	41.24	70.99	39.85	113.08	42.83	28.63	28.96	47.29	-	0.76	0.05	0.03	0.84	0.54	0.62	0.14	0.23	0.42	0.28
<i>Simalia oenpelliensis</i>	111.73	50.16	52.89	62.95	81.47	43.62	44.20	37.37	43.23	59.61	46.05	55.42	53.54	42.68	73.37	37.40	91.60	35.41	26.16	34.47	31.17	41.80	-	0.12	0.09	0.81	0.72	0.90	0.33	0.39	0.69	0.39
<i>Bothrochilus boa</i>	58.79	52.43	71.10	55.10	52.47	52.75	41.99	57.42	63.11	20.14	35.39	35.33	37.57	57.00	48.58	52.87	89.43	54.51	73.74	66.83	57.07	87.57	73.23	-	0.28	0.00	0.00	0.06	0.06	0.02	0.09	0.00
<i>Leiopython albertisii</i>	49.54	52.19	82.41	57.90	46.56	49.32	51.63	65.88	69.12	22.26	41.77	41.21	41.05	60.64	45.74	59.01	73.66	59.61	78.45	73.26	64.01	94.17	77.77	20.13	-	0.00	0.00	0.03	0.00	0.00	0.04	0.00
<i>Aspidites melanocephalus</i>	108.89	53.91	37.53	61.20	90.95	38.90	35.46	28.63	32.11	58.66	36.16	45.16	41.30	19.18	54.06	19.02	97.80	19.15	13.54	13.36	24.24	28.44	29.71	68.18	72.91	-	0.76	0.66	0.02	0.06	0.50	0.05
<i>Aspidites ramsayi</i>	96.17	44.25	45.32	56.57	80.03	29.68	32.42	31.37	34.57	47.29	28.66	38.79	32.82	17.58	45.37	18.89	87.58	19.16	22.99	23.06	25.63	39.89	33.18	58.75	60.22	15.21	-	0.49	0.02	0.06	0.80	0.21
<i>Liasis fuscus</i>	109.36	45.68	34.11	43.58	76.84	40.31	33.75	19.33	26.48	62.83	50.12	61.85	59.63	38.36	65.64	35.39	101.17	35.85	25.63	34.55	20.95	45.22	29.11	70.98	78.16	30.03	35.33	-	0.38	0.51	0.58	0.16
<i>Liasis mackloti</i>	81.64	44.42	46.16	34.68	59.05	36.26	14.30	25.38	33.45	33.94	30.82	38.70	40.73	38.06	49.48	33.25	99.23	33.97	49.24	45.48	28.57	67.84	51.76	34.12	44.51	45.75	41.29	40.10	-	0.80	0.49	0.00
<i>Liasis olivaceus</i>	86.60	42.30	36.18	39.91	66.85	36.25	13.01	20.10	28.16	39.17	29.66	37.99	39.31	29.89	42.95	25.90	101.43	29.02	40.73	37.38	21.79	57.83	48.30	40.66	50.24	36.82	33.16	35.01	14.19	-	0.74	0.01
<i>Liasis papuana</i>	89.04	39.35	44.37	49.16	70.23	30.24	19.39	27.03	34.64	34.00	17.33	29.77	25.85	22.89	43.81	17.56	93.57	20.56	32.91	29.65	23.26	49.47	37.72	43.10	48.94	26.58	18.28	36.06	26.29	20.11	-	0.45
<i>Boa constrictor</i>	81.68	46.82	53.85	64.67	78.72	33.23	40.49	44.88	47.69	40.88	25.81	31.06	25.94	25.57	36.22	27.49	81.95	29.07	37.83	33.54	38.19	51.94	46.31	50.09	49.46	31.87	20.82	51.85	45.50	38.80	24.41	-

Table S5. Body shape slope angle differences. Pairwise comparisons of the angle between the slopes (direction of allometry) for body shape data in degrees (bottom triangle), and *P*-values of the difference between them computed with 10,000 iterations (upper triangle). Significant values indicating different slope angles are highlighted in green. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Similia amethystina</i>	<i>Similia boeleni</i>	<i>Similia clastolepis</i>	<i>Similia kinghorni</i>	<i>Similia nauta</i>	<i>Similia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.99	0.95	0.95	0.95	1.00	0.95	0.84	0.65	0.73	0.13	0.75	0.71	0.04	0.37	0.05	0.77	0.21	0.14	0.15	0.53	0.03	0.01	0.87	0.95	0.13	0.42	0.13	0.56	0.07	0.84	0.82
<i>Python bivittatus</i>	10.09	-	0.75	0.61	0.94	0.99	0.54	0.52	0.44	0.25	0.00	0.37	0.11	0.00	0.15	0.00	0.26	0.02	0.01	0.01	0.05	0.01	0.00	0.35	0.86	0.00	0.04	0.04	0.04	0.00	0.69	0.47
<i>Python brongersmai</i>	20.67	29.40	-	0.94	0.71	0.86	0.82	0.70	0.58	0.74	0.27	0.71	0.76	0.15	0.47	0.20	0.59	0.44	0.41	0.42	0.83	0.09	0.01	0.78	0.70	0.27	0.54	0.32	0.74	0.20	0.73	0.64
<i>Python curtus</i>	14.49	19.07	18.86	-	0.78	0.79	0.24	0.15	0.21	0.10	0.00	0.13	0.04	0.00	0.08	0.00	0.07	0.01	0.02	0.01	0.12	0.01	0.00	0.12	0.21	0.00	0.01	0.07	0.03	0.00	0.85	0.08
<i>Python molurus</i>	17.56	13.41	35.01	20.72	-	0.90	0.62	0.49	0.33	0.36	0.03	0.35	0.23	0.00	0.12	0.00	0.44	0.05	0.03	0.02	0.24	0.01	0.01	0.38	0.72	0.05	0.14	0.07	0.19	0.01	0.96	0.40
<i>Python regius</i>	6.28	5.82	23.89	15.45	15.28	-	0.72	0.57	0.42	0.36	0.01	0.46	0.20	0.00	0.16	0.00	0.29	0.03	0.02	0.01	0.13	0.01	0.00	0.48	0.84	0.00	0.08	0.06	0.10	0.00	0.73	0.49
<i>Python sebae</i>	13.83	17.79	25.16	26.64	24.08	15.21	-	0.91	0.30	0.84	0.03	0.76	0.61	0.00	0.25	0.00	0.63	0.09	0.06	0.04	0.22	0.02	0.01	0.83	0.78	0.01	0.23	0.06	0.40	0.00	0.38	0.33
<i>Malayopython reticulatus</i>	20.63	20.99	32.11	34.17	29.86	20.30	10.24	-	0.52	0.91	0.07	0.98	0.83	0.01	0.40	0.00	0.70	0.14	0.07	0.06	0.14	0.02	0.01	0.95	0.88	0.02	0.60	0.06	0.38	0.01	0.25	0.81
<i>Malayopython timoriensis</i>	32.00	30.06	41.55	41.15	42.73	31.68	33.96	28.37	-	0.27	0.02	0.58	0.34	0.03	0.64	0.01	0.32	0.05	0.04	0.04	0.04	0.01	0.00	0.54	0.48	0.01	0.18	0.03	0.10	0.01	0.18	0.76
<i>Antaresia childreni</i>	25.05	28.21	29.90	36.55	34.79	25.57	12.02	11.03	37.29	-	0.20	0.94	0.93	0.02	0.38	0.01	0.49	0.37	0.17	0.18	0.38	0.05	0.02	0.77	0.46	0.09	0.86	0.12	0.82	0.03	0.21	0.32
<i>Antaresia maculosa</i>	56.69	60.48	54.30	66.05	63.70	57.75	43.55	42.07	64.74	32.85	-	0.12	0.06	0.23	0.23	0.78	0.03	0.96	0.62	0.70	0.14	0.32	0.12	0.02	0.00	0.57	0.27	0.25	0.24	0.96	0.02	0.00
<i>Antaresia perthensis</i>	24.76	26.19	31.56	37.19	36.31	24.65	15.11	7.61	27.22	10.78	39.62	-	0.96	0.03	0.54	0.01	0.53	0.24	0.12	0.14	0.17	0.04	0.01	0.94	0.67	0.03	0.81	0.08	0.46	0.02	0.19	0.79
<i>Antaresia stimsoni</i>	24.18	28.63	27.52	36.15	37.49	25.97	13.73	11.55	31.50	8.84	36.51	8.27	-	0.00	0.49	0.00	0.35	0.21	0.13	0.12	0.12	0.03	0.01	0.87	0.21	0.01	0.51	0.07	0.48	0.00	0.12	0.18
<i>Morelia bredli</i>	68.31	70.35	63.02	76.81	79.01	67.86	57.48	51.80	61.29	45.88	31.26	45.52	46.07	-	0.30	0.20	0.00	0.34	0.31	0.40	0.00	0.45	0.12	0.00	0.00	0.01	0.05	0.21	0.00	0.07	0.00	0.00
<i>Morelia carinata</i>	49.86	53.33	49.55	60.63	64.64	52.35	44.02	38.33	32.93	39.51	48.10	33.21	32.03	42.77	-	0.15	0.34	0.33	0.32	0.38	0.11	0.11	0.03	0.46	0.22	0.05	0.38	0.06	0.28	0.16	0.06	0.34
<i>Morelia spilota</i>	62.36	66.74	55.65	69.98	71.41	63.25	50.32	48.66	68.07	39.01	12.86	44.42	41.47	23.23	48.98	-	0.00	0.88	0.69	0.79	0.01	0.43	0.10	0.00	0.00	0.07	0.01	0.30	0.00	0.55	0.00	0.00
<i>Morelia viridis</i>	22.54	25.26	35.60	36.30	29.96	25.42	14.96	15.80	33.85	20.15	44.89	20.96	18.86	61.22	39.65	53.94	-	0.06	0.05	0.03	0.05	0.01	0.01	0.63	0.42	0.00	0.10	0.03	0.22	0.00	0.20	0.18
<i>Similia amethystina</i>	51.66	56.72	45.80	59.66	61.24	53.10	39.74	39.23	60.43	29.05	10.79	35.60	31.47	29.67	44.22	11.44	43.48	-	0.83	0.94	0.34	0.32	0.08	0.09	0.02	0.54	0.45	0.33	0.49	0.88	0.04	0.02
<i>Similia boeleni</i>	62.99	70.59	50.37	67.66	74.97	65.96	54.03	55.55	71.88	45.61	27.50	51.28	45.25	37.50	49.37	21.27	57.02	21.01	-	0.97	0.29	0.51	0.08	0.06	0.02	0.30	0.17	0.43	0.28	0.73	0.03	0.02
<i>Similia clastolepis</i>	57.01	63.36	46.74	63.49	69.26	59.15	46.89	46.62	62.91	37.00	21.01	41.64	36.77	28.25	42.11	14.17	50.59	12.52	11.75	-	0.21	0.40	0.06	0.05	0.01	0.22	0.21	0.34	0.25	0.69	0.02	0.01
<i>Similia kinghorni</i>	32.27	38.96	24.97	34.64	39.37	34.00	26.34	33.50	56.79	24.66	36.00	33.82	28.77	54.77	56.62	39.30	36.47	29.74	38.10	35.20	-	0.08	0.01	0.07	0.03	0.21	0.12	0.31	0.53	0.03	0.28	0.01
<i>Similia nauta</i>	102.55	106.69	90.46	106.06	110.27	102.71	91.82	90.01	104.37	80.62	52.14	84.96	82.93	43.80	80.40	42.40	96.24	53.23	46.19	48.72	74.55	-	0.59	0.02	0.01	0.22	0.08	0.64	0.06	0.35	0.01	0.01
<i>Similia oenpelliensis</i>	126.99	124.15	129.72	134.86	120.79	124.73	114.45	110.25	125.50	105.41	77.99	109.56	110.92	77.45	108.80	77.42	112.30	86.59	89.09	89.67	106.27	52.52	-	0.01	0.00	0.11	0.03	0.21	0.02	0.12	0.01	0.00
<i>Bothrochilus boa</i>	18.06	21.55	27.16	31.47	31.48	19.91	10.54	8.24	25.69	13.67	44.30	9.40	8.71	53.45	34.14	50.02	14.62	39.96	53.41	45.35	33.07	91.54	116.39	-	0.65	0.00	0.25	0.04	0.24	0.00	0.20	0.63
<i>Leiopython albertisii</i>	13.36	10.59	30.56	26.68	20.75	11.57	11.17	10.66	26.76	19.57	51.72	16.63	19.91	61.49	45.24	58.39	17.95	48.61	63.93	55.75	36.44	99.35	117.26	12.94	-	0.00	0.08	0.04	0.05	0.00	0.39	0.74
<i>Aspidites melanocephalus</i>	53.68	56.85	52.28	59.76	55.41	53.91	42.38	44.57	72.01	35.03	20.33	44.86	42.00	46.67	64.27	27.12	47.13	23.50	37.10	34.01	28.20	58.18	78.50	48.12	51.04	-	0.06	0.37	0.10	0.29	0.05	0.00
<i>Aspidites ramsayi</i>	35.22	36.74	38.17	46.21	44.11	34.64	22.91	17.77	39.85	11.49	27.56	13.91	15.47	35.45	37.64	32.19	28.93	24.64	43.45	32.94	30.92	72.47	97.22	21.71	27.51	33.82	-	0.13	0.36	0.03	0.07	0.06
<i>Liasis fuscus</i>	75.61	78.97	63.17	72.16	78.59	74.36	70.81	73.82	92.37	64.64	53.84	71.14	69.44	55.23	87.14	46.51	82.79	50.00	48.63	49.59	48.69	44.37	79.43	75.72	77.64	45.15	61.54	-	0.12	0.22	0.12	0.03
<i>Liasis mackloti</i>	29.74	35.76	29.18	39.15	39.66	32.20	18.19	21.79	46.31	12.27	27.95	21.59	15.17	47.38	41.90	34.57	23.15	23.26	36.82	30.67	17.85	76.06	104.03	21.20	28.76	29.42	19.21	61.23	-	0.04	0.13	0.01
<i>Liasis olivaceus</i>	61.44	66.46	56.67	69.89	69.20	63.30	48.96	48.58	70.39	38.99	8.82	46.00	41.65	34.26	50.27	13.12	49.51	13.19	21.58	18.76	18.37	48.30	77.06	49.61	58.05	23.26	34.96	53.41	31.76	-	0.01	0.00
<i>Liasis papuana</i>	24.64	23.48	34.16	18.07	14.39	22.65	33.03	40.43	52.42	42.73	69.41	45.58	45.84	84.53	74.40	75.30	41.89	65.61	76.51	72.46	38.82	109.42	123.80	41.23	32.05	57.68	51.85	71.40	45.59	74.02	-	0.19
<i>Boa constrictor</i>	19.47	17.27	32.54	31.75	29.66	18.02	17.35	11.64	18.21	21.42	52.51	13.28	18.81	56.61	38.11	57.62	22.05	48.75	63.57	54.39	41.44	97.45	118.05	12.18	9.96	55.57	26.28	79.67	31.89	58.98	40.07	-

Table S6. Head shape slope length differences. Pairwise comparisons of the differences in slope length, i.e., amount of shape change per unit of log centroid size change (bottom triangle), and *P*-values of the difference between them computed with 10,000 iterations (upper triangle). Significant values denoting differences in magnitude of shape change per unit of size are highlighted in green. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsoyi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.59	0.73	0.48	0.90	0.54	0.93	0.87	0.70	0.70	0.87	0.94	0.87	0.29	0.88	0.60	0.46	0.56	0.17	0.09	0.64	0.00	0.68	0.56	0.49	0.26	0.43	0.12	0.98	0.77	0.89	0.68
<i>Python bivittatus</i>	0.04	-	0.44	0.75	0.51	0.87	0.13	0.10	0.83	0.76	0.21	0.41	0.11	0.00	0.35	0.01	0.63	0.03	0.01	0.00	0.04	0.00	0.36	0.93	0.70	0.00	0.00	0.02	0.22	0.07	0.48	0.71
<i>Python brongersmai</i>	0.03	0.07	-	0.36	0.64	0.40	0.77	0.82	0.50	0.51	0.83	0.67	0.82	0.56	0.83	0.95	0.36	0.90	0.37	0.23	0.99	0.01	0.96	0.43	0.39	0.51	0.75	0.28	0.73	0.90	0.64	0.51
<i>Python curtus</i>	0.06	0.01	0.09	-	0.40	0.88	0.13	0.10	0.65	0.57	0.16	0.31	0.10	0.00	0.28	0.02	0.94	0.03	0.01	0.00	0.05	0.00	0.29	0.79	0.94	0.00	0.01	0.01	0.18	0.07	0.37	0.51
<i>Python molurus</i>	0.01	0.03	0.04	0.05	-	0.46	0.71	0.63	0.73	0.70	0.67	0.94	0.64	0.06	0.72	0.28	0.32	0.28	0.05	0.01	0.37	0.00	0.57	0.47	0.34	0.05	0.15	0.04	0.80	0.51	0.99	0.64
<i>Python regius</i>	0.05	0.01	0.08	0.01	0.04	-	0.14	0.11	0.74	0.67	0.20	0.37	0.13	0.00	0.32	0.02	0.79	0.03	0.01	0.00	0.05	0.00	0.32	0.93	0.89	0.00	0.01	0.02	0.22	0.09	0.45	0.62
<i>Python sebae</i>	0.01	0.05	0.03	0.06	0.02	0.05	-	0.84	0.44	0.31	0.87	0.75	0.83	0.01	0.91	0.13	0.03	0.26	0.06	0.00	0.37	0.00	0.69	0.09	0.01	0.01	0.05	0.06	0.88	0.62	0.66	0.12
<i>Malayopython reticulatus</i>	0.01	0.05	0.02	0.07	0.02	0.06	0.01	-	0.38	0.25	0.97	0.65	0.99	0.02	0.98	0.22	0.02	0.32	0.07	0.00	0.47	0.00	0.73	0.06	0.01	0.01	0.08	0.07	0.74	0.75	0.58	0.08
<i>Malayopython timoriensis</i>	0.03	0.01	0.06	0.03	0.02	0.02	0.04	0.04	-	0.98	0.43	0.67	0.38	0.04	0.51	0.17	0.57	0.17	0.03	0.00	0.22	0.00	0.43	0.78	0.62	0.03	0.09	0.03	0.51	0.31	0.72	1.00
<i>Antaresia childreni</i>	0.03	0.01	0.06	0.03	0.02	0.02	0.04	0.04	0.00	-	0.35	0.60	0.26	0.00	0.48	0.05	0.45	0.08	0.02	0.00	0.11	0.00	0.43	0.70	0.49	0.00	0.02	0.03	0.43	0.19	0.69	0.98
<i>Antaresia maculosa</i>	0.01	0.05	0.02	0.07	0.02	0.06	0.01	0.00	0.04	0.04	-	0.69	0.98	0.09	1.00	0.48	0.09	0.47	0.08	0.01	0.61	0.00	0.76	0.17	0.09	0.06	0.24	0.08	0.79	0.84	0.63	0.25
<i>Antaresia perthensis</i>	0.01	0.04	0.04	0.05	0.00	0.04	0.01	0.02	0.02	0.02	0.02	-	0.65	0.04	0.75	0.23	0.21	0.25	0.04	0.00	0.34	0.00	0.59	0.35	0.22	0.03	0.10	0.05	0.85	0.52	0.93	0.52
<i>Antaresia stimsoni</i>	0.01	0.05	0.02	0.07	0.02	0.06	0.01	0.00	0.04	0.04	0.00	0.02	-	0.02	0.99	0.28	0.03	0.35	0.07	0.00	0.49	0.00	0.74	0.08	0.01	0.02	0.11	0.08	0.74	0.77	0.58	0.10
<i>Morelia bredli</i>	0.09	0.13	0.05	0.14	0.10	0.14	0.08	0.08	0.12	0.12	0.07	0.09	0.08	-	0.22	0.09	0.00	0.27	0.55	0.16	0.15	0.02	0.54	0.00	0.00	0.86	0.46	0.42	0.02	0.06	0.03	0.00
<i>Morelia carinata</i>	0.01	0.05	0.02	0.07	0.02	0.06	0.01	0.00	0.04	0.04	0.00	0.02	0.00	0.07	-	0.61	0.24	0.58	0.13	0.04	0.69	0.00	0.76	0.33	0.26	0.19	0.38	0.11	0.84	0.88	0.70	0.43
<i>Morelia spilota</i>	0.04	0.08	0.01	0.09	0.05	0.09	0.03	0.03	0.07	0.07	0.03	0.04	0.03	0.05	0.03	-	0.00	0.84	0.14	0.02	0.88	0.01	0.99	0.00	0.00	0.06	0.38	0.14	0.18	0.51	0.21	0.00
<i>Morelia viridis</i>	0.06	0.02	0.09	0.00	0.05	0.01	0.06	0.07	0.03	0.03	0.07	0.05	0.07	0.15	0.07	0.10	-	0.01	0.00	0.00	0.01	0.00	0.28	0.67	0.84	0.00	0.00	0.01	0.08	0.02	0.28	0.32
<i>Simalia amethystina</i>	0.04	0.09	0.01	0.10	0.05	0.09	0.04	0.03	0.08	0.07	0.03	0.05	0.03	0.04	0.03	0.01	0.10	-	0.19	0.03	0.77	0.01	0.92	0.02	0.01	0.20	0.64	0.17	0.25	0.51	0.23	0.03
<i>Simalia boeleni</i>	0.12	0.16	0.09	0.17	0.13	0.17	0.11	0.11	0.15	0.15	0.11	0.12	0.11	0.03	0.11	0.08	0.18	0.07	-	0.55	0.14	0.03	0.35	0.01	0.01	0.63	0.28	0.79	0.05	0.09	0.04	0.01
<i>Simalia clastolepis</i>	0.15	0.19	0.12	0.21	0.16	0.20	0.15	0.14	0.18	0.18	0.14	0.16	0.14	0.07	0.14	0.11	0.21	0.11	0.03	-	0.02	0.08	0.21	0.00	0.00	0.21	0.05	0.81	0.00	0.01	0.00	0.00
<i>Simalia kinghorni</i>	0.03	0.08	0.00	0.09	0.04	0.08	0.03	0.02	0.06	0.06	0.02	0.04	0.02	0.05	0.02	0.00	0.09	0.01	0.08	0.12	-	0.01	0.96	0.02	0.01	0.10	0.42	0.13	0.35	0.71	0.31	0.04
<i>Simalia nauta</i>	0.32	0.36	0.29	0.37	0.33	0.37	0.31	0.31	0.35	0.35	0.31	0.33	0.31	0.23	0.31	0.28	0.38	0.27	0.20	0.17	0.29	-	0.01	0.00	0.00	0.02	0.01	0.05	0.00	0.00	0.00	0.00
<i>Simalia oenpelliensis</i>	0.04	0.08	0.00	0.09	0.05	0.09	0.03	0.03	0.07	0.07	0.02	0.04	0.03	0.05	0.03	0.00	0.10	0.01	0.08	0.11	0.00	0.28	-	0.34	0.31	0.49	0.76	0.26	0.65	0.83	0.56	0.42
<i>Bothrochilus boa</i>	0.04	0.00	0.08	0.01	0.03	0.00	0.05	0.06	0.01	0.01	0.06	0.04	0.06	0.13	0.06	0.08	0.01	0.09	0.16	0.20	0.08	0.36	0.08	-	0.77	0.00	0.00	0.02	0.17	0.05	0.43	0.61
<i>Leiopython albertisii</i>	0.05	0.01	0.09	0.00	0.04	0.00	0.06	0.06	0.02	0.02	0.07	0.05	0.06	0.14	0.07	0.09	0.01	0.10	0.17	0.21	0.09	0.37	0.09	0.01	-	0.00	0.00	0.01	0.06	0.01	0.29	0.30
<i>Aspidites melanocephalus</i>	0.09	0.14	0.06	0.15	0.10	0.14	0.09	0.08	0.12	0.12	0.08	0.10	0.08	0.01	0.08	0.06	0.15	0.05	0.02	0.06	0.06	0.23	0.06	0.14	0.15	-	0.34	0.48	0.01	0.04	0.03	0.00
<i>Aspidites ramsoyi</i>	0.06	0.10	0.03	0.12	0.07	0.11	0.06	0.05	0.09	0.09	0.05	0.07	0.05	0.03	0.05	0.02	0.12	0.02	0.06	0.09	0.03	0.26	0.02	0.11	0.11	0.03	-	0.23	0.07	0.21	0.10	0.00
<i>Liasis fuscus</i>	0.14	0.18	0.10	0.19	0.15	0.18	0.13	0.13	0.17	0.17	0.12	0.14	0.12	0.05	0.12	0.10	0.20	0.09	0.02	0.02	0.10	0.18	0.10	0.18	0.19	0.04	0.08	-	0.06	0.09	0.04	0.02
<i>Liasis mackloti</i>	0.00	0.04	0.03	0.06	0.01	0.05	0.00	0.01	0.03	0.03	0.01	0.01	0.01	0.09	0.01	0.04	0.06	0.04	0.12	0.15	0.03	0.32	0.04	0.05	0.05	0.09	0.06	0.13	-	0.57	0.77	0.27
<i>Liasis olivaceus</i>	0.02	0.06	0.01	0.08	0.03	0.07	0.01	0.01	0.05	0.05	0.01	0.03	0.01	0.07	0.01	0.02	0.08	0.02	0.10	0.13	0.01	0.30	0.02	0.07	0.07	0.07	0.04	0.12	0.02	-	0.46	0.07
<i>Liasis papuana</i>	0.01	0.03	0.04	0.04	0.00	0.04	0.02	0.02	0.02	0.02	0.02	0.00	0.02	0.10	0.02	0.05	0.05	0.06	0.13	0.16	0.04	0.33	0.05	0.03	0.04	0.10	0.07	0.15	0.01	0.03	-	0.61
<i>Boa constrictor</i>	0.03	0.01	0.06	0.03	0.02	0.02	0.04	0.04	0.00	0.00	0.04	0.02	0.04	0.12	0.04	0.07	0.03	0.08	0.15	0.18	0.06	0.35	0.07	0.01	0.02	0.12	0.09	0.17	0.03	0.05	0.02	-

Table S7. Body shape slope length differences. Pairwise comparisons of the differences in slope length, i.e., amount of shape change per unit of log centroid size change (bottom triangle), and *P*-values of the difference between them computed with 10,000 iterations (upper triangle). Significant values denoting differences in magnitude of shape change per unit of size are highlighted in green. Black boxes outline comparisons within clades.

	Python										Antaresia										Simalia										Leiopython										Aspidites										Liasis										Boa									
	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsi</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>																																						
<i>Python anchietae</i>	-	0.03	0.36	0.90	0.30	0.97	0.04	0.02	0.06	0.03	0.01	0.03	0.10	0.00	0.01	0.00	0.03	0.01	0.06	0.02	0.01	0.28	0.54	0.12	0.00	0.01	0.00	0.20	0.04	0.02	0.02	0.01																																						
<i>Python bivittatus</i>	0.28	-	0.44	0.00	0.16	0.00	0.81	0.59	0.84	0.96	0.23	0.95	0.17	0.01	0.31	0.00	0.97	0.18	0.85	0.73	0.27	0.57	0.48	0.13	0.00	0.08	0.01	0.63	0.93	0.47	0.50	0.23																																						
<i>Python brongersmai</i>	0.16	0.12	-	0.36	0.90	0.34	0.49	0.32	0.51	0.45	0.21	0.43	0.78	0.09	0.17	0.09	0.44	0.18	0.53	0.35	0.24	0.88	0.89	0.83	0.08	0.16	0.12	0.79	0.46	0.31	0.25	0.26																																						
<i>Python curtus</i>	0.01	0.27	0.15	-	0.21	0.89	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.30	0.59	0.01	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00																																						
<i>Python molurus</i>	0.14	0.14	0.02	0.13	-	0.18	0.19	0.08	0.29	0.17	0.03	0.16	0.50	0.00	0.06	0.00	0.14	0.02	0.31	0.12	0.03	0.77	0.96	0.58	0.00	0.01	0.01	0.65	0.16	0.06	0.08	0.03																																						
<i>Python regius</i>	0.01	0.28	0.16	0.01	0.14	-	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.28	0.57	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.00																																						
<i>Python sebae</i>	0.27	0.01	0.11	0.25	0.13	0.26	-	0.41	0.96	0.86	0.14	0.79	0.19	0.00	0.26	0.00	0.77	0.11	0.96	0.59	0.15	0.63	0.53	0.15	0.00	0.03	0.00	0.69	0.85	0.28	0.41	0.08																																						
<i>Malayopython reticulatus</i>	0.32	0.04	0.16	0.31	0.18	0.32	0.05	-	0.56	0.57	0.51	0.65	0.05	0.03	0.49	0.01	0.58	0.39	0.58	0.91	0.62	0.43	0.39	0.04	0.01	0.24	0.08	0.46	0.49	0.92	0.76	0.63																																						
<i>Malayopython timoriensis</i>	0.26	0.02	0.10	0.25	0.12	0.26	0.00	0.06	-	0.87	0.29	0.82	0.51	0.04	0.30	0.03	0.81	0.22	1.00	0.66	0.33	0.65	0.53	0.45	0.03	0.16	0.08	0.72	0.88	0.49	0.45	0.34																																						
<i>Antaresia childreni</i>	0.28	0.00	0.12	0.26	0.14	0.27	0.01	0.04	0.02	-	0.23	0.93	0.21	0.01	0.31	0.00	0.93	0.18	0.87	0.71	0.26	0.59	0.49	0.16	0.00	0.07	0.02	0.64	0.97	0.45	0.48	0.23																																						
<i>Antaresia maculosa</i>	0.37	0.09	0.21	0.36	0.23	0.37	0.10	0.05	0.11	0.09	-	0.29	0.01	0.18	0.79	0.12	0.23	0.81	0.31	0.50	0.85	0.28	0.29	0.01	0.09	0.69	0.38	0.29	0.17	0.53	0.85	0.73																																						
<i>Antaresia perthensis</i>	0.29	0.00	0.13	0.27	0.15	0.28	0.02	0.03	0.02	0.01	0.08	-	0.21	0.01	0.35	0.01	0.98	0.22	0.82	0.78	0.35	0.56	0.47	0.17	0.00	0.12	0.03	0.61	0.89	0.56	0.54	0.34																																						
<i>Antaresia stimsoni</i>	0.20	0.08	0.04	0.19	0.06	0.20	0.06	0.12	0.06	0.08	0.17	0.08	-	0.00	0.11	0.00	0.11	0.02	0.53	0.16	0.01	0.93	0.73	0.82	0.00	0.00	0.00	0.97	0.12	0.01	0.14	0.00																																						
<i>Morelia bredli</i>	0.47	0.19	0.31	0.45	0.33	0.46	0.20	0.15	0.21	0.19	0.10	0.18	0.27	-	0.58	0.99	0.00	0.34	0.06	0.06	0.10	0.11	0.16	0.00	0.78	0.28	0.54	0.10	0.00	0.02	0.25	0.03																																						
<i>Morelia carinata</i>	0.40	0.12	0.24	0.39	0.26	0.40	0.13	0.08	0.14	0.12	0.03	0.12	0.20	0.07	-	0.56	0.33	0.93	0.30	0.47	0.70	0.22	0.22	0.09	0.47	0.98	0.79	0.24	0.29	0.51	0.71	0.63																																						
<i>Morelia spilota</i>	0.47	0.19	0.31	0.45	0.33	0.46	0.20	0.15	0.21	0.19	0.10	0.18	0.27	0.00	0.07	-	0.00	0.29	0.05	0.04	0.04	0.12	0.17	0.00	0.67	0.17	0.42	0.10	0.00	0.00	0.23	0.00																																						
<i>Morelia viridis</i>	0.28	0.00	0.12	0.27	0.14	0.28	0.02	0.04	0.02	0.01	0.09	0.00	0.08	0.18	0.12	0.18	-	0.18	0.82	0.74	0.26	0.57	0.48	0.09	0.00	0.05	0.01	0.61	0.89	0.45	0.50	0.19																																						
<i>Simalia amethystina</i>	0.39	0.11	0.23	0.38	0.25	0.39	0.12	0.07	0.13	0.11	0.02	0.11	0.19	0.08	0.01	0.08	0.11	-	0.24	0.38	0.66	0.23	0.25	0.01	0.22	0.93	0.60	0.24	0.14	0.41	0.71	0.55																																						
<i>Simalia boeleni</i>	0.26	0.02	0.10	0.25	0.12	0.26	0.01	0.06	0.00	0.02	0.11	0.02	0.06	0.21	0.14	0.21	0.02	0.13	-	0.65	0.36	0.66	0.53	0.47	0.04	0.19	0.10	0.73	0.88	0.52	0.47	0.37																																						
<i>Simalia clastolepis</i>	0.31	0.03	0.15	0.30	0.17	0.31	0.04	0.01	0.05	0.03	0.06	0.02	0.11	0.16	0.09	0.16	0.03	0.08	0.05	-	0.59	0.47	0.41	0.13	0.03	0.29	0.13	0.50	0.67	0.84	0.71	0.62																																						
<i>Simalia kinghorni</i>	0.36	0.07	0.20	0.34	0.22	0.35	0.09	0.04	0.09	0.08	0.01	0.07	0.15	0.11	0.05	0.11	0.07	0.04	0.09	0.05	-	0.32	0.32	0.01	0.03	0.51	0.21	0.34	0.19	0.64	0.96	0.90																																						
<i>Simalia nauta</i>	0.19	0.09	0.03	0.17	0.05	0.18	0.08	0.13	0.08	0.09	0.18	0.10	0.02	0.28	0.21	0.28	0.10	0.20	0.07	0.12	0.17	-	0.78	0.98	0.10	0.22	0.16	0.91	0.60	0.41	0.34	0.35																																						
<i>Simalia oenpelliensis</i>	0.13	0.15	0.03	0.11	0.01	0.12	0.14	0.19	0.13	0.15	0.24	0.16	0.07	0.34	0.27	0.34	0.16	0.26	0.13	0.18	0.23	0.06	-	0.77	0.15	0.25	0.21	0.71	0.51	0.38	0.30	0.34																																						
<i>Bothrochilus boa</i>	0.19	0.09	0.03	0.18	0.05	0.19	0.07	0.13	0.07	0.09	0.18	0.09	0.01	0.28	0.21	0.28	0.09	0.20	0.07	0.12	0.16	0.00	0.06	-	0.00	0.00	0.00	0.91	0.10	0.01	0.12	0.00																																						
<i>Leiopython albertsi</i>	0.49	0.20	0.33	0.47	0.35	0.48	0.22	0.17	0.22	0.21	0.11	0.20	0.28	0.02	0.08	0.02	0.20	0.09	0.22	0.17	0.13	0.30	0.36	0.29	-	0.13	0.30	0.08	0.00	0.00	0.18	0.00																																						
<i>Aspidites melanocephalus</i>	0.40	0.12	0.24	0.39	0.26	0.39	0.13	0.08	0.14	0.12	0.03	0.11	0.20	0.07	0.00	0.07	0.11	0.01	0.14	0.09	0.04	0.21	0.27	0.21	0.09	-	0.57	0.22	0.04	0.22	0.64	0.33																																						
<i>Aspidites ramsayi</i>	0.43	0.15	0.27	0.42	0.29	0.43	0.16	0.11	0.17	0.15	0.06	0.15	0.23	0.04	0.03	0.04	0.15	0.04	0.17	0.12	0.08	0.24	0.30	0.24	0.05	0.03	-	0.15	0.00	0.05	0.42	0.08																																						
<i>Liasis fuscus</i>	0.21	0.07	0.05	0.19	0.07	0.20	0.06	0.11	0.05	0.07	0.16	0.08	0.01	0.26	0.19	0.26	0.08	0.18	0.05	0.10	0.15	0.02	0.08	0.02	0.28	0.19	0.22	-	0.65	0.44	0.36	0.36																																						
<i>Liasis mackloti</i>	0.28	0.01	0.12	0.26	0.14	0.27	0.01	0.04	0.01	0.00	0.09	0.01	0.07	0.19	0.13	0.19	0.01	0.12	0.01	0.03	0.08	0.09	0.15	0.08	0.21	0.12	0.16	0.07	-	0.34	0.46	0.11																																						
<i>Liasis olivaceus</i>	0.33	0.04	0.17	0.31	0.19	0.32	0.06	0.01	0.06	0.05	0.04	0.04	0.12	0.14	0.08	0.14	0.04	0.07	0.06	0.02	0.03	0.14	0.20	0.13	0.16	0.07	0.11	0.12	0.05	-	0.81	0.65																																						
<i>Liasis papuana</i>	0.35	0.07	0.19	0.34	0.21	0.35	0.08	0.03	0.09	0.07	0.02	0.07	0.15	0.12	0.05	0.12	0.07	0.04	0.09	0.04	0.00	0.16	0.22	0.16	0.13	0.05	0.08	0.14	0.07	0.02	-	0.98																																						
<i>Boa constrictor</i>	0.35	0.07	0.19	0.33	0.21	0.34	0.08	0.03	0.09	0.07	0.02	0.06	0.14	0.12	0.05	0.12	0.06	0.04	0.09	0.04	0.01	0.16	0.22	0.16	0.14	0.05	0.08	0.14	0.07	0.02	0.00	-																																						

Table S8. Head shape intercept differences. Pairwise differences in the intercept of the allometric regressions (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 iterations (upper triangle). This test only applies to pairs of taxa for which the null hypothesis of common slopes has not been rejected. Cells highlighted in green correspond to species where they have a common slope but different intercept (parallel allometric trajectories). Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreii</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oepelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsi</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.39	-	0.41	0.75	0.31	-	-	-	0.28	0.40	0.30	0.16	-	0.84	-	0.60	-	-	-	-	0.58	0.55	0.38	-	-	-	0.19	-	-	0.73	-
<i>Python bivittatus</i>	0.19	-	0.68	0.41	0.59	0.59	-	-	0.73	0.54	-	-	-	-	0.68	-	-	-	0.45	-	0.51	0.82	0.64	0.68	0.82	0.80	0.82	0.85	0.94	0.80	0.81	-
<i>Python brongersmai</i>	-	0.21	-	0.63	0.43	0.72	0.90	0.95	0.92	0.52	0.66	0.59	0.60	0.86	0.76	0.83	-	0.82	0.91	0.81	0.90	0.51	0.82	0.64	0.68	0.82	0.80	0.82	0.85	0.94	0.80	0.81
<i>Python curtus</i>	0.18	0.11	0.19	-	0.60	0.59	0.22	0.19	0.86	-	-	-	-	-	0.60	-	-	-	0.41	-	0.10	0.50	-	-	-	-	-	0.30	0.31	0.20	0.41	-
<i>Python molurus</i>	0.15	0.11	0.28	0.12	-	0.49	-	-	-	0.41	-	-	-	-	0.76	-	-	-	-	-	-	0.36	0.59	0.45	-	-	-	0.08	-	-	-	-
<i>Python regius</i>	0.18	0.08	0.19	0.09	0.13	-	0.33	0.20	0.91	0.60	0.65	0.51	-	0.48	0.72	0.42	-	0.15	0.48	0.11	0.16	0.02	0.57	-	-	0.51	0.44	0.33	0.59	0.31	0.66	0.60
<i>Python sebae</i>	-	-	0.15	0.15	-	0.12	-	0.55	0.77	-	0.30	0.04	-	0.65	0.51	-	-	0.61	0.75	0.39	0.65	0.16	0.81	-	-	-	-	0.41	0.83	0.80	0.65	-
<i>Malayopython reticulatus</i>	-	-	0.12	0.15	-	0.13	0.07	-	0.78	-	0.10	-	0.54	0.44	-	-	-	0.50	0.74	0.36	0.82	0.14	0.82	-	-	0.40	-	0.60	0.45	0.83	0.41	-
<i>Malayopython timoriensis</i>	-	0.10	0.15	0.09	-	0.07	0.10	0.10	-	0.55	0.65	0.49	0.51	0.76	0.94	0.72	-	0.53	0.59	0.42	0.58	0.20	0.72	-	-	0.60	0.59	0.48	0.80	0.71	0.70	0.73
<i>Antaresia childreii</i>	0.19	0.07	0.23	-	0.12	0.08	-	-	0.11	-	0.95	0.72	0.38	-	0.50	-	-	-	0.39	-	-	0.02	0.45	0.77	0.90	-	-	0.04	0.19	0.03	0.81	-
<i>Antaresia maculosa</i>	0.20	-	0.22	-	-	0.09	0.12	0.16	0.12	0.04	-	0.98	0.88	0.42	0.61	0.45	-	0.25	0.48	0.12	0.16	0.08	0.67	0.82	-	0.60	0.64	0.26	0.56	0.30	0.96	0.90
<i>Antaresia perthensis</i>	0.20	-	0.23	-	-	0.10	0.14	-	0.13	0.05	0.03	-	0.54	0.26	0.42	0.18	-	0.07	0.41	0.07	0.04	0.02	0.55	0.58	0.72	0.52	0.42	0.08	0.18	0.05	0.82	0.62
<i>Antaresia stimsoni</i>	0.23	-	0.21	-	-	-	-	-	0.12	0.06	0.04	0.05	-	0.41	0.41	-	-	0.12	0.49	0.12	-	0.03	0.59	-	-	-	-	0.09	-	-	0.90	0.45
<i>Morelia bredli</i>	-	-	0.18	-	-	0.12	0.08	0.10	0.12	-	0.12	0.13	0.10	-	0.60	0.76	-	0.83	0.87	0.55	0.65	0.31	0.85	-	-	0.78	0.70	0.60	0.78	0.76	0.77	0.42
<i>Morelia carinata</i>	0.16	0.12	0.23	0.14	0.14	0.11	0.17	0.18	0.11	0.12	0.13	0.14	0.15	0.15	-	0.54	-	0.35	0.54	0.36	0.41	0.18	0.57	0.60	0.59	0.53	0.60	0.30	0.48	0.41	0.78	0.55
<i>Morelia spilota</i>	-	-	0.17	-	-	0.10	-	-	0.10	-	0.08	0.10	-	0.05	0.14	-	-	0.56	0.71	0.30	0.52	0.16	0.82	-	-	0.70	0.52	0.47	-	0.59	0.85	-
<i>Morelia viridis</i>	0.15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Simalia amethystina</i>	-	-	0.18	-	-	0.17	0.09	0.10	0.16	-	0.16	0.18	0.13	0.07	0.21	0.09	-	-	0.92	0.82	0.73	0.23	0.90	-	-	0.59	0.51	0.64	0.60	0.81	0.54	0.20
<i>Simalia boeleni</i>	-	0.22	0.19	0.27	-	0.21	0.16	0.15	0.20	0.22	0.20	0.21	0.18	0.12	0.25	0.13	-	0.11	-	0.97	0.82	0.60	0.98	-	-	0.75	0.76	0.91	0.73	0.83	0.58	0.64
<i>Simalia clastolepis</i>	-	-	0.22	-	-	0.26	0.18	0.18	0.24	-	0.24	0.25	0.21	0.15	0.30	0.17	-	0.10	0.10	-	0.50	0.59	0.90	-	-	0.40	0.33	0.76	0.33	0.52	0.28	0.16
<i>Simalia kinghorni</i>	-	-	0.15	0.19	-	0.16	0.08	0.06	0.13	-	0.17	0.18	-	0.09	0.19	0.09	-	0.08	0.12	0.15	-	0.16	0.87	-	-	0.48	0.33	0.70	0.59	0.91	0.45	-
<i>Simalia nauta</i>	-	0.47	0.37	0.50	-	0.47	0.39	0.38	0.45	0.47	0.44	0.45	0.42	0.38	0.51	0.39	-	0.34	0.30	0.27	0.38	-	0.51	-	-	0.26	0.22	0.48	0.09	0.16	0.14	0.09
<i>Simalia oepelliensis</i>	-	0.22	0.23	0.27	0.29	0.23	0.17	0.17	0.23	0.22	0.21	0.22	0.20	0.17	0.29	0.16	-	0.14	0.13	0.16	0.14	0.32	-	0.54	0.59	0.82	0.87	0.95	0.78	0.82	0.78	0.78
<i>Bothrochilus boa</i>	0.17	-	0.24	-	0.12	-	-	-	-	0.04	0.05	0.05	-	0.12	-	-	-	-	-	-	-	-	0.25	-	0.56	-	-	0.09	0.10	-	0.76	-
<i>Leiopython albertsii</i>	0.20	-	0.20	-	0.13	-	-	-	-	0.03	-	0.05	-	-	0.12	-	-	-	-	-	-	-	0.21	0.06	-	-	-	-	-	-	-	-
<i>Aspidites melanocephalus</i>	-	-	0.18	-	0.12	-	0.13	0.13	-	0.09	0.10	-	0.07	0.16	0.06	-	-	0.12	0.12	0.17	0.13	0.37	0.18	-	-	-	0.90	0.59	-	0.59	0.82	0.76
<i>Aspidites ramsayi</i>	-	-	0.21	-	0.12	-	-	-	0.14	-	0.08	0.09	-	0.08	0.15	0.07	-	0.12	0.13	0.19	0.13	0.39	0.17	-	-	0.05	-	0.51	-	0.44	0.94	0.70
<i>Liasis fuscus</i>	-	0.26	0.20	0.28	0.34	0.26	0.19	0.16	0.24	0.27	0.27	0.28	0.25	0.19	0.32	0.20	-	0.16	0.13	0.15	0.15	0.29	0.12	0.31	-	0.21	0.22	-	0.18	0.46	0.42	0.33
<i>Liasis mackloti</i>	0.25	-	0.16	0.15	-	0.09	0.04	0.08	0.09	0.09	0.09	0.10	-	0.07	0.15	-	-	0.09	0.15	0.18	0.09	0.40	0.17	0.12	-	-	-	0.20	-	0.59	0.80	-
<i>Liasis olivaceus</i>	-	-	0.13	0.17	-	0.14	0.05	0.05	0.12	0.15	0.15	0.17	-	0.08	0.18	0.07	-	0.07	0.13	0.15	0.05	0.37	0.16	-	-	0.11	0.13	0.17	0.07	-	0.60	-
<i>Liasis papuana</i>	-	0.09	0.21	0.17	-	0.11	0.11	0.15	0.13	0.07	0.05	0.07	0.06	0.10	0.13	0.07	-	0.15	0.17	0.22	0.14	0.43	0.21	0.08	-	0.07	0.06	0.26	0.08	0.13	-	0.95
<i>Boa constrictor</i>	0.23	-	0.19	-	-	0.08	-	-	0.11	-	0.05	0.06	0.06	0.10	0.14	-	-	0.14	0.17	0.21	-	0.42	0.18	-	-	0.07	0.06	0.23	-	-	0.06	-

Table S9. Body shape intercept differences. Pairwise differences in the intercept of the allometric regressions (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 iterations (upper triangle). Details as in Table S8.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Antaresia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.71	0.98	0.67	0.98	0.79	0.52	0.31	0.63	0.12	0.10	0.13	0.24	-	0.54	0.02	0.21	0.27	0.27	0.27	0.27	-	-	0.47	0.21	0.08	0.17	0.28	0.21	0.07	0.56	0.44
<i>Python bivittatus</i>	0.48	-	0.86	0.24	0.67	0.28	0.64	0.35	0.71	0.17	-	0.24	0.27	-	0.29	-	0.16	-	-	-	0.25	-	0.48	0.11	-	-	-	-	-	-	0.61	0.70
<i>Python brongersmai</i>	0.43	0.74	-	0.88	0.95	0.95	0.73	0.62	0.82	0.41	0.40	0.46	0.52	0.50	0.63	0.24	0.50	0.64	0.63	0.65	0.64	0.59	-	0.75	0.46	0.35	0.53	0.63	0.52	0.44	0.80	0.67
<i>Python curtus</i>	0.74	1.15	0.55	-	0.64	0.64	0.10	0.17	0.44	0.01	-	0.01	-	-	0.31	-	0.06	-	-	-	0.24	-	0.08	0.03	-	-	0.44	-	-	0.53	0.03	
<i>Python molurus</i>	0.31	0.47	0.62	0.87	-	0.74	0.49	0.29	0.51	0.09	-	0.11	0.22	-	0.34	-	0.19	0.27	-	-	0.26	-	0.37	0.18	0.08	0.18	0.27	0.17	-	0.59	0.47	
<i>Python regius</i>	0.48	0.85	0.49	0.41	0.56	-	0.12	0.23	0.35	0.02	-	0.01	0.01	-	0.23	-	0.10	-	-	-	0.24	-	0.09	0.06	-	0.01	0.38	0.07	-	0.48	0.05	
<i>Python sebae</i>	0.65	0.30	0.91	1.36	0.63	1.05	-	0.74	0.63	0.26	-	0.29	0.42	-	0.41	-	0.28	0.26	0.29	-	0.29	-	0.63	0.12	-	0.24	0.35	0.23	-	0.63	0.30	
<i>Malayopython reticulatus</i>	0.95	0.58	1.21	1.67	0.93	1.36	0.32	-	0.60	0.52	0.52	0.48	0.63	-	0.66	-	0.64	0.28	0.48	0.30	0.33	-	0.70	0.29	-	0.44	0.34	0.59	-	0.54	0.38	
<i>Malayopython timoriensis</i>	0.86	0.46	1.06	1.47	0.91	1.19	0.53	0.59	-	0.36	-	0.63	0.63	-	0.62	-	0.42	0.30	-	-	-	-	0.88	0.34	-	0.61	-	0.37	-	0.52	0.90	
<i>Antaresia childreni</i>	1.01	0.59	1.18	1.67	0.97	1.41	0.45	0.40	0.59	-	0.80	0.71	0.68	-	0.59	-	0.27	0.28	0.26	0.19	0.33	-	0.27	0.86	0.28	0.68	0.30	0.43	-	0.79	0.19	
<i>Antaresia maculosa</i>	1.19	-	1.34	-	-	-	-	0.59	-	0.25	-	0.44	0.31	0.49	0.68	0.34	-	0.51	0.44	0.35	0.53	0.43	0.47	-	-	0.76	0.63	0.61	0.29	-	-	
<i>Antaresia perthensis</i>	0.86	0.41	1.04	1.51	0.83	1.24	0.37	0.44	0.42	0.22	0.39	-	0.79	-	0.39	-	0.26	0.27	0.21	0.11	0.30	-	0.45	0.49	-	0.71	0.36	0.30	-	0.74	0.38	
<i>Antaresia stimsoni</i>	0.85	0.44	1.04	-	0.85	1.26	0.31	0.33	0.45	0.20	0.43	0.15	-	-	0.57	-	0.23	0.23	0.28	0.17	0.27	-	0.52	0.31	-	0.36	0.34	0.24	-	0.68	0.12	
<i>Morelia bredli</i>	-	-	1.88	-	-	-	-	-	-	-	0.60	-	-	-	0.61	0.82	-	0.47	0.46	0.27	-	0.30	0.44	-	-	-	0.28	0.43	-	0.26	-	
<i>Morelia carinata</i>	1.40	0.97	1.62	2.09	1.37	1.82	0.80	0.56	0.79	0.50	0.55	0.62	0.59	0.49	-	0.74	0.75	0.63	0.81	0.64	0.59	0.28	-	0.63	0.64	0.62	0.58	0.46	0.97	0.44	0.59	0.44
<i>Morelia spilota</i>	1.64	-	1.82	-	-	-	-	-	-	-	0.55	-	-	0.20	0.44	-	-	0.49	0.50	0.35	-	0.33	0.32	-	-	0.52	-	0.44	-	0.21	-	
<i>Morelia viridis</i>	1.07	0.70	1.38	1.79	1.00	1.50	0.51	0.35	0.71	0.49	-	0.53	0.49	-	0.49	-	-	0.21	-	-	0.22	-	0.30	0.12	-	0.27	-	0.32	-	0.52	0.17	
<i>Simalia amethystina</i>	1.84	-	2.03	-	1.81	-	1.23	0.96	1.40	0.96	0.95	1.16	1.08	0.62	0.71	0.51	0.97	-	0.98	0.98	0.64	0.57	0.38	0.27	-	0.45	0.35	0.68	0.52	0.99	-	-
<i>Simalia boeleni</i>	1.64	-	1.78	-	-	1.09	0.88	-	0.88	0.95	1.07	0.95	0.85	0.85	0.73	0.70	-	0.43	-	0.99	0.99	0.72	0.61	0.34	-	0.46	0.29	0.77	0.74	0.81	-	-
<i>Simalia clastolepis</i>	1.63	-	1.81	-	-	-	0.76	-	0.82	0.88	1.01	0.90	0.68	0.61	0.57	-	-	0.27	0.29	-	0.85	0.52	0.52	-	-	0.29	0.22	0.63	0.62	0.74	-	-
<i>Simalia kinghorni</i>	1.47	1.17	1.62	2.13	1.44	1.89	0.92	0.74	-	0.69	0.73	0.89	0.80	-	0.68	-	0.78	0.49	0.32	0.39	-	0.31	-	0.26	-	0.54	0.36	0.69	0.52	-	0.46	-
<i>Simalia nauta</i>	-	-	2.80	-	-	-	-	-	-	-	1.66	-	-	1.21	1.57	1.20	-	0.96	1.25	1.19	1.31	-	0.74	-	-	0.33	0.33	0.80	0.30	0.53	-	-
<i>Simalia oenpelliensis</i>	-	-	-	-	-	-	-	-	-	-	2.40	-	-	1.98	-	2.02	-	2.06	2.44	2.32	-	1.46	-	-	-	0.34	-	0.54	-	0.34	-	-
<i>Bothrochilus boa</i>	0.78	0.39	1.02	1.47	0.81	1.20	0.28	0.34	0.34	0.40	-	0.29	0.23	-	0.64	-	0.46	1.19	1.04	-	0.93	-	-	-	0.14	-	0.24	-	0.22	-	0.62	0.28
<i>Leiopython albertisii</i>	1.15	0.71	1.32	1.80	1.07	1.52	0.59	0.49	0.68	0.18	-	0.33	0.36	-	0.47	-	0.52	-	-	-	-	-	0.54	-	-	0.77	-	-	-	-	0.82	0.20
<i>Aspidites melanocephalus</i>	1.42	-	1.56	-	1.34	-	-	-	0.46	0.32	-	-	-	-	0.55	0.36	-	0.74	0.77	0.73	0.54	1.42	2.21	-	-	-	0.29	0.53	0.40	0.23	-	-
<i>Aspidites ramsayi</i>	1.05	-	1.17	-	1.00	1.40	0.60	0.62	0.58	0.26	0.28	0.25	0.34	0.78	0.64	-	0.69	1.15	1.09	1.04	0.91	1.87	-	0.53	0.27	0.55	-	0.49	0.32	-	0.87	0.29
<i>Liasis fuscus</i>	1.92	-	1.91	2.43	1.87	2.22	1.44	1.33	-	1.15	1.05	1.32	1.28	1.01	1.28	0.97	-	0.98	1.01	1.02	0.89	1.08	2.12	-	-	0.90	1.20	-	0.34	0.48	0.52	-
<i>Liasis mackloti</i>	1.29	-	1.49	-	1.26	1.71	0.66	0.41	0.80	0.38	0.45	0.55	0.48	-	0.26	-	0.46	0.62	0.61	0.49	0.49	1.50	-	0.59	-	0.44	0.59	1.10	-	0.53	-	-
<i>Liasis olivaceus</i>	1.90	-	2.09	-	-	-	-	-	-	-	0.95	-	-	0.56	0.72	0.46	-	0.13	0.55	0.39	-	0.91	1.94	-	-	0.73	-	1.00	-	-	-	-
<i>Liasis papuana</i>	1.13	0.80	1.24	1.70	1.04	1.51	0.74	0.77	0.93	0.43	-	0.52	0.56	-	0.77	-	0.74	-	-	-	0.77	-	-	0.74	0.42	-	0.45	1.12	0.67	-	-	0.63
<i>Boa constrictor</i>	0.74	0.28	0.95	1.34	0.68	1.04	0.43	0.59	0.36	0.52	-	0.33	0.42	-	0.87	-	0.69	-	-	-	-	-	0.42	0.58	-	0.47	-	-	-	-	0.77	-

Table S10. Head shape peramorphosis test. Pairwise comparisons of the predicted head shape differences at maximum per-group body size (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 iterations (upper triangle). This test only applies to pairs of taxa for which the null hypothesis of common slope and common intercept has not been rejected. Cells highlighted in green correspond to species where they have a common slope and intercept but different predicted head shape at maximum per group size (peramorphosis/paedomorphosis). Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.47	-	0.67	0.38	0.71	-	-	0.07	0.07	0.04	0.09	-	-	0.17	-	0.15	-	-	-	-	-	0.05	0.05	-	-	-	0.06	-	-	-	0.19
<i>Python bivittatus</i>	0.05	-	0.04	0.10	0.35	0.02	-	-	0.05	0.00	-	-	-	-	0.00	-	-	-	0.00	-	0.04	0.06	0.16	-	-	-	0.01	0.00	0.02	0.01	0.05	
<i>Python brongersmai</i>	-	0.05	-	0.78	0.02	0.10	0.02	0.01	0.09	0.00	0.00	0.00	0.01	0.00	0.06	0.00	-	0.36	0.00	0.02	0.04	0.06	0.16	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	0.05
<i>Python curtus</i>	0.04	0.05	0.02	-	0.05	0.47	0.03	0.03	0.14	-	-	-	-	-	0.02	-	-	-	0.00	-	0.12	-	0.11	-	-	-	0.02	0.00	0.02	0.02	-	
<i>Python molurus</i>	0.06	0.03	0.05	0.05	-	0.01	-	-	-	0.00	-	-	-	-	0.00	-	-	0.05	0.00	0.00	0.02	-	0.05	0.00	0.00	-	0.19	0.00	0.00	0.00	0.00	
<i>Python regius</i>	0.04	0.05	0.04	0.03	0.06	-	0.00	0.01	0.12	0.00	0.00	0.00	-	0.00	0.01	0.00	-	0.05	0.00	0.00	0.02	-	0.02	-	-	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Python sebae</i>	-	-	0.06	0.06	-	0.07	-	0.07	0.03	-	0.01	-	-	0.00	0.01	-	-	0.00	0.00	0.00	0.00	0.01	0.00	-	-	-	0.03	0.00	0.04	0.03	-	
<i>Malayopython reticulatus</i>	-	-	0.07	0.06	-	0.07	0.05	-	0.20	-	0.04	-	-	0.02	0.01	-	-	0.02	0.03	0.07	0.12	0.03	0.00	-	-	0.02	-	0.00	0.00	0.00	0.40	-
<i>Malayopython timoriensis</i>	-	0.06	0.06	0.05	-	0.05	0.08	0.05	-	0.00	0.03	0.00	0.00	0.03	0.05	0.02	-	0.25	0.11	0.22	0.70	0.34	0.06	-	-	0.01	0.09	0.02	0.00	0.27	0.00	
<i>Antaresia childreni</i>	0.08	0.06	0.05	-	0.06	0.07	-	0.08	-	0.00	0.00	0.11	-	0.00	-	-	-	-	0.00	-	-	-	0.06	0.00	0.00	-	-	0.00	-	0.00	-	
<i>Antaresia maculosa</i>	0.09	-	0.06	-	-	0.07	0.05	0.05	0.06	0.06	-	0.00	0.00	0.00	0.00	0.00	-	0.01	0.00	0.00	0.00	0.03	0.00	0.01	-	0.00	0.00	0.00	0.00	0.02	0.00	
<i>Antaresia perthensis</i>	0.09	-	0.07	-	-	0.08	0.07	-	0.08	0.04	0.04	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	-	-	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia stimsoni</i>	0.07	-	0.05	-	-	-	-	0.08	0.02	0.05	0.04	-	-	0.00	0.00	-	-	0.00	0.00	0.00	-	-	0.07	-	-	-	0.00	-	-	0.00	0.00	0.00
<i>Morelia bredli</i>	-	-	0.09	-	-	0.10	0.10	0.07	0.08	-	0.08	0.11	0.11	-	0.16	0.22	-	0.01	0.01	0.46	0.01	0.18	0.00	-	-	0.00	0.03	0.00	0.00	0.01	0.00	
<i>Morelia carinata</i>	0.09	0.10	0.08	0.08	0.12	0.09	0.11	0.10	0.08	0.10	0.09	0.11	0.09	0.07	-	0.04	-	0.10	0.01	0.32	0.03	0.59	0.04	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.11
<i>Morelia spilota</i>	-	-	0.09	-	-	0.09	-	0.07	-	0.07	0.10	-	-	0.02	0.07	-	-	0.00	0.00	0.27	0.00	0.07	0.00	-	-	0.00	0.00	0.00	0.01	-	-	-
<i>Morelia viridis</i>	0.07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Simalia amethystina</i>	-	-	0.03	-	-	0.05	0.07	0.06	0.05	-	0.05	0.07	0.06	0.08	0.07	0.07	-	-	0.01	0.03	0.23	0.09	0.03	-	-	0.00	0.00	0.00	0.00	0.00	0.04	0.01
<i>Simalia boeleni</i>	-	0.11	0.12	0.11	-	0.11	0.12	0.08	0.07	0.14	0.10	0.13	0.14	0.08	0.11	0.07	-	0.10	-	0.15	0.01	0.17	0.00	-	-	0.12	0.05	0.00	0.00	0.00	0.03	0.00
<i>Simalia clastolepis</i>	-	-	0.08	-	-	0.09	0.09	0.06	0.06	-	0.07	0.09	0.10	0.03	0.06	0.03	-	0.07	0.06	-	0.06	0.47	0.01	-	-	0.01	0.17	0.00	0.00	0.00	0.07	0.00
<i>Simalia kinghorni</i>	-	-	0.05	0.04	-	0.05	0.06	0.04	0.03	-	0.05	0.08	-	0.07	0.08	0.07	-	0.03	0.08	0.06	-	0.09	0.01	-	-	0.00	0.02	0.00	0.00	0.00	0.17	-
<i>Simalia nauta</i>	-	0.08	0.08	0.07	-	0.07	0.09	0.08	0.06	0.09	0.07	0.09	0.08	0.07	0.05	0.07	-	0.07	0.08	0.05	0.06	-	0.02	-	-	0.02	0.11	0.00	0.00	0.00	0.07	0.01
<i>Simalia oenpelliensis</i>	-	0.06	0.04	0.05	0.06	0.06	0.08	0.10	0.08	0.04	0.08	0.06	0.04	0.12	0.09	0.12	-	0.06	0.14	0.11	0.07	0.09	-	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	0.00
<i>Bothrochilus boa</i>	0.11	-	0.08	-	0.08	-	-	-	0.05	0.05	0.03	-	-	-	0.12	-	-	-	-	-	-	-	0.08	-	0.00	-	-	0.04	0.03	-	0.00	-
<i>Leiopython albertisii</i>	0.11	-	0.09	-	0.08	-	-	-	0.07	-	0.09	-	-	-	0.14	-	-	-	-	-	-	-	0.08	0.09	-	-	-	-	-	-	-	-
<i>Aspidites melanocephalus</i>	-	-	0.13	-	-	0.12	-	0.09	0.08	-	0.11	0.14	-	0.08	0.12	0.08	-	0.11	0.04	0.07	0.09	0.09	0.16	-	-	-	0.01	0.00	-	0.00	0.00	0.00
<i>Aspidites ramsayi</i>	-	-	0.09	-	-	0.09	-	-	0.06	-	0.08	0.11	-	0.05	0.09	0.05	-	0.08	0.05	0.04	0.06	0.07	0.12	-	-	0.05	-	0.00	-	0.00	0.07	0.00
<i>Liasis fuscus</i>	-	0.06	0.08	0.08	0.04	0.09	0.05	0.09	0.09	0.05	0.07	0.06	0.07	0.14	0.13	0.13	-	0.09	0.15	0.12	0.09	0.12	0.07	0.05	-	0.16	0.12	-	0.49	0.07	0.02	0.00
<i>Liasis mackloti</i>	0.10	-	0.08	0.09	-	0.10	0.06	0.10	0.10	0.05	0.08	0.06	-	0.14	0.14	-	-	0.09	0.16	0.13	0.10	0.13	0.07	0.05	-	-	0.02	-	0.02	0.00	-	
<i>Liasis olivaceus</i>	-	-	0.06	0.07	-	0.08	0.05	0.09	0.10	0.05	0.08	0.07	-	0.13	0.12	0.12	-	0.08	0.16	0.12	0.09	0.11	0.06	-	-	0.17	0.12	0.04	0.04	-	0.01	-
<i>Liasis papuana</i>	-	0.07	0.08	0.07	-	0.08	0.07	0.04	0.04	0.09	0.05	0.08	0.09	0.08	0.10	0.07	-	0.06	0.06	0.06	0.04	0.07	0.10	0.08	-	0.07	0.05	0.09	0.10	0.10	-	0.00
<i>Boa constrictor</i>	0.07	-	0.04	-	-	0.07	-	0.08	-	0.08	0.09	0.07	0.08	0.06	-	-	-	0.05	0.13	0.08	-	0.08	0.07	-	-	0.14	0.10	0.10	-	-	0.10	-

Table S11. Body shape peramorphosis test. Pairwise comparisons of the predicted body shape differences at maximum per-group body size (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 iterations (upper triangle). Details as in Table S10.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsoyi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>	
<i>Python anchietae</i>	-	0.30	0.06	0.29	0.68	0.26	0.68	0.20	0.58	0.26	0.22	0.06	0.67	-	0.40	-	0.10	0.14	0.66	0.59	0.12	-	-	0.66	0.10	0.09	0.25	0.26	0.13	0.13	0.17	0.92	
<i>Python bivittatus</i>	0.35	-	0.00	0.01	0.95	0.00	0.30	0.24	0.34	0.08	-	0.00	0.03	-	0.17	-	0.16	-	-	-	0.06	-	-	0.12	0.24	-	-	-	-	-	0.06	0.06	
<i>Python brongersmai</i>	0.62	0.78	-	0.78	0.01	0.12	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.01	0.02	0.00	0.03	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	-	
<i>Python curtus</i>	0.55	0.70	0.13	-	0.08	0.34	0.01	0.01	0.06	-	-	-	-	0.06	-	-	0.00	-	-	-	0.01	-	-	0.01	-	-	-	0.03	-	-	0.01	0.01	
<i>Python molurus</i>	0.29	0.08	0.73	0.64	-	0.02	0.70	0.23	0.53	0.16	-	0.02	0.19	-	0.33	-	0.13	0.07	-	-	0.04	-	-	0.31	0.19	0.03	0.02	0.34	0.05	-	0.07	0.33	
<i>Python regius</i>	0.40	0.58	0.24	0.20	0.51	-	0.00	0.01	0.01	-	-	-	-	-	0.01	-	0.00	-	-	-	0.00	-	-	0.00	0.00	-	-	0.00	0.00	-	0.00	-	
<i>Python sebae</i>	0.21	0.19	0.76	0.67	0.14	0.53	-	0.16	0.23	0.31	-	-	0.13	-	0.04	-	0.01	0.01	0.19	-	0.02	-	-	0.50	0.01	-	0.01	0.19	0.07	-	0.02	0.13	
<i>Malayopython reticulatus</i>	0.44	0.25	0.98	0.90	0.29	0.76	0.27	-	0.41	-	0.05	0.00	0.00	0.01	-	0.17	-	0.44	0.11	0.04	0.27	0.15	-	-	0.13	0.25	-	0.01	0.22	0.05	-	0.23	0.02
<i>Malayopython timoriensis</i>	0.32	0.21	0.81	0.74	0.22	0.59	0.24	0.21	-	0.03	-	0.00	0.06	-	0.42	-	0.15	0.03	-	-	-	-	-	0.19	0.18	-	0.00	-	0.00	-	0.02	0.10	
<i>Antaresia childreni</i>	0.26	0.22	0.77	0.69	0.20	0.54	0.14	0.28	0.24	-	0.00	0.00	0.07	-	0.00	-	0.00	0.00	0.04	0.02	0.00	-	-	0.62	0.00	0.01	0.00	0.00	0.00	-	0.00	0.01	
<i>Antaresia maculosa</i>	0.32	-	0.46	-	-	-	-	0.60	-	0.34	-	0.00	0.00	0.00	0.00	0.00	0.00	-	0.01	0.00	0.00	0.00	0.00	-	0.00	0.05	0.00	0.00	0.00	-	-	-	
<i>Antaresia perthensis</i>	0.40	0.27	0.62	0.55	0.27	0.43	0.36	0.47	0.32	0.31	0.27	-	0.00	-	0.00	-	0.00	0.00	0.05	0.00	0.00	-	-	0.00	0.00	-	0.00	0.00	0.00	-	0.00	0.00	
<i>Antaresia stimsoni</i>	0.18	0.26	0.65	-	0.22	0.42	0.18	0.37	0.25	0.13	0.25	0.26	-	-	0.00	-	0.00	0.00	0.09	0.01	0.00	-	-	0.07	0.00	-	0.01	0.00	0.00	-	0.00	0.08	
<i>Morelia bredli</i>	-	-	0.96	-	-	-	-	-	-	-	0.61	-	-	-	0.09	0.47	-	0.00	0.01	0.71	-	0.16	0.00	-	-	-	-	0.00	0.01	-	0.00	-	
<i>Morelia carinata</i>	0.54	0.31	0.94	0.88	0.37	0.76	0.44	0.30	0.25	0.45	0.64	0.42	0.47	0.24	-	0.09	0.38	0.04	0.14	0.36	0.02	0.58	-	0.04	0.23	0.00	0.00	0.02	0.00	0.01	0.00	0.02	
<i>Morelia spilota</i>	0.43	-	0.92	-	-	-	-	-	-	-	0.55	-	-	0.08	0.28	-	-	0.00	0.01	0.80	-	0.04	0.00	-	-	0.00	-	0.09	-	0.00	-	-	
<i>Morelia viridis</i>	0.45	0.21	0.94	0.86	0.27	0.74	0.30	0.16	0.22	0.34	-	0.44	0.40	-	0.20	-	-	0.00	-	-	0.00	-	-	0.00	0.17	-	0.00	-	0.00	-	0.00	0.00	
<i>Simalia amethystina</i>	0.74	-	1.27	-	0.56	-	0.57	0.32	0.49	0.59	0.90	0.72	0.68	0.37	0.40	0.40	0.33	-	0.00	0.01	0.16	0.25	0.10	0.00	-	0.00	0.00	0.00	0.00	0.00	-	-	
<i>Simalia boeleni</i>	0.29	-	0.70	-	-	0.23	0.34	-	0.19	0.32	0.20	0.19	0.30	0.30	0.35	0.24	-	0.61	-	0.47	0.00	0.05	0.01	0.15	-	0.00	0.01	0.02	0.00	0.00	-	-	
<i>Simalia clastolepis</i>	0.39	-	0.86	-	-	-	0.23	-	0.30	0.52	0.37	0.34	0.10	0.24	0.09	-	0.44	0.21	-	0.00	0.23	0.02	-	-	0.00	0.00	0.25	0.01	0.02	-	-	-	
<i>Simalia kinghorni</i>	0.67	0.49	1.24	1.15	0.54	1.02	0.51	0.29	-	0.53	0.86	0.73	0.63	-	0.48	-	0.33	0.19	0.58	0.42	-	0.07	-	0.01	-	0.00	0.00	0.02	0.00	-	0.78	-	
<i>Simalia nauta</i>	-	-	1.12	-	-	-	-	-	-	-	0.78	-	-	0.22	0.22	0.29	-	0.21	0.47	0.29	0.29	-	0.02	-	-	0.00	0.00	0.04	0.00	0.02	-	-	
<i>Simalia oenpelliensis</i>	-	-	-	-	-	-	-	-	-	-	1.00	-	-	0.52	-	0.54	-	0.25	0.74	0.58	-	0.40	-	-	-	-	0.00	-	0.00	-	0.00	-	
<i>Bothrochilus boa</i>	0.24	0.26	0.81	0.73	0.25	0.58	0.14	0.28	0.26	0.09	-	0.39	0.17	-	0.47	-	0.34	0.58	0.23	-	0.50	-	-	-	0.00	-	0.00	-	0.02	-	0.01	0.03	
<i>Leiopython albertisii</i>	0.46	0.18	0.92	0.84	0.23	0.71	0.30	0.18	0.20	0.34	-	0.40	0.39	-	0.20	-	0.12	-	-	-	-	-	-	0.37	-	-	0.00	-	-	0.00	0.00		
<i>Aspidites melanocephalus</i>	0.41	-	0.88	-	0.35	-	-	-	-	0.20	0.43	-	-	-	0.58	0.36	-	0.64	0.32	0.40	0.55	0.59	0.69	-	-	-	0.00	0.00	0.00	0.00	-	-	
<i>Aspidites ramsoyi</i>	0.32	-	0.61	-	0.36	0.39	0.34	0.53	0.43	0.25	0.16	0.29	0.20	0.57	0.62	-	0.56	0.83	0.29	0.49	0.78	0.73	-	0.30	0.55	0.30	-	0.00	0.00	-	0.00	0.00	
<i>Liasis fuscus</i>	0.44	-	0.95	0.85	0.27	0.74	0.26	0.26	-	0.29	0.56	0.47	0.39	0.24	0.43	0.17	-	0.43	0.32	0.24	0.35	0.39	0.54	-	-	0.30	0.50	-	0.06	0.13	0.00	-	
<i>Liasis mackloti</i>	0.44	-	1.01	-	0.39	0.79	0.30	0.34	0.46	0.36	0.63	0.62	0.45	-	0.58	-	0.38	0.51	0.45	0.39	0.37	0.51	-	0.30	-	0.34	0.56	0.21	-	-	0.00	-	
<i>Liasis olivaceus</i>	0.50	-	1.06	-	-	-	-	-	-	-	0.67	-	-	0.28	0.43	0.26	-	0.31	0.43	0.31	-	0.33	0.37	-	-	0.38	-	0.19	-	-	-	-	
<i>Liasis papuana</i>	0.62	0.47	1.21	1.12	0.51	0.98	0.46	0.26	0.46	0.47	-	0.70	0.58	-	0.49	-	0.34	-	-	-	0.10	-	-	0.43	0.40	-	0.72	0.33	0.33	-	-	0.00	
<i>Boa constrictor</i>	0.15	0.27	0.57	0.49	0.22	0.35	0.22	0.43	0.29	0.24	-	0.26	0.15	-	0.47	-	0.41	-	-	-	-	-	-	0.26	0.41	-	0.27	-	-	-	0.64	-	

Table S12. Head size-shape space overlap (ontogenetic scaling) tests for heterochrony (Tfh1). Pairwise tests with the null hypothesis that species overlap in size-shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 iterations at upper triangle. The hypothesis of interest is the null in this case. Cells highlighted in green correspond to pairs of taxa that have overlapping trajectories in size-shape space and no difference in slope. Cells with numbers in red correspond to pairs of taxa where they overlap in size-shape space with phenotype at maximum size differs, confirming strong ontogenetic scaling. Low sample numbers for comparisons with *Morelia carinata* call for extra caution. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.00	-	0.01	0.02	0.01	-	-	-	0.00	0.00	0.00	0.00	-	0.03	-	0.00	-	-	-	-	-	0.00	0.00	-	-	-	-	0.00	-	-	0.00
<i>Python bivittatus</i>	0.04	-	0.00	0.00	0.35	0.00	-	-	0.02	0.00	-	-	-	-	0.00	-	-	-	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	-
<i>Python brongersmai</i>	-	0.06	-	0.52	0.01	0.02	0.01	0.13	0.07	0.01	0.00	0.00	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Python curtus</i>	0.02	0.05	0.04	-	0.00	0.03	0.00	0.00	0.09	-	-	-	-	-	0.01	-	-	-	0.00	-	0.00	0.00	0.00	-	-	-	0.00	0.00	0.00	0.00	0.00	-
<i>Python molurus</i>	0.01	0.05	0.03	0.03	-	0.00	-	-	0.00	-	0.00	0.00	-	-	0.01	-	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python regius</i>	0.05	0.09	0.07	0.07	0.06	-	0.00	0.00	0.16	0.00	0.00	0.00	-	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python sebae</i>	-	-	0.12	0.12	-	0.15	-	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	-	0.00	0.00	0.00	0.00	0.00	-
<i>Malayopython reticulatus</i>	-	-	0.11	0.11	-	0.14	0.19	-	0.00	-	0.00	-	-	0.00	0.09	-	-	0.00	0.00	0.00	0.00	0.01	0.00	-	-	0.00	-	0.00	0.00	0.00	0.00	-
<i>Malayopython timoriensis</i>	-	0.05	0.03	0.03	-	0.06	0.11	0.10	-	0.00	0.00	0.00	0.00	0.00	0.09	0.00	-	0.00	0.19	0.00	0.00	0.04	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia childreni</i>	0.11	0.14	0.12	-	0.11	0.15	-	-	0.12	-	0.00	0.00	0.02	-	0.00	-	-	0.00	-	-	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	-
<i>Antaresia maculosa</i>	0.09	-	0.10	-	-	0.13	0.18	0.17	0.10	0.19	-	0.21	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia perthensis</i>	0.09	-	0.11	-	-	0.14	0.19	-	0.10	0.19	0.17	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia stimsoni</i>	0.14	-	0.16	-	-	-	-	-	0.15	0.24	0.22	0.23	-	0.00	0.00	-	-	0.00	0.00	0.00	-	0.00	0.00	-	-	-	-	0.00	-	-	0.00	0.00
<i>Morelia bredli</i>	-	-	0.06	-	-	0.09	0.14	0.13	0.06	-	0.13	0.13	0.18	-	0.07	0.04	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Morelia carinata</i>	0.01	0.04	-	0.02	0.01	0.05	0.10	0.00	0.01	0.11	0.09	0.09	0.14	0.04	-	0.04	-	0.00	0.00	0.00	0.00	0.04	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Morelia spilota</i>	-	-	0.36	-	-	0.39	-	-	0.35	-	0.42	0.43	-	0.38	0.34	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	-	0.00	0.00	-
<i>Morelia viridis</i>	0.13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Simalia amethystina</i>	-	-	0.08	-	-	0.11	0.16	0.15	0.07	-	0.14	0.15	0.20	0.10	-	0.40	-	-	0.00	0.00	0.12	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia boeleni</i>	-	0.07	0.05	0.05	-	0.08	0.13	0.12	0.05	0.14	0.12	0.12	0.17	0.08	0.04	0.37	-	0.09	-	0.00	0.00	0.01	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>Simalia clastolepis</i>	-	-	0.03	-	-	0.06	0.11	0.10	0.02	-	0.10	0.10	0.15	0.05	0.01	0.35	-	0.07	0.05	-	0.00	0.20	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia kinghorni</i>	-	-	0.08	0.08	-	0.11	0.16	0.15	0.08	-	0.15	0.15	-	0.11	-	0.40	-	0.12	0.10	0.08	-	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia nauta</i>	-	0.05	0.03	0.03	-	0.06	0.11	0.10	0.02	0.11	0.10	0.10	0.15	0.05	0.01	0.35	-	0.07	0.04	0.02	0.07	-	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia oenpelliensis</i>	-	0.05	0.03	0.03	0.02	0.06	0.11	0.10	0.03	0.12	0.10	0.10	0.15	0.06	0.01	0.35	-	0.07	0.05	0.02	0.08	0.02	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Bothrochilus boa</i>	0.06	-	0.07	-	0.06	-	-	-	0.16	0.14	0.15	-	-	0.06	-	-	-	-	-	-	-	0.07	-	0.00	-	-	-	-	-	-	-	-
<i>Leiopython albertisii</i>	0.12	-	0.13	-	0.12	-	-	-	0.22	-	0.20	-	-	-	-	-	-	-	-	-	-	-	0.17	-	-	-	-	-	-	-	-	-
<i>Aspidites melanocephalus</i>	-	-	0.16	-	-	0.19	-	0.23	0.15	-	0.22	0.23	-	0.18	0.14	0.48	-	0.20	0.17	0.15	0.20	0.15	0.15	-	-	-	0.00	0.00	-	0.00	0.00	0.00
<i>Aspidites ramsayi</i>	-	-	0.12	-	-	0.15	-	0.12	-	0.19	0.19	-	0.15	0.11	0.44	-	-	0.16	0.14	0.12	0.17	0.12	0.12	-	-	0.24	-	0.00	-	0.00	0.00	0.00
<i>Liasis fuscus</i>	-	0.08	0.06	0.06	0.05	0.09	0.14	0.13	0.05	0.14	0.12	0.13	0.18	0.08	0.04	0.38	-	0.10	0.07	0.05	0.10	0.05	0.05	0.10	-	0.18	0.14	-	0.01	0.00	0.00	0.00
<i>Liasis mackloti</i>	0.07	-	0.08	0.08	-	0.11	0.16	0.15	0.08	0.17	0.15	0.15	-	0.11	0.07	-	-	0.12	0.10	0.08	0.13	0.07	0.08	0.12	-	-	-	0.10	-	0.00	0.00	-
<i>Liasis olivaceus</i>	-	-	0.07	0.07	-	0.11	0.16	0.15	0.07	0.16	0.14	0.15	-	0.10	-	0.40	-	0.11	0.09	0.07	0.12	0.07	0.07	-	-	0.20	0.16	0.10	0.12	-	0.00	-
<i>Liasis papuana</i>	-	0.07	0.05	0.05	-	0.08	0.13	0.12	0.04	0.13	0.11	0.12	0.17	0.07	0.03	0.37	-	0.09	0.06	0.04	0.09	0.04	0.04	0.08	-	0.17	0.13	0.07	0.09	0.08	-	0.00
<i>Boa constrictor</i>	0.13	-	0.15	-	-	0.18	-	-	0.14	-	0.22	0.22	0.27	0.17	0.13	-	-	0.19	0.16	0.14	-	0.14	0.14	-	-	0.27	0.23	0.17	-	-	0.16	-

Table S13. Head shape space overlap tests for heterochrony (Tfh2). Pairwise tests with the null hypothesis that species overlap in shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 iterations at upper triangle. The hypothesis of interest is the null in this case. Cells highlighted in green and with white borders correspond to pairs of taxa that have overlapping trajectories in shape space only and not in size-shape, therefore heterochrony by size-shape dissociation. Cells highlighted in green without borders are pairs of taxa where the null has been accepted but they also overlap in size-shape space (tested in Thf1). Low sample numbers for comparisons with *Morelia carinata* call for extra caution. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.00	-	0.04	0.08	0.01	-	-	0.00	0.00	0.00	0.00	0.00	0.09	0.01	-	-	-	-	-	-	-	0.00	0.00	-	-	-	-	-	-	-	0.00
<i>Python bivittatus</i>	0.04	-	0.00	0.00	0.26	0.00	-	-	0.06	0.40	-	-	-	-	0.00	-	-	-	0.00	-	-	0.00	0.00	-	-	-	-	0.00	-	-	-	0.00
<i>Python brongersmai</i>	-	0.05	-	0.33	0.00	0.01	0.02	0.36	0.08	0.09	0.00	0.00	0.00	0.00	0.01	0.00	-	0.12	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Python curtus</i>	0.02	0.05	0.03	-	0.05	0.07	0.00	0.00	0.11	-	-	-	-	-	0.02	-	-	-	0.00	0.00	0.00	0.00	0.01	-	-	-	0.00	0.00	0.00	0.00	0.00	-
<i>Python molurus</i>	0.01	0.04	0.02	0.02	-	0.00	-	-	-	0.02	-	-	-	-	0.04	-	-	-	-	-	-	-	0.00	0.00	0.00	-	-	0.00	-	-	-	-
<i>Python regius</i>	0.04	0.07	0.05	0.06	0.05	-	0.00	0.00	0.58	0.05	0.00	0.00	-	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python sebae</i>	-	-	0.09	0.09	-	0.12	-	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	-	-	0.00	0.00	0.00	0.00	0.07	-	-	-	0.00	0.00	0.00	0.00	0.00	-
<i>Malayopython reticulatus</i>	-	-	0.08	0.08	-	0.11	0.14	-	0.04	-	0.00	-	-	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.01	0.01	-	-	0.00	-	0.00	0.00	0.00	-
<i>Malayopython timoriensis</i>	-	0.04	0.02	0.02	-	0.05	0.09	0.08	-	1.00	0.01	0.71	0.00	0.00	0.04	0.00	-	0.00	0.05	0.00	0.01	0.00	0.01	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia childreni</i>	0.10	0.13	0.11	-	0.10	0.14	-	0.10	-	-	0.45	0.00	0.51	-	0.07	-	-	-	1.00	-	-	0.06	0.01	0.00	0.07	-	-	0.00	0.00	0.00	1.00	-
<i>Antaresia maculosa</i>	0.07	-	0.08	-	-	0.11	0.15	0.14	0.08	0.17	-	1.00	0.00	0.00	0.01	0.00	-	0.00	0.01	0.10	0.00	0.00	0.09	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia perthensis</i>	0.08	-	0.09	-	-	0.12	0.15	-	0.09	0.17	0.15	-	0.00	-	0.01	0.12	-	0.00	0.99	0.39	0.00	0.00	0.00	0.02	0.00	0.13	0.69	0.00	0.00	0.00	0.49	0.00
<i>Antaresia stimsoni</i>	0.11	-	0.13	-	-	-	-	0.12	0.21	0.18	0.19	-	-	0.99	0.01	-	-	0.00	0.00	0.99	-	0.01	0.00	-	-	-	-	0.00	-	-	0.00	0.00
<i>Morelia bredli</i>	-	-	0.04	-	-	0.07	0.10	0.09	0.03	-	0.10	0.10	0.14	-	0.00	0.10	-	0.00	0.00	0.02	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Morelia carinata</i>	0.00	0.03	0.02	0.02	0.01	0.04	0.08	0.07	0.01	0.10	0.07	0.08	0.11	0.03	-	0.01	-	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Morelia spilota</i>	-	-	0.23	-	-	0.26	-	0.23	-	0.29	0.30	-	-	0.25	0.22	-	-	0.00	0.00	0.37	0.00	0.01	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Morelia viridis</i>	0.11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Simalia amethystina</i>	-	-	0.05	-	-	0.08	0.12	0.11	0.05	-	0.11	0.12	0.15	0.07	0.04	0.26	-	-	0.00	0.00	0.04	0.00	0.09	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia boeleni</i>	-	0.05	0.03	0.03	-	0.06	0.09	0.09	0.03	0.11	0.09	0.09	0.13	0.04	0.02	0.24	-	0.06	-	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>Simalia clastolepis</i>	-	-	0.02	-	-	0.05	0.08	0.08	0.02	-	0.08	0.08	0.12	0.03	0.01	0.23	-	0.05	0.03	-	0.00	0.03	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Simalia kinghorni</i>	-	-	0.06	0.06	-	0.08	0.12	0.11	0.05	-	0.11	0.12	-	0.07	0.04	0.26	-	0.08	0.06	0.05	-	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia nauta</i>	-	0.04	0.02	0.02	-	0.04	0.08	0.07	0.01	0.10	0.07	0.08	0.12	0.03	0.01	0.22	-	0.04	0.02	0.01	0.05	-	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia oenpelliensis</i>	-	0.04	0.02	0.03	0.02	0.05	0.09	0.08	0.02	0.11	0.08	0.09	0.12	0.04	0.01	0.23	-	0.05	0.03	0.02	0.05	0.01	-	0.00	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00
<i>Bothrochilus boa</i>	0.06	-	0.07	-	0.06	-	-	-	-	0.15	0.12	0.13	-	-	0.05	-	-	-	-	-	-	-	0.06	-	0.00	-	-	0.00	0.00	-	0.02	-
<i>Leiopython albertisii</i>	0.11	-	0.12	-	0.11	-	-	-	-	0.20	-	0.18	-	-	0.11	-	-	-	-	-	-	-	0.12	0.16	-	-	-	-	-	-	-	-
<i>Aspidites melanocephalus</i>	-	-	0.09	-	-	0.12	-	0.15	0.09	-	0.15	0.16	-	0.10	0.08	0.30	-	0.12	0.10	0.09	0.12	0.08	0.09	-	-	-	0.00	-	0.00	0.00	0.00	0.00
<i>Aspidites ramsayi</i>	-	-	0.09	-	-	0.12	-	-	0.09	-	0.15	0.15	-	0.10	0.08	0.30	-	0.12	0.09	0.08	0.12	0.08	0.09	-	-	0.16	-	0.00	-	0.00	0.01	0.00
<i>Liasis fuscus</i>	-	0.06	0.04	0.04	0.04	0.07	0.10	0.10	0.04	0.12	0.10	0.10	0.14	0.05	0.03	0.25	-	0.07	0.04	0.03	0.07	0.03	0.04	0.08	-	0.11	0.10	-	0.00	0.00	0.00	0.00
<i>Liasis mackloti</i>	0.06	-	0.07	0.07	-	0.09	0.13	0.12	0.06	0.15	0.12	0.13	-	0.08	0.05	-	-	0.09	0.07	0.06	0.09	0.06	0.06	0.11	-	-	-	0.08	-	0.00	0.00	-
<i>Liasis olivaceus</i>	-	-	0.06	0.06	-	0.09	0.12	0.11	0.05	0.14	0.12	0.12	-	0.07	0.05	0.26	-	0.09	0.06	0.05	0.09	0.05	0.06	-	-	0.12	0.12	0.07	0.10	-	0.00	-
<i>Liasis papuana</i>	-	0.06	0.04	0.04	-	0.06	0.10	0.09	0.03	0.12	0.09	0.10	0.14	0.05	0.03	0.24	-	0.06	0.04	0.03	0.07	0.03	0.03	0.08	-	0.10	0.10	0.05	0.08	0.07	-	0.00
<i>Boa constrictor</i>	0.11	-	0.12	-	-	0.14	-	-	0.11	-	0.17	0.18	0.21	0.13	0.10	-	-	0.14	0.12	0.11	-	0.11	0.11	-	-	0.18	0.18	0.13	-	-	0.13	-

Table S14. Body size-shape space overlap tests for heterochrony (Tfh1). Pairwise tests with the null hypothesis that species overlap in size-shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 iterations at upper triangle. Details as in Table S12.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.00	0.00	0.00	0.23	0.00	0.03	0.00	0.00	0.00	0.03	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13
<i>Python bivittatus</i>	0.66	-	0.00	0.00	0.17	0.00	0.07	0.00	0.09	0.00	-	0.00	0.00	-	0.00	-	0.00	-	0.00	-	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	0.00	0.00	0.00
<i>Python brongersmai</i>	0.46	1.00	-	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python curtus</i>	0.43	0.97	0.77	-	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	-	-	0.00	-	0.00	-	-	-	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	0.00	0.00	0.00
<i>Python molurus</i>	0.32	0.86	0.66	0.63	-	0.00	0.17	0.00	0.09	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	-	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13
<i>Python regius</i>	1.18	1.73	1.52	1.50	1.39	-	0.00	0.00	0.00	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	-	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python sebae</i>	1.66	2.20	1.99	1.97	1.86	2.72	-	0.00	0.18	0.00	-	0.00	0.00	-	0.04	-	0.00	0.00	0.00	-	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Malayopython reticulatus</i>	2.12	2.67	2.46	2.44	2.33	3.19	3.66	-	0.03	0.00	0.00	0.00	0.00	-	0.33	-	0.00	0.00	0.01	0.07	0.00	-	0.00	0.01	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Malayopython timoriensis</i>	0.27	0.81	0.61	0.58	0.47	1.34	1.81	2.27	-	0.00	-	0.00	0.00	-	0.16	-	0.00	0.00	-	-	-	-	0.00	0.07	-	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Antaresia childreni</i>	2.32	2.86	2.66	2.63	2.52	3.38	3.85	4.32	2.47	-	0.00	0.00	0.00	-	0.00	-	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia maculosa</i>	2.45	-	2.78	-	-	-	4.45	-	4.65	-	0.01	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.01	0.00	0.00	0.00	0.00	-	-
<i>Antaresia perthensis</i>	1.73	2.27	2.07	2.04	1.93	2.80	3.27	3.74	1.88	3.93	4.06	-	0.00	-	0.00	-	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	-	0.05	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia stimsoni</i>	2.89	3.44	3.23	-	3.09	3.96	4.43	4.90	3.04	5.09	5.22	4.50	-	-	0.00	-	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Morelia bredli</i>	-	-	1.06	-	-	-	-	-	-	-	3.05	-	-	-	0.02	0.62	-	0.00	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	-
<i>Morelia carinata</i>	0.07	0.61	0.41	0.38	0.27	1.14	1.61	2.08	0.22	2.27	2.40	1.68	2.84	0.67	-	0.29	0.58	0.00	0.52	0.20	0.05	0.00	-	0.00	0.19	0.00	0.00	0.06	0.00	0.00	0.00	0.00
<i>Morelia spilota</i>	8.56	-	8.89	-	-	-	-	-	-	-	10.88	-	-	9.16	8.51	-	-	0.00	0.00	0.06	-	0.00	0.00	-	0.00	-	0.00	-	0.00	0.00	-	-
<i>Morelia viridis</i>	2.58	3.12	2.92	2.89	2.78	3.65	4.12	4.59	2.73	4.78	-	4.19	5.35	-	2.53	-	0.00	-	-	0.00	-	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	0.00	0.00
<i>Simalia amethystina</i>	1.00	-	1.34	-	1.20	-	2.54	3.01	1.15	3.20	3.33	2.61	3.78	1.60	0.95	9.44	3.46	-	0.00	0.00	0.36	0.06	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia boeleni</i>	1.10	-	1.43	-	-	2.63	3.10	-	3.30	3.43	2.71	3.87	1.70	1.05	9.53	-	1.98	-	0.07	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia clastolepis</i>	0.29	-	0.62	-	-	-	2.29	-	2.49	2.62	1.90	3.06	0.89	0.24	8.72	-	1.17	1.26	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia kinghorni</i>	1.63	2.17	1.97	1.94	1.83	2.70	3.17	3.64	-	3.83	3.96	3.24	4.40	-	1.58	-	4.09	2.51	2.61	1.80	-	0.05	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia nauta</i>	-	-	0.65	-	-	-	-	-	-	2.64	-	-	0.91	0.26	8.75	-	1.20	1.29	0.48	1.82	-	0.00	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia oenpelliensis</i>	-	-	-	-	-	-	-	-	-	2.65	-	-	0.92	-	8.76	-	1.21	1.30	0.49	-	0.52	-	-	-	0.00	-	0.00	-	0.00	0.00	0.00	-
<i>Bothrochilus boa</i>	1.38	1.92	1.71	1.69	1.58	2.44	2.91	3.38	1.53	3.58	-	2.99	4.15	-	1.33	-	3.84	2.26	2.35	-	2.89	-	-	-	0.00	-	0.00	-	0.00	0.00	0.00	0.00
<i>Leiopython albertisii</i>	3.04	3.58	3.38	3.35	3.24	4.10	4.57	5.04	3.19	5.24	-	4.65	5.81	-	2.99	-	5.50	-	-	-	-	-	-	4.30	-	-	0.00	-	0.00	0.00	0.00	0.00
<i>Aspidites melanocephalus</i>	3.00	-	3.34	-	3.20	-	-	-	5.20	5.33	-	-	2.95	11.44	-	-	3.88	3.98	3.17	4.51	3.19	3.20	-	-	-	0.00	-	0.00	0.00	0.00	-	-
<i>Aspidites ramsayi</i>	2.36	-	2.69	-	2.56	3.42	3.89	4.36	2.51	4.56	4.68	3.97	5.13	2.96	2.31	-	4.82	3.24	3.33	2.52	3.87	2.55	-	3.61	5.28	5.24	-	0.00	0.00	0.00	0.00	0.00
<i>Liasis fuscus</i>	1.62	-	1.96	1.93	1.82	2.68	3.15	3.62	-	3.82	3.95	3.23	4.39	2.22	1.57	10.06	-	2.50	2.60	1.79	3.13	1.81	1.82	-	4.50	3.86	-	0.00	0.00	0.00	0.00	-
<i>Liasis mackloti</i>	1.79	-	2.13	-	1.99	2.86	3.33	3.80	1.94	3.99	4.12	3.40	4.56	-	1.74	-	4.25	2.67	2.77	1.96	3.30	1.98	-	3.05	-	4.67	4.03	3.29	-	0.00	0.00	-
<i>Liasis olivaceus</i>	1.23	-	1.57	-	-	-	-	-	-	3.56	-	-	-	1.83	1.18	9.67	-	2.11	2.21	1.40	-	1.42	1.43	-	-	4.11	-	2.73	-	-	-	-
<i>Liasis papuana</i>	0.43	0.97	0.77	0.74	0.63	1.50	1.97	2.44	0.58	2.63	-	2.04	3.21	-	0.38	-	2.89	-	-	-	1.94	-	-	1.69	3.35	-	2.67	1.93	2.10	-	-	0.00
<i>Boa constrictor</i>	3.64	4.19	3.98	3.96	3.85	4.71	5.18	5.65	3.80	5.84	-	5.26	6.42	-	3.60	-	6.11	-	-	-	-	-	-	4.90	6.56	-	5.88	-	-	-	3.96	-

Table S15. Body shape space overlap tests for heterochrony (Tfh2). Pairwise tests with the null hypothesis that species overlap in shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 iterations at upper triangle. Details as in Table S13.

	Python anchietae	Python bivittatus	Python brongersmai	Python curtus	Python molurus	Python regius	Python sebae	Malayopython reticulatus	Malayopython timoriensis	Antaresia childreni	Antaresia maculosa	Antaresia perthensis	Antaresia stimsoni	Morelia bredli	Morelia carinata	Morelia spilota	Morelia viridis	Simalia amethystina	Simalia boeleni	Simalia clastolepis	Simalia kinghorni	Simalia nauta	Simalia oenpelliensis	Bothrochilus boa	Leiopython albertisii	Aspidites melanocephalus	Aspidites ramsayi	Liasis fuscus	Liasis mackloti	Liasis olivaceus	Liasis papuana	Boa constrictor
Python anchietae	-	0.00	0.01	0.00	0.334	0.00	0.07	0.00	0.03	0.00	0.07	0.01	0.01	-	0.00	0.00	0.00	0.00	0.02	0.00	0.01	-	-	0.00	0.05	0.03	0.46	0.08	0.00	0.00	0.01	0.93
Python bivittatus	0.50	-	0.00	0.00	0.23	0.00	0.16	0.00	0.662	0.002	-	0.00	0.00	-	0.00	-	0.002	-	-	-	0.00	-	-	0.00	0.01	-	-	-	-	-	0.01	0.00
Python brongersmai	0.39	0.81	-	0.52	0.02	0.02	0.00	0.002	0.002	0.002	0.21	0.00	0.00	0.00	0.02	0.002	0.002	0.002	0.002	0.002	0.00	0.002	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Python curtus	0.28	0.70	0.58	-	0.00	0.008	0.00	0.00	0.002	0.00	-	0.00	-	-	0.00	-	0.002	-	-	-	0.00	-	-	0.00	0.00	-	0.002	-	-	-	0.00	0.00
Python molurus	0.28	0.70	0.59	0.48	-	0.00	0.31	0.00	0.29	0.00	-	0.29	0.02	-	0.00	-	0.002	0.002	-	-	0.00	-	0.02	0.07	0.00	0.07	0.04	0.00	-	0.02	0.40	
Python regius	0.88	1.30	1.19	1.08	1.09	-	0.00	0.00	0.002	0.00	-	0.00	0.00	-	0.00	-	0.002	-	-	-	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00
Python sebae	1.46	1.88	1.76	1.65	1.66	2.26	-	0.00	0.22	0.00	-	0.00	0.00	-	0.058	-	0.002	0.002	0.002	0.002	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00
Malayopython reticulatus	1.81	2.23	2.12	2.01	2.01	2.61	3.18	-	0.08	0.00	0.00	0.32	0.00	-	0.676	-	0.002	0.002	0.15	0.16	0.00	-	-	0.00	0.43	-	0.00	0.00	0.00	-	0.21	0.00
Malayopython timoriensis	0.21	0.63	0.51	0.40	0.41	1.01	1.58	1.94	-	0.002	-	0.89	0.01	-	0.126	-	0.002	0.002	-	-	-	-	-	0.06	0.12	-	0.00	-	0.00	-	0.00	0.03
Antaresia childreni	1.91	2.33	2.21	2.11	2.11	2.71	3.28	3.64	2.03	-	0.002	0.00	0.002	-	0.002	-	0.002	0.002	0.002	0.002	0.00	-	-	0.00	0.002	1	0.002	0.00	0.00	-	0.002	0.00
Antaresia maculosa	2.09	-	2.39	-	-	-	-	3.82	-	3.92	-	0.22	0.00	0.00	0.00	0.00	-	0.10	0.02	0.002	0.85	0.00	0.944	-	-	0.03	0.02	0.03	0.00	0.00	-	-
Antaresia perthensis	1.45	1.87	1.75	1.64	1.65	2.25	2.82	3.18	1.57	3.27	3.45	-	0.11	-	0.002	-	0.002	0.00	0.036	0.002	0.04	-	-	0.00	1.00	-	0.096	0.01	0.002	-	0.096	0.00
Antaresia stimsoni	2.23	2.65	2.53	-	2.43	3.03	3.60	3.96	2.35	4.05	4.23	3.59	-	-	0.002	-	0.002	0.00	0.00	0.002	0.00	-	0.00	0.00	-	0.00	0.00	0.002	-	0.00	0.00	
Morelia bredli	-	-	0.81	-	-	-	-	-	-	-	2.52	-	-	-	0.02	0.426	-	0.00	0.00	0.07	-	0.00	0.00	-	-	0.00	0.00	0.00	0.002	-	-	
Morelia carinata	0.05	0.47	0.36	0.25	0.25	0.85	1.42	1.78	0.18	1.88	2.06	1.42	2.20	0.48	-	0.21	0.64	0.01	0.60	0.46	0.09	0.03	-	0.00	0.10	0.064	0.00	0.144	0.03	0.02	0.102	0.00
Morelia spilota	6.80	-	7.10	-	-	-	-	-	-	-	8.81	-	-	7.23	6.77	-	-	0.00	0.06	0.86	-	0.02	0.00	-	-	0.002	-	0.002	-	0.002	-	-
Morelia viridis	2.25	2.67	2.55	2.44	2.45	3.05	3.62	3.98	2.37	4.07	-	3.61	4.39	-	2.22	-	-	0.00	-	-	0.00	-	-	0.00	0.00	-	0.002	-	0.002	-	0.02	0.002
Simalia amethystina	0.73	-	1.04	-	0.94	-	2.11	2.46	0.86	2.56	2.74	2.10	2.88	1.16	0.70	7.45	2.90	-	0.00	0.00	0.22	0.12	0.004	0.002	-	0.00	0.00	0.00	0.00	0.00	-	-
Simalia boeleni	0.95	-	1.25	-	-	2.32	2.68	-	2.77	2.96	2.31	3.09	1.38	0.92	7.67	-	-	1.60	-	0.18	0.00	0.03	0.00	0.008	-	0.00	0.00	0.00	0.00	0.00	-	-
Simalia clastolepis	0.24	-	0.55	-	-	-	-	1.97	-	2.07	2.25	1.61	2.39	0.67	0.21	6.96	-	0.90	1.11	-	0.00	0.004	0.00	-	-	0.00	0.00	0.01	0.00	0.00	-	-
Simalia kinghorni	1.36	1.78	1.66	1.56	1.56	2.16	2.73	3.09	-	3.19	3.37	2.72	3.50	-	1.33	-	3.52	2.01	2.23	1.52	-	0.12	-	0.002	-	0.00	0.00	0.00	0.00	-	0.05	-
Simalia nauta	-	-	0.55	-	-	-	-	-	-	-	2.25	-	-	0.67	0.22	6.96	-	0.90	1.11	0.41	1.52	-	0.00	-	-	0.00	0.00	0.00	0.00	0.02	-	-
Simalia oenpelliensis	-	-	-	-	-	-	-	-	-	-	2.25	-	-	0.67	-	6.96	-	0.89	1.11	0.40	-	0.41	-	-	-	0.002	-	0.01	-	0.002	-	-
Bothrochilus boa	1.16	1.58	1.46	1.35	1.36	1.96	2.53	2.89	1.28	2.98	-	2.52	3.30	-	1.13	-	3.32	1.81	2.02	-	2.43	-	-	-	0.00	-	0.002	-	0.002	-	0.00	0.00
Leiopython albertisii	2.63	3.05	2.93	2.83	2.83	3.43	4.00	4.36	2.75	4.45	-	3.99	4.77	-	2.60	-	4.79	-	-	-	-	-	-	-	3.70	-	-	0.002	-	-	0.10	0.00
Aspidites melanocephalus	2.39	-	2.69	-	2.59	-	-	-	-	4.22	4.40	-	-	-	2.36	9.11	-	3.04	3.26	2.55	3.67	2.55	2.55	-	-	-	0.00	-	0.00	0.00	-	-
Aspidites ramsayi	1.87	-	2.17	-	2.07	2.67	3.24	3.60	1.99	3.69	3.87	3.23	4.01	2.29	1.84	-	4.03	2.52	2.73	2.03	3.14	2.03	-	2.94	4.41	4.17	-	0.00	0.00	-	0.002	0.002
Liasis fuscus	1.31	-	1.61	1.51	1.51	2.11	2.68	3.04	-	3.13	3.32	2.67	3.45	1.74	1.28	8.03	-	1.96	2.17	1.47	2.59	1.47	1.47	-	-	3.62	3.09	-	0.03	0.002	0.002	-
Liasis mackloti	1.36	-	1.66	-	1.56	2.16	2.73	3.09	1.48	3.18	3.36	2.72	3.50	-	1.33	-	3.52	2.01	2.22	1.52	2.63	1.52	-	2.43	-	3.67	3.14	2.58	-	-	0.002	-
Liasis olivaceus	0.91	-	1.21	-	-	-	-	-	-	-	2.91	-	-	1.33	0.88	7.62	-	1.56	1.77	1.07	-	1.07	1.07	-	-	3.21	-	2.13	-	-	-	-
Liasis papuana	0.36	0.78	0.66	0.56	0.56	1.16	1.73	2.09	0.48	2.19	-	1.72	2.50	-	0.33	-	2.52	-	-	-	1.64	-	-	1.43	2.91	-	2.14	1.59	1.63	-	-	0.00
Boa constrictor	2.89	3.31	3.19	3.09	3.09	3.69	4.26	4.62	3.01	4.71	-	4.25	5.03	-	2.86	-	5.05	-	-	-	-	-	-	3.96	5.43	-	4.67	-	-	-	3.16	-

Figure S1. Landmark and semilandmark configuration used to describe dorsal head shape in pythons. Description of numbered landmarks (large red dots) and semilandmarks (small red dots) is as follows: 1, tip of the snout; 2-3 anterior most points of the nostrils; 4-5, anterior most points of the eyes; 6-7, posterior most points of the eyes; 8-9, corners of the mouth; 10-22 and 23-35, semi-landmark curves describing the outline of the head going from the tip of the snout to the corner of the mouth for each side.

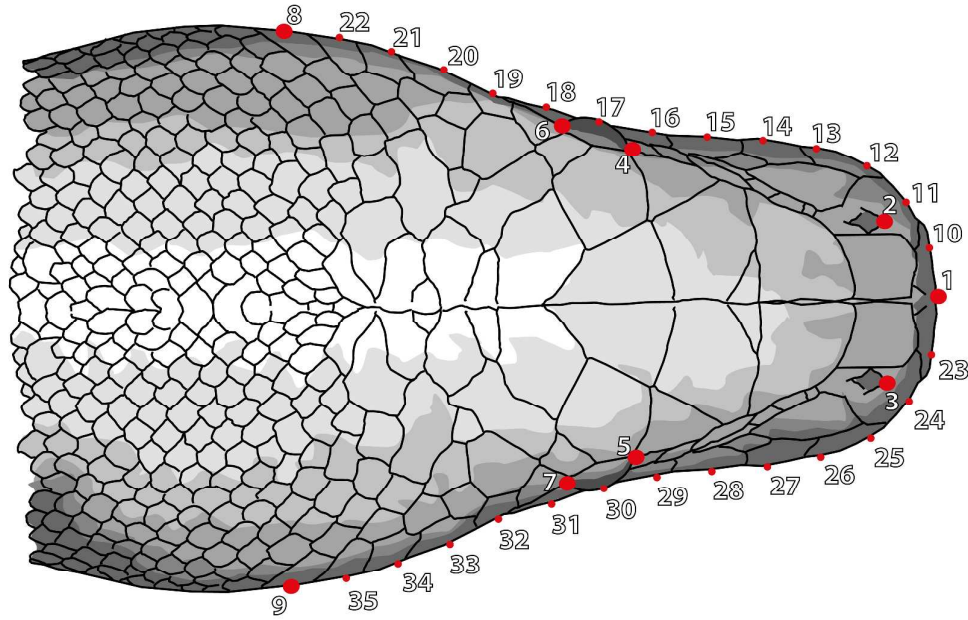


Figure S2. Regression scores (top), common allometric components (CAC; middle) and Principal Component Analysis (PCA; bottom) of python head shape (left) and body shape (right). Dots are colored according to their species and clades as in Figs. 2 and 3. Dot size is proportional to size. The x axis of size in the Regression score and CAC plots corresponds to log-transformed centroid size and log-transformed size for head and body shape, respectively. Principal component axes labels include the percentage of variance they each explain.

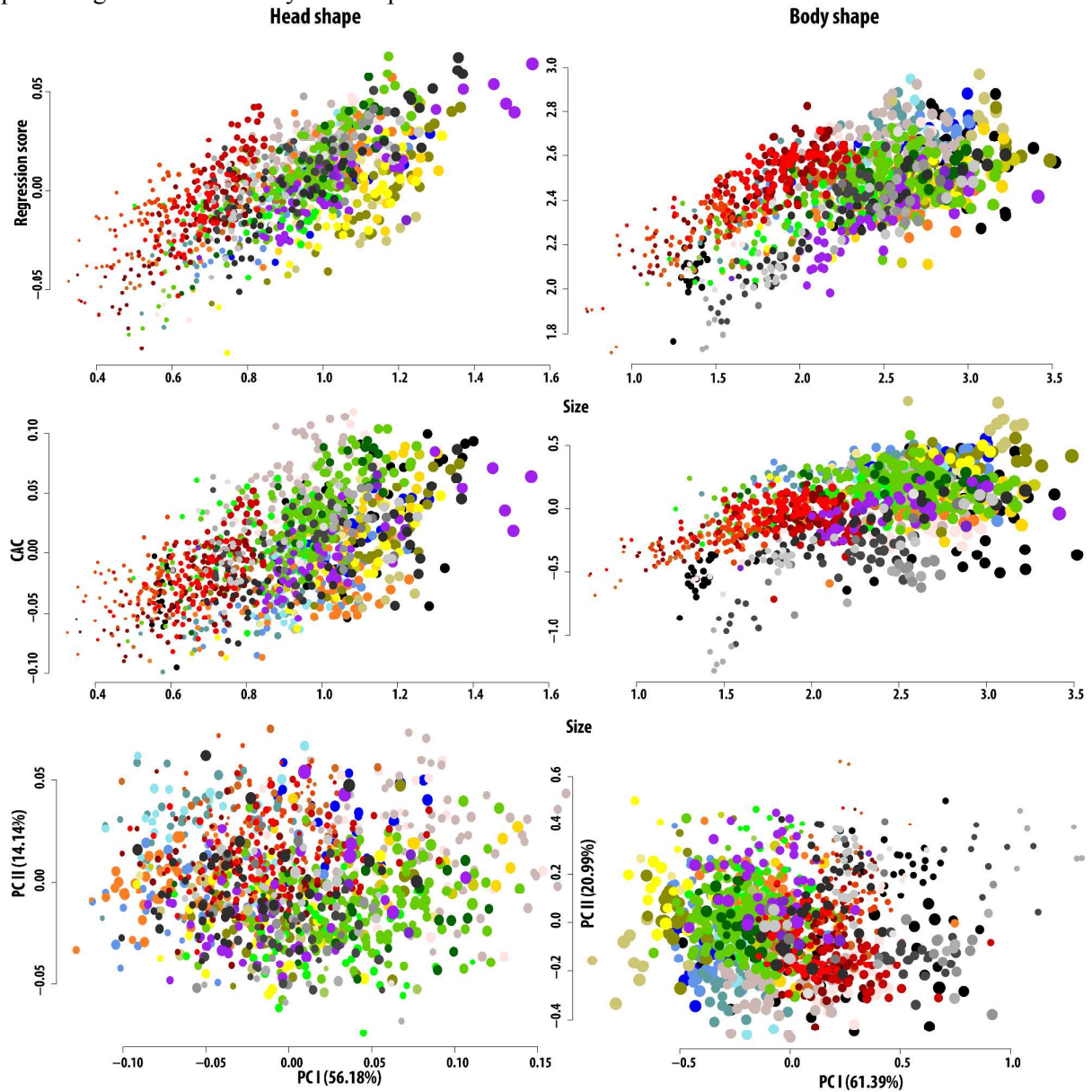


Figure S3. Regression scores, CAC and PCA as described in Fig. S2 for head and body shape, separated by clade.

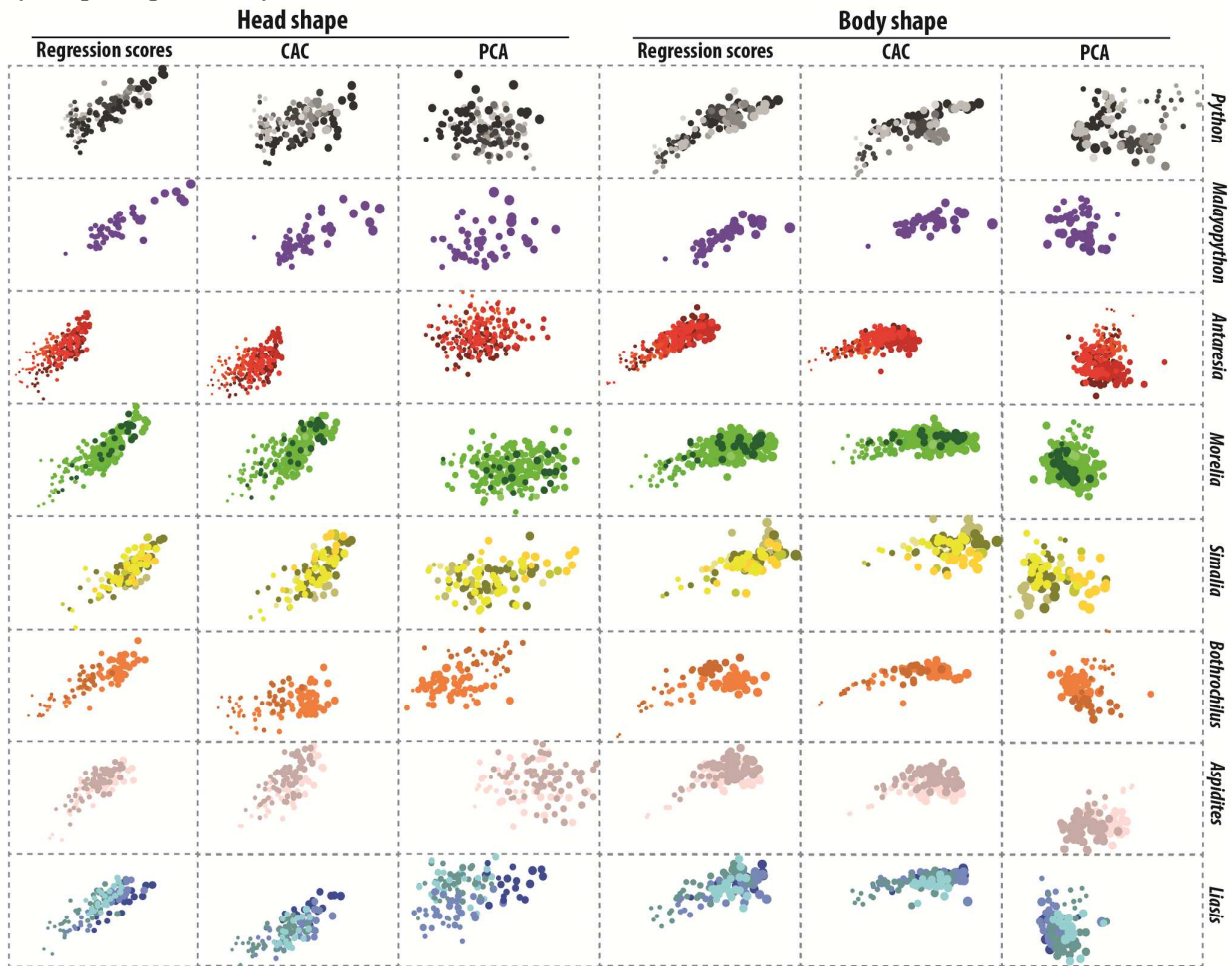


Figure S4. Slope vector lengths (the magnitude of shape change with unit of size change) for each species of python for head and body shape.

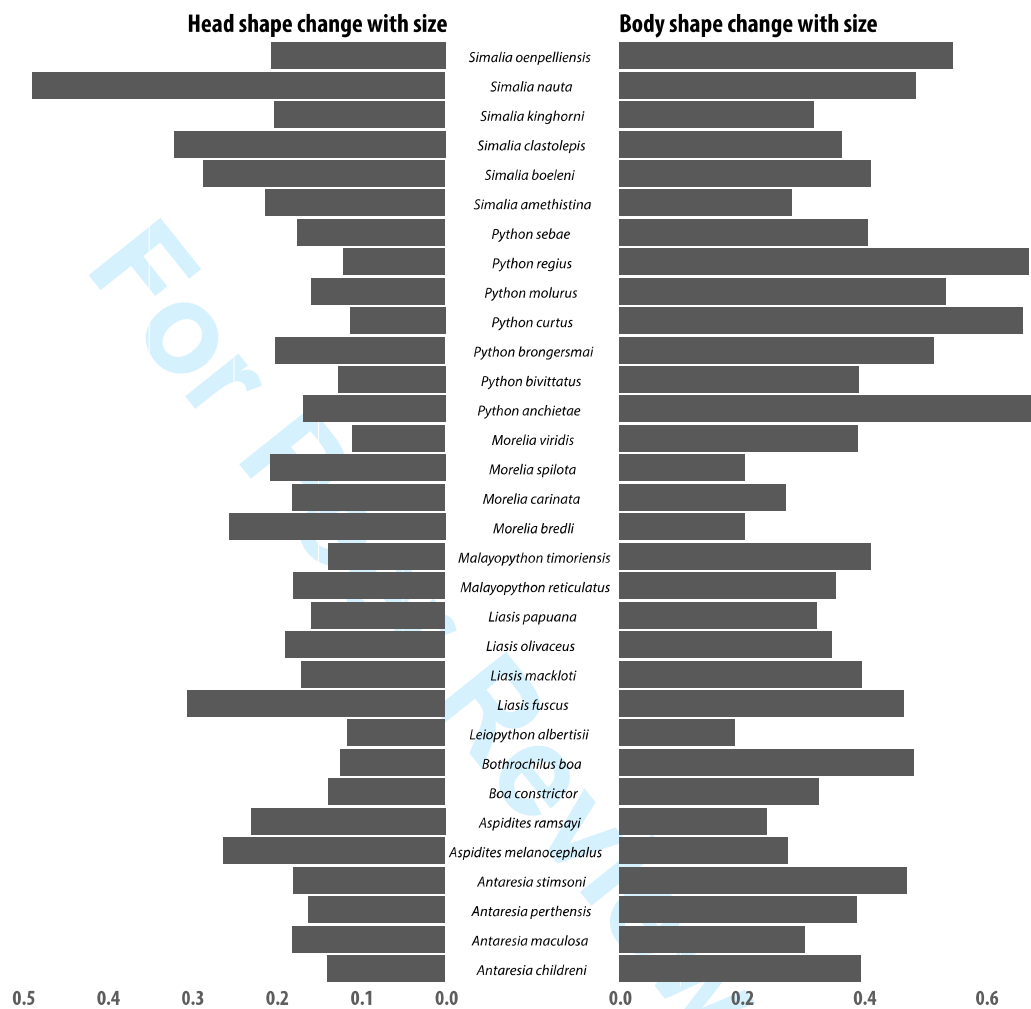


Figure S5. Maximum clade credibility time-calibrated tree of the pythons used in this study. Black circles at the nodes indicate a node supported with a posterior probability of 0.95 or higher. Blue bars at the nodes indicate the 95% highest posterior density of the divergence time estimated for that node. The scale at the bottom indicates the time frame in millions of years for the divergence of the nodes. From top to bottom, the scale indicates the geological ages, epochs and periods as a reference.

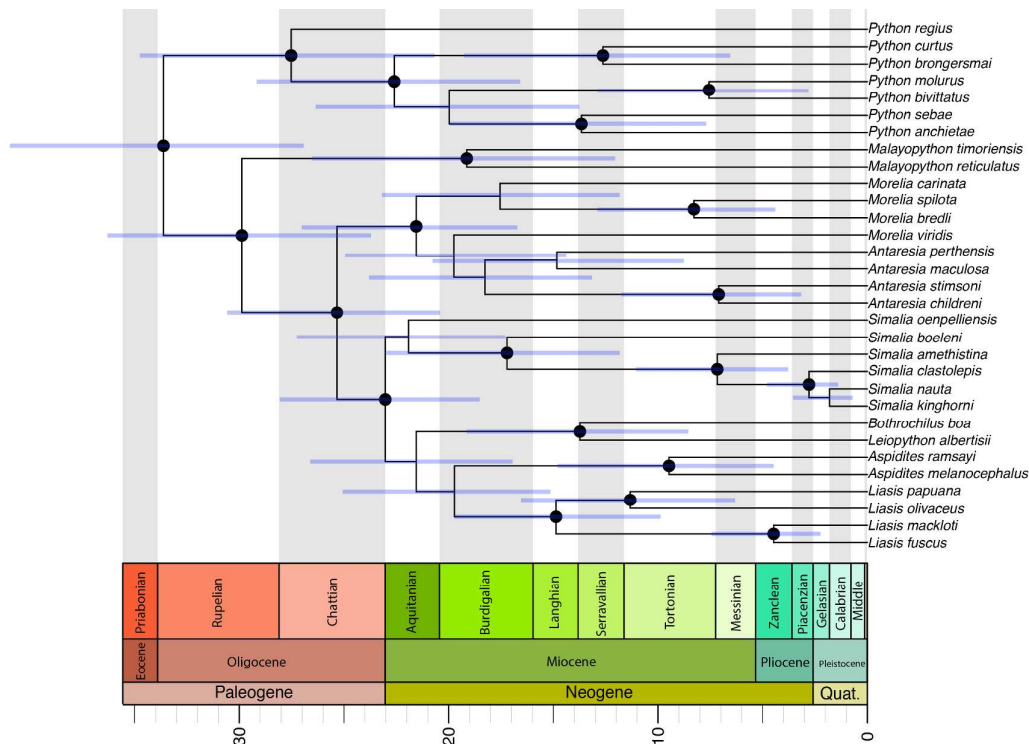
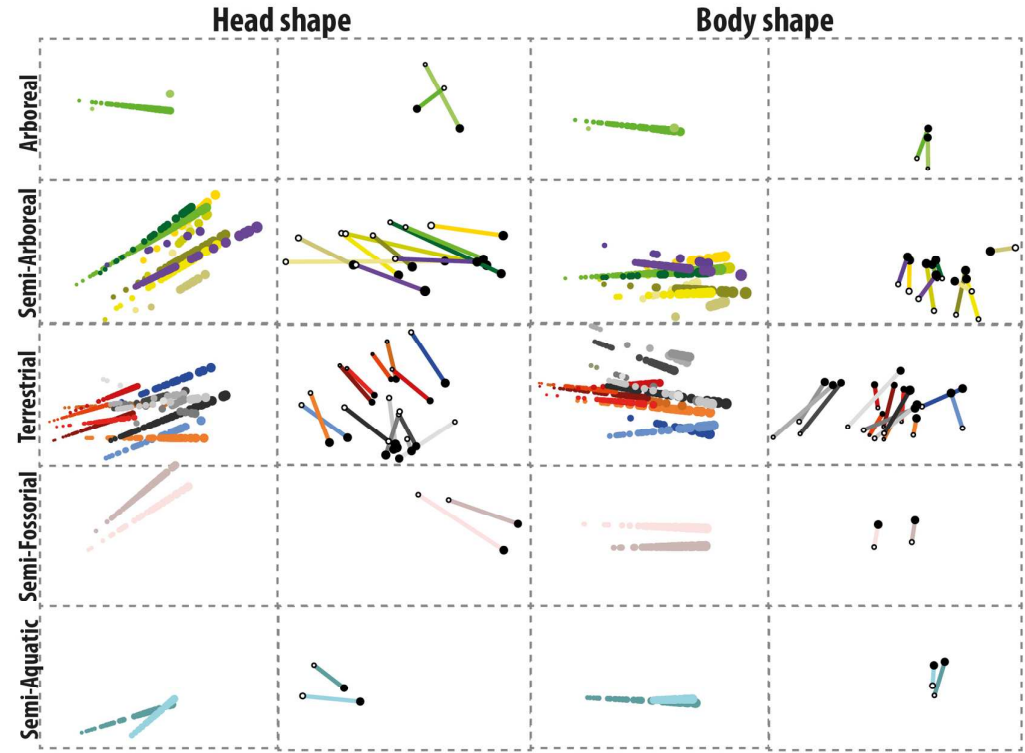


Figure S6. Ontogenetic allometric trajectories derived from the HOS (first and third columns) and PTA (second and fourth columns) tests, of head and body shape of the pythons, separated by micro-habitat choice. These are the same trajectories illustrated in Figures 2 and 3; see the respective legends for details.



Abstract

Ontogenetic allometry, how species change with size through their lives, and heterochony, a decoupling between shape, size and age, are major contributors to biological diversity. However, macro-evolutionary allometric and heterochronic trends remain poorly understood because previous studies have focused on small groups of closely related species. Here we focus on testing hypotheses about the evolution of allometry and how allometry and heterochrony drive morphological diversification at the level of an entire species-rich and diverse clade. Pythons are a useful system due to their remarkably diverse and well-adapted phenotypes and extreme size disparity. We collected detailed phenotype data on 40 of the 44 species of python from 1,191 specimens. We used a suite of analyses to test for shifts in trajectories that modify morphological diversity. Heterochrony is the main driver of initial divergence within python clades, and shifts in the slopes of allometric trajectories make exploration of novel phenotypes possible later in divergence history. We found that allometric coefficients are highly evolvable and there is an association between ontogenetic allometry and ecology, suggesting that allometry is both labile and adaptive rather than a constraint on possible phenotypes.

17
18 **Introduction**

19

20 Allometry, the relationship between biological traits and size ([Huxley and Teissier 1936](#))(~~Huxley and~~
21 ~~Teissier 1936~~), and its role as both a contributor and constrainer of phenotypic diversity, has been a central
22 focus in evolutionary biology for the last century ([Huxley and Teissier 1936](#); [Gould 1966](#); [Mosimann 1970](#);
23 [Klingenberg 1998](#); [2016](#))(~~Huxley and Teissier 1936~~; ~~Gould 1966~~; ~~Mosimann 1970~~; ~~Klingenberg 1998~~;
24 ~~2016~~). Ontogenetic allometry, the relationship between biological traits and size through ontogeny ([Alberch](#)
25 ~~et al. 1979~~; [Voje et al. 2013](#))(~~Alberch et al. 1979~~; ~~Voje et al. 2013~~) is likely also a major contributor to
26 biological diversity but it is comparatively less well understood. The few studies that have evaluated it
27 among closely related species have concluded that it has played a major role in that clade’s phenotypic
28 diversity through ontogeny ([Zelditch et al. 2003](#); [Adams and Nistri 2010](#); [Piras et al. 2011](#))(~~Zelditch et al.~~
29 ~~2003~~; ~~Adams and Nistri 2010~~; ~~Piras et al. 2011~~). The evolutionary mechanisms that cause ontogenetic
30 allometric trajectories to shift during evolution (see below), thus impacting phenotypic diversity at different
31 developmental stages, remain unclear ([Zelditch et al. 2003](#); [Klingenberg 2010](#); [Pélabon et al. 2014](#))(~~Zelditch~~
32 ~~et al. 2003~~; ~~Klingenberg 2010~~; ~~Pélabon et al. 2014~~). However, extrinsic forces like selective pressures or
33 phenotypic plasticity imposed by ecological factors can affect the intrinsic forces of development ([Frankino](#)
34 ~~et al. 2005~~)(~~Frankino et al. 2005~~). Allometry and size-shape relationships have been considered constraints
35 that size and growth impose to the morphologies that organisms can adopt ([Simpson 1944](#); [Gould and](#)
36 [Lewontin 1979](#); [Maynard Smith et al. 1985](#))(~~Simpson 1944~~; ~~Gould and Lewontin 1979~~; ~~Maynard Smith et~~
37 ~~al. 1985~~). Yet, allometric trajectories themselves can be biological traits under selection and not just
38 constraints ([Weber 1990](#); [Frankino et al. 2005](#); [Adams and Nistri 2010](#); [Wilson and Sanchez-Villagra 2010](#);
39 [Klingenberg 2010](#); [Urošević et al. 2013](#); [Porto et al. 2013](#); [Voje et al. 2013](#); [Giannini 2014](#))(~~Weber 1990~~;
40 ~~Frankino et al. 2005~~; ~~Adams and Nistri 2010~~; ~~Wilson and Sanchez Villagra 2010~~; ~~Klingenberg 2010~~;
41 ~~Urošević et al. 2013~~; ~~Porto et al. 2013~~; ~~Voje et al. 2013~~; ~~Giannini 2014~~).

42

There are several properties of ontogenetic allometric trajectories that can shift the array of phenotypes observed in a clade at any given ontogenetic stage ([Zelditch et al. 2012; Sheets and Zelditch 2013](#))(~~Zelditch et al. 2012; Sheets and Zelditch 2013~~). [When examined in a statistical regression framework](#). For example, modifications in the slopes of the allometric regressions, which define the magnitude and direction of shape change with size, can lead to patterns like ontogenetic convergence or divergence. In some European plethodontid salamanders, juveniles start off with very different feet shape but converge onto a similar foot morphology as they grow, which is thought to be an adaptation to climbing ([Adams and Nistri 2010](#))(~~Adams and Nistri 2010~~). Conversely, damselfishes show a conserved larval skeletal morphology while they inhabit the homogeneous oceanic environment but diverge into a disparate array of adult morphologies in order to use the more complex and diverse coral reefs as micro-habitat ([Frédérich and Vandewalle 2011](#))(~~Frédérich and Vandewalle 2011~~). Trajectories can shift in their [regression](#) intercept, producing parallel trajectories that have the same direction of shape change but never share the same phenotype ([Frédérich and Vandewalle 2011; Hipsley and Müller 2017](#))(~~Frédérich and Vandewalle 2011; Hipsley and Müller 2017~~). If trajectories overlap ([share an intercept and slope](#)), heterochronic changes, where a decoupling between shape, size and age happens, can induce profound changes in morphological diversity ([Gould 1977; Gerber et al. 2008; Bhullar et al. 2012; Foth et al. 2016](#))(~~Gould 1977; Zelditch et al. 2003; Gerber et al. 2008; Piras et al. 2011; Bhullar et al. 2012; Foth et al. 2016~~). ~~Whereas~~ Size is the independent variable used in studies of ontogenetic allometry, ~~while~~ and time is the independent variable in studies of heterochrony. ~~W~~~~without data on the age of the individuals, it is not possible to inferring~~ information on rates of change, or establishing heterochronic processes driving evolution, ~~is not possible~~ {Godfrey:1995gw}. Nevertheless, using size as a proxy of age, it is possible to detect the observable outcomes of heterochrony, like paedomorphosis and peramorphosis, where species become more juvenile or adult looking in respect to the other, respectively ([Piras et al. 2011; Gerber and Hopkins 2011](#)). In ontogenetic scaling, a special form of heterochrony, [species overlap in size-shape space, where](#) the relationship between size and shape is maintained (i.e. same allometric regression equation), and changes in growth rate will change the juvenile and adult morphologies along the same trajectory ([Mitteroecker et al. 2005; Zelditch et al. 2012](#))(~~Mitteroecker et al. 2005; Zelditch~~

et al. 2012). Heterochronic changes therefore produce forms that are more ~~adult-like~~ (peramorphic) or ~~juvenile-like~~ (paedomorphic) in respect to the ancestor (Gould 1977; Alberch et al. 1979; Piras et al. 2011; Gerber and Hopkins 2011)(Gould 1977; Alberch et al. 1979; Piras et al. 2011; Gerber and Hopkins 2011).

Figure 1 illustrates examples of these patterns, and the workflow used to detect them.

Pythons are a family of Old World constrictor snakes that include 44 species distributed in Africa, Asia, Melanesia and Australia. They exhibit their maximum taxonomic, phenotypic and ecological diversity in the Australasian region (Barker et al. 2015)(Barker et al. 2015). Several aspects of this family make them an excellent model for the study of morphological diversity, adaptation and allometry. They display one of the most extreme size ranges among any animal family, ranging from the pygmy python (*Antaresia perthensis*) that reach only 65 cm (Esquerré, unpublished data) to the reticulated python (*Malayopython reticulatus*), the longest snake on Earth that can reach almost 9 m in length (Murphy and Henderson 1997)(Murphy and Henderson 1997) – with difference in mass that spans three orders of magnitude. Their remarkable ecological diversity, particularly in micro-habitat choice, has provided diverging selective pressures driving an equally remarkable head shape diversity (Esquerré and Keogh 2016)(Esquerré and Keogh 2016). This combination of features provides an ideal scenario to test hypotheses on the contributions of allometry to clade diversity and how allometry interacts with ecological factors.

Our study focuses on ontogenetic allometry and observable products of heterochrony ~~of in~~ python head and body shape. Here we examine diversity in post-natal ontogenetic allometric trajectories in regard to direction, length (magnitude) and intercept at the family level, and at a genus or clade level, to estimate if closely related species would be more constrained to change shape in the same direction and have similar ontogenetic trajectories. Additionally, we test if among-species morphological disparity increases (indicating ontogenetic divergence) or decreases (indicating ontogenetic convergence) over ontogeny at the whole family level and for each clade separately. In clades where trajectories are overlapping, we explore how the array of phenotypic mega-diversity in pythons is affected by changes along a common ontogenetic

trajectory, with the ambition of finding patterns that can be explained by [processes of](#) heterochrony. Then, by incorporating ontogenetic allometry into a phylogenetic framework we evaluate how direction and magnitude of shape change with size evolves. This is achieved by mapping those traits on a phylogeny and treating allometry itself as an evolvable trait ([Gerber et al. 2008](#))([Gerber et al. 2008](#)). Finally, we determine if selection on micro-habitat use, which is known to strongly affect adult head morphology ([Esquerré and Keogh 2016](#))([Esquerré and Keogh 2016](#)), impacts the diversity of ontogenetic trajectories directing phenotypic change through growth in pythons.

Material and methods

Sampling

We visited nine major natural history collections (see Table S1) and sampled 1,191 specimens spanning 40 of the 44 recognized species of Pythonidae ([Barker et al. 2015](#))([Barker et al. 2015](#)), plus *Boa constrictor* from Boidae to have a comparison with this snake family that shows strong convergent evolution with pythons ([Esquerré and Keogh 2016](#))([Esquerré and Keogh 2016](#)). We measured an average of 32.2 specimens per species (range 3-153; see Table S1 for details on sampling). To increase statistical power, we considered some species that are phenotypically and ecologically extremely similar, and have shallow or unassessed genetic divergence, to be a single unit for analyses. This gave us more complete size ranges ~~and also~~ and did not change our interpretation of ~~our~~ the results. Specifically, we ~~lumped-grouped~~ *Python breitensteini* with *P. curtus*, *P. natalensis* with *P. sebae*, *Morelia imbricata* with *M. spilota*, *Morelia azurea* with *M. viridis*, all the *Leiopython* species with *L. albertisii*, and *Boa imperator* with *B. constrictor*.

Morphometrics

The head of each specimen was photographed in the dorsal view with a Canon 7D camera with a Canon 100 mm f/2.8 macro lens and a Canon Twin Lite macro flash, mounted on a tripod. We placed a scale-bar next to each specimen to quantify size. On each photograph, we digitized a configuration of 9 landmarks and 26 semilandmarks to ~~describe~~ [characterize](#) head shape (Fig. S1), as described in Esquerré & Keogh (2016). We

digitized the landmark and semilandmark coordinates using tpsDig v.2.17 (Rohlf 2015)(Rohlf 2015). Semilandmarks were permitted to slide in order to ~~minimise~~minimize bending energy (Gunz and Mitteroecker 2013)(Gunz and Mitteroecker 2013) on tpsRelw v.1.54 (Rohlf 2015)(Rohlf 2015). To retain only shape variation between the landmark coordinates, the effects of location, scale and orientation were removed with a generalized Procrustes analysis (Rohlf and Slice 1990)(Rohlf and Slice 1990) taking into account object symmetry (Klingenberg et al. 2002)(Klingenberg et al. 2002), performed with the function *bilat.symmetry* in the R package *geomorph* 3.0 (Adams et al. 2016)(Adams et al. 2016). Head size was calculated as ~~the~~ centroid size, the square root of the sum of the squared distance of every landmark to the centroid or ‘center’ of the landmark configuration.

For body shape analyses, we measured head length (from the posterior edge of the jaw, marked with a pin on the specimen, to the tip of the snout) and head width (between the posterior edges of the jaw) from the photographs using tpsDig v.2.17 (Rohlf 2015)(Rohlf 2015). For each specimen where the body was preserved and in good condition, we measured the snout-vent length (SVL), tail length, mid-body girth (measured at half of the SVL) and neck girth (measured just posterior to the skull), using a thread that was then measured against a ruler. To avoid overlapping body measurements we subtracted head length from SVL to get a body length measure. To remove the effect of size while maintaining allometric effects, we calculated the log-shape ratios of the body measurements (Mosimann and James 1979; Claude 2013)(Mosimann and James 1979; Claude 2013) where, for each individual, we first computed size as the geometric mean of all measurements. Then, each measurement for each specimen was divided by this size estimation to obtain the shape ratios and then log-transformed. These were used as the data for the subsequent analyses. The log-transformed geometric mean was used as size for the analyses of body shape allometry because it uses all of the body measurements as an estimation of size (Mosimann 1970; Claude 2008)(Mosimann 1970; Claude 2008), rather than just SVL. ~~We also performed all the analyses stated on in this paper with non-log-transformed size variables and SVL as the size variable for the body shape analyses, which gave us qualitatively identical results and are thus not reported.~~ Before performing the analyses stated below, we tested for the presence of sexual dimorphism with a distance-based ANOVA (Goodall 1991;

~~Anderson 2001~~)(~~Goodall 1991; Anderson 2001~~) on both head and body shape, and found none. This was performed with the function *procD.lm* in *geomorph*.

Analyses of allometric ontogenetic trajectories

To study allometry at a shallower evolutionary scale and to compare between lineages, we grouped the species in clades which correspond to their genera, except for *Bothrochilus* and *Leiopython* which are sister taxa grouped together here. The following analyses follow the schematic Figure 1, in a step by step procedure where changes in allometry and heterochrony are identified. ~~All of All~~ the analyses were performed on head shape and body shape variables separately. First, we determined if any species displayed isometric growth (no change in shape with size) by fitting individual regressions for each species of size on shape using *procD.lm* from the R package ~~geomorph~~ *geomorph* and assessing the significance with 10,000-999 iterations. A significant association rejects the null hypothesis of isometry and reveals that there is allometry and therefore the species lacks isometry. A non-significant relationship indicates isometry or lack of sufficient sampling to provide statistical power to detect allometry. We then assessed the relationship of shape and log-transformed size (i.e. allometry) for all species of pythons using two complementary approaches: 1) a homogeneity of slopes test, and 2) a phenotypic trajectory analyses, which are described in detail below. They are both used to establish the patterns of direction and magnitude of shape change with size, by testing for differences in the slope angle and length. The tests differ in that the first considers size as a continuous variable and the second considers size as a proxy for estimating ontogenetic stage as a categorical variable. It is useful to perform both because together they provide a robust statistical framework and visualize different aspects of the results, the first being a size-shape space and the second a morphospace visualization.

We performed an homogeneity of slopes (HOS) test, using a distance-based ANCOVA on both head and body shape including size, species and the interaction of the two terms(~~Collyer and Adams 2013~~)(~~Collyer and Adams 2013~~). The test performs statistical assessment of the terms in the model using distances among

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specimens, rather than explained covariance matrices among variables ([Anderson 2001](#))(~~Anderson 2001~~). It quantifies the amount of shape variation explained by size, computes the allometric slopes for each species, and performs pairwise comparisons for the slope angles (direction of shape change with size) and slope lengths (amount of shape change with size). Statistical significance was evaluated with a residual randomization permutation procedure with ~~9,999~~10,000-iterations. This was performed using the *advanced.procD.lm* function in *geomorph*. For a simple visualization of the diverse ontogenetic allometric trajectories among the species, we plotted the first principal component (PC1) of the matrix of predicted shapes from the multivariate regression ([Adams and Nistri 2010](#))(~~Adams and Nistri 2010~~).

We performed a phenotypic trajectory analysis (PTA) ([Adams and Collyer 2009; Collyer and Adams 2013](#))(~~Adams and Collyer 2009; Collyer and Adams 2013~~), a procedure that quantifies the variation of different attributes of a shape change trajectory between two or more points. We used species as the groups and juveniles and adults as the trajectory points. First, for each species we chose the specimens that clearly represented juveniles or adults (sexually mature), leaving out specimens where sexual maturity was uncertain. We compared the direction and size of the trajectories between juveniles and adults between all taxa and assessed the significance of these comparisons with 10,000~~9,999~~ permutations. This analysis was performed with the function *trajectory.analysis* in *geomorph*. To visualize the ontogenetic phenotypic trajectories, we plotted the first two PCs of shape variation. To enable biological interpretation of the PCs from the PTA analysis and the above multivariate regression of head shape data we used thin plate spline deformation grids ([Bookstein 1991](#))(~~Bookstein 1991~~). For body shape analyses we examined the PC loadings.

When pairwise species comparisons of slope angle did not reject the null hypothesis of parallel allometric slopes, indicating similar slopes, we performed an additional test to evaluate whether the slopes are overlapping (H_0) or parallel (H_1). This was done by assessing whether there is a shift on the intercept along the Y (shape) axis using pairwise comparisons of the intercepts of the allometric regression of each species.

Significance was assessed by comparing the difference to a set of 9,99910,000 permutations, with the *int.test* R function developed by Piras *et al.* (Piras et al. 2011)(~~Piras et al. 2011~~). For species where the null hypothesis of parallel trajectories was rejected, we then investigated the possibility of heterochrony.

It is important to note that due to the limitations of a study using wild-caught rare species, the ontogenetic sampling for all of the species is not complete. This mainly influences the results on magnitude of shape change with size. The broad patterns across the family is clear, but specific comparisons, particularly with *Simalia nauta*, *S. oenpelliensis* and *Liasis fuscus*, where small juveniles could not be measured, should be taken with caution.

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Heterochrony

We performed a test to identify patterns of peramorphosis/paedomorphosis with the null hypothesis that two species do not differ in predicted shape at the maximum size of the species being compared using the R function *peram.test* developed by Piras *et al.* (Piras et al. 2011)(~~Piras et al. 2011~~). A rejection of the null is interpreted as one of them being peramorphic (more ‘adult-like’) or paedomorphic (more ‘juvenile-like’) with respect to the other. Statistical significance was assessed by comparing to a randomly generated distribution of the data with 9,99910,000 permutations.

Finally, we performed two tests developed by (Gerber and Hopkins 2011)(~~Gerber and Hopkins 2011~~), and based on (Mitteroecker et al. 2005)(~~Mitteroecker et al. 2005~~), to further examine heterochrony by assessing the species trajectories overlap in shape and size-shape space. These tests rely on the fact that heterochrony requires the species shape change trajectories to overlap. They are both based on computing multivariate regressions of shape on size for the species being compared. The first one (Tfh1) is used to identify heterochrony by ontogenetic scaling (maintaining an overlap in size-shape space), which is translated into an extension or truncation of the ontogenetic trajectory. It uses the sum of the squared residuals from the regression as a tests statistic. The second one (Tfh2) is used to identify heterochrony with a size-shape

dissociation, and uses the sum of squared distances from each specimen to its nearest point on the regression curve as a test statistic. Statistical significance was assessed with ~~10,000~~9,999 permutations for Tfh1 and ~~499-500~~ permutations for Thf2.

The number of pairwise comparisons from the intercept and peramorphosis tests requires that the *P*-values are corrected with a Benjamini-Hochberg or ‘false discovery rate’ correction (~~Benjamini and Hochberg 1995~~)(~~Benjamini and Hochberg 1995~~). The *P*-values from the Tfh1 and Tfh2 tests from heterochrony were not corrected since we are interested in accepting the null hypothesis and therefore type II error is a bigger concern than type I error. The *P*-values from the slope angle and length tests were not corrected since the tests are not independent and do not require correction. For all the tests we considered a *P*-value below 0.05 (5%) as the threshold for statistical significance.

Ontogenetic convergence and divergence

Slopes that differ in their angular direction, as defined by the HOS test, may be the result of ontogenetic convergence (e.g., Adams and Nistri 2010) or divergence (i.e. allometric repatterning (~~Webster and Zelditch 2005~~)(~~Webster and Zelditch 2005~~)). For pythons as a whole, and for each clade where not all species had the same slope, we assessed whether their ontogenetic allometric trajectories display a convergent or divergent pattern, against a null hypothesis of ontogenetic consistency, by comparing the variation among juveniles versus the variation among adults. We calculated and summed the pairwise Euclidean distances between all specimens, using the first principal component of the predicted morphologies in both ontogenetic stages separately, to calculate the $D = D_{\text{juv}} - D_{\text{adult}}$ statistic. A positive result implies adults are more similar to each other than juveniles are (convergence) and a negative result implies juveniles more similar to each other than adults are (divergence). The significance of the statistic was assessed with ~~9,999~~10,000 permutations of the data where depending on the hypothesis of convergence or divergence, a *P*-value was obtained based on the proportion of iterated *D* statistics that were below or above the observed *D*, respectively (~~Adams and Nistri 2010~~)(~~Adams and Nistri 2010~~).

Phylogenetic hypothesis

To examine variation in ontogenetic allometry in an evolutionary context we constructed a time-calibrated ultrametric phylogenetic tree of the pythons. We used the alignment provided for the most recent and complete phylogenetic analysis that included this group (Reynolds et al. 2014)(Reynolds et al. 2014). This dataset corresponds to a supermatrix of three mitochondrial and eight nuclear loci of most pythons and boas. Details on how we reconstructed the phylogeny can be found in the Supplementary Information.

Evolution of ontogenetic allometric trajectories

There are currently no methods to perform the preceding statistical analyses for allometric ontogenetic trajectories in a phylogenetic comparative context, taking into account the statistical non-independence of species data when within-species variation is the feature of interest (rather than species averages). Thus, we present a novel approach to visualize the evolution of the parameters of the allometric trajectories in a phylogenetic context, ~~using ancestral state reconstruction and a tree projection approach similar to the phylomorphospace (sensu Sidlauskas 2008). Similarly to what is done in a traditional morphospace visualization, this method is based on plotting the first two principal components of the allometric vector describing the multivariate slopes of the trajectories, similar to what has been called an allometric space (Klingenberg and Froese 1991; Wilson and Sanchez-Villagra 2010). However, in addition to the terminal taxa, we also added the reconstructed ancestral state of each node using a maximum likelihood approach, and the tree topology connecting these, making it analogous to a phylomorphospace (sensu Sidlauskas 2008). We propose this visualization be termed phyloallomspace. This analysis~~ ~~We performed an ancestral state reconstruction on the vector describing the allometric trajectory for each species using maximum likelihood to reconstruct the evolution of the direction of allometric shape change. The trajectories of the tree tips and reconstructed nodes are then subjected to principal components analysis and visualised in a biplot of the first two axes with the tree projected into the space to show the inferred evolutionary histories of ontogenetic slope change. This~~ was implemented with the function *plotGMPhyloMorphoSpace* of

geomorph. To reconstruct the evolution of the magnitude of allometric shape change, we used the slope vector length, or magnitude of shape change per unit of size, to perform an ancestral state reconstruction using maximum likelihood. This was performed with the function *contMap* in the R package *phytools* (Revell 2012)(Revell 2012). We also removed the three species with missing early ontogenetic stages from the evolutionary analysis, to avoid creating any bias in the results.

Ecological influence on ontogenetic allometry

Finally, to test the effect of ecology on ontogenetic allometry, and accounting for phylogenetic relationships, we performed a phylogenetic ANOVA that uses a generalization of phylogenetic generalized least squares (PGLS) for high-dimensional and multivariate data (Adams 2014)(Adams 2014). This was first performed on the allometric slopes using microhabitat use as the predictor variable, first as coded in Esquerré & Keogh (2016) where *Aspidites melanocephalus* and *A. ramsayi* are considered semi-fossorial and *Liasis mackloti* and *L. fuscus* as semi-aquatic, and second where we lumped the semi-fossorial and semi-aquatic taxa as terrestrial, because these shifts only occur a single time in both cases. This was performed with the *procD.pgls* function in *geomorph* (Adams 2014)(Adams 2014). To have a visualization of the coupling between the evolution of ecology and allometric coefficients, we performed an ancestral state reconstruction of micro-habitat use by using stochastic character mapping (Huelsenbeck et al. 2003). We ran 10,000 independent stochastic character maps to have an estimate of uncertainty (Revell 2014). This was done using the R package *phytools*.

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Results

Ontogenetic allometry

Most of the species displayed allometric growth (i.e. lack of isometry). The species that did display non-significant relationships between size and shape had low samples numbers, so we call caution interpreting results regarding them, namely *Morelia carinata*, *Simalia oenpelliensis*, *S. nauta*, *Python anchietae*, *P. brongersmai* and *L. fuscus* (Table S3). Size, species and the interaction of the two strongly influence python

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head shape (ANCOVA, size $F_{(1, 1127)} = 320.663$, $P < 0.0001$; species $F_{(31, 1127)} = 47.007$, $P < 0.0001$; size*species $F_{(31, 1127)} = 4.243108$, $P < 0.0001$) and body shape (size $F_{(1, 1040)} = 560.549$, $P < 0.0001$, species $F_{(1, 1040)} = 69.167$, $P < 0.0001$; size*species $F_{(31, 1040)} = 4.096$, $P < 0.0001$). These results indicate that there is clear ontogenetic allometry in both head and body shape and that allometry differs between species in both head and body shape. The pattern is clearly observed on the difference in slopes of trajectories in both head and body shape (Figs. 2 and 3). The raw regression scores, common allometric component (Adams et al. 2013) and raw principal components for all the species and separated by clade can be seen in Figs. S2 and S3.

The head shape changes associated with increasing size, as described by a multivariate regression of shape on log-transformed size (Fig. 2) and by PC1 of the PTA (Fig. 3), involve a broadening of the snout and eyes that become smaller and more dorsally situated. PC2 of the PTA represents a massive enlargement and lateralization of the eyes and a transition to a shorter and more pointed snout. For body shape, PC1 of the PTA represents an elongation of the tail (tail length eigenvector = 0.8) and a slimming of the body (mid-body girth eigenvector = -0.35). PC2 of the PTA mainly represents a thickening of the body (mid-body girth eigenvector = 0.63), an elongation of the body (body length eigenvector = 0.47) and a proportional reduction in head size (head length eigenvector = -0.41; head width eigenvector = -0.43).

Both the HOS test and PTA analyses show equivalent differences of direction and magnitude of shape change in head and body shape, and therefore we only present the results from the first. Head and body shape ontogenetic allometric trajectory diversity is extremely large in pythons. The slope vector lengths and the trajectory path distances, which both translate into the amount of shape change given size, can be seen in Fig S42, but easily interpreted by looking at the steepness of the slopes of shape on size in Fig. 2 and the length of the PTA trajectories on Fig. 3. Pairwise comparison of slope angles and slope vector lengths for head and body shape can be seen in Tables S43-76. Because of the large number of taxa included in these analyses and the great diversity in observed patterns, the results are also summarized on a clade-by-clade

basis in Fig. 4. The main findings supported by the pairwise species comparisons and the visualization of the results can be broken down as follows.

Direction of shape change with size

In general, species within the same genus or clade tended to differ very little in angle of shape change with size, implying parallel or overlapping allometric trajectories within clades (Fig. 4, Tables [S3-S4](#) and [S4S5](#)). The broad pattern is that pythons tend to get broader heads and proportionally smaller and more dorsally situated eyes as they grow. There are a few exceptions, but the most contrasting is *Morelia viridis* which has a significantly different head shape slope orientation from almost all of the species. There are also slope differences in head shape within *Python* and body shape within *Morelia* and *Liasis*.

Magnitude of shape change with size

Similarly to what is observed with the direction of shape change, species within the same clade tend to differ very little in the amount of shape change they go through with size, implying a strong phylogenetic effect on the magnitude of change (Tables [S5-S6](#) and [S6S7](#)). *Simalia clastolepis* has a significantly larger head shape change than most other pythons (Fig. [S42](#) and Table [S5S6](#)). Species in *Simalia* and *Aspidites* tend to show larger amounts of head shape change, whereas other taxa like *Leiopython albertisii*, *Bothrochilus boa* and *Python curtus* display little head shape change with size, getting closer to isometry (Fig. [S2-S4](#) and Table [S5S6](#)), which in multivariate allometry is represented as a flat line parallel to the x-axis (Fig. 4). *Python curtus*, *P. regius* and *P. anchietae* display large amounts of body shape change with size, whereas *Leiopython albertisii*, *Morelia spilota*, *M. bredli* and the two species in the genus *Aspidites* display small amounts of change (Fig. [S2-S4](#) and Table [S6S7](#)).

Intercepts of ontogenetic allometry

Among the species with a similar allometric slope, we did not identify parallel allometric trajectories (different allometric intercepts) within clades for head or body shape, but there were a few cases among

species of different clades (Tables [S7-S8](#) and [S8-S9](#)). This indicates that most species with a shared allometric slope have overlapping trajectories.

Heterochrony

Within clades, the most common pattern explaining morphological diversity in pythons is peramorphosis/paedomorphosis (Tables [S9-S10](#) and [S10-S11](#)), where slopes and intercepts between species are equivalent but they differ on the maximum size phenotype, one being more “adult-like” or peramorphic than the other. Between clades, both differences in slopes and shifts along the ontogenetic trajectories are responsible for changes in phenotypes. However, within clades many species pairs have equivalent ontogenetic trajectories. The Thf1 and Tfh2 tests found overlapping trajectories in size-shape and shape space mostly within clades. These tests were more conservative in their results, and most species pairs do not display heterochrony according to the test’s definition of heterochrony. However, in both head and body shape, some similar and closely related species pairs within *Python*, *Antaresia*, *Morelia* and *Simalia*, some display ontogenetic scaling and others/or heterochrony via size-shape space dissociation. Furthermore, *Antaresia maculosa* / *A. perthensis* (the largest and smallest species within their clade) and *Simalia boeleni* / *S. clastolepis* display overlap in size-shape space and significantly different maximum size phenotypes in head and body shape respectively, suggesting a strong case of ontogenetic scaling (Tables [S11-S12](#)-[S14-S15](#)).

Ontogenetic convergence and divergence

In the test for ontogenetic convergence/divergence we find convergence in head shape within *Python*, and convergence in body shape within *Morelia* and *Liasis* (Table 1), which is clearly observable from the ontogenetic trajectories (Fig. 4), and from the fact that there is divergence in slopes in those clades (Tables [S3-S4](#) and [S4-S5](#)). This means that juveniles of these species are very different to each other but they become very similar as they approach adulthood. More broadly, species with stocky and short-tailed body shapes as juveniles (e.g., *Python curtus*, *P. brongersmai* and *P. regius*) elongate as they grow while species that are

thin and long-tailed as juveniles (e.g. *Simalia*) get stockier and ~~more~~ shorter tailed with size, almost converging on body shape with the former.

Phylogenetic hypothesis

Unsurprisingly, the topology recovered by our analysis is identical to the one recovered by (Reynolds et al. 2014)(Reynolds et al. 2014). The basal split between the Afro-Asian *Python* genus and the rest of the Pythonidae is dated at the early Oligocene with 33.62 my, with a 95% highest posterior density interval between 26.85 and 40.9 my. ~~The majority of~~ Most the nodes are supported with a posterior probability higher than 0.95. *Morelia viridis* is not recovered with *Morelia* but with its sister clade *Antaresia* (with low posterior probability). However, preliminary results from a phylogenomic analysis using hundreds of nuclear loci supports the inclusion of this species in *Morelia* (Esquerré et al. *in prep*), therefore it is considered with this clade in the analyses of this paper. For details on the tree topology, divergence times and support see Fig. S3S5.

Evolution of ontogenetic allometry

The biplot of the inferred evolutionary history of direction of allometric shape change (Fig. 5) highlights the phylogenetic structure found on the grouping of the slopes. For both head and body shape, the genus *Python*, which is sister to all other pythons, displays a distinct set of slopes from the rest, despite being itself very diverse. On both head and body shape, other clades like *Simalia*, *Aspidites* and *Morelia* (except again by *Morelia viridis*) occupy the opposite side of the biplot, while the clades *Antaresia*, *Malayopython*, *Bothrochilus/Leiopython* and most of *Liasis* occupy a middle area of the space.

The ancestral state reconstruction of the magnitude of shape change with size shows a similar pattern of separation in groups of clades as the evolution of direction of shape change. *Simalia*, *Aspidites* and *Morelia* (except *M. viridis*) experience a great amount of head shape change but generally small amounts of body

shape change with size. The opposite is true for *Python*, and again, the other clades show intermediate amount of phenotypic change with growth.

Ecological influence on allometry

Microhabitat use was found to have a significant effect on the variation of allometric slopes in head shape with the original micro-habitat codings from Esquerré & Keogh (2016) ($F_{(4, 23)} = 1.736$, $P = \mathbf{0.0062}$) and considering the semi-fossorial and semi-aquatic species as terrestrial ($F_{(4, 25)} = 2.376$, $P = \mathbf{0.0033}$).

Microhabitat use was not found to have significant effect on body shape allometric slopes ($F_{(4, 23)} = 0.759$, $P = 0.232$) nor when semi-fossorial and semi-aquatic species are coded as terrestrial ($F_{(4, 25)} = 1.087$, $P = 0.076$). The stochastic mapping of micro-habitat shows predicts terrestriality as the ancestral state of pythons, with at least three independent origins of semi-arboreality, two of arboreality and one of semi-aquatic and semi-fossorial micro-habitat preferences (Fig. 5). Comparing the plots representing the evolution of allometry and ecology in Fig. 5 reveals that there is a tendency of species that have the same ecology to share regions of allometric space and patterns of magnitude of shape change with size. Fig. S6 displays the ontogenetic allometric trajectories separated by ecology, showing how there are trends of allometry for each micro-habitat choice.

Discussion

Pythons are a morphologically and ecologically mega-diverse group of vertebrates that display phenotypes that are highly adapted to their ecological lifestyle (Esquerré and Keogh 2016)(Esquerré and Keogh 2016).

We have revealed that their post-natal ontogenetic allometry is evolutionarily labile and they have great diversity in developmental trajectories. Other published studies of ontogenetic allometric trajectories have focused on variation within genera or closely related species; as far as we are aware, this is the first study looking into the evolution ontogenetic allometry at a family level incorporating almost every taxon. Within the Pythonidae we observe that the shifts in ontogenetic allometric trajectories that change a groups'

morphological diversity are not consistent across all clades. Some clades show ontogenetic convergence, others equivalent trajectories, but most often the differences observed among phenotypes of a clade are derived from heterochronic processes (i.e. peramorphosis/paedomorphosis). By the sheer diversity and lability of allometry, and its correlation with ecology in pythons, we suggest that allometry is a highly labile, evolvable and adaptive trait.

Studies within genera normally observe one type of ontogenetic trajectory shift driving the phenotypic diversity: for example ontogenetic convergence in plethodontid salamander foot morphology (Adams and Nistri 2010)(Adams and Nistri 2010) or heterochrony in *Podarcis* lizard head shape (Piras et al. 2011)(Piras et al. 2011). The species-rich and phenotypically conserved old world lacertid lizards also display conserved ontogenetic allometries (Hipsley and Müller 2017)(Hipsley and Müller 2017). Pythons exhibit these and other patterns too, suggesting that different ontogenetic allometric changes can generate morphological diversity in a relatively short time period. Our data demonstrates that patterns in allometric trajectories in pythons differ within and between clades. Within clades there is a strong pattern of overlapping (similar) trajectories between species, where changes are mostly heterochronic and along the same trajectories. Between clades however, there are discernible shifts in both the direction and magnitude of ontogenetic allometry. This is in agreement with the hypothesis that allometries evolve at million-year time scales and closely related species will tend to show less divergence in their trajectories (Voje et al. 2013)(Voje et al. 2013). For some clades, like lacertid lizards, phenotypic differences between species are developed prenatally (observed as shifts in their allometric intercepts), and in others like pythons, differences mostly develop after birth (observed as conserved intercepts but shifts in the extension or slope of the trajectories). In pythons, there is also strong variation in the magnitude of shape change, where some *Python* species experience great body shape transformation as they grow while some *Morelia* and *Aspidites* species experience milder changes.

Heterochronic changes are capable of increasing phenotypic diversity in a short period of time, and induce deep changes in the morphology of lineages (Gould 1977)(Gould 1977). Birds evolved their unique cranial morphologies by combination of cranial paedomorphosis and beak peramorphosis in relation to theropod dinosaurs (Bhullar et al. 2012; Foth et al. 2016)(Bhullar et al. 2012; Foth et al. 2016) and heterochrony is a common feature in morphological evolution in squamate reptiles (Piras et al. 2011)(Piras et al. 2011). Exploring allometric trajectories in size-shape space makes it possible to infer heterochronic products of processes like paedomorphosis and peramorphosis (Piras et al. 2011)(Piras et al. 2011) and to distinguish between heterochrony by ontogenetic scaling (with species sharing size-shape space) or by size-shape dissociation (Mitteroecker et al. 2005; Gerber and Hopkins 2011)(Mitteroecker et al. 2005; Gerber and Hopkins 2011). We identified these two types of heterochrony within four python genera. Most notably, *Antaresia perthensis*, the smallest python in the world, is completely paedomorphic in relation to *Antaresia maculosa*, the largest species within its clade. We identify that the most common form of developmental change fueling initial evolution of pythonid morphologies are heterochronic changes along the trajectories determining the shape at maximum size, where a species changes its phenotype by growing ~~more or less bigger or smaller~~. Without information on the age of individual specimens though, we can only identify the products and not the processes of heterochronic perturbations (Klingenberg and Spence 1993; Godfrey and Sutherland 1995; Piras et al. 2011)(Klingenberg and Spence 1993; Godfrey and Sutherland 1995; Piras et al. 2011), because paedomorphosis or peramorphosis can originate from modifications on age at onset, age at offset and/or growth rate (Reilly et al. 1997)(Reilly et al. 1997). However, snakes generally display indeterminate growth (Andrews 1982; Shine et al. 1998)(Andrews 1982; Shine et al. 1998) and size is strongly correlated with age (Gignac and Gregory 2005)(Gignac and Gregory 2005), which make them a much better model for detecting heterochrony than most animal groups. Our data suggests that heterochrony is the process responsible for morphological evolution at the early stages of diversification, since it is responsible for divergence within clades. It seems that longer evolutionary times are required for allometric slopes to evolve, allowing the ontogenetic allometric trajectories to explore new areas of morphological space (Weston 2003; Wilson and Sánchez-Villagra 2011)(Weston 2003; Wilson and Sánchez-Villagra

2014). Similarly, some closely related dinosaur species tend to have more similar and conserved ontogenies and that these diverge as phylogenetic relatedness decreases (Bhullar et al. 2012; Mallon et al. 2015)(Bhullar et al. 2012; Mallon et al. 2015). Shifts in ontogenetic allometric slopes increases the disparity in a group and aids in finding new phenotypes that better suit the selective pressures.

The analyses of allometric slope, intercept and peramorphosis/paedomorphosis reveal a clear pattern of conserved allometric trajectories and hypermorphosis where differences in the shape attained at maximum size suggest that heterochrony is the mostly the cause of morphological evolution at the start of divergence. On the other hand, the Tfh1 and Tfh2 analyses of overlap in size-shape and shape space suggest a much weaker pattern of heterochrony. Nonetheless, given the strong support of heterochronic patterns found by the previous battery of analyses, and the clear morphological differences in phenotypes between most species of pythons of the same clades, we conclude that the Tfh1 and Tfh2 tests are very conservative in detecting patterns of heterochrony.

Studies of static allometry, where size-phenotype relationships are studied across different organisms at the same developmental stage, have proposed that size imposes strong limitations and constrains on phenotypes (Huxley 1932; Simpson 1944; Gould and Lewontin 1979). What we observe as developmental constraints in studies of ontogenetic allometry and development, can be expressions of different processes, like a common development-genetic architecture or limitations in the number of ways development can be produced due to physiological/mechanical limitations (Sanger et al. 2012). Nevertheless, in recent years, studies of ontogenetic allometry (where size-phenotype relationships are studied across developmental stages within a species), have compared the ontogenetic allometric trends between species. Some authors (Wilson and Sanchez-Villagra 2010; Klingenberg 2010; Voje et al. 2013)(Wilson:2010ke, Klingenberg:2010el, Voje:2013bg) of these studies have concluded that allometry has been observed and referred to as can be an adaptive and evolvable trait that can lead to complex patterns of phenotypic diversity, rather than a constraint on phenotypes imposed by size and ontogeny (Wilson:2010ke, Klingenberg:2010el).

~~Voje 2013b~~ (Wilson and Sanchez-Villagra 2010; Klingenberg 2010). Evaluating allometric coefficients in the context of a phylogeny can provide insights into how it evolves and how it is constrained by phylogenetic relatedness (Giannini 2014)(Giannini 2014). Methods do not exist yet that allow for a proper incorporation of phylogenetic information into analyses comparing within-species patterns like ontogenetic allometry, where there are often more individuals than taxa. Nevertheless, examining the evolution of the patterns of allometric trajectories under a phylogenetic framework we observe that the developmental patterns of head and body shape change differ greatly and that there are clade-specific trends that seem to be related to their ecology. For example, the species in the lineage that includes the terrestrial Afro-Asian *Python*, which is sister to all other pythons, display small amounts of head shape change but immense body shape transformation as they grow, including an elongation of the tail and decrease in body girth. The opposite direction and magnitude of allometric shape change is observed in some of the Australo-Papuan clades including the semi-arboreal *Simalia*, *Morelia*, and the semi-fossorial *Aspidites*. These results suggest that allometric coefficients are more labile than previously thought. More studies at a macro-evolutionary scale are needed to better understand exactly how evolvable allometry is, and how important it is in shaping the diversity of a group.

The lability of allometry provides evidence that it can be highly evolvable (Pélabon et al. 2014)(Pélabon et al. 2014), but a correlation with ecology suggests it also may be adaptive. In pythons, micro-habitat use drives phenotypic evolution (Esquerré and Keogh 2016)(Esquerré and Keogh 2016) and our results suggest that it also can have an effect on ontogenetic allometry. In the Australo-Papuan genus *Morelia* two semi-arboreal species, *Morelia spilota* and *M. bredli*, show the same ontogenetic allometric trajectory. The closely related *Morelia viridis* on the other hand, is unique among pythons in most aspects of its ecology and phenotype. It is the only completely arboreal species in the family and it goes through an extreme ontogenetic color change from bright red or yellow juveniles to completely green adults. This coloration change has been found to be strongly associated with changes in head shape allometry and dietary shift from ectothermic to endothermic prey (Natusch and Lyons 2012)(Natusch and Lyons 2012). This is accompanied by a shift in micro-habitat use, from the edge of rainforest closer to the ground to the upper and inner

rainforest canopy ([Wilson et al. 2007](#))(~~Wilson et al. 2007~~). This ontogenetic shift towards arboreality is the opposite to what is commonly observed on other python species which get increasingly terrestrial with size and age ([Stafford 1986; Luiselli et al. 2007](#))(~~Stafford 1986; Luiselli et al. 2007~~). Since head shape is predicted by micro-habitat, it is expected under the hypothesis that allometry is a trait under natural selection that the head shape ontogenetic trajectories of *M. viridis* and the rest of the pythons also go in opposite directions. As additional evidence, the enigmatic *M. carinata* has been described as ecologically intermediate between *M. viridis* and *M. spilota/M. bredli* ([Porter et al. 2012](#))(~~Porter et al. 2012~~) and it also has an intermediate ontogenetic trajectory between the two.

Phenotypic adaptations to terrestrial and semi-arboreal ecological niches have evolved independently more than once in pythons, but the remaining ecologies have a single origin. To fully appreciate the role of ecological factors on the evolution of ontogeny, a comparative study with the boas, a group that has convergently evolved the same ecomorphological diversity observed in pythons ([Esquerré and Keogh 2016](#))(~~Esquerré and Keogh 2016~~), would shed further light on this topic.

Data on the ontogeny of ecology in pythons is still anecdotal and incomplete for many species. It is understood that many pythons, and snakes in general, display a dietary shift from ectothermic to endothermic prey as they grow ([Slip and Shine 1988; Greer 1997; Shine et al. 1998; Luiselli and Angelici 1998; Natusch and Lyons 2012](#))(~~Slip and Shine 1988; Greer 1997; Shine et al. 1998; Luiselli and Angelici 1998; Natusch and Lyons 2012~~), but detailed studies on habitat use and other ecological factors are necessary. Several findings of this study need this information to establish the mechanisms behind shifts in ontogenetic trajectories. For example, the strong ontogenetic convergence in *Python* head shape and *Morelia* body shape, where juvenile phenotypes are disparate but adults are extremely similar, needs to be understood in the light of the way their natural history changes with growth, like ontogenetic convergence driven by adaptation in European plethodontid salamanders ([Adams and Nistri 2010](#))(~~Adams and Nistri 2010~~). Nevertheless, our study adds to a growing body of evidence. Artificial selection on insect allometry

has shown that the direction of change with growth can be shifted by evolution ([e.g. Weber 1990; Wilkinson 1993; Emlen 1996; Frankino et al. 2005](#))(~~e.g. Weber 1990; Wilkinson 1993; Emlen 1996; Frankino et al. 2005~~) and adaptive shifts in the allometries of organisms to match their ecomorphological needs ([Adams and Nistri 2010](#))(~~Adams and Nistri 2010~~) demonstrate the possible adaptive properties of allometry.

Pythons are not only immensely diverse in their shapes and ecologies, but as we have demonstrated here, also in the way they transform their phenotypes through their lives. Different clades of pythons that display different ecological attributes also have different ontogenetic allometric trajectories. Some of them display strong ontogenetic convergence for example, others have very similar trajectories and many evolve their differences by extending or truncating their trajectories evolving forms that are paedomorphic or peramorphic. As we compare between clades, the slopes of the trajectories change, suggesting it is more challenging for biological forms to shift the direction of their change rather than the starting and finishing points or the rate of change. This enabled pythons to evolve more novel forms as they also shifted in their ecologies, requiring phenotypes better adapted to their needs. Maybe the remarkably diverse array of developmental pathways of pythons is not particularly unique. This calls for studies on broader taxonomic groups on the evolution of ontogenetic allometry and post-natal development. It may be that allometry is generally more evolvable, and that the constraints it imposes are often adaptations ~~in reality~~. This would underscore the notion that allometry is often only a static constraint that funnels phenotypic variation in a certain direction, and highlight its role in increasing phenotypic diversity in living organisms. This study provides strong evidence of ontogenetic allometry as a highly evolvable trait and calls to evolutionary biologists, to rethink 'allometry as a universal constraint on biological traits' and instead as a trait by itself ([Klingenberg 2010](#))(~~Klingenberg 2010~~).

References

[Adams, D. C. 2014. A method for assessing phylogenetic least squares models for shape and other high-dimensional multivariate data. *Evolution* 68:2675–2688.](#)

588 [Adams, D. C., and A. Nistri. 2010. Ontogenetic convergence and evolution of foot morphology in European](#)
589 [cave salamanders \(Family: Plethodontidae\). BMC Evol. Biol. 10:216.](#)

590 [Adams, D. C., and M. L. Collyer. 2009. A general framework for the analysis of phenotypic trajectories in](#)
591 [evolutionary studies. Evolution 63:1143–1154.](#)

592 [Adams, D. C., F. J. Rohlf, and D. E. Slice. 2013. A field comes of age: geometric morphometrics in the 21st](#)
593 [century. Hystrix 24:7–14.](#)

594 [Adams, D. C., M. L. Collyer, A. Kaliontzopoulou, and E. Sherratt. 2016. Geomorph \(Version 3.0.2.\):](#)
595 [Geometric Morphometric Analyses of 2D/3D Landmark Data.](#)

596 [Alberch, P., S. J. Gould, G. F. Oster, and D. B. Wake. 1979. Size and shape in ontogeny and phylogeny.](#)
597 [Paleobiology 5:269–317.](#)

598 [Anderson, M. J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecol.](#)
599 [26:32–46.](#)

600 [Andrews, R. M. 1982. Patterns of growth in reptiles. Pp. 273–320 in C. Gans and F. H. Pough, eds. Biology](#)
601 [of the Reptilia Volume 13, Physiology D: Physiological Ecology.](#)

602 [Barker, D. G., T. M. Barker, M. A. Davis, and G. W. Schuett. 2015. A review of the systematics and](#)
603 [taxonomy of Pythonidae: an ancient serpent lineage. Zool. J. Linnean Soc. 175:1–19.](#)

604 [Benjamini, Y., and Y. Hochberg. 1995. Controlling the false discovery rate: a practical and powerful](#)
605 [approach to multiple testing. J R Stat Soc Series B Stat Methodol 57:289–300. J Royal Statistical Society.](#)

606 [Bhullar, B.-A. S., J. Marugán-Lobón, F. Racimo, G. S. Bever, T. B. Rowe, M. A. Norell, and A. Abzhanov.](#)
607 [2012. Birds have paedomorphic dinosaur skulls. Nature 487:223–226.](#)

608 [Bookstein, F. L. 1991. Morphometric tools for landmark data: geometry and biology. Cambridge University](#)
609 [Press, New York.](#)

610 [Claude, J. 2013. Log-shape ratios, Procrustes superimposition, elliptic Fourier analysis: three worked](#)
611 [examples in R. Hystrix 24:94–102.](#)

612 [Claude, J. 2008. Morphometrics with R. Springer, New York, USA.](#)

613 [Collyer, M. L., and D. C. Adams. 2013. Phenotypic trajectory analysis: comparison of shape change patterns](#)
614 [in evolution and ecology. Hystrix 24:75–83.](#)

615 [Emlen, D. J. 1996. Artificial selection on horn length-body size allometry in the horned beetle *Onthophagus*](#)
616 [*acuminatus* \(Coleoptera: Scarabaeidae\). Evolution 50:1219–1230.](#)

617 [Esquerré, D., and J. S. Keogh. 2016. Parallel selective pressures drive convergent diversification of](#)
618 [phenotypes in pythons and boas. Ecol. Lett. 19:800–809.](#)

619 [Foth, C., B. P. Hedrick, and M. D. Ezcurra. 2016. Cranial ontogenetic variation in early saurischians and the](#)
620 [role of heterochrony in the diversification of predatory dinosaurs. PeerJ 4:e1589.](#)

621 [Frankino, W. A., B. J. Zwaan, D. L. Stern, and P. M. Brakefield. 2005. Natural selection and developmental](#)
622 [constraints in the evolution of allometries. Science 307:718–720.](#)

623 [Frédérich, B., and P. Vandewalle. 2011. Bipartite life cycle of coral reef fishes promotes increasing shape](#)

- disparity of the head skeleton during ontogeny: an example from damselfishes (Pomacentridae). *BMC Evol. Biol.* 11:1–21.
- Gerber, S., and M. J. Hopkins. 2011. Mosaic heterochrony and evolutionary modularity: the trilobite genus *Zacanthopsis* as a case study. *Evolution* 65:3241–3252.
- Gerber, S., G. J. Eble, and P. Neige. 2008. Allometric space and allometric disparity: a developmental perspective in the macroevolutionary analysis of morphological disparity. *Evolution* 62:1450–1457.
- Giannini, N. P. 2014. Quantitative developmental data in a phylogenetic framework. *J. Exp. Zool. B Mol. Dev. Evol.* 322:558–566.
- Gignac, A., and P. T. Gregory. 2005. The effects of body size, age, and food intake during pregnancy on reproductive traits of a viviparous snake, *Thamnophis ordinoides*. *Écoscience* 12:236–243.
- Godfrey, L. R., and M. R. Sutherland. 1995. Flawed inference: why size-based tests of heterochronic processes do not work. *J. Theor. Biol.* 172:43–61.
- Goodall, C. 1991. Procrustes Methods in the Statistical Analysis of Shape. *J R Stat Soc Series B Stat Methodol* 53:285–339.
- Gould, S. J. 1966. Allometry and size in ontogeny and phylogeny. *Biol Rev Camb Philos Soc* 41:587–640.
- Gould, S. J. 1977. *Ontogeny and phylogeny*. Harvard University Press, Cambridge, MA, USA.
- Gould, S. J., and R. C. Lewontin. 1979. The spandrels of San Marco and the Panglossian paradigm: a critique of the adaptationist programme. *Philos Trans R Soc Lond B Biol Sci* 205:581–598.
- Greer, A. E. 1997. *The biology and evolution of Australian snakes*. Surrey Beatty & Sons Pty Limited, Chipping Norton, Australia.
- Gunz, P., and P. Mitteroecker. 2013. Semilandmarks: a method for quantifying curves and surfaces. *Hystrix* 24:103–109.
- Hipsley, C. A., and J. Müller. 2017. Developmental dynamics of ecomorphological convergence in a transcontinental lizard radiation. *Evolution* 63:685.
- Huelsenbeck, J. P., R. Nielsen, and J. P. Bollback. 2003. Stochastic mapping of morphological characters. *Syst. Biol.* 52:131–158.
- Huxley, J. S. 1932. *Problems of relative growth*. L. MacVeagh, New York.
- Huxley, J. S., and G. Teissier. 1936. Terminology of relative growth. *Nature* 137:780–781.
- Klingenberg, C. 2010. There's something afoot in the evolution of ontogenies. *BMC Evol. Biol.* 10:221.
- Klingenberg, C. P. 1998. Heterochrony and allometry: the analysis of evolutionary change in ontogeny. *Biol. Rev.* 73:79–123.
- Klingenberg, C. P. 2016. Size, shape, and form: concepts of allometry in geometric morphometrics. *Dev. Genes Evol.* 226:1–25.
- Klingenberg, C. P., and J. R. Spence. 1993. Heterochrony and allometry: lessons from the water strider genus *Limnoporus*. *Evolution* 47:1834–1853.

659 [Klingenberg, C. P., and R. Froese. 1991. A multivariate comparison of allometric growth patterns. Syst.](#)
660 [Biol. 40:410–419.](#)

661 [Klingenberg, C. P., M. Barluenga, and A. Meyer. 2002. Shape analysis of symmetric structures: quantifying](#)
662 [variation among individuals and asymmetry. Evolution 56:1909–1920.](#)

663 [Luiselli, L., and F. M. Angelici. 1998. Sexual size dimorphism and natural history traits are correlated with](#)
664 [intersexual dietary divergence in royal pythons \(*Python regius*\) from the rainforests of southeastern Nigeria.](#)
665 [Ital. J. Zool. 65:183–185.](#)

666 [Luiselli, L., G. C. Akani, E. A. Eniang, and E. Politano. 2007. Comparative ecology and ecological](#)
667 [modeling of sympatric pythons, *Python regius* and *Python sebae*. Pp. 89–100 in R. W. Henderson and R.](#)
668 [Powell, eds. Biology of the boas and pythons. Eagle Mountain Publishing, Eagle Mountain, Utah, USA.](#)

669 [Mallon, J. C., M. J. Ryan, and J. A. Campbell. 2015. Skull ontogeny in *Arrhinoceratops brachyops*](#)
670 [\(Ornithischia: Ceratopsidae\) and other horned dinosaurs. Zool. J. Linnean Soc. 175:910–929.](#)

671 [Maynard Smith, J., R. Burian, S. Kauffman, P. Alberch, J. Campbell, B. Goodwin, R. Lande, D. Raup, and](#)
672 [L. Wolpert. 1985. Developmental Constraints and Evolution: A Perspective from the Mountain Lake](#)
673 [Conference on Development and Evolution. Q. Rev. Biol. 60:265–287.](#)

674 [Mitteroecker, P., P. Gunz, and F. L. Bookstein. 2005. Heterochrony and geometric morphometrics: a](#)
675 [comparison of cranial growth in *Pan paniscus* versus *Pan troglodytes*. Evol. Dev. 7:244–258.](#)

676 [Mosimann, J. E. 1970. Size allometry: size and shape variables with characterizations of the lognormal and](#)
677 [generalized gamma distributions. J. Am. Stat. Assoc. 65:930–945.](#)

678 [Mosimann, J. E., and F. C. James. 1979. New statistical methods for allometry with application to Florida](#)
679 [red-winged blackbirds. Evolution 33:444–459.](#)

680 [Murphy, J. C., and R. W. Henderson. 1997. Tales of giant snakes. Krieger Publishing Company, Malabar,](#)
681 [FL, USA.](#)

682 [Natusch, D. J. D., and J. A. Lyons. 2012. Relationships between ontogenetic changes in prey selection, head](#)
683 [shape, sexual maturity, and colour in an Australasian python \(*Morelia viridis*\). Biol. J. Linnean Soc.](#)
684 [107:269–276.](#)

685 [Pélabon, C., C. Firmat, G. H. Bolstad, K. L. Voje, D. Houle, J. Cassara, A. L. Rouzic, and T. F. Hansen.](#)
686 [2014. Evolution of morphological allometry. Ann. N. Y. Acad. Sci. 1320:58–75.](#)

687 [Piras, P., D. Salvi, G. Ferrara, L. Maiorino, M. Delfino, L. Pedde, and T. Kotsakis. 2011. The role of post-](#)
688 [natal ontogeny in the evolution of phenotypic diversity in Podarcis lizards. J. Evol. Biol. 24:2705–2720.](#)

689 [Porter, R., J. Weigel, and R. Shine. 2012. Natural history of the rough-scaled python, *Morelia carinata*](#)
690 [\(Serpentes: Pythonidae\). Aust. Zool. 36:137–142.](#)

691 [Porto, A., L. T. Shirai, F. B. de Oliveira, and G. Marroig. 2013. Size variation, growth strategies, and the](#)
692 [evolution of modularity in the mammalian skull. Evolution 67:3305–3322.](#)

693 [Reilly, S. M., E. O. Wiley, and D. J. Meinhardt. 1997. An integrative approach to heterochrony: the](#)
694 [distinction between interspecific and intraspecific phenomena. Biol. J. Linnean Soc. 60:119–143.](#)

695 [Revell, L. J. 2014. Graphical methods for visualizing comparative data on phylogenies. Pp. 77–103 in L. Z.](#)
696 [Garamszegi, ed. Modern phylogenetic comparative methods and their application in evolutionary biology.](#)

- [Springer Berlin Heidelberg, Berlin, Heidelberg.](#)
- [Revell, L. J. 2012. phytools: an R package for phylogenetic comparative biology \(and other things\). *Methods Ecol. Evol.* 3:217–223.](#)
- [Reynolds, G. R., M. L. Niemiller, and L. J. Revell. 2014. Toward a tree-of-life for the boas and pythons: Multilocus species-level phylogeny with unprecedented taxon sampling. *Mol Phylogenet Evol* 71:201–213.](#)
- [Rohlf, F. J. 2015. The tps series of software. *Hystrix* 26:1–4.](#)
- [Rohlf, F. J., and D. Slice. 1990. Extensions of the Procrustes method for the optimal superimposition of landmarks. *Syst. Biol.* 39:40–59.](#)
- [Sanger, T. J., L. J. Revell, J. J. Gibson-Brown, and J. B. Losos. 2012. Repeated modification of early limb morphogenesis programmes underlies the convergence of relative limb length in *Anolis* lizards. *Proc. R. Soc. B* 279:739–748.](#)
- [Sheets, H. D., and M. L. Zelditch. 2013. Studying ontogenetic trajectories using resampling methods and landmark data. *Hystrix* 24:67–73.](#)
- [Shine, R., P. S. Harlow, J. S. Keogh, and Boeadi. 1998. The influence of sex and body size on food habits of a giant tropical snake, *Python reticulatus*. *Funct. Ecol.* 12:248–258.](#)
- [Sidlauskas, B. 2008. Continuous and arrested morphological diversification in sister clades of characiform fishes: a phylomorphospace approach. *Evolution* 62:3135–3156.](#)
- [Simpson, G. G. 1944. Tempo and mode in evolution. Columbia Univ. Press, New York.](#)
- [Slip, D. J., and R. Shine. 1988. Feeding habits of the Diamond Python, *Morelia s. spilota*: ambush predation by a boid snake. *J. Herpetol.* 22:323–330.](#)
- [Stafford, P. J. 1986. Pythons and boas. T.F.H. Publications, Neptune City, NJ, U.S.A.](#)
- [Urošević, A., K. Ljubišavljević, and A. Ivanović. 2013. Patterns of cranial ontogeny in lacertid lizards: morphological and allometric disparity. *J. Evol. Biol.* 26:399–415.](#)
- [Voje, K. L., T. F. Hansen, C. K. Egset, G. H. Bolstad, and C. Pélabon. 2013. Allometric constraints and the evolution of allometry. *Evolution* 68:866–885.](#)
- [Weber, K. E. 1990. Selection on wing allometry in *Drosophila melanogaster*. *Genetics* 126:975–989.](#)
- [Webster, M., and M. L. Zelditch. 2005. Evolutionary modifications of ontogeny: heterochrony and beyond. *Paleobiology* 31:354–372.](#)
- [Weston, E. M. 2003. Evolution of ontogeny in the hippopotamus skull: using allometry to dissect developmental change. *Biol. J. Linnean Soc.* 80:625–638.](#)
- [Wilkinson, G. S. 1993. Artificial sexual selection alters allometry in the stalk-eyed fly *Cyrtodiopsis dalmanni* \(Diptera: Diopsidae\). *Genet. Res.* 62:213–222.](#)
- [Wilson, D., R. Heinsohn, and J. A. Endler. 2007. The adaptive significance of ontogenetic colour change in a tropical python. *Biol. Lett.* 3:40–43.](#)
- [Wilson, L. A. B., and M. R. Sanchez-Villagra. 2010. Diversity trends and their ontogenetic basis: an](#)

[exploration of allometric disparity in rodents. Proc. R. Soc. B 277:1227–1234.](#)

[Wilson, L. A. B., and M. R. Sánchez-Villagra. 2011. Evolution and Phylogenetic Signal of Growth Trajectories: The Case of Chelid Turtles. J. Exp. Zool. B Mol. Dev. Evol. 316B:50–60.](#)

[Zelditch, M. L., D. L. Swiderski, and H. D. Sheets. 2012. Geometric morphometrics for biologists: a primer. Second Edition. Academic Press, London, UK.](#)

[Zelditch, M. L., H. D. Sheets, and W. L. Fink. 2003. The ontogenetic dynamics of shape disparity. Paleobiology 29:139–156.](#)

Table 1. Test for ontogenetic convergence/divergence in head and body shapes in all pythons (Pythonidae) and each clade that displays allometric slope differences, separately. A positive D statistic means that juveniles are more variable than adults (convergence) and a negative D statistic means that adults are more variable than juveniles (divergence). *P*-values are drawn from the number of times out of 10,000 ~~9,999~~ permutations that the observed D is higher (P_{con} , for convergence) and lower (P_{div} , for divergence) than the randomized D.

Clade	Head shape			Body shape			Conclusions
	D	P_{con}	P_{div}	D	P_{con}	P_{div}	
Pythonidae	-1,489	0.0001	1	3,594	0.14	0.86	Overall no convergence or divergence
<i>Python</i>	55.66	0.0005	1	-	-	-	Convergence in head shape
<i>Morelia</i>	15.39	0.99	0.008	184.83	0.024	0.98	Convergence on body shape
<i>Simalia</i>	-	-	-	-321.6	0.86	0.14	No convergence or divergence in body shape
<i>Liasis</i>	-	-	-	36.78	0.014	0.99	Divergence on head shape

Figure 1. Schematic of the workflow to identify the different processes and patterns of ontogenetic allometric and heterochronic changes. See Materials and Methods for details on each step and the analyses. Below, a phenotype vs. body size illustration of a hypothetical example of patterns our study seeks to uncover. Having the gray triangles as a reference trajectory, the green ones illustrate ontogenetic divergence; the red ones ontogenetic convergence; the blue ones parallel ontogenetic trajectories or shifts in the intercept; the ochre ones heterochrony, with the ochre triangles being peramorphic or the gray triangles being paedomorphic, in respect to the each other.

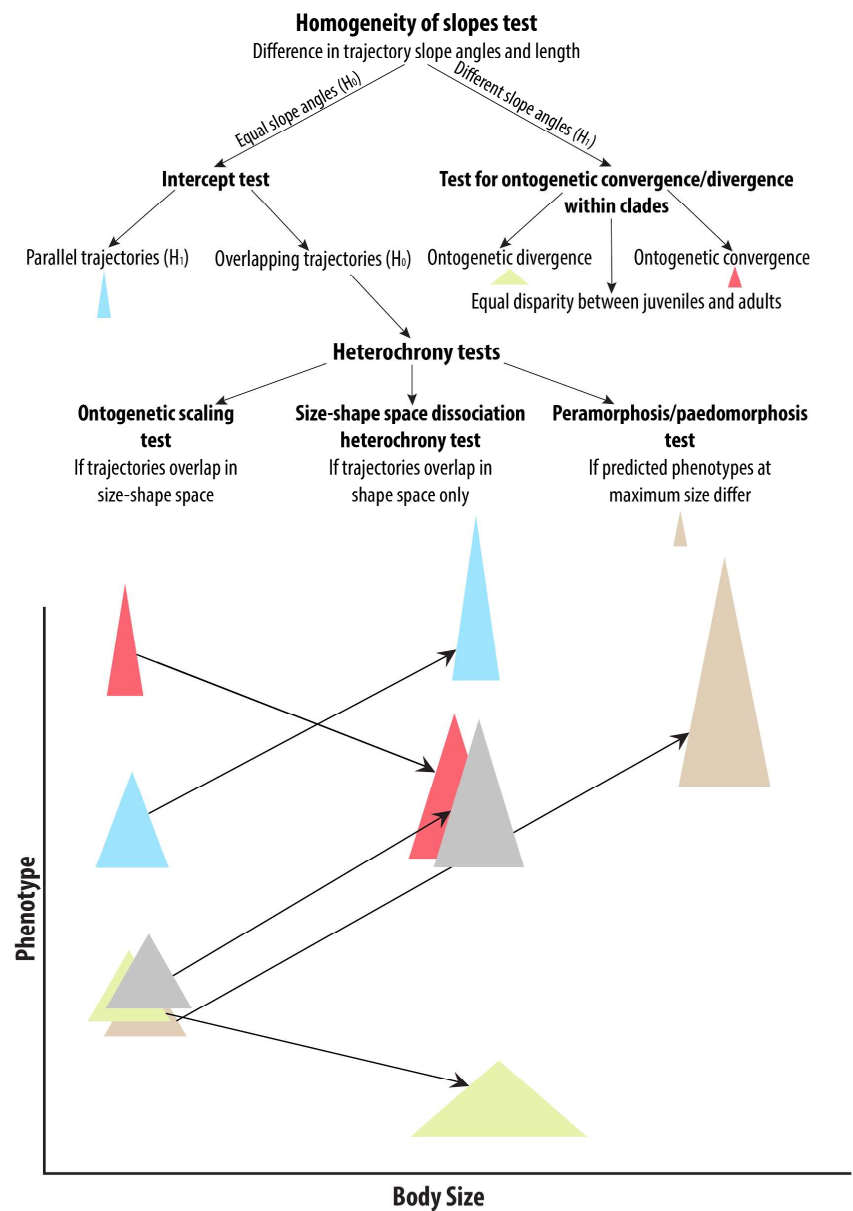


Figure 2. Ontogenetic allometric trajectories derived from the HOS test of head (above) and body (below) shape. The x-axis represents log-transformed centroid size for head and log geometric mean for body. The y-axis on both plots is the first principal component of the predicted values of the multivariate regression of shape on size. Each line of dots represents the predicted allometric trajectory for each species, as per the colored legend between the two plots. The size of the dots for each specimen is proportional to its size. On the head shape plot, thin plate spline deformation grids show the shape change from the mean shape of the dataset to the highest (above) and the lowest (below) specimen on the y-axis. Similarly, on the body shape plot illustrations based on the specimens that are highest and lowest on the y-axis represent the shape difference along the y-axis.

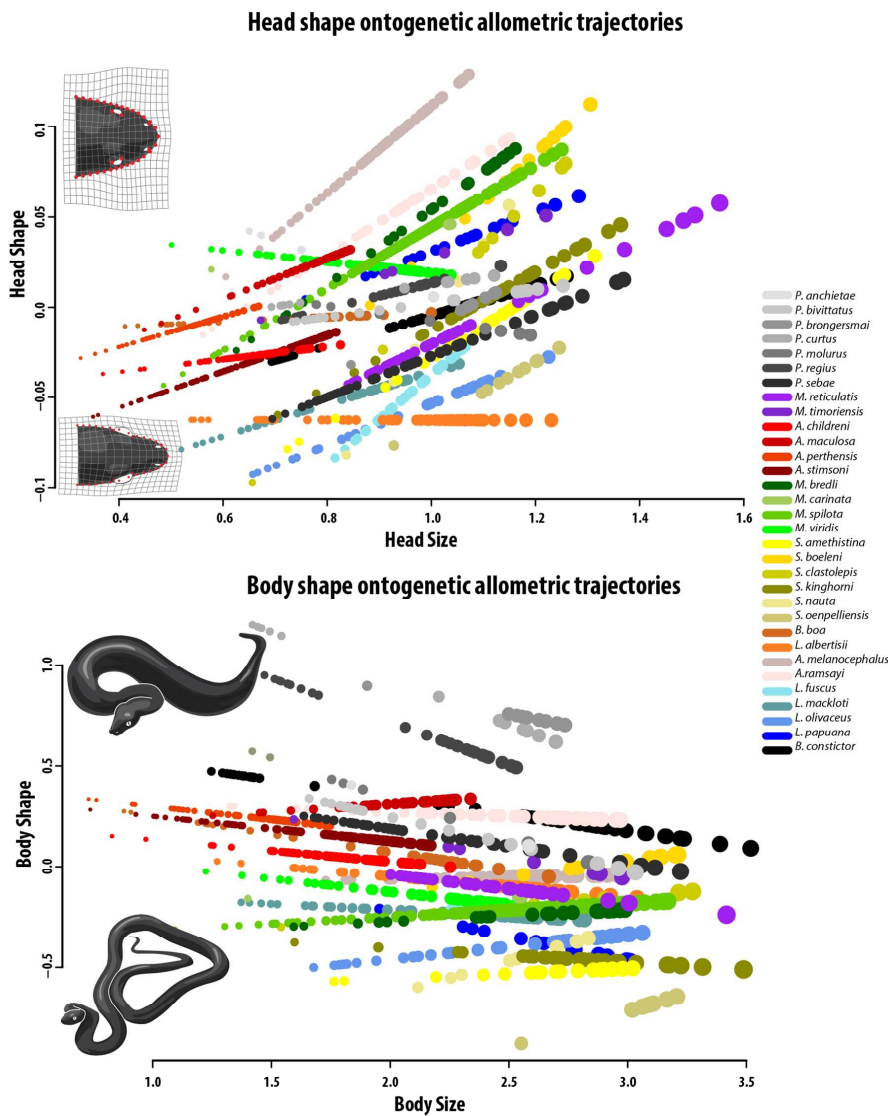


Figure 3. Ontogenetic allometric trajectories derived from the PTA, of head (above) and body (below) shape. The specimens are plotted on a morphospace represented by principal components (PC) 1 and 2 on the x- and y-axes respectively. White dots represent the average shape of juveniles and the black dots the average shape of adults. The lines between them are what we define as trajectories. The color of each line represents the species according to the legend. The gray dots in the background represent the total variation within the sample. The size of the dots for each specimen is proportional to its size. Thin plate spline deformation grids and body shape plot illustrations show the extremes of variation represented by each PC axis.

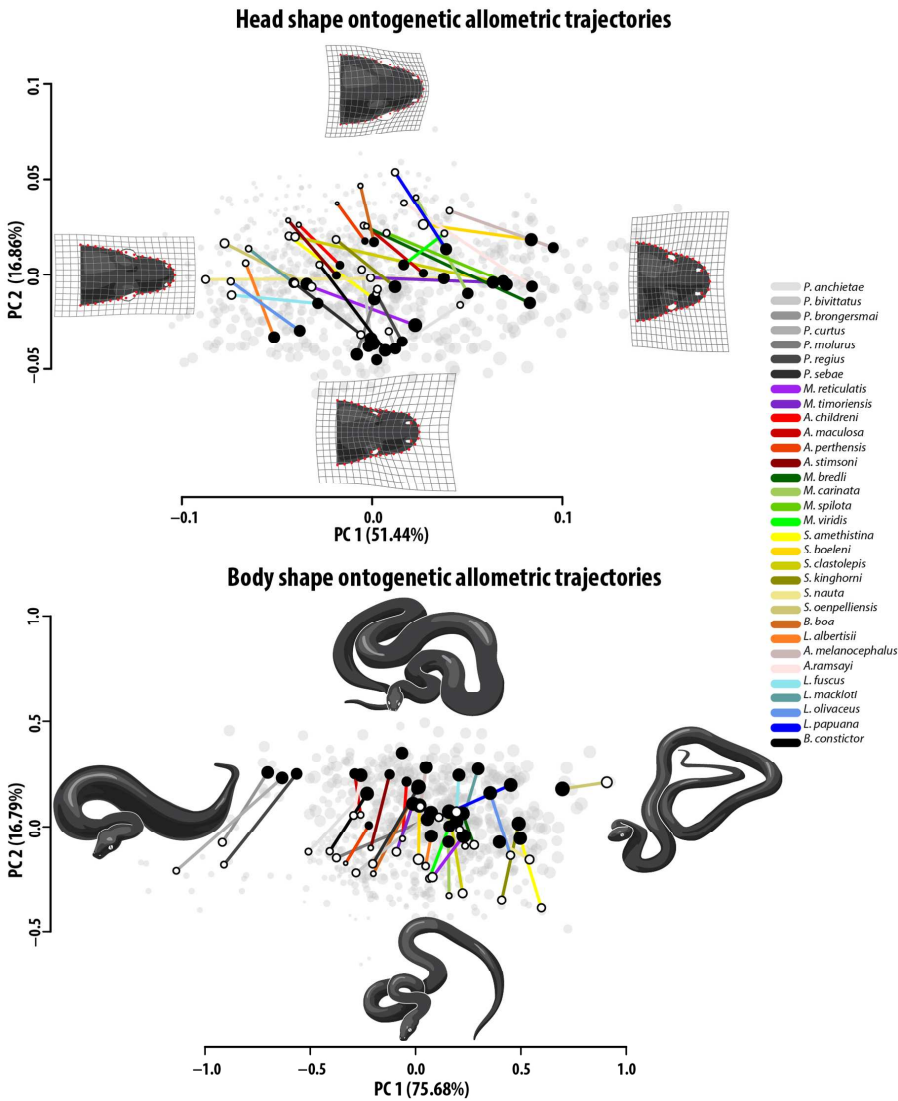
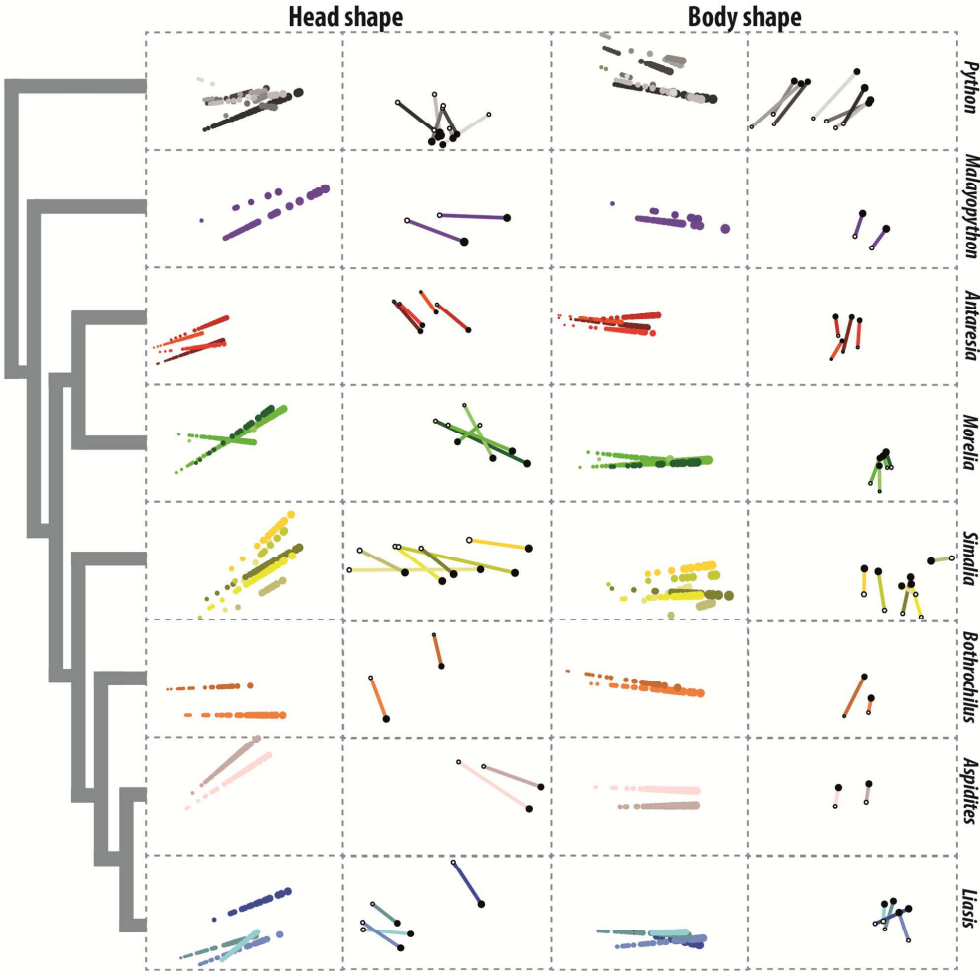
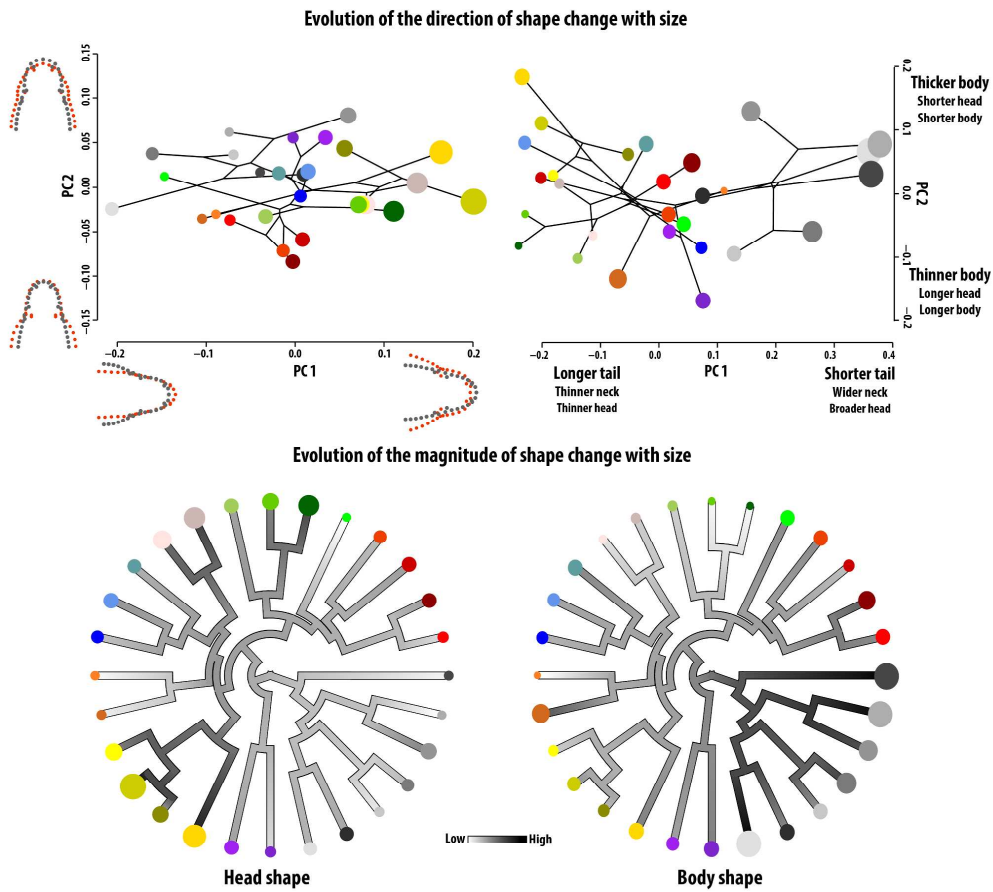


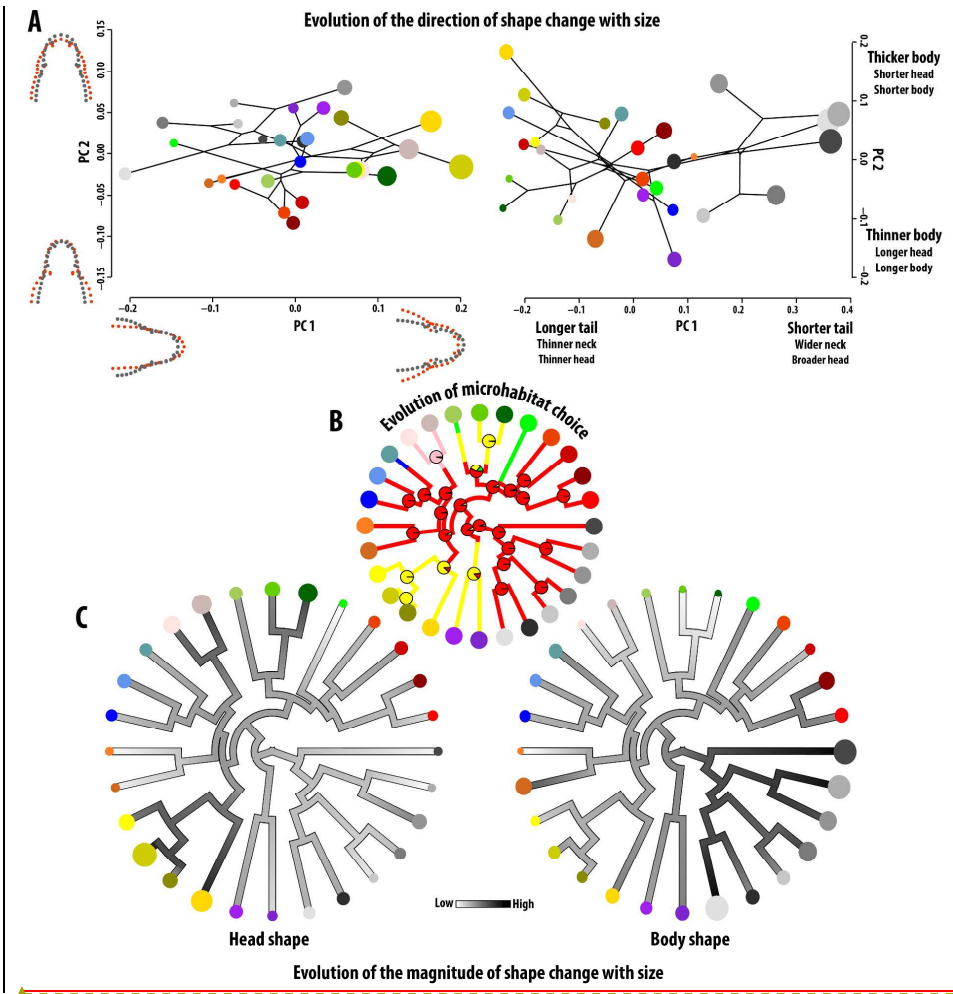
Figure 4. Ontogenetic allometric trajectories derived from the HOS (first and third columns) and PTA (second and fourth columns) tests, of head and body shape of the pythons, separated by clade. The rows of figures at each tip of the tree based on our phylogenetic analysis represent the trajectories of the python species within the clade that is labelled on the right edge of the figure. These are the same trajectories illustrated in Figures 2 and 3 therefore for details on the meaning of the axes and how to interpret them see the respective legends.



797 **Figure 5.** Above: Phylomorphospace and ancestral state reconstruction of the slopes of allometric shape
798 change in each python species, left side shows head shape and right side shows body shape. The phylogeny
799 and reconstructed ancestors, as the position of the nodes, ancestral nodes are plotted on a PC1 vs PC2 plot.
800 Besides the PC axes for head shape are On the left side one illustrations at each end of the axes illustrate the
801 direction of head shape change the slopes closer to that extreme represent, going from the gray to red
802 shapes describing the shape changes from the mean configuration (gray) to the extremes (red) of each axis.
803 Besides the PC axes for body shape are summaries of the On the right side one the texts at each end of the
804 axes inform on the body shape changes that occur occurrences with size from the mean shape to the extremes
805 of each axis, on the slopes closer to that end, with the amount of change approximately proportional to the
806 size of the text. B: Stochastic character mapping of the evolution of ecology in pythons. The base tree is a
807 random of 10,000 replicates and the pie-charts represent the percentage of time each state is reconstructed at
808 that node. Tips are colored according to species and clade as in Figures 2 & 3. Branch and node colors
809 (except for tips which are colored according to species and clade as in the other plots) correspond to green:
810 arboreal, yellow: semi-arboreal, red: terrestrial, blue: semi-aquatic and pink: semi-fossorial. Below C:
811 Ancestral state reconstruction of the slope vector length (or magnitude of shape change with size), with
812 black representing high phenotypic change and white representing low phenotypic change. As above, left
813 side one is for head shape on left and right side one for body shape on right. On both set of plots the dots
814 are colored according to the species as in Fig. 2 and they are sized proportionally to the magnitude of shape
815 change with size. Tips in all figures are colored according to species and clade as in Figures 2 & 3 and on A
816 and C they are sized proportionally to the magnitude of shape change with size.



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SUPPORTING INFORMATION

Phylogenetic hypothesis

Using PartitionFinder v.1.1.1 ([Lanfear et al. 2012](#))(~~Lanfear et al. 2012~~), we found the best partitioning scheme is between mitochondrial and nuclear loci, and that best substitution model for both partitions is GTR+I+G. However, we decided to use GTR+G instead, since the gamma distribution (G) with an alpha parameter can already allow for a proportion of sites with very low rates of evolution, and several problems have been know with using a proportion of invariant sites parameter (I) ([Yang 2006](#))(~~Yang 2006~~). To estimate the phylogenetic tree and divergence times we used a Bayesian inference with node calibration on BEAST v.2.4.2 ([Bouckaert et al. 2014](#))(~~Bouckaert et al. 2014~~). We used a relaxed lognormal molecular clock for the rate variation in each partition and Yule model of speciation for the branching of the tree. See Table S2 for node calibrations, based on Head (2015). We ran two independent Markov chain Monte Carlo chains for 200 million generations. Details on how we set the parameters can be obtained from the xml file that can be found on the dryad repository. We assessed proper mixing and convergence of the chains using the program Tracer v.1.6.0 ([Rambaut et al. 2014](#))(~~Rambaut et al. 2014~~) and checked that the effective sample sizes were >200 for every parameter. We also ensured that both runs converged on tree topologies using the R package *rwty* ([Warren et al. 2017](#))(~~Warren et al. 2017~~). We combined the results of both runs on LogCombiner v.2.4.2 and summarized a maximum clade credibility tree keeping the median heights on TreeAnnotator v.2.4.2. Finally, we pruned the tree to include only the taxa present on this study with the R package *ape* ([Paradis et al. 2004](#))(~~Paradis et al. 2004~~).

References

- Bouckaert, R., J. Heled, D. Kühnert, T. Vaughan, C.-H. Wu, D. Xie, M. A. Suchard, A. Rambaut, and A. J. Drummond. 2014. BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. *PLoS Comp Biol* 10:e1003537.
- Head, J.J. 2015. Fossil calibration dates for molecular phylogenetic analysis of snakes 1: Serpentes, Alethinophidia, Boidae, Pythonidae. *Paleontol. Electronica* 18.1.6FC:1-17.
- Lanfear, R., B. Calcott, S. Y. W. Ho, and S. Guindon. 2012. Partitionfinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Mol. Biol. Evol.* 29:1695–1701.
- Paradis, E., J. Claude, and K. Strimmer. 2004. APE: analyses of phylogenetics and evolution in R language.

852 Bioinformatics 20:289–290.

853 Rambaut, A., M. A. Suchard, D. Xie, and A. J. Drummond. 2014. Tracer v1.6, Available from
854 <http://beast.bio.ed.ac.uk/Tracer>.

855 Warren, D. L., A. J. Geneva, and R. Lanfear. 2017. RWTY (R We There Yet): An R Package for Examining
856 Convergence of Bayesian Phylogenetic Analyses. *Mol. Biol. Evol.* 34:1016–1020.

857 Yang, Z. 2006. *Computational Molecular Evolution*. Oxford University Press, Oxford, UK.

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Table S1. Summary of the species used in this study, the sample size for each species, their snout-vent length (SVL) range and head size range. SVL ranges with an asterisk mean that the largest specimen(s) of that species did not have its body preserved. ~~Therefore~~Therefore, for head shape analyses the SVL range is an underrepresentation of the range sampled for that species. All specimens were measured in the following collections: the Queensland Museum, the Museum and Art Gallery of the Northern Territory, the South Australian Museum, the Western Australian Museum, the Australian Museum, the California Academy of Sciences, the University of Texas at Arlington, the American Museum of Natural History and the Museum of Comparative Zoology.

Species	Sample size	SVL range (cm)	Head size range (cm)
<i>Python anchietae</i>	4	72-180	2.15-5.11
<i>Python bivittatus</i>	24	54-274	2.88-8.67
<i>Python brongersmai</i>	10	65-163	3.08-7.06
<i>Python curtus</i>	13	36-151	2.41-6.11
<i>Python molurus</i>	9	51-214*	3.1-8.56
<i>Python regius</i>	31	36-155*	2.43-7.34
<i>Python sebae</i>	48	45-310*	2.49-12.73
<i>Malayopython reticulatus</i>	47	70-718	3.57-19.19
<i>Malayopython timoriensis</i>	7	45-292	2.4-8.41
<i>Antaresia childreni</i>	70	23-131	1.24-3.5
<i>Antaresia maculosa</i>	42	40-132	1.41-4.01
<i>Antaresia perthensis</i>	55	19-67	1.07-2.5
<i>Antaresia stimsoni</i>	88	19-135	1.1-3.37
<i>Morelia bredli</i>	25	52-242	2.17-7.12
<i>Morelia carinata</i>	3	42-156	1.8-5.54
<i>Morelia spilota</i>	153	26-294	1.5-8.62
<i>Morelia viridis</i>	53	33-180	1.53-5.54
<i>Simalia amethystina</i>	29	68-309	2.76-10.5
<i>Simalia boeleni</i>	15	112-306	3.65-9.18
<i>Simalia clastolepis</i>	9	52-344	2.29-9.47
<i>Simalia kinghorni</i>	36	65-469	2.55-12.03
<i>Simalia nauta</i>	8	111-242	3.77-7.26
<i>Simalia oenpelliensis</i>	10	210-406	4.63-9.11
<i>Bothrochilus boa</i>	33	20-185	1.31-5.25
<i>Leiopython albertisii</i>	67	35-283	1.86-9.21
<i>Aspidites melanocephalus</i>	69	68-245	2.15-6.8
<i>Aspidites ramsayi</i>	45	37-258	1.84-7.56
<i>Liasis fuscus</i>	26	116-205	3.18-6.3
<i>Liasis mackloti</i>	44	39-207	1.73-6.15
<i>Liasis olivaceus</i>	37	64-302	2.5-9.26
<i>Liasis papuana</i>	20	93-378	2.83-9.54
<i>Boa constrictor</i>	61	45-269	2.46-9.39

Table S2: Fossil calibrations used for the time-calibrated phylogeny. These calibrations are based on Head (2015). Minimum ages given as millions of years ago (MY).

Taxon	Clade	Minimum age (MY)
<i>Coniophis</i> sp.	Serpentes / (Iguania + Anguimorpha)	98.32
<i>Haasophis terrasactus</i>	(Aniliidae + Tropidophiinae) / Macrostromata	93.9
<i>Australophis anilioides</i>	Aniliidae / Tropidophiidae	72.1
<i>Titanoboa cerrejonensis</i>	Boinae / Erycinae	58
<i>Corallus priscus</i>	<i>Corallus</i> / (<i>Chilabothrus</i> +(<i>Epicrates</i> + <i>Eunectes</i>))	50.2
<i>Eunectes stirtoni</i>	<i>Epicrates</i> / <i>Eunectes</i>	12.375
<i>Calamagras weigeli</i>	Ungaliophiinae / Charininae	35.2
Unnamed taxon (UNSM 125562)	<i>Charina</i> / <i>Lichanura</i>	18.7
<i>Ogmophis compactus</i>	Loxocemidae / Pythonidae	35.2
<i>Morelia riversleighensis</i>	Malayopython / Australo-Papuan Pythonidae	12.5

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Table S3. Tests statistics and *P* values from the test for isometry allometry for each species. Isometry is the null hypothesis: here, so *P* values greater/less than 0.05 suggest/reject the null hypothesis, isometry.

Species	Head shape							Body shape						
	Df	SS	MS	Rsq	F	Z	P	Df	SS	MS	Rsq	F	Z	P
<i>Python anchietae</i>	2	0.002	0.002	0.388	1.268	1.102	0.3092	2	0.387	0.387	0.865	12.856	2.087	0.0644
<i>Python bivittatus</i>	22	0.012	0.012	0.243	7.053	4.551	<0.0001	20	0.712	0.712	0.542	23.631	8.385	<0.0001
<i>Python brongersmai</i>	8	0.002	0.002	0.108	0.966	0.771	0.3709	7	0.131	0.131	0.248	2.312	1.548	0.1874
<i>Python curtus</i>	11	0.005	0.005	0.208	2.893	2.071	0.0369	11	1.621	1.621	0.814	47.982	6.413	<0.0001
<i>Python molurus</i>	7	0.006	0.006	0.399	4.640	2.778	0.0003	5	0.393	0.393	0.600	7.511	2.808	0.0024
<i>Python regius</i>	29	0.007	0.007	0.118	3.868	2.908	0.0081	27	1.801	1.801	0.616	43.233	12.507	<0.0001
<i>Python sebae</i>	46	0.055	0.055	0.356	25.377	12.701	<0.0001	36	1.163	1.163	0.422	26.255	12.266	<0.0001
<i>Malavopython reticulatus</i>	45	0.051	0.051	0.362	25.566	12.736	<0.0001	38	0.500	0.500	0.195	9.210	6.063	<0.0001
<i>Malavopython timoriensis</i>	5	0.004	0.004	0.248	1.649	1.254	0.1993	5	0.244	0.244	0.536	5.785	2.509	0.0195
<i>Antaresia childreni</i>	68	0.010	0.010	0.088	6.550	5.075	0.0002	65	0.640	0.640	0.221	18.407	11.588	<0.0001
<i>Antaresia maculosa</i>	40	0.013	0.013	0.133	6.144	4.358	0.0015	40	0.286	0.286	0.107	4.795	3.521	0.0025
<i>Antaresia perthensis</i>	53	0.010	0.010	0.099	5.834	4.492	0.0003	53	0.481	0.481	0.223	15.240	9.653	<0.0001
<i>Antaresia stimsoni</i>	86	0.039	0.039	0.220	24.188	15.192	<0.0001	82	2.366	2.366	0.455	68.495	27.127	<0.0001
<i>Morelia bredli</i>	23	0.047	0.047	0.522	25.130	8.888	<0.0001	22	0.190	0.190	0.224	6.334	4.099	0.0020
<i>Morelia carinata</i>	1	0.005	0.005	0.692	2.252	1.298	0.2460	1	0.065	0.065	0.851	5.724	1.532	0.0813
<i>Morelia spilota</i>	151	0.148	0.148	0.304	65.816	32.371	<0.0001	149	0.998	0.998	0.105	17.502	12.469	<0.0001
<i>Morelia viridis</i>	51	0.011	0.011	0.078	4.303	3.124	0.0101	50	0.955	0.955	0.275	18.924	11.456	<0.0001
<i>Simalia amethystina</i>	27	0.027	0.027	0.320	12.732	7.005	<0.0001	16	0.182	0.182	0.162	3.089	2.150	0.0408
<i>Simalia boeleni</i>	13	0.015	0.015	0.306	5.741	3.234	0.0091	12	0.214	0.214	0.171	2.472	1.915	0.0430
<i>Simalia clastolepis</i>	7	0.030	0.030	0.724	18.353	4.207	<0.0001	6	0.299	0.299	0.568	7.891	3.175	0.0005
<i>Simalia kinghorni</i>	34	0.031	0.031	0.325	16.360	8.827	<0.0001	27	0.447	0.447	0.221	7.670	4.835	0.0004
<i>Simalia nauta</i>	6	0.017	0.017	0.612	9.456	2.956	0.0125	6	0.114	0.114	0.310	2.702	1.825	0.0646
<i>Simalia oenpelliensis</i>	8	0.003	0.003	0.185	1.818	1.468	0.1211	7	0.087	0.087	0.249	2.318	1.669	0.0778
<i>Aspidites melanocephalus</i>	67	0.049	0.049	0.259	23.478	13.012	<0.0001	66	0.390	0.390	0.117	8.759	6.268	<0.0001
<i>Aspidites ramsayi</i>	43	0.052	0.052	0.332	21.358	11.265	<0.0001	42	0.396	0.396	0.147	7.243	5.036	<0.0001
<i>Bothrochilus boa</i>	31	0.014	0.014	0.195	7.524	5.044	0.0002	31	1.851	1.851	0.585	43.610	13.648	<0.0001
<i>Leiopython albertisii</i>	65	0.031	0.031	0.214	17.690	11.131	<0.0001	52	0.330	0.330	0.100	5.760	4.100	0.0016
<i>Liasis fuscus</i>	24	0.012	0.012	0.232	7.264	4.515	0.0008	22	0.127	0.127	0.076	1.798	1.543	0.0905
<i>Liasis mackloti</i>	42	0.025	0.025	0.283	16.543	9.878	<0.0001	41	1.269	1.269	0.423	30.030	13.624	<0.0001
<i>Liasis olivaceus</i>	35	0.032	0.032	0.362	19.854	10.364	<0.0001	33	0.806	0.806	0.408	22.704	10.630	<0.0001
<i>Liasis papuana</i>	18	0.008	0.008	0.223	5.155	3.595	0.0008	12	0.135	0.135	0.266	4.345	2.999	0.0016
<i>Boa constrictor</i>	59	0.041	0.041	0.240	18.665	10.982	<0.0001	54	1.540	1.540	0.300	23.196	12.506	<0.0001

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Table S3S4. Head shape slope angle differences. Pairwise comparisons of the angle between the slopes (direction of allometry) for head shape data in degrees (bottom triangle), and *P*-values of the difference between them computed with 10,000 9,999 iterations (upper triangle). Significant values indicating different slope angles are highlighted in green. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python malurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clostolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.11	0.04	0.10	0.43	0.08	0.03	0.01	0.03	0.18	0.05	0.06	0.06	0.02	0.27	0.01	0.27	0.02	0.00	0.01	0.02	0.00	0.02	0.21	0.30	0.00	0.02	0.01	0.06	0.05	0.04	0.06
<i>Python bivittatus</i>	72.11	-	0.25	0.09	0.14	0.11	0.01	0.01	0.12	0.06	0.03	0.01	0.00	0.01	0.15	0.00	0.00	0.01	0.10	0.02	0.02	0.10	0.37	0.01	0.00	0.00	0.02	0.28	0.02	0.02	0.15	0.01
<i>Python brongersmai</i>	108.28	62.47	-	0.34	0.06	0.34	0.59	0.82	0.82	0.17	0.37	0.30	0.24	0.67	0.45	0.62	0.00	0.59	0.82	0.81	0.78	0.76	0.61	0.17	0.10	0.68	0.49	0.85	0.49	0.70	0.59	0.33
<i>Python curtus</i>	76.90	43.21	57.94	-	0.17	0.15	0.07	0.10	0.38	0.05	0.04	0.01	0.01	0.02	0.14	0.01	0.00	0.03	0.09	0.03	0.07	0.07	0.23	0.02	0.01	0.01	0.02	0.40	0.20	0.11	0.11	0.00
<i>Python malurus</i>	50.82	44.80	94.84	48.76	-	0.05	0.02	0.01	0.03	0.13	0.02	0.01	0.01	0.00	0.06	0.00	0.03	0.00	0.01	0.00	0.01	0.00	0.10	0.07	0.09	0.00	0.00	0.06	0.04	0.02	0.02	0.00
<i>Python regius</i>	79.82	38.99	56.92	41.89	60.06	-	0.08	0.09	0.35	0.11	0.21	0.09	0.04	0.18	0.26	0.07	0.00	0.27	0.33	0.18	0.23	0.18	0.53	0.02	0.02	0.11	0.25	0.45	0.13	0.13	0.46	0.11
<i>Python sebae</i>	90.93	44.99	39.89	41.26	67.49	36.43	-	0.17	0.41	0.04	0.27	0.11	0.01	0.08	0.16	0.02	0.00	0.18	0.23	0.17	0.24	0.24	0.44	0.01	0.00	0.03	0.03	0.49	0.67	0.76	0.70	0.00
<i>Malayopython reticulatus</i>	100.05	47.31	30.47	38.91	74.86	35.43	19.96	-	0.94	0.01	0.07	0.03	0.00	0.12	0.13	0.02	0.00	0.26	0.52	0.32	0.91	0.32	0.59	0.00	0.00	0.11	0.04	0.92	0.15	0.33	0.38	0.00
<i>Malayopython timoriensis</i>	97.20	49.80	34.54	38.67	77.36	38.05	30.40	15.45	-	0.07	0.21	0.10	0.07	0.54	0.32	0.35	0.00	0.56	0.66	0.53	0.88	0.41	0.61	0.04	0.02	0.45	0.34	0.86	0.39	0.56	0.50	0.10
<i>Antaresia childreni</i>	63.55	41.20	72.49	51.76	48.73	41.37	39.37	52.55	57.70	-	0.46	0.32	0.18	0.02	0.23	0.01	0.00	0.04	0.05	0.03	0.02	0.07	0.25	0.61	0.37	0.01	0.02	0.11	0.14	0.07	0.32	0.03
<i>Antaresia maculosa</i>	84.96	49.89	55.13	58.12	72.78	37.73	27.52	38.95	45.93	28.08	-	0.90	0.92	0.35	0.32	0.41	0.00	0.55	0.29	0.34	0.17	0.30	0.48	0.16	0.05	0.17	0.32	0.26	0.27	0.30	0.90	0.32
<i>Antaresia perthensis</i>	83.04	61.60	60.54	68.53	78.42	47.25	36.08	49.11	56.01	32.93	17.04	-	0.79	0.17	0.27	0.15	0.00	0.30	0.17	0.22	0.06	0.25	0.33	0.18	0.06	0.07	0.11	0.13	0.13	0.13	0.51	0.19
<i>Antaresia stimsoni</i>	81.70	55.42	62.23	64.38	76.80	43.73	37.36	48.90	53.78	30.30	13.50	17.26	-	0.07	0.24	0.01	0.00	0.12	0.12	0.13	0.01	0.23	0.29	0.02	0.00	0.02	0.04	0.11	0.01	0.01	0.45	0.06
<i>Morelia bredli</i>	96.71	54.46	38.04	55.64	87.00	34.69	30.52	28.11	29.27	51.10	29.06	37.09	33.34	-	0.38	0.80	0.00	0.84	0.74	0.87	0.32	0.53	0.51	0.00	0.00	0.61	0.63	0.44	0.05	0.16	0.65	0.15
<i>Morelia carinata</i>	66.42	53.23	56.77	59.58	75.47	48.15	50.83	54.25	50.42	49.29	45.22	48.82	44.58	39.07	-	0.21	0.02	0.21	0.22	0.22	0.17	0.22	0.20	0.20	0.20	0.16	0.24	0.19	0.19	0.29	0.37	0.38
<i>Morelia spilota</i>	99.84	53.43	38.12	55.73	84.50	35.53	25.68	25.29	31.46	46.64	22.85	31.86	30.27	12.20	45.07	-	0.00	0.91	0.68	0.85	0.22	0.49	0.57	0.00	0.00	0.36	0.25	0.42	0.02	0.08	0.74	0.00
<i>Morelia viridis</i>	54.43	72.08	119.35	85.64	61.94	73.40	102.80	102.46	96.41	78.33	94.01	96.51	90.47	96.72	83.45	101.42	-	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia amethystina</i>	99.12	54.79	42.52	54.80	83.33	32.03	27.10	24.94	29.87	46.54	24.59	32.73	31.52	15.21	49.45	10.86	95.95	-	0.74	0.87	0.56	0.51	0.69	0.01	0.00	0.67	0.61	0.52	0.12	0.21	0.77	0.12
<i>Simalia boeleni</i>	113.44	55.39	35.02	61.11	92.73	40.77	39.95	29.14	33.02	64.37	43.51	52.15	49.66	24.82	58.28	23.98	99.66	25.36	-	0.98	0.76	0.89	0.93	0.02	0.01	0.98	0.77	0.89	0.14	0.25	0.58	0.26
<i>Simalia clostolepis</i>	110.43	61.84	34.01	64.18	96.87	43.00	36.10	29.88	34.39	60.43	35.71	41.74	40.70	17.48	54.02	15.95	105.09	17.81	15.32	-	0.54	0.86	0.77	0.01	0.00	0.96	0.62	0.63	0.10	0.20	0.56	0.21
<i>Simalia kinghorni</i>	99.00	44.39	33.22	44.87	75.21	31.69	22.87	10.80	19.17	49.95	35.56	45.55	45.86	25.22	52.04	21.50	97.54	20.86	24.11	26.18	-	0.39	0.78	0.00	0.00	0.36	0.24	0.90	0.18	0.42	0.62	0.02
<i>Simalia nauta</i>	131.27	73.85	43.31	82.32	113.11	65.24	56.14	49.69	53.21	80.08	55.60	60.04	57.51	41.24	70.99	39.85	113.08	42.83	28.63	28.96	47.29	-	0.76	0.05	0.03	0.84	0.54	0.62	0.14	0.23	0.42	0.28
<i>Simalia oenpelliensis</i>	111.73	50.16	52.89	62.95	81.47	43.62	44.20	37.37	43.23	59.61	46.05	55.42	53.54	42.68	73.37	37.40	91.60	35.41	26.16	34.47	31.17	41.80	-	0.12	0.09	0.81	0.72	0.90	0.33	0.39	0.69	0.39
<i>Bothrochilus boa</i>	58.79	52.43	71.10	55.10	52.47	52.75	41.99	57.42	63.11	20.14	35.39	35.33	37.57	57.00	48.58	52.87	89.43	54.51	73.74	66.83	57.07	87.57	73.23	-	0.28	0.00	0.00	0.06	0.06	0.02	0.09	0.00
<i>Leiopython albertisii</i>	49.54	52.19	82.41	57.90	46.56	49.32	51.63	65.88	69.12	22.26	41.77	41.21	41.05	60.64	45.74	59.01	73.66	59.61	78.45	73.26	64.01	94.17	77.77	20.13	-	0.00	0.00	0.03	0.00	0.00	0.04	0.00
<i>Aspidites melanocephalus</i>	108.89	53.91	37.53	61.20	90.95	38.90	35.46	28.63	32.11	58.66	36.16	45.16	41.30	19.18	54.06	19.02	97.80	19.15	13.54	13.36	24.24	28.44	29.71	68.18	72.91	-	0.76	0.66	0.02	0.06	0.50	0.05
<i>Aspidites ramsayi</i>	96.17	44.25	45.32	56.57	80.03	29.68	32.42	31.37	34.57	47.29	28.66	38.79	32.82	17.58	45.37	18.89	87.58	19.16	22.99	23.06	25.63	39.89	33.18	58.75	60.22	15.21	-	0.49	0.02	0.06	0.80	0.21
<i>Liasis fuscus</i>	109.36	45.68	34.11	43.58	76.84	40.31	33.75	19.33	26.48	62.83	50.12	61.85	59.63	38.36	65.64	35.39	101.17	35.85	25.63	34.55	20.95	45.22	29.11	70.98	78.16	30.03	35.33	-	0.38	0.51	0.58	0.16
<i>Liasis mackloti</i>	81.64	44.42	46.16	34.68	59.05	36.26	14.30	25.38	33.45	33.94	30.82	38.70	40.73	38.06	49.48	33.25	99.23	33.97	49.24	45.48	28.57	67.84	51.76	34.12	44.51	45.75	41.29	40.10	-	0.80	0.49	0.00
<i>Liasis olivaceus</i>	86.60	42.30	36.18	39.91	66.85	36.25	13.01	20.10	28.16	39.17	29.66	37.99	39.31	29.89	42.95	25.90	101.43	29.02	40.73	37.38	21.79	57.83	48.30	40.66	50.24	36.82	33.16	35.01	14.19	-	0.74	0.01
<i>Liasis papuana</i>	89.04	39.35	44.37	49.16	70.23	30.24	19.39	27.03	34.64	34.00	17.33	29.77	25.85	22.89	43.81	17.56	93.57	20.56	32.91	29.65	23.26	49.47	37.72	43.10	48.94	26.58	18.28	36.06	26.29	20.11	-	0.45
<i>Boa constrictor</i>	81.68	46.82	53.85	64.67	78.72	33.23	40.49	44.88	47.69	40.88	25.81	31.06	25.94	25.57	36.22	27.49	81.95	29.07	37.83	33.54	38.19	51.94	46.31	50.09	49.46	31.87	20.82	51.85	45.50	38.80	24.41	-

Table S4S5. Body shape slope angle differences. Pairwise comparisons of the angle between the slopes (direction of allometry) for body shape data in degrees (bottom triangle), and *P*-values of the difference between them computed with 10,000 9,999 iterations (upper triangle). Significant values indicating different slope angles are highlighted in green. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia pertherensis</i>	<i>Antaresia maculosa</i>	<i>Antaresia stimsoni</i>	<i>Antaresia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsi</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivacea</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.99	0.95	0.95	0.95	1.00	0.95	0.84	0.65	0.73	0.13	0.75	0.71	0.04	0.37	0.05	0.77	0.21	0.14	0.15	0.53	0.03	0.01	0.87	0.95	0.13	0.42	0.13	0.56	0.07	0.84	0.82
<i>Python bivittatus</i>	10.09	-	0.75	0.61	0.94	0.99	0.54	0.52	0.44	0.25	0.00	0.37	0.11	0.00	0.15	0.00	0.26	0.02	0.01	0.01	0.05	0.01	0.00	0.35	0.86	0.00	0.04	0.04	0.04	0.00	0.69	0.47
<i>Python brongersmai</i>	20.67	29.40	-	0.94	0.71	0.86	0.82	0.70	0.58	0.74	0.27	0.71	0.76	0.15	0.47	0.20	0.59	0.44	0.41	0.42	0.83	0.09	0.01	0.78	0.70	0.27	0.54	0.32	0.74	0.20	0.73	0.64
<i>Python curtus</i>	14.49	19.07	18.86	-	0.78	0.79	0.24	0.15	0.21	0.10	0.00	0.13	0.04	0.00	0.08	0.00	0.07	0.01	0.02	0.01	0.12	0.01	0.00	0.12	0.21	0.00	0.01	0.07	0.03	0.00	0.85	0.08
<i>Python molurus</i>	17.56	13.41	35.01	20.72	-	0.90	0.62	0.49	0.33	0.36	0.03	0.35	0.23	0.00	0.12	0.00	0.44	0.05	0.03	0.02	0.24	0.01	0.01	0.38	0.72	0.05	0.14	0.07	0.19	0.01	0.96	0.40
<i>Python regius</i>	6.28	5.82	23.89	15.45	15.28	-	0.72	0.57	0.42	0.36	0.01	0.46	0.20	0.00	0.16	0.00	0.29	0.03	0.02	0.01	0.13	0.01	0.00	0.48	0.84	0.00	0.08	0.06	0.10	0.00	0.73	0.49
<i>Python sebae</i>	13.83	17.79	25.16	26.64	24.08	15.21	-	0.91	0.30	0.84	0.03	0.76	0.61	0.00	0.25	0.00	0.63	0.09	0.06	0.04	0.22	0.02	0.01	0.83	0.78	0.01	0.23	0.06	0.40	0.00	0.38	0.33
<i>Malayopython reticulatus</i>	20.63	20.99	32.11	34.17	29.86	20.30	10.24	-	0.52	0.91	0.07	0.98	0.83	0.01	0.40	0.00	0.70	0.14	0.07	0.06	0.14	0.02	0.01	0.95	0.88	0.02	0.60	0.06	0.38	0.01	0.25	0.81
<i>Malayopython timoriensis</i>	32.00	30.06	41.55	41.15	42.73	31.68	33.96	28.37	-	0.27	0.02	0.58	0.34	0.03	0.64	0.01	0.32	0.05	0.04	0.04	0.04	0.01	0.00	0.54	0.48	0.01	0.18	0.03	0.10	0.01	0.18	0.76
<i>Antaresia childreni</i>	25.05	28.21	29.90	36.55	34.79	25.57	12.02	11.03	37.29	-	0.20	0.94	0.93	0.02	0.38	0.01	0.49	0.37	0.17	0.18	0.38	0.05	0.02	0.77	0.46	0.09	0.86	0.12	0.82	0.03	0.21	0.32
<i>Antaresia maculosa</i>	56.69	60.48	54.30	66.05	63.70	57.75	43.55	42.07	64.74	32.85	-	0.12	0.06	0.23	0.23	0.78	0.03	0.96	0.62	0.70	0.14	0.32	0.12	0.02	0.00	0.57	0.27	0.25	0.24	0.96	0.02	0.00
<i>Antaresia pertherensis</i>	24.76	26.19	31.56	37.19	36.31	24.65	15.11	7.61	27.22	10.78	39.62	-	0.96	0.03	0.54	0.01	0.53	0.24	0.12	0.14	0.17	0.04	0.01	0.94	0.67	0.03	0.81	0.08	0.46	0.02	0.19	0.79
<i>Antaresia stimsoni</i>	24.18	28.63	27.52	36.15	37.49	25.97	13.73	11.55	31.50	8.84	36.51	8.27	-	0.00	0.49	0.00	0.35	0.21	0.13	0.12	0.12	0.03	0.01	0.87	0.21	0.01	0.51	0.07	0.48	0.00	0.12	0.18
<i>Morelia bredli</i>	68.31	70.35	63.02	76.81	79.01	67.86	57.48	51.80	61.29	45.88	31.26	45.52	46.07	-	0.30	0.20	0.00	0.34	0.31	0.40	0.00	0.45	0.12	0.00	0.00	0.01	0.05	0.21	0.00	0.07	0.00	0.00
<i>Morelia carinata</i>	49.86	53.33	49.55	60.63	64.64	52.35	44.02	38.33	32.93	39.51	48.10	33.21	32.03	42.77	-	0.15	0.30	0.33	0.32	0.38	0.11	0.11	0.03	0.46	0.22	0.05	0.38	0.06	0.28	0.16	0.06	0.34
<i>Morelia spilota</i>	62.36	66.74	55.65	69.98	71.41	63.25	50.32	48.66	68.07	39.01	12.86	44.42	41.47	23.23	48.98	-	0.00	0.88	0.69	0.79	0.01	0.43	0.10	0.00	0.00	0.07	0.01	0.30	0.00	0.55	0.00	0.00
<i>Morelia viridis</i>	22.54	25.26	35.60	36.30	29.96	25.42	14.96	15.80	33.85	20.15	44.89	20.96	18.86	61.22	39.65	53.94	-	0.06	0.05	0.03	0.05	0.01	0.01	0.63	0.42	0.00	0.10	0.03	0.22	0.00	0.20	0.18
<i>Simalia amethystina</i>	51.66	56.72	45.80	59.66	61.24	53.10	39.74	39.23	60.43	29.05	10.79	35.60	31.47	29.67	44.22	11.44	43.48	-	0.83	0.94	0.34	0.32	0.08	0.09	0.02	0.54	0.45	0.33	0.49	0.88	0.04	0.02
<i>Simalia boeleni</i>	62.99	70.59	50.37	67.66	74.97	65.96	54.03	55.55	71.88	45.61	27.50	51.28	45.25	37.50	49.37	21.27	57.02	21.01	-	0.97	0.29	0.51	0.08	0.06	0.02	0.30	0.17	0.43	0.28	0.73	0.03	0.02
<i>Simalia clastolepis</i>	57.01	63.36	46.74	63.49	69.26	59.15	46.89	46.62	62.91	37.00	21.01	41.64	36.77	28.25	42.11	14.17	50.59	12.52	11.75	-	0.21	0.40	0.06	0.05	0.01	0.22	0.21	0.34	0.25	0.69	0.02	0.01
<i>Simalia kinghorni</i>	32.27	38.96	24.97	34.64	39.37	34.00	26.34	33.50	56.79	24.66	36.00	33.82	28.77	54.77	56.62	39.30	36.47	29.74	38.10	35.20	-	0.08	0.01	0.07	0.03	0.21	0.12	0.31	0.53	0.03	0.28	0.01
<i>Simalia nauta</i>	102.55	106.69	90.46	106.06	110.27	102.71	91.82	90.01	104.37	80.62	52.14	84.96	82.93	43.80	80.40	42.40	96.24	53.23	46.19	48.72	74.55	-	0.59	0.02	0.01	0.22	0.08	0.64	0.06	0.35	0.01	0.01
<i>Simalia oenpelliensis</i>	126.99	124.15	129.72	134.86	120.79	124.73	114.45	110.25	125.50	105.41	77.99	109.56	110.92	77.45	108.80	77.42	112.30	86.59	89.09	89.67	106.27	52.52	-	0.01	0.00	0.11	0.03	0.21	0.02	0.12	0.01	0.00
<i>Bothrochilus boa</i>	18.06	21.55	27.16	31.47	31.48	19.91	10.54	8.24	25.69	13.67	44.30	9.40	8.71	53.45	34.14	50.02	14.62	39.96	53.41	45.35	33.07	91.54	116.39	-	0.65	0.00	0.25	0.04	0.24	0.00	0.20	0.63
<i>Leiopython albertsi</i>	13.36	10.59	30.56	26.68	20.75	11.57	11.17	10.66	26.76	19.57	51.72	16.63	19.91	61.49	45.24	58.39	17.95	48.61	63.93	55.75	36.44	99.35	117.26	12.94	-	0.00	0.08	0.04	0.05	0.00	0.39	0.74
<i>Aspidites melanocephalus</i>	53.68	56.85	52.28	59.76	55.41	53.91	42.38	44.57	72.01	35.03	20.33	44.86	42.00	46.67	64.27	27.12	47.13	23.50	37.10	34.01	28.20	58.18	78.50	48.12	51.04	-	0.06	0.37	0.10	0.29	0.05	0.00
<i>Aspidites ramsayi</i>	35.22	36.74	38.17	46.21	44.11	34.64	22.91	17.77	39.85	11.49	27.56	13.91	15.47	35.45	37.64	32.19	28.93	24.64	43.45	32.94	30.92	72.47	97.22	21.71	27.51	33.82	-	0.13	0.36	0.03	0.07	0.06
<i>Liasis fuscus</i>	75.61	78.97	63.17	72.16	78.59	74.36	70.81	73.82	92.37	64.64	53.84	71.14	69.44	55.23	87.14	46.51	82.79	50.00	48.63	49.59	48.69	44.37	79.43	75.72	77.64	45.15	61.54	-	0.12	0.22	0.12	0.03
<i>Liasis mackloti</i>	29.74	35.76	29.18	39.15	39.66	32.20	18.19	21.79	46.31	12.27	27.95	21.59	15.17	47.38	41.90	34.57	23.15	23.26	36.82	30.67	17.85	76.06	104.03	21.20	28.76	29.42	19.21	61.23	-	0.04	0.13	0.01
<i>Liasis olivacea</i>	61.44	66.46	56.67	69.89	69.20	63.30	48.96	48.58	70.39	38.99	8.82	46.00	41.65	34.26	50.27	13.12	49.51	13.19	21.58	18.76	38.17	48.30	77.06	49.61	58.05	23.26	34.96	53.41	31.76	-	0.01	0.00
<i>Liasis papuana</i>	24.64	23.48	34.16	18.07	14.39	22.65	33.03	40.43	52.42	42.73	69.41	45.58	45.84	84.53	74.40	75.30	41.89	65.61	76.51	72.46	38.82	109.42	123.80	41.23	32.05	57.68	51.85	71.40	45.59	74.02	-	0.19
<i>Boa constrictor</i>	19.47	17.27	32.54	31.75	29.66	18.02	17.35	11.64	18.21	21.42	52.51	13.28	18.81	56.61	38.11	57.62	22.05	48.75	63.57	54.39	41.44	97.45	118.05	12.18	9.96	55.57	26.28	79.67	31.89	58.98	40.07	-

Table S5S6. Head shape slope length differences. Pairwise comparisons of the differences in slope length, i.e., amount of shape change per unit of log centroid size change (bottom triangle), and *P*-values of the difference between them computed with 10,000 9,999 iterations (upper triangle). Significant values denoting differences in magnitude of shape change per unit of size are highlighted in green. Black boxes outline comparisons within clades.

	Python anchietae										Python bivittatus										Python brongersmai										Python curtus										Python molurus										Python regius										Python sebae										Malayopython reticulatus												Malayopython timoriensis												Antaresia childreni												Antaresia macleayi												Antaresia perthensis												Antaresia stimsoni												Morelia bredli												Morelia carinata												Morelia spilota												Morelia viridis												Similia amethystina												Similia boeleni												Similia clastolepis												Similia kinghorni												Similia nauta												Similia oenpelliensis												Bothrochilus boa												Leiopython albertisi												Aspidites melanocephalus												Aspidites ramsayi												Liasis fuscus												Liasis mackloti												Liasis olivaceus												Liasis papuana												Boa constrictor													
Python anchietae	-	0.59	0.73	0.48	0.90	0.54	0.93	0.87	0.70	0.70	0.87	0.94	0.87	0.29	0.88	0.60	0.46	0.56	0.17	0.09	0.64	0.00	0.68	0.56	0.49	0.26	0.43	0.12	0.98	0.77	0.89	0.68	0.04	0.44	0.31	0.87	0.75	0.83	0.01	0.91	0.13	0.03	0.26	0.06	0.00	0.37	0.00	0.69	0.09	0.01	0.01	0.05	0.06	0.88	0.62	0.66	0.12																																																																																																																																																																																																																																																																																																																											
Python bivittatus	0.04	-	0.44	0.75	0.51	0.87	0.13	0.10	0.83	0.76	0.21	0.41	0.11	0.00	0.35	0.01	0.63	0.03	0.01	0.00	0.04	0.00	0.36	0.93	0.70	0.00	0.00	0.02	0.22	0.07	0.48	0.71	0.03	0.07	-	0.36	0.64	0.40	0.77	0.82	0.50	0.51	0.83	0.67	0.82	0.56	0.83	0.95	0.36	0.90	0.37	0.23	0.99	0.01	0.96	0.43	0.39	0.51	0.75	0.28	0.73	0.90	0.64	0.51																																																																																																																																																																																																																																																																																																																				
Python brongersmai	0.03	0.07	-	0.36	0.64	0.40	0.77	0.10	0.65	0.57	0.16	0.31	0.10	0.00	0.28	0.02	0.94	0.03	0.01	0.00	0.05	0.00	0.29	0.79	0.94	0.00	0.01	0.01	0.18	0.07	0.37	0.51	0.06	0.01	0.09	-	0.40	0.88	0.13	0.10	0.65	0.57	0.16	0.31	0.10	0.00	0.28	0.02	0.94	0.03	0.01	0.00	0.05	0.00	0.29	0.79	0.94	0.00	0.01	0.01	0.18	0.07	0.37	0.51																																																																																																																																																																																																																																																																																																																				
Python curtus	0.06	0.01	0.09	-	0.40	0.88	0.13	0.10	0.65	0.57	0.16	0.31	0.10	0.00	0.28	0.02	0.94	0.03	0.01	0.00	0.05	0.00	0.29	0.79	0.94	0.00	0.01	0.01	0.18	0.07	0.37	0.51	0.06	0.01	0.09	-	0.40	0.88	0.13	0.10	0.65	0.57	0.16	0.31	0.10	0.00	0.28	0.02	0.94	0.03	0.01	0.00	0.05	0.00	0.29	0.79	0.94	0.00	0.01	0.01	0.18	0.07	0.37	0.51																																																																																																																																																																																																																																																																																																																				
Python molurus	0.01	0.03	0.04	0.05	-	0.46	0.71	0.63	0.73	0.70	0.67	0.94	0.64	0.06	0.72	0.28	0.32	0.28	0.05	0.01	0.37	0.00	0.57	0.47	0.34	0.05	0.15	0.04	0.80	0.51	0.99	0.64	0.01	0.03	0.04	0.05	-	0.46	0.71	0.63	0.73	0.70	0.67	0.94	0.64	0.06	0.72	0.28	0.32	0.28	0.05	0.01	0.37	0.00	0.57	0.47	0.34	0.05	0.15	0.04	0.80	0.51	0.99	0.64																																																																																																																																																																																																																																																																																																																				
Python regius	0.05	0.01	0.08	0.01	0.04	-	0.14	0.11	0.74	0.67	0.20	0.37	0.13	0.00	0.32	0.02	0.79	0.03	0.01	0.00	0.05	0.00	0.32	0.93	0.89	0.00	0.01	0.02	0.22	0.09	0.45	0.62	0.01	0.05	0.08	0.01	0.04	-	0.14	0.11	0.74	0.67	0.20	0.37	0.13	0.00	0.32	0.02	0.79	0.03	0.01	0.00	0.05	0.00	0.32	0.93	0.89	0.00	0.01	0.02	0.22	0.09	0.45	0.62																																																																																																																																																																																																																																																																																																																				
Python sebae	0.01	0.05	0.03	0.06	0.02	0.05	-	0.84	0.44	0.31	0.87	0.75	0.83	0.01	0.91	0.13	0.03	0.26	0.06	0.00	0.37	0.00	0.69	0.09	0.01	0.01	0.05	0.06	0.88	0.62	0.66	0.12	0.01	0.05	0.08	0.01	0.04	-	0.14	0.11	0.74	0.67	0.20	0.37	0.13	0.00	0.32	0.02	0.79	0.03	0.01	0.00	0.05	0.00	0.32	0.93	0.89	0.00	0.01	0.02	0.22	0.09	0.45	0.62																																																																																																																																																																																																																																																																																																																				
Malayopython reticulatus	0.01	0.05	0.02	0.07	0.02	0.06	0.01	-	0.38	0.25	0.97	0.65	0.99	0.02	0.98	0.22	0.02	0.32	0.07	0.00	0.47	0.00	0.73	0.06	0.01	0.01	0.08	0.07	0.74	0.75	0.58	0.08	0.03	0.01	0.06	0.02	0.05	-	0.38	0.25	0.97	0.65	0.99	0.02	0.98	0.22	0.02	0.32	0.07	0.00	0.47	0.00	0.73	0.06	0.01	0.01	0.08	0.07	0.74	0.75	0.58	0.08																																																																																																																																																																																																																																																																																																																						
Malayopython timoriensis	0.03	0.01	0.06	0.03	0.02	0.02	0.04	0.04	0.00	-	0.35	0.60	0.26	0.00	0.51	0.17	0.57	0.17	0.03	0.00	0.22	0.00	0.43	0.78	0.62	0.03	0.09	0.03	0.51	0.31	0.72	1.00	0.03	0.01	0.06	0.03	0.02	0.04	-	0.38	0.25	0.97	0.65	0.99	0.02	0.98	0.22	0.02	0.32	0.07	0.00	0.47	0.00	0.73	0.06	0.01	0.01	0.08	0.07	0.74	0.75	0.58	0.08																																																																																																																																																																																																																																																																																																																					
Antaresia childreni	0.03	0.01	0.06	0.03	0.02	0.02	0.04	0.04	0.00	-	0.35	0.60	0.26	0.00	0.48	0.05	0.45	0.08	0.02	0.00	0.11	0.00	0.43	0.70	0.49	0.00	0.02	0.03	0.43	0.19	0.69	0.98	0.25	0.01	0.04	0.05	0.00	0.04	0.01	0.02	0.02	-	0.65	0.04	0.75	0.23	0.21	0.25	0.04	0.00	0.34	0.00	0.59	0.35	0.22	0.03	0.10	0.05	0.85	0.52	0.93	0.52																																																																																																																																																																																																																																																																																																																						
Antaresia macleayi	0.01	0.05	0.02	0.07	0.02	0.06	0.01	0.00	0.04	0.04	-	0.69	0.98	0.09	1.00	0.48	0.09	0.47	0.08	0.01	0.61	0.00	0.76	0.17	0.09	0.06	0.24	0.08	0.79	0.84	0.63	0.25	0.01	0.04	0.04	0.05	0.00	0.04	0.01	0.02	0.02	-	0.65	0.04	0.75	0.23	0.21	0.25	0.04	0.00	0.34	0.00	0.59	0.35	0.22	0.03	0.10	0.05	0.85	0.52	0.93	0.52																																																																																																																																																																																																																																																																																																																						
Antaresia perthensis	0.01	0.04	0.04	0.05	0.00	0.04	0.01	0.00	0.04	0.04	0.00	0.02	-	0.02	0.99	0.28	0.03	0.35	0.07	0.00	0.49	0.00	0.74	0.08	0.01	0.02	0.11	0.08	0.74	0.77	0.58	0.10	0.01	0.04	0.05	0.00	0.04	0.01	0.02	0.02	-	0.65	0.04	0.75	0.23	0.21	0.25	0.04	0.00	0.34	0.00	0.59	0.35	0.22	0.03	0.10	0.05	0.85	0.52	0.93	0.52																																																																																																																																																																																																																																																																																																																							
Antaresia stimsoni	0.01	0.05	0.02	0.07	0.02	0.06	0.01	0.00	0.04	0.04	0.00	0.02	-	0.02	0.99	0.28	0.03	0.35	0.07	0.00	0.49	0.00	0.74	0.08	0.01	0.02	0.11	0.08	0.74	0.77	0.58	0.10	0.01	0.04	0.05	0.00	0.04	0.01	0.02	0.02	-	0.65	0.04	0.75	0.23	0.21	0.25	0.04	0.00	0.34	0.00	0.59	0.35	0.22	0.03	0.10	0.05	0.85	0.52	0.93	0.52																																																																																																																																																																																																																																																																																																																							
Morelia bredli	0.09	0.13	0.05	0.14	0.10	0.14	0.08	0.08	0.12	0.12	0.07	0.09	0.08	-	0.22	0.09	0.00	0.27	0.55	0.16	0.15	0.02	0.54	0.00	0.00	0.86	0.46	0.42	0.02	0.06	0.03	0.00	0.09	0.13	0.05	0.14	0.10	0.14	0.08	0.08	0.12	0.12	0.07	0.09	0.08	-	0.22	0.09	0.00	0.27	0.55	0.16	0.15	0.02	0.54	0.00	0.00	0.86	0.46	0.42	0.02	0.06	0.03	0.00	0.09	0.13	0.05	0.14	0.10	0.14	0.08	0.08	0.12	0.12	0.07	0.09	0.08																																																																																																																																																																																																																																																																																																							
Morelia carinata	0.01	0.05	0.02	0.07	0.02	0.06	0.01	0.00	0.04	0.04	0.00	0.02	0.00	0.07	-	0.61	0.24	0.58	0.13	0.04	0.69	0.00	0.76	0.33	0.26	0.19	0.38	0.11	0.84	0.88	0.70	0.43	0.01	0.04	0.05	0.00	0.04	0.01	0.02	0.05	0.07	0.15	0.07	0.10	-	0.01	0.00	0.00	0.01	0.00	0.28	0.67	0.84	0.00	0.00	0.01	0.08	0.02	0.28	0.32																																																																																																																																																																																																																																																																																																																								
Morelia spilota	0.04	0.08	0.01	0.09	0.05	0.09	0.03	0.03	0.07	0.07	0.03	0.04	0.03	0.05	0.03	-	0.00	0.84	0.14	0.02	0.88	0.01	0.99	0.00	0.00	0.06	0.38	0.14	0.18	0.51	0.21	0.00	0.06	0.02	0.09	0.00	0.05	0.01	0.06	0.07	0.03	0.03	0.07	0.05	0.07	0.15	0.07	0.10	-	0.01	0.00	0.00	0.01	0.00	0.28	0.67	0.84	0.00	0.00	0.01	0.08	0.02	0.28	0.32																																																																																																																																																																																																																																																																																																																				
Morelia viridis	0.06	0.02	0.09	0.00	0.05	0.01	0.06	0.07	0.0																																																																																																																																																																																																																																																																																																																																																																											

Table S6S7. Body shape slope length differences. Pairwise comparisons of the differences in slope length, i.e., amount of shape change per unit of log centroid size change (bottom triangle), and *P*-values of the difference between them computed with 10,000 9,999 iterations (upper triangle). Significant values denoting differences in magnitude of shape change per unit of size **-**are highlighted in green. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.03	0.36	0.90	0.30	0.97	0.04	0.02	0.06	0.03	0.01	0.03	0.10	0.00	0.01	0.00	0.03	0.01	0.06	0.02	0.01	0.28	0.54	0.12	0.00	0.01	0.00	0.20	0.04	0.02	0.02	0.01
<i>Python bivittatus</i>	0.28	-	0.44	0.00	0.16	0.00	0.81	0.59	0.84	0.96	0.23	0.95	0.17	0.01	0.31	0.00	0.97	0.18	0.85	0.73	0.27	0.57	0.48	0.13	0.00	0.08	0.01	0.63	0.93	0.47	0.50	0.23
<i>Python brongersmai</i>	0.16	0.12	-	0.36	0.90	0.34	0.49	0.32	0.51	0.45	0.21	0.43	0.78	0.09	0.17	0.09	0.44	0.18	0.53	0.35	0.24	0.88	0.89	0.83	0.08	0.16	0.12	0.79	0.46	0.31	0.25	0.26
<i>Python curtus</i>	0.01	0.27	0.15	-	0.21	0.89	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.30	0.59	0.01	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00
<i>Python molurus</i>	0.14	0.14	0.02	0.13	-	0.18	0.19	0.08	0.29	0.17	0.03	0.16	0.50	0.00	0.06	0.00	0.14	0.02	0.31	0.12	0.03	0.77	0.96	0.58	0.00	0.01	0.01	0.65	0.16	0.06	0.08	0.03
<i>Python regius</i>	0.01	0.28	0.16	0.01	0.14	-	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.28	0.57	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.00
<i>Python sebae</i>	0.27	0.01	0.11	0.25	0.13	0.26	-	0.41	0.96	0.86	0.14	0.79	0.19	0.00	0.26	0.00	0.77	0.11	0.96	0.59	0.15	0.63	0.53	0.15	0.00	0.03	0.00	0.69	0.85	0.28	0.41	0.08
<i>Malayopython reticulatus</i>	0.32	0.04	0.16	0.31	0.18	0.32	0.05	-	0.56	0.57	0.51	0.65	0.05	0.03	0.49	0.01	0.58	0.39	0.58	0.91	0.62	0.43	0.39	0.04	0.01	0.24	0.08	0.46	0.49	0.92	0.76	0.63
<i>Malayopython timoriensis</i>	0.26	0.02	0.10	0.25	0.12	0.26	0.06	0.06	-	0.87	0.29	0.82	0.51	0.04	0.30	0.03	0.81	0.22	1.00	0.66	0.33	0.65	0.53	0.45	0.03	0.16	0.08	0.72	0.88	0.49	0.45	0.34
<i>Antaresia childreni</i>	0.28	0.00	0.12	0.26	0.14	0.27	0.01	0.04	0.02	-	0.23	0.93	0.21	0.01	0.31	0.00	0.93	0.18	0.87	0.71	0.26	0.59	0.49	0.16	0.00	0.07	0.02	0.64	0.97	0.45	0.48	0.23
<i>Antaresia maculosa</i>	0.37	0.09	0.21	0.36	0.23	0.37	0.10	0.05	0.11	0.09	-	0.29	0.01	0.18	0.79	0.12	0.23	0.81	0.31	0.50	0.85	0.28	0.29	0.01	0.09	0.69	0.38	0.29	0.17	0.53	0.85	0.73
<i>Antaresia perthensis</i>	0.29	0.00	0.13	0.27	0.15	0.28	0.02	0.03	0.02	0.01	0.08	-	0.21	0.01	0.35	0.01	0.98	0.22	0.82	0.78	0.35	0.56	0.47	0.17	0.00	0.12	0.03	0.61	0.89	0.56	0.54	0.34
<i>Antaresia stimsoni</i>	0.20	0.08	0.04	0.19	0.06	0.20	0.06	0.12	0.06	0.08	0.17	0.08	-	0.00	0.11	0.00	0.11	0.02	0.53	0.16	0.01	0.93	0.73	0.82	0.00	0.00	0.00	0.97	0.12	0.01	0.14	0.00
<i>Morelia bredli</i>	0.47	0.19	0.31	0.45	0.33	0.46	0.20	0.15	0.21	0.19	0.10	0.18	0.27	-	0.58	0.99	0.00	0.34	0.06	0.06	0.10	0.11	0.16	0.00	0.78	0.28	0.54	0.10	0.00	0.02	0.25	0.03
<i>Morelia carinata</i>	0.40	0.12	0.24	0.39	0.26	0.40	0.13	0.08	0.14	0.12	0.03	0.12	0.20	0.07	-	0.56	0.33	0.93	0.30	0.47	0.70	0.22	0.22	0.09	0.47	0.98	0.79	0.24	0.29	0.51	0.71	0.63
<i>Morelia spilota</i>	0.47	0.19	0.31	0.45	0.33	0.46	0.20	0.15	0.21	0.19	0.10	0.18	0.27	0.00	0.07	-	0.00	0.29	0.05	0.04	0.04	0.12	0.17	0.00	0.67	0.17	0.42	0.10	0.00	0.00	0.23	0.00
<i>Morelia viridis</i>	0.28	0.00	0.12	0.27	0.14	0.28	0.02	0.04	0.02	0.01	0.09	0.00	0.08	0.18	0.12	0.18	-	0.18	0.82	0.74	0.26	0.57	0.48	0.09	0.00	0.05	0.01	0.61	0.89	0.45	0.50	0.19
<i>Simalia amethystina</i>	0.39	0.11	0.23	0.38	0.25	0.39	0.12	0.07	0.13	0.11	0.02	0.11	0.19	0.08	0.01	0.08	0.11	-	0.24	0.38	0.66	0.23	0.25	0.01	0.22	0.93	0.60	0.24	0.14	0.41	0.71	0.55
<i>Simalia boeleni</i>	0.26	0.02	0.10	0.25	0.12	0.26	0.01	0.06	0.00	0.02	0.11	0.02	0.06	0.21	0.14	0.21	0.02	0.13	-	0.65	0.36	0.66	0.53	0.47	0.04	0.19	0.10	0.73	0.88	0.52	0.47	0.37
<i>Simalia clastolepis</i>	0.31	0.03	0.15	0.30	0.17	0.31	0.04	0.01	0.05	0.03	0.06	0.02	0.11	0.16	0.09	0.16	0.03	0.08	0.05	-	0.59	0.47	0.41	0.13	0.03	0.29	0.13	0.50	0.67	0.84	0.71	0.62
<i>Simalia kinghorni</i>	0.36	0.07	0.20	0.34	0.22	0.35	0.09	0.04	0.09	0.08	0.01	0.07	0.15	0.11	0.05	0.11	0.07	0.04	0.09	0.05	-	0.32	0.32	0.01	0.03	0.51	0.21	0.34	0.19	0.64	0.96	0.90
<i>Simalia nauta</i>	0.19	0.09	0.03	0.17	0.05	0.18	0.08	0.13	0.08	0.09	0.18	0.10	0.02	0.28	0.21	0.28	0.10	0.20	0.07	0.12	0.17	-	0.78	0.98	0.10	0.22	0.16	0.91	0.60	0.41	0.34	0.35
<i>Simalia oenpelliensis</i>	0.13	0.15	0.03	0.11	0.01	0.12	0.14	0.19	0.13	0.15	0.24	0.16	0.07	0.34	0.27	0.34	0.16	0.26	0.13	0.18	0.23	0.06	-	0.77	0.15	0.25	0.21	0.71	0.51	0.38	0.30	0.34
<i>Bothrochilus boa</i>	0.19	0.09	0.03	0.18	0.05	0.19	0.07	0.13	0.07	0.09	0.18	0.09	0.01	0.28	0.21	0.28	0.09	0.20	0.07	0.12	0.16	0.00	0.06	-	0.00	0.00	0.00	0.91	0.10	0.01	0.12	0.00
<i>Leiopython albertisii</i>	0.49	0.20	0.33	0.47	0.35	0.48	0.22	0.17	0.22	0.21	0.11	0.20	0.28	0.02	0.08	0.02	0.20	0.09	0.22	0.17	0.13	0.30	0.36	0.29	-	0.13	0.30	0.08	0.00	0.00	0.18	0.00
<i>Aspidites melanocephalus</i>	0.40	0.12	0.24	0.39	0.26	0.39	0.13	0.08	0.14	0.12	0.03	0.11	0.20	0.07	0.00	0.07	0.11	0.01	0.14	0.09	0.04	0.21	0.27	0.21	0.09	-	0.57	0.22	0.04	0.22	0.64	0.33
<i>Aspidites ramsayi</i>	0.43	0.15	0.27	0.42	0.29	0.43	0.16	0.11	0.17	0.15	0.06	0.15	0.23	0.04	0.03	0.04	0.15	0.04	0.17	0.12	0.08	0.24	0.30	0.24	0.05	0.03	-	0.15	0.00	0.05	0.42	0.08
<i>Liasis fuscus</i>	0.21	0.07	0.05	0.19	0.07	0.20	0.06	0.11	0.05	0.07	0.16	0.08	0.01	0.26	0.19	0.26	0.08	0.18	0.05	0.10	0.15	0.02	0.08	0.02	0.28	0.19	0.22	-	0.65	0.44	0.36	0.36
<i>Liasis mackloti</i>	0.28	0.01	0.12	0.26	0.14	0.27	0.01	0.04	0.01	0.00	0.09	0.01	0.07	0.19	0.13	0.19	0.01	0.12	0.01	0.03	0.08	0.09	0.15	0.08	0.21	0.12	0.16	0.07	-	0.34	0.46	0.11
<i>Liasis olivaceus</i>	0.33	0.04	0.17	0.31	0.19	0.32	0.06	0.01	0.06	0.05	0.04	0.04	0.12	0.14	0.08	0.14	0.04	0.07	0.06	0.02	0.03	0.14	0.20	0.13	0.16	0.07	0.11	0.12	0.05	-	0.81	0.65
<i>Liasis papuana</i>	0.35	0.07	0.19	0.34	0.21	0.35	0.08	0.03	0.09	0.07	0.02	0.07	0.15	0.12	0.05	0.12	0.07	0.04	0.09	0.04	0.00	0.16	0.22	0.16	0.13	0.05	0.08	0.14	0.07	0.02	-	0.98
<i>Boa constrictor</i>	0.35	0.07	0.19	0.33	0.21	0.34	0.08	0.03	0.09	0.07	0.02	0.06	0.14	0.12	0.05	0.12	0.06	0.04	0.09	0.04	0.01	0.16	0.22	0.16	0.14	0.05	0.08	0.14	0.07	0.02	0.00	-

Table S7S8. Head shape intercept differences. Pairwise differences in the intercept of the allometric regressions (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 9,999-iterations (upper triangle). This test only applies to pairs of taxa for which the null hypothesis of common slopes has not been rejected. Cells highlighted in green correspond to species where they have a common slope but different intercept (parallel allometric trajectories). Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsi</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>		
<i>Python anchietae</i>	-	0.39	-	0.41	0.75	0.31	-	-	0.28	0.40	0.30	0.16	-	0.84	-	0.60	-	-	-	-	-	-	0.55	0.38	-	-	-	0.19	-	-	0.73	-		
<i>Python bivittatus</i>	0.19	-	0.68	0.41	0.59	0.59	-	0.73	0.54	-	-	-	-	0.68	-	-	-	0.45	-	0.82	0.91	0.81	0.90	0.51	0.82	0.64	0.68	0.82	0.80	0.82	0.85	0.94	0.80	0.81
<i>Python brongersmai</i>	-	0.21	-	0.63	0.43	0.72	0.90	0.95	0.92	0.52	0.66	0.59	0.60	0.86	0.76	0.83	-	0.82	0.91	0.81	0.90	0.51	0.82	0.64	0.68	0.82	0.80	0.82	0.85	0.94	0.80	0.81		
<i>Python curtus</i>	0.18	0.11	0.19	-	0.60	0.59	0.22	0.19	0.86	-	-	-	-	0.60	0.76	-	-	0.41	-	0.10	0.10	0.04	0.50	-	-	-	0.30	0.31	0.20	0.41	-	-		
<i>Python molurus</i>	0.15	0.11	0.28	0.12	-	0.49	-	-	0.41	-	-	-	-	0.76	-	-	-	-	-	-	-	-	0.36	0.59	0.45	-	-	0.08	-	-	-	-		
<i>Python regius</i>	0.18	0.08	0.19	0.09	0.13	-	0.33	0.20	0.91	0.60	0.65	0.51	-	0.48	0.72	0.42	-	0.15	0.48	0.11	0.16	0.02	0.57	-	-	0.51	0.44	0.33	0.59	0.31	0.66	0.60		
<i>Python sebae</i>	-	-	0.15	0.15	-	0.12	-	0.55	0.77	-	0.30	0.04	-	0.65	0.51	-	-	0.61	0.75	0.39	0.65	0.16	0.81	-	-	-	0.41	0.83	0.80	0.65	-	-		
<i>Malayopython reticulatus</i>	-	-	0.12	0.15	-	0.13	0.07	-	0.78	-	0.10	-	-	0.54	0.44	-	-	0.50	0.74	0.36	0.82	0.14	0.82	-	-	0.40	-	0.60	0.45	0.83	0.41	-		
<i>Malayopython timoriensis</i>	-	0.10	0.15	0.09	-	0.07	0.10	0.10	-	0.55	0.65	0.49	0.51	0.76	0.94	0.72	-	0.53	0.59	0.42	0.58	0.20	0.72	-	-	0.60	0.59	0.48	0.80	0.71	0.70	0.73		
<i>Antaresia childreni</i>	0.19	0.07	0.23	-	0.12	0.08	-	-	0.11	-	0.95	0.72	0.38	-	0.50	-	-	-	0.39	-	-	0.02	0.45	0.77	0.90	-	0.04	0.19	0.03	0.81	-	-		
<i>Antaresia maculosa</i>	0.20	-	0.22	-	-	0.09	0.12	0.16	0.12	0.04	-	0.98	0.88	0.42	0.61	0.45	-	0.25	0.48	0.12	0.16	0.08	0.67	0.82	-	0.60	0.64	0.26	0.56	0.30	0.96	0.90		
<i>Antaresia perthensis</i>	0.20	-	0.23	-	-	0.10	0.14	-	0.13	0.05	0.03	-	0.54	0.26	0.42	0.18	-	0.07	0.41	0.07	0.04	0.02	0.55	0.58	0.72	0.52	0.42	0.08	0.18	0.05	0.82	0.62		
<i>Antaresia stimsoni</i>	0.23	-	0.21	-	-	-	-	0.12	0.06	0.04	0.05	-	0.41	0.41	-	-	-	0.12	0.49	0.12	-	0.03	0.59	-	-	-	0.09	-	-	-	0.90	0.45		
<i>Morelia bredli</i>	-	-	0.18	-	-	0.12	0.08	0.10	0.12	-	0.12	0.13	0.10	-	0.60	0.76	-	0.83	0.87	0.55	0.65	0.31	0.85	-	-	0.78	0.70	0.60	0.78	0.76	0.77	0.42		
<i>Morelia carinata</i>	0.16	0.12	0.23	0.14	0.14	0.11	0.17	0.18	0.11	0.12	0.13	0.14	0.15	0.15	-	0.54	-	0.35	0.54	0.36	0.41	0.18	0.57	0.60	0.59	0.53	0.60	0.30	0.48	0.41	0.78	0.55		
<i>Morelia spilota</i>	-	-	0.17	-	-	0.10	-	0.10	-	0.08	0.10	-	-	0.05	0.14	-	-	0.56	0.71	0.30	0.52	0.16	0.82	-	-	0.70	0.52	0.47	-	0.59	0.85	-		
<i>Morelia viridis</i>	0.15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
<i>Simalia amethystina</i>	-	-	0.18	-	-	0.17	0.09	0.10	0.16	-	0.16	0.18	0.13	0.07	0.21	0.09	-	-	0.92	0.82	0.73	0.23	0.90	-	-	0.59	0.51	0.64	0.60	0.81	0.54	0.20		
<i>Simalia boeleni</i>	-	0.22	0.19	0.27	-	0.21	0.16	0.15	0.20	0.22	0.20	0.21	0.18	0.12	0.25	0.13	-	0.11	-	0.97	0.82	0.60	0.98	-	-	0.75	0.76	0.91	0.73	0.83	0.58	0.64		
<i>Simalia clastolepis</i>	-	-	0.22	-	-	0.26	0.18	0.18	0.24	-	0.24	0.25	0.21	0.15	0.30	0.17	-	0.10	0.10	-	0.50	0.59	0.90	-	-	0.40	0.33	0.76	0.33	0.52	0.28	0.16		
<i>Simalia kinghorni</i>	-	-	0.15	0.19	-	0.16	0.08	0.06	0.13	-	0.17	0.18	-	0.09	0.19	0.09	-	0.08	0.12	0.15	-	0.16	0.87	-	-	0.48	0.33	0.70	0.59	0.91	0.45	-		
<i>Simalia nauta</i>	-	0.47	0.37	0.50	-	0.47	0.39	0.38	0.45	0.47	0.44	0.45	0.42	0.38	0.51	0.39	-	0.34	0.30	0.27	0.38	-	0.51	-	-	0.26	0.22	0.48	0.09	0.16	0.14	0.09		
<i>Simalia oenpelliensis</i>	-	0.22	0.23	0.27	0.29	0.23	0.17	0.17	0.23	0.22	0.21	0.22	0.20	0.17	0.29	0.16	-	0.14	0.13	0.16	0.14	0.32	-	0.54	0.59	0.82	0.87	0.95	0.78	0.82	0.78	0.78		
<i>Bothrochilus boa</i>	0.17	-	0.24	-	0.12	-	-	-	0.04	0.05	0.05	-	-	0.12	-	-	-	-	-	-	-	-	0.25	-	-	-	0.09	0.10	-	-	0.76	-		
<i>Leiopython albertsi</i>	0.20	-	0.20	-	0.13	-	-	-	0.03	-	0.05	-	-	0.12	-	-	-	-	-	-	-	-	0.21	0.06	-	-	-	-	-	-	-	-		
<i>Aspidites melanocephalus</i>	-	-	0.18	-	-	0.12	-	0.13	0.13	-	0.09	0.10	-	0.07	0.16	0.06	-	0.12	0.12	0.17	0.13	0.37	0.18	-	-	-	0.90	0.59	-	0.59	0.82	0.76		
<i>Aspidites ramsayi</i>	-	-	0.21	-	-	0.12	-	0.14	-	0.08	0.09	-	0.08	0.15	0.07	-	-	0.12	0.13	0.19	0.13	0.39	0.17	-	-	0.05	-	0.51	-	0.44	0.94	0.70		
<i>Liasis fuscus</i>	-	0.26	0.20	0.28	0.34	0.26	0.19	0.16	0.24	0.27	0.27	0.28	0.25	0.19	0.32	0.20	-	0.16	0.13	0.15	0.15	0.29	0.12	0.31	-	0.21	0.22	-	0.18	0.46	0.42	0.33		
<i>Liasis mackloti</i>	0.25	-	0.16	0.15	-	0.09	0.04	0.08	0.09	0.09	0.09	0.10	-	0.07	0.15	-	-	0.09	0.15	0.18	0.09	0.40	0.17	0.12	-	-	-	0.20	-	0.59	0.80	-		
<i>Liasis olivaceus</i>	-	-	0.13	0.17	-	0.14	0.05	0.05	0.12	0.15	0.15	0.17	-	0.08	0.18	0.07	-	0.07	0.13	0.15	0.05	0.37	0.16	-	-	0.11	0.13	0.17	0.07	-	0.60	-		
<i>Liasis papuana</i>	-	0.09	0.21	0.17	-	0.11	0.11	0.15	0.13	0.07	0.05	0.07	0.06	0.10	0.13	0.07	-	0.15	0.17	0.22	0.14	0.43	0.21	0.08	-	0.07	0.06	0.26	0.08	0.13	-	0.95		
<i>Boa constrictor</i>	0.23	-	0.19	-	-	0.08	-	-	0.11	-	0.05	0.06	0.06	0.10	0.14	-	-	0.14	0.17	0.21	-	0.42	0.18	-	-	0.07	0.06	0.23	-	-	0.06	-		

Table S8S9. Body shape intercept differences. Pairwise differences in the intercept of the allometric regressions (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 9,999-iterations (upper triangle). Details as in Table S7S8.

	Python anchietae	Python bivittatus	Python brongersmai	Python curtus	Python molurus	Python sebae	Malayopython reticulatus	Malayopython timoriensis	Antaresia childreni	Antaresia maculosa	Antaresia perthensis	Antaresia stimsoni	Morelia bredli	Morelia carinata	Morelia spilota	Morelia viridis	Simalia amethystina	Simalia boeleni	Simalia kinghorni	Simalia clostolepis	Simalia nauta	Simalia oenpelliensis	Bothrochilus boa	Leiopython albertsi	Aspidites melanocephalus	Aspidites ramsayi	Liasis fuscus	Liasis mackloti	Liasis olivaceus	Liasis papuana	Boa constrictor	
Python anchietae	-	0.71	0.98	0.67	0.98	0.79	0.52	0.31	0.63	0.12	0.10	0.13	0.24	-	0.54	0.02	0.21	0.27	0.27	0.27	0.27	-	0.47	0.21	0.08	0.17	0.28	0.21	0.07	0.56	0.44	
Python bivittatus	0.48	-	0.86	0.24	0.67	0.78	0.64	0.35	0.71	0.17	-	0.24	0.27	-	0.29	-	0.16	-	-	0.25	-	-	0.48	0.11	-	-	-	-	-	-	0.61	0.70
Python brongersmai	0.43	0.74	-	0.88	0.95	0.95	0.73	0.62	0.82	0.41	0.40	0.46	0.52	0.50	0.63	0.24	0.50	0.64	0.63	0.65	0.64	0.59	-	0.75	0.46	0.35	0.53	0.63	0.52	0.44	0.80	0.67
Python curtus	0.74	1.15	0.55	-	0.64	0.64	0.10	0.17	0.44	0.01	-	0.01	-	-	0.31	-	0.06	-	-	0.24	-	-	0.08	0.03	-	-	-	0.44	-	-	0.53	0.03
Python molurus	0.31	0.47	0.62	0.87	-	0.74	0.49	0.29	0.51	0.09	-	0.11	0.22	-	0.34	-	0.10	0.27	-	-	0.26	-	0.37	0.18	0.08	0.18	0.27	0.17	-	0.59	0.47	
Python regius	0.48	0.85	0.49	0.41	0.56	-	0.12	0.23	0.53	0.02	-	0.01	0.01	-	0.23	-	0.10	-	-	-	0.24	-	0.09	0.06	-	0.01	0.28	0.07	-	0.48	0.05	
Python sebae	0.65	0.30	0.91	1.36	0.63	1.05	-	0.74	0.63	0.26	-	0.29	0.42	-	0.41	-	0.28	0.26	0.29	-	0.29	-	0.63	0.12	-	0.24	0.35	0.23	-	0.63	0.30	
Malayopython reticulatus	0.95	0.58	1.21	1.67	0.93	1.36	0.32	-	0.60	0.52	0.52	0.48	0.63	-	0.66	-	0.64	0.28	0.48	0.30	0.33	-	0.70	0.29	-	0.44	0.34	0.59	-	0.54	0.38	
Malayopython timoriensis	0.86	0.46	1.06	1.47	0.91	1.19	0.53	0.59	-	0.36	-	0.63	0.63	-	0.62	-	0.62	0.42	0.30	-	-	-	0.88	0.34	-	0.61	-	0.37	-	0.52	0.90	
Antaresia childreni	1.01	0.59	1.18	1.67	0.97	1.41	0.45	0.40	0.59	-	0.80	0.71	0.68	-	0.59	-	0.27	0.28	0.26	0.19	0.33	-	0.27	0.86	0.28	0.68	0.30	0.43	-	0.79	0.19	
Antaresia maculosa	1.19	-	1.34	-	-	-	-	0.59	-	0.25	-	0.44	0.31	0.49	0.68	0.34	-	0.51	0.44	0.35	0.53	0.43	0.47	-	0.76	0.66	0.63	0.61	0.29	-	-	
Antaresia perthensis	0.86	0.41	1.04	1.51	0.83	1.24	0.37	0.44	0.42	0.22	0.39	-	0.79	-	0.39	-	0.26	0.27	0.21	0.11	0.30	-	0.45	0.49	-	0.71	0.36	0.30	-	0.74	0.38	
Antaresia stimsoni	0.85	0.44	1.04	-	0.85	1.26	0.31	0.33	0.45	0.20	0.43	0.15	-	-	0.57	-	0.23	0.23	0.28	0.17	0.27	-	0.52	0.31	-	0.36	0.34	0.24	-	0.68	0.12	
Morelia bredli	-	-	1.88	-	-	-	-	-	0.60	-	-	-	-	-	0.61	0.82	-	0.47	0.46	0.27	-	0.30	0.44	-	-	-	0.28	0.43	-	0.26	-	
Morelia carinata	1.40	0.97	1.62	2.09	1.37	1.82	0.80	0.56	0.79	0.50	0.55	0.62	0.59	0.49	-	0.74	0.75	0.63	0.81	0.64	0.59	0.28	-	0.63	0.64	0.62	0.58	0.46	0.97	0.44	0.59	0.44
Morelia spilota	1.64	-	1.82	-	-	-	-	-	0.55	-	-	-	-	0.20	0.44	-	-	0.49	0.50	0.35	-	0.33	0.32	-	-	0.52	-	0.44	-	0.21	-	
Morelia viridis	1.07	0.70	1.38	1.79	1.00	1.50	0.51	0.35	0.71	0.49	-	0.53	0.49	-	0.49	-	-	0.21	-	0.22	-	-	0.30	0.12	-	0.27	-	0.32	-	0.52	0.17	
Simalia amethystina	1.84	-	2.03	-	1.81	-	1.23	0.96	1.40	0.96	0.95	1.16	1.08	0.62	0.71	0.51	0.97	-	0.98	0.98	0.64	0.57	0.38	0.27	-	0.45	0.35	0.68	0.52	0.99	-	-
Simalia boeleni	1.64	-	1.78	-	-	1.09	0.88	-	0.88	0.95	1.07	0.95	0.85	0.73	0.70	-	-	0.43	-	0.99	0.99	0.72	0.61	0.34	-	0.46	0.29	0.77	0.74	0.81	-	-
Simalia clostolepis	1.63	-	1.81	-	-	-	-	0.76	-	0.82	0.88	1.01	0.90	0.68	0.61	0.57	-	0.27	0.29	-	0.85	0.52	0.52	-	0.29	0.22	0.63	0.62	0.74	0.84	-	-
Simalia kinghorni	1.47	1.17	1.62	2.13	1.44	1.89	0.92	0.74	-	0.69	0.73	0.89	0.80	-	0.68	-	0.78	0.49	0.32	0.39	-	0.31	-	0.26	-	0.54	0.36	0.69	0.52	-	0.46	-
Simalia nauta	-	-	2.80	-	-	-	-	-	-	-	-	-	-	1.21	1.57	1.20	-	0.96	1.25	1.19	1.31	-	0.74	-	0.33	0.33	0.80	0.30	0.53	-	-	
Simalia oenpelliensis	-	-	-	-	-	-	-	-	-	1.66	-	-	-	1.98	2.02	-	-	2.06	2.44	2.32	-	1.46	-	-	-	0.34	-	0.54	-	0.34	-	-
Bothrochilus boa	0.78	0.39	1.02	1.47	0.81	1.20	0.28	0.34	0.34	0.40	-	0.29	0.23	0.64	-	0.46	1.19	1.04	-	0.93	-	-	-	0.14	-	0.24	-	0.22	-	0.62	0.28	
Leiopython albertsi	1.15	0.71	1.32	1.80	1.07	1.52	0.59	0.49	0.68	0.18	-	0.33	0.36	-	0.47	0.52	-	-	-	-	-	0.54	-	-	0.77	-	-	-	0.82	0.20	-	
Aspidites melanocephalus	1.42	-	1.56	-	1.34	-	-	-	0.46	0.32	-	-	-	0.55	0.36	-	0.74	0.77	0.73	0.54	1.42	2.21	-	-	-	0.29	0.53	0.40	0.23	-	-	
Aspidites ramsayi	1.05	-	1.17	-	1.00	1.40	0.60	0.62	0.58	0.26	0.28	0.25	0.34	0.78	0.64	-	0.69	1.15	1.09	1.04	0.91	1.87	-	0.53	0.27	0.55	-	0.49	0.32	-	0.87	0.29
Liasis fuscus	1.92	-	1.91	2.43	1.87	2.22	1.44	1.33	-	1.15	1.05	1.32	1.28	1.01	1.28	0.97	-	0.98	1.01	1.02	0.89	1.08	2.12	-	0.90	1.20	-	0.34	0.48	0.52	-	-
Liasis mackloti	1.29	-	1.49	-	1.26	1.71	0.66	0.41	0.80	0.38	0.45	0.55	0.48	-	0.26	-	0.46	0.62	0.61	0.49	0.49	1.50	-	0.59	-	0.44	0.59	1.10	-	0.53	-	
Liasis olivaceus	1.90	-	2.09	-	-	-	-	-	-	0.95	-	-	-	0.56	0.72	0.46	-	0.13	0.55	0.39	-	0.91	1.94	-	0.73	-	-	-	-	-	-	-
Liasis papuana	1.13	0.80	1.24	1.70	1.04	1.51	0.74	0.77	0.93	0.43	-	0.52	0.56	-	0.77	-	0.74	-	-	-	0.77	-	0.74	0.42	-	0.45	-	1.12	0.67	-	0.63	
Boa constrictor	0.74	0.28	0.95	1.34	0.68	1.04	0.43	0.59	0.36	0.52	-	0.33	0.42	-	0.87	-	0.69	-	-	-	-	-	0.42	0.58	-	0.47	-	-	-	-	0.77	-

Table S9S10. Head shape peramorphosis test. Pairwise comparisons of the predicted head shape differences at maximum per-group body size (bottom triangle), and the Benjamini-Hochberg corrected P -values of the difference between them computed with 10,000 ~~9,999~~ iterations (upper triangle). This test only applies to pairs of taxa for which the null hypothesis of common slope and common intercept has not been rejected. Cells highlighted in green correspond to species where they have a common slope and intercept but different predicted head shape at maximum per group size (peramorphosis/paedomorphosis). Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python bongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Similia amethystina</i>	<i>Similia boeleni</i>	<i>Similia clastolepis</i>	<i>Similia kinghorni</i>	<i>Similia nauta</i>	<i>Similia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>	
<i>Python anchietae</i>	-	0.47		0.67	0.38	0.71				0.07	0.07	0.04	0.09		0.17		0.15							0.05	0.05				0.06			0.19	
<i>Python bivittatus</i>	0.05	-	0.04	0.10	0.35	0.02			0.05	0.00				0.00	0.06	0.00		0.36	0.00	0.02	0.04	0.06	0.16	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	0.05	
<i>Python bongersmai</i>		0.05	-	0.78	0.02	0.10	0.02	0.01	0.09	0.00	0.00	0.00	0.01	0.00	0.06	0.00			0.00	0.02	0.04	0.06	0.16	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	0.05	
<i>Python curtus</i>	0.04	0.05	0.02	-	0.05	0.47	0.03	0.03	0.14					0.02					0.00		0.12		0.11				0.02	0.00	0.02	0.02			
<i>Python molurus</i>	0.06	0.03	0.05	0.05		0.01			0.00						0.00				0.00				0.05	0.00	0.00			0.19					
<i>Python regius</i>	0.04	0.05	0.04	0.03	0.06		0.00	0.01	0.12	0.00	0.00	0.00		0.00	0.01	0.00	0.05	0.00	0.00	0.02		0.02			0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Python sebae</i>			0.06	0.06		0.07		0.07	0.03		0.01				0.00	0.01			0.00	0.00	0.00	0.01	0.00				0.03	0.00	0.04	0.03			
<i>Malayopython reticulatus</i>			0.07	0.06		0.07	0.05		0.20		0.04			0.02	0.01		0.02	0.03	0.07	0.12	0.03	0.00	0.00		0.02		0.00	0.00	0.00	0.40			
<i>Malayopython timoriensis</i>		0.06	0.06	0.05		0.05	0.08	0.05		0.00	0.03	0.00	0.00	0.03	0.05	0.02		0.25	0.11	0.22	0.70	0.34	0.06		0.01	0.09	0.02	0.00	0.00	0.27	0.00		
<i>Antaresia childreni</i>	0.08	0.06	0.05		0.06	0.07		0.08		0.00	0.00	0.11			0.00				0.00				0.06	0.00	0.00			0.00	-	0.00	-	0.00	
<i>Antaresia maculosa</i>	0.09	-	0.06	-	-	0.07	0.05	0.05	0.06	0.06	-	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.03	0.00	0.01	-	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	
<i>Antaresia perthensis</i>	0.09	-	0.07	-	-	0.08	0.07	-	0.08	0.04	0.04	-	0.00	0.00	0.00	0.00		0.00	0.00	0.00	-	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Antaresia stimsoni</i>	0.07	-	0.05	-	-	-	-	-	0.08	0.02	0.05	0.04	-	0.00	0.00			0.00	0.00	0.00	-	0.07					0.00	-	0.00	-	0.00	0.00	
<i>Morelia bredli</i>		-	0.09	-	-	0.10	0.10	0.07	0.08	-	0.08	0.11	0.11	-	0.16	0.22		0.01	0.01	0.46	0.01	0.18	0.00				0.00	0.03	0.00	0.00	0.00	0.01	0.00
<i>Morelia carinata</i>	0.09	0.10	0.08	0.08	0.12	0.09	0.11	0.10	0.08	0.10	0.09	0.11	0.09	0.07	-	0.04		0.10	0.01	0.32	0.03	0.59	0.04	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.11	
<i>Morelia spilota</i>		-	0.09	-	-	0.09	-	-	0.07	-	0.07	0.10	-	0.02	0.07	-		0.00	0.00	0.27	0.00	0.07	0.00				0.00	0.00	-	0.00	0.01	-	
<i>Morelia viridis</i>	0.07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		-	0.01	0.03	0.23	0.09	0.03				0.00	0.00	0.00	0.00	0.04	0.01	
<i>Similia amethystina</i>		-	0.03	-	-	0.05	0.07	0.06	0.05	-	0.05	0.07	0.06	0.08	0.07	0.07	-	-	0.01	0.03	0.23	0.09	0.03				0.00	0.00	0.00	0.00	0.00	0.04	0.01
<i>Similia boeleni</i>	-	0.11	0.12	0.11	-	0.11	0.12	0.08	0.07	0.14	0.10	0.13	0.14	0.08	0.11	0.07	-	0.10	-	0.15	0.01	0.17	0.00				0.12	0.05	0.00	0.00	0.03	0.00	
<i>Similia clastolepis</i>	-	-	0.08	-	-	0.09	0.09	0.06	0.06	-	0.07	0.09	0.10	0.03	0.06	0.03	-	0.07	0.06	-	0.06	0.47	0.01	-			0.01	0.17	0.00	0.00	0.07	0.00	
<i>Similia kinghorni</i>	-	-	0.05	0.04	-	0.05	0.06	0.04	0.03	-	0.05	0.08	-	0.07	0.08	0.07	-	0.03	0.08	0.06	-	0.09	0.01	-			0.00	0.02	0.00	0.00	0.17	-	
<i>Similia nauta</i>	-	0.08	0.08	0.07	-	0.07	0.09	0.08	0.06	0.09	0.07	0.09	0.08	0.07	0.05	0.07	-	0.07	0.08	0.05	0.06	-	0.02	-			0.02	0.11	0.00	0.00	0.07	0.01	
<i>Similia oenpelliensis</i>	-	0.06	0.04	0.05	0.06	0.06	0.08	0.10	0.08	0.04	0.08	0.06	0.04	0.12	0.09	0.12	-	0.06	0.14	0.11	0.07	0.09	-	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	0.00	
<i>Bothrochilus boa</i>	0.11	-	0.08	-	0.08	-	-	-	0.05	0.05	0.03	-	-	0.12	-	-	-	-	-	-	-	-	0.08	-	0.00	-		0.04	0.03	-	0.00	-	
<i>Leiopython albertisii</i>	0.11	-	0.09	-	0.08	-	-	-	0.07	-	0.09	-	-	0.14	-	-	-	-	-	-	-	-	0.08	-	0.09	-		-	-	-	-	-	
<i>Aspidites melanocephalus</i>	-	-	0.13	-	-	0.12	-	0.09	0.08	-	0.11	0.14	-	0.08	0.12	0.08	-	0.11	0.04	0.07	0.09	0.09	0.16	-	-	-	0.01	0.00	-	0.00	0.00	0.00	
<i>Aspidites ramsayi</i>	-	-	0.09	-	-	0.09	-	-	0.06	-	0.08	0.11	-	0.05	0.09	0.05	-	0.08	0.05	0.04	0.06	0.07	0.12	-	-	0.05	-	0.00	-	0.00	0.07	0.00	
<i>Liasis fuscus</i>	-	0.06	0.08	0.08	0.04	0.09	0.05	0.09	0.09	0.05	0.07	0.06	0.07	0.14	0.13	0.13	-	0.09	0.15	0.12	0.09	0.12	0.07	0.05	-	0.16	0.12	-	0.49	0.07	0.02	0.00	
<i>Liasis mackloti</i>	0.10	-	0.08	0.09	-	0.10	0.06	0.10	0.10	0.05	0.08	0.06	-	0.14	0.14	-	-	0.09	0.16	0.13	0.10	0.13	0.07	0.05	-	-	0.02	-	0.02	0.00	-		
<i>Liasis olivaceus</i>	-	-	0.06	0.07	-	0.08	0.05	0.09	0.10	0.05	0.08	0.07	-	0.13	0.12	0.12	-	0.08	0.16	0.12	0.09	0.11	0.06	-	-	0.17	0.12	0.04	0.04	-	0.01	-	
<i>Liasis papuana</i>	-	0.07	0.08	0.07	-	0.08	0.07	0.04	0.04	0.09	0.05	0.08	0.09	0.08	0.10	0.07	-	0.06	0.06	0.06	0.04	0.07	0.10	0.08	-	0.07	0.05	0.09	0.10	0.10	-	0.00	
<i>Boa constrictor</i>	0.07	-	0.04	-	-	0.07	-	-	0.08	-	0.08	0.09	0.07	0.08	0.06	-	-	0.05	0.13	0.08	-	0.08	0.07	-	-	0.14	0.10	0.10	-	-	0.10	-	

Table S4S11. Body shape peramorphosis test. Pairwise comparisons of the predicted body shape differences at maximum per-group body size (bottom triangle), and the Benjamini-Hochberg corrected *P*-values of the difference between them computed with 10,000 ~~9,999~~ iterations (upper triangle). Details as in Table ~~S9S10~~.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>	
<i>Python anchietae</i>	-	0.30	0.06	0.29	0.68	0.26	0.68	0.20	0.58	0.26	0.22	0.06	0.67	-	0.40	-	0.10	0.14	0.66	0.59	0.12	-	-	0.66	0.10	0.09	0.25	0.26	0.13	0.13	0.17	0.92	
<i>Python bivittatus</i>	0.35	-	0.00	0.01	0.95	0.00	0.30	0.24	0.34	0.08	-	0.00	0.03	-	0.17	-	0.16	-	-	-	0.06	-	-	0.12	0.24	-	-	-	-	-	-	0.06	0.06
<i>Python brongersmai</i>	0.62	0.78	-	0.78	0.01	0.12	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.02	0.00	0.03	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	
<i>Python curtus</i>	0.55	0.70	0.13	-	0.08	0.34	0.01	0.01	0.06	-	-	-	-	-	0.06	-	0.00	-	-	-	0.01	-	-	0.01	-	-	-	-	0.03	-	0.01	0.01	
<i>Python molurus</i>	0.29	0.08	0.73	0.64	-	0.02	0.70	0.23	0.53	0.16	-	0.02	0.19	-	0.33	-	0.13	0.07	-	-	0.04	-	-	0.31	0.19	0.03	0.02	0.34	0.05	-	0.07	0.33	
<i>Python regius</i>	0.40	0.58	0.24	0.20	0.51	-	0.00	0.01	0.01	-	-	-	-	-	0.01	-	0.00	-	-	-	0.00	-	-	0.00	0.00	-	-	0.00	0.00	-	0.00	-	
<i>Python sebae</i>	0.21	0.19	0.76	0.67	0.14	0.53	-	0.16	0.23	0.31	-	-	0.00	0.13	-	0.04	-	0.01	0.01	0.19	-	0.02	-	0.50	0.01	-	-	0.01	0.19	0.07	-	0.02	0.13
<i>Malayopython reticulatus</i>	0.44	0.25	0.98	0.90	0.29	0.76	0.27	-	0.41	0.05	0.00	0.00	0.01	-	0.17	-	0.44	0.11	0.04	0.27	0.15	-	-	0.13	0.25	-	0.01	0.19	0.07	-	0.02	0.13	
<i>Malayopython timoriensis</i>	0.32	0.21	0.81	0.74	0.22	0.59	0.24	0.21	-	0.03	-	0.00	0.06	-	0.42	-	0.15	0.03	-	-	-	-	-	0.13	0.25	-	0.01	0.22	0.05	-	0.23	0.02	
<i>Antaresia childreni</i>	0.26	0.22	0.77	0.69	0.20	0.54	0.14	0.28	0.24	-	0.00	0.00	0.07	-	0.00	-	0.00	0.00	0.04	0.02	0.00	-	-	0.19	0.18	-	0.00	-	0.00	-	0.02	0.10	
<i>Antaresia maculosa</i>	0.32	-	0.46	-	-	-	-	0.60	-	0.34	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.05	0.00	0.00	0.00	-	
<i>Antaresia perthensis</i>	0.40	0.27	0.62	0.55	0.27	0.43	0.36	0.47	0.32	0.31	0.27	-	0.00	-	0.00	-	0.00	0.00	0.05	0.00	0.00	-	-	0.00	0.00	-	0.00	0.00	0.00	-	0.00	0.00	
<i>Antaresia stimsoni</i>	0.18	0.26	0.65	-	0.22	0.42	0.18	0.37	0.25	0.13	0.25	0.26	-	-	0.00	-	0.00	0.00	0.09	0.01	0.00	-	-	0.07	0.00	-	0.01	0.00	0.00	-	0.00	0.08	
<i>Morelia bredli</i>	-	-	0.96	-	-	-	-	-	-	-	0.61	-	-	-	0.09	0.47	-	-	0.00	0.01	0.71	-	0.16	0.00	-	-	-	0.00	0.01	-	-	-	
<i>Morelia carinata</i>	0.54	0.31	0.94	0.88	0.37	0.76	0.44	0.30	0.25	0.45	0.64	0.42	0.47	0.24	-	0.09	0.38	0.04	0.14	0.36	0.02	0.58	-	0.04	0.23	0.00	0.00	0.02	0.00	0.01	0.00	0.02	
<i>Morelia spilota</i>	0.43	-	0.92	-	-	-	-	-	-	-	0.55	-	-	0.08	0.28	-	-	0.00	0.01	0.80	-	0.04	0.00	-	-	0.00	-	0.09	-	0.00	-	-	
<i>Morelia viridis</i>	0.45	0.21	0.94	0.86	0.27	0.74	0.30	0.16	0.22	0.34	-	0.44	0.40	-	0.20	-	-	0.00	-	-	0.00	-	-	0.00	0.17	-	0.00	-	0.00	-	0.00	0.00	
<i>Simalia amethystina</i>	0.74	-	1.27	-	0.56	-	0.57	0.32	0.49	0.59	0.90	0.72	0.68	0.37	0.40	0.40	0.33	-	0.00	0.01	0.16	0.25	0.10	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-	
<i>Simalia boeleni</i>	0.29	-	0.70	-	-	0.23	0.34	-	0.19	0.32	0.20	0.19	0.30	0.35	0.24	-	0.61	-	0.47	0.00	0.05	0.01	0.15	-	0.00	0.01	0.02	0.00	0.00	-	-	-	
<i>Simalia clastolepis</i>	0.39	-	0.86	-	-	-	0.23	-	0.30	0.52	0.37	0.34	0.10	0.24	0.09	-	0.44	0.21	-	0.00	0.23	0.02	-	-	0.00	0.00	0.25	0.01	0.02	-	-	-	
<i>Simalia kinghorni</i>	0.67	0.49	1.24	1.15	0.54	1.02	0.51	0.29	-	0.53	0.86	0.73	0.63	-	0.48	-	0.33	0.19	0.58	0.42	-	0.07	-	0.01	-	0.00	0.00	0.02	0.00	-	0.78	-	
<i>Simalia nauta</i>	-	-	1.12	-	-	-	-	-	-	-	0.78	-	-	0.22	0.22	0.29	-	0.21	0.47	0.29	0.29	-	0.02	-	0.00	0.00	0.04	0.00	0.02	-	-	-	
<i>Simalia oenpelliensis</i>	-	-	-	-	-	-	-	-	-	-	1.00	-	-	0.52	-	0.54	-	0.25	0.74	0.58	-	0.40	-	-	-	0.00	-	0.00	-	0.00	-	-	
<i>Bothrochilus boa</i>	0.24	0.26	0.81	0.73	0.25	0.58	0.14	0.28	0.26	0.09	-	0.39	0.17	-	0.47	-	0.34	0.58	0.23	-	0.50	-	-	-	0.37	-	0.00	-	0.02	-	0.01	0.03	
<i>Leiopython albertisii</i>	0.46	0.18	0.92	0.84	0.23	0.71	0.30	0.18	0.20	0.34	-	0.40	0.39	-	0.20	-	0.12	-	-	-	-	-	-	0.37	-	0.00	-	0.00	-	0.00	0.00		
<i>Aspidites melanocephalus</i>	0.41	-	0.88	-	0.35	-	-	-	0.20	0.43	-	-	-	-	0.58	0.36	-	0.64	0.32	0.40	0.55	0.59	0.69	-	-	-	0.00	0.00	0.00	-	-	-	
<i>Aspidites ramsayi</i>	0.32	-	0.61	-	0.36	0.39	0.34	0.53	0.43	0.25	0.16	0.29	0.20	0.57	0.62	-	0.56	0.83	0.29	0.49	0.78	0.73	-	0.30	0.55	0.30	-	0.00	0.00	-	0.00	0.00	
<i>Liasis fuscus</i>	0.44	-	0.95	0.85	0.27	0.74	0.26	0.26	-	0.29	0.56	0.47	0.39	0.24	0.43	0.17	-	0.43	0.32	0.24	0.35	0.39	0.54	-	-	0.30	0.50	-	0.06	0.13	0.00		
<i>Liasis mackloti</i>	0.44	-	1.01	-	0.39	0.79	0.30	0.34	0.46	0.36	0.63	0.62	0.45	-	0.58	-	0.38	0.51	0.45	0.39	0.37	0.51	-	0.30	-	0.34	0.56	-	0.21	-	0.00		
<i>Liasis olivaceus</i>	0.50	-	1.06	-	-	-	-	-	-	-	0.67	-	-	0.28	0.43	0.26	-	0.31	0.43	0.31	-	0.33	0.37	-	-	0.38	-	0.19	-	-	-	-	
<i>Liasis papuana</i>	0.62	0.47	1.21	1.12	0.51	0.98	0.46	0.26	0.46	0.47	-	0.70	0.58	-	0.49	-	0.34	-	-	-	0.10	-	-	0.43	0.40	-	0.72	0.33	0.33	-	-	0.00	
<i>Boa constrictor</i>	0.15	0.27	0.57	0.49	0.22	0.35	0.22	0.43	0.29	0.24	-	0.26	0.15	-	0.47	-	0.41	-	-	-	-	-	-	0.26	0.41	-	0.27	-	-	-	-	0.64	

Table S4S12. Head size-shape space overlap (ontogenetic scaling) tests for heterochrony (Tfh1). Pairwise tests with the null hypothesis that species overlap in size-shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 9,999-iterations at upper triangle. The hypothesis of interest is the null in this case. Cells highlighted in green correspond to pairs of taxa that have overlapping trajectories in size-shape space and no difference in slope. Cells with numbers in red correspond to pairs of taxa where they overlap in size-shape space with phenotype at maximum size differs, confirming strong ontogenetic scaling. Low sample numbers for comparisons with *Morelia carinata* call for extra caution. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertisii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.00	-	0.01	0.02	0.01	-	-	-	0.00	0.00	0.00	0.00	0.03	-	0.00	-	-	-	-	-	-	-	0.00	0.00	-	-	-	0.00	-	-	0.00
<i>Python bivittatus</i>	0.04	-	0.00	0.00	0.35	0.00	-	-	0.02	0.00	-	-	-	0.00	-	-	-	0.00	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Python brongersmai</i>	-	0.06	-	0.52	0.01	0.02	0.01	0.13	0.07	0.01	0.00	0.00	0.00	0.00	-	0.00	-	0.00	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python curtus</i>	0.02	0.05	0.04	-	0.00	0.03	0.00	0.00	0.09	-	-	-	-	0.01	-	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Python molurus</i>	0.01	0.05	0.03	0.03	-	0.00	-	-	-	0.00	-	-	-	0.01	-	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Python regius</i>	0.05	0.09	0.07	0.07	0.06	-	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python sebae</i>	-	-	0.12	0.12	-	0.15	-	0.00	0.00	0.00	-	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Malayopython reticulatus</i>	-	-	0.11	0.11	-	0.14	0.19	-	0.00	-	0.00	-	-	0.09	0.09	-	0.00	0.00	0.00	0.00	0.01	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Malayopython timoriensis</i>	-	0.05	0.03	0.03	-	0.06	0.11	0.10	-	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.19	0.00	0.00	0.00	0.04	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia childreni</i>	0.11	0.14	0.12	-	0.11	0.15	-	0.12	-	0.00	0.00	0.02	-	0.00	-	-	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia maculosa</i>	0.09	-	0.10	-	0.13	0.18	0.17	0.10	0.19	-	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia perthensis</i>	0.09	-	0.11	-	-	0.14	0.19	-	0.10	0.19	0.17	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia stimsoni</i>	0.14	-	0.16	-	-	-	-	0.15	-	0.24	0.22	0.23	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Morelia bredli</i>	-	-	0.06	-	-	0.09	0.14	0.13	0.06	-	0.13	0.13	0.18	-	0.07	0.04	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Morelia carinata</i>	0.01	0.04	-	0.02	0.01	0.05	0.10	0.00	0.01	0.11	0.09	0.09	0.14	0.04	-	0.04	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Morelia spilota</i>	-	-	0.36	-	-	0.39	-	0.35	-	0.42	0.43	-	-	0.38	0.34	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Morelia viridis</i>	0.13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Simalia amethystina</i>	-	-	0.08	-	-	0.11	0.16	0.15	0.07	-	0.14	0.15	0.20	0.10	-	0.40	-	-	0.00	0.00	0.12	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia boeleni</i>	-	0.07	0.05	0.05	-	0.08	0.13	0.12	0.05	0.14	0.12	0.12	0.17	0.08	0.04	0.37	-	0.09	-	0.00	0.00	0.01	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>Simalia clastolepis</i>	-	-	0.03	-	-	0.06	0.11	0.10	0.02	-	0.10	0.10	0.15	0.05	0.01	0.35	-	0.07	0.05	-	0.00	0.20	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia kinghorni</i>	-	-	0.08	0.08	-	0.11	0.16	0.15	0.08	-	0.15	0.15	-	0.11	-	0.40	-	0.12	0.10	0.08	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia nauta</i>	-	0.05	0.03	0.03	-	0.06	0.11	0.10	0.02	0.11	0.10	0.10	0.15	0.05	0.01	0.35	-	0.07	0.04	0.02	0.07	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia oenpelliensis</i>	-	0.05	0.03	0.03	0.02	0.06	0.11	0.10	0.03	0.12	0.10	0.10	0.15	0.06	0.01	0.35	-	0.07	0.05	0.02	0.08	0.02	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Bothrochilus boa</i>	0.06	-	0.07	-	0.06	-	-	-	0.16	0.14	0.15	-	-	0.06	-	-	-	-	-	-	-	-	0.07	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00
<i>Leiopython albertisii</i>	0.12	-	0.13	-	0.12	-	-	0.22	-	0.20	-	0.20	-	-	-	-	-	-	-	-	-	-	0.13	-	0.17	-	-	-	-	-	-	-
<i>Aspidites melanocephalus</i>	-	-	0.16	-	-	0.19	-	0.23	0.15	-	0.22	0.23	-	0.18	0.14	0.48	-	0.20	0.17	0.15	0.20	0.15	0.15	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aspidites ramsayi</i>	-	-	0.12	-	-	0.15	-	0.12	-	0.19	0.19	-	0.15	0.11	0.44	-	0.16	0.14	0.12	0.17	0.12	0.12	-	0.24	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Liasis fuscus</i>	-	0.08	0.06	0.06	0.05	0.09	0.14	0.13	0.05	0.14	0.12	0.13	0.18	0.08	0.04	0.38	-	0.10	0.07	0.05	0.10	0.05	0.05	0.10	-	0.18	0.14	-	0.01	0.00	0.00	0.00
<i>Liasis mackloti</i>	0.07	-	0.08	0.08	-	0.11	0.16	0.15	0.08	0.17	0.15	0.15	-	0.11	0.07	-	0.12	0.10	0.08	0.13	0.07	0.08	0.12	-	-	0.10	-	0.00	0.00	-	-	-
<i>Liasis olivaceus</i>	-	-	0.07	0.07	-	0.11	0.16	0.15	0.07	0.16	0.14	0.15	-	0.10	-	0.40	-	0.11	0.09	0.07	0.12	0.07	0.07	-	0.20	0.16	0.10	0.12	-	0.00	-	-
<i>Liasis papuana</i>	-	0.07	0.05	0.05	-	0.08	0.13	0.12	0.04	0.13	0.11	0.12	0.17	0.07	0.03	0.37	-	0.09	0.06	0.04	0.09	0.04	0.04	0.08	-	0.17	0.13	0.07	0.09	0.08	-	0.00
<i>Boa constrictor</i>	0.13	-	0.15	-	-	0.18	-	0.14	-	0.22	0.22	0.27	0.17	0.13	-	-	0.19	0.16	0.14	-	0.14	0.14	-	0.27	0.23	0.17	-	-	0.16	-	-	-

Table S12S13. Head shape space overlap tests for heterochrony (Tfh2). Pairwise tests with the null hypothesis that species overlap in shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 9,999-iterations at upper triangle. The hypothesis of interest is the null in this case. Cells highlighted in green and with white borders correspond to pairs of taxa that have overlapping trajectories in shape space only and not in size-shape, therefore heterochrony by size-shape dissociation. Cells highlighted in green without borders are pairs of taxa where the null has been accepted but they also overlap in size-shape space (tested in Thf1). Low sample numbers for comparisons with *Morelia carinata* call for extra caution. Black boxes outline comparisons within clades.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilata</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsii</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>	
<i>Python anchietae</i>	-	0.00	0.04	0.08	0.01	-	-	-	-	0.00	0.00	0.00	0.00	-	0.09	-	0.01	-	-	-	-	-	-	0.00	0.00	-	-	0.00	-	-	-	0.00	
<i>Python bivittatus</i>	0.04	-	0.00	0.00	0.26	0.00	-	-	-	0.06	0.40	-	-	-	0.00	-	-	0.00	-	0.00	-	0.00	0.00	-	-	-	0.00	-	-	-	-	0.00	
<i>Python brongersmai</i>	-	0.05	-	0.33	0.00	0.01	0.02	0.36	0.08	0.09	0.00	0.00	0.00	0.00	0.01	0.00	0.12	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	
<i>Python curtus</i>	0.02	0.05	0.03	-	0.05	0.07	0.00	0.00	0.11	-	-	-	-	0.02	-	-	-	-	-	0.00	0.00	0.01	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	
<i>Python molurus</i>	0.01	0.04	0.02	0.02	-	0.00	-	-	0.02	-	0.05	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	
<i>Python regius</i>	0.04	0.07	0.05	0.06	0.05	-	0.00	0.00	0.58	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Python sebae</i>	-	-	0.09	0.09	-	0.12	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.07	-	-	0.00	0.00	0.01	0.00	-	-	-	-	
<i>Malayopython reticulatus</i>	-	-	0.08	0.08	-	0.11	0.14	-	0.04	-	0.00	-	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.01	0.01	-	-	0.00	0.00	0.00	0.00	0.00	0.00	-	-	
<i>Malayopython timoriensis</i>	-	0.04	0.02	0.02	-	0.05	0.09	0.08	-	1.00	0.01	0.71	0.00	0.00	0.04	0.00	-	0.00	0.05	0.00	0.01	0.00	0.01	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Antaresia childreni</i>	0.10	0.13	0.11	-	0.10	0.14	-	0.10	-	0.45	0.00	0.51	-	0.07	-	-	-	1.00	0.01	0.10	0.00	0.00	0.06	0.01	0.07	-	0.00	0.00	0.00	1.00	-	-	
<i>Antaresia maculosa</i>	0.07	-	0.08	-	-	0.11	0.15	0.14	0.08	0.17	-	1.00	0.00	0.00	0.01	0.00	-	0.00	0.01	0.10	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Antaresia perthensis</i>	0.08	-	0.09	-	-	0.12	0.15	-	0.09	0.17	0.15	-	0.00	0.01	0.12	0.00	-	0.00	0.99	0.39	0.00	0.00	0.00	0.02	0.00	0.13	0.69	0.00	0.00	0.49	0.00	0.00	
<i>Antaresia stimsoni</i>	0.11	-	0.13	-	-	-	-	0.12	0.21	0.18	0.19	-	0.99	0.01	-	-	0.00	0.00	0.99	-	0.01	0.00	-	-	0.00	-	0.00	-	0.00	0.00	0.00	0.00	
<i>Morelia bredli</i>	-	-	0.04	-	0.07	0.10	0.09	0.03	-	0.10	0.10	0.14	-	0.00	0.10	-	0.00	0.00	0.00	0.02	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Morelia carinata</i>	0.00	0.03	0.02	0.02	0.01	0.04	0.08	0.07	0.01	0.10	0.07	0.08	0.11	0.03	-	0.01	-	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	
<i>Morelia spilata</i>	-	-	0.23	-	-	0.26	-	0.23	-	0.29	0.30	-	-	0.25	0.22	-	-	0.00	0.00	0.37	0.00	0.01	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	
<i>Morelia viridis</i>	0.11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
<i>Simalia amethystina</i>	-	-	0.05	-	-	0.08	0.12	0.11	0.05	-	0.11	0.12	0.15	0.07	0.04	0.26	-	-	0.00	0.00	0.04	0.00	0.09	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Simalia boeleni</i>	-	0.05	0.03	0.03	-	0.06	0.09	0.09	0.03	0.11	0.09	0.09	0.13	0.04	0.02	0.24	-	0.06	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	
<i>Simalia clastolepis</i>	-	-	0.02	-	-	0.05	0.08	0.08	0.02	-	0.08	0.08	0.12	0.03	0.01	0.23	-	0.05	0.03	-	0.00	0.03	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	
<i>Simalia kinghorni</i>	-	-	0.06	0.06	-	0.08	0.12	0.11	0.05	-	0.11	0.12	-	0.07	0.04	0.26	-	0.08	0.06	0.05	-	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Simalia nauta</i>	-	0.04	0.02	0.02	-	0.04	0.08	0.07	0.01	0.10	0.07	0.08	0.12	0.03	0.01	0.22	-	0.04	0.02	0.01	0.05	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Simalia oenpelliensis</i>	-	0.04	0.02	0.03	0.02	0.05	0.09	0.08	0.02	0.11	0.08	0.09	0.12	0.04	0.01	0.23	-	0.05	0.03	0.02	0.05	0.01	-	0.00	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00	
<i>Bothrochilus boa</i>	0.06	-	0.07	-	0.06	-	-	-	0.15	0.12	0.13	-	-	0.05	-	-	-	-	-	-	-	0.06	-	0.00	-	0.00	-	0.00	0.00	-	0.02	-	
<i>Leiopython albertsii</i>	0.11	-	0.12	-	0.11	-	-	0.20	-	0.18	-	-	-	0.11	-	-	-	-	-	-	-	0.12	-	0.16	-	-	-	0.00	-	-	-	-	
<i>Aspidites melanocephalus</i>	-	-	0.09	-	-	0.12	-	0.15	0.09	-	0.15	0.16	-	0.10	0.08	0.30	-	0.12	0.10	0.09	0.12	0.08	0.09	-	-	-	0.00	-	0.00	0.00	0.00	0.00	
<i>Aspidites ramsayi</i>	-	-	0.09	-	-	0.12	-	0.09	-	0.15	0.15	-	-	0.10	0.08	0.30	-	0.12	0.09	0.08	0.12	0.08	0.09	-	-	0.16	-	0.00	0.00	0.00	0.01	0.00	
<i>Liasis fuscus</i>	-	0.06	0.04	0.04	0.04	0.07	0.10	0.10	0.04	0.12	0.10	0.10	0.14	0.05	0.03	0.25	-	0.07	0.04	0.03	0.07	0.03	0.04	0.08	-	0.11	0.10	-	0.00	0.00	0.00	0.00	
<i>Liasis mackloti</i>	0.06	-	0.07	0.07	-	0.09	0.13	0.12	0.06	0.15	0.12	0.13	-	0.08	0.05	-	-	0.09	0.07	0.06	0.09	0.06	0.06	0.11	-	-	-	0.08	-	0.00	0.00	0.00	
<i>Liasis olivaceus</i>	-	-	0.06	0.06	-	0.09	0.12	0.11	0.05	0.14	0.12	0.12	-	0.07	0.05	0.26	-	0.09	0.06	0.05	0.09	0.05	0.06	-	0.12	0.12	0.07	0.10	-	0.00	0.00	0.00	
<i>Liasis papuana</i>	-	0.06	0.04	0.04	-	0.06	0.10	0.09	0.03	0.12	0.09	0.10	0.14	0.05	0.03	0.24	-	0.06	0.04	0.03	0.07	0.03	0.03	0.08	-	0.10	0.10	0.05	0.08	0.07	-	0.00	
<i>Boa constrictor</i>	0.11	-	0.12	-	-	0.14	-	-	0.11	-	0.17	0.18	0.21	0.13	0.10	-	-	0.14	0.12	0.11	-	0.11	0.11	-	-	0.18	0.18	0.13	-	-	0.13	-	0.00

Table S4S14. Body size-shape space overlap tests for heterochrony (Tfh1). Pairwise tests with the null hypothesis that species overlap in size-shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the P -values of the of size-shape dissociation computed with 10,000 9,999 iterations at upper triangle. Details as in Table S4S12.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsi</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.00	0.00	0.00	0.23	0.00	0.03	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13
<i>Python bivittatus</i>	0.66	-	0.00	0.00	0.17	0.00	0.07	0.00	0.09	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python brongersmai</i>	0.46	1.00	-	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python curtus</i>	0.43	0.97	0.77	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python molurus</i>	0.32	0.86	0.66	0.63	-	0.00	0.17	0.00	0.09	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13
<i>Python regius</i>	1.18	1.73	1.52	1.50	1.39	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Python sebae</i>	1.66	2.20	1.99	1.97	1.86	2.72	-	0.00	0.18	0.00	-	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Malayopython reticulatus</i>	2.12	2.67	2.46	2.44	2.33	3.19	3.66	-	0.03	0.00	0.00	0.00	0.00	0.33	0.00	0.00	0.01	0.07	0.00	-	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Malayopython timoriensis</i>	0.27	0.81	0.61	0.58	0.47	1.34	1.81	2.27	-	0.00	-	0.00	0.00	0.16	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.01
<i>Antaresia childreni</i>	2.32	2.86	2.66	2.63	2.52	3.38	3.85	4.32	2.47	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Antaresia maculosa</i>	2.45	-	2.78	-	-	-	-	4.45	-	4.65	-	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	-
<i>Antaresia perthensis</i>	1.73	2.27	2.07	2.04	1.93	2.80	3.27	3.74	1.88	3.93	4.06	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00
<i>Antaresia stimsoni</i>	2.89	3.44	3.23	-	3.09	3.96	4.43	4.90	3.04	5.09	5.22	4.50	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Morelia bredli</i>	-	-	1.06	-	-	-	-	-	-	3.05	-	-	-	0.02	0.62	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Morelia carinata</i>	0.07	0.61	0.41	0.38	0.27	1.14	1.61	2.08	0.22	2.27	2.40	1.68	2.84	0.67	-	0.29	0.58	0.00	0.52	0.20	0.05	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.06	0.00	0.00	0.00
<i>Morelia spilota</i>	8.56	-	8.89	-	-	-	-	-	-	10.88	-	-	-	9.16	8.51	-	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Morelia viridis</i>	2.58	3.12	2.92	2.89	2.78	3.65	4.12	4.59	2.73	4.78	-	4.19	5.35	2.53	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Simalia amethystina</i>	1.00	-	1.34	-	1.20	-	2.54	3.01	1.15	3.20	3.33	2.61	3.78	1.60	0.95	9.44	3.46	-	0.00	0.00	0.36	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia boeleni</i>	1.10	-	1.43	-	-	2.63	3.10	-	3.30	3.43	2.71	3.87	1.70	1.05	9.53	-	1.98	-	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia clastolepis</i>	0.29	-	0.62	-	-	-	2.29	-	2.49	2.62	1.90	3.06	0.89	0.24	8.72	-	1.17	1.26	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia kinghorni</i>	1.63	2.17	1.97	1.94	1.83	2.70	3.17	3.64	-	3.83	3.96	3.24	4.40	1.58	-	4.09	2.51	2.61	1.80	-	0.05	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia nauta</i>	-	-	0.65	-	-	-	-	-	-	2.64	-	-	-	0.91	0.26	8.75	-	1.20	1.29	0.48	1.82	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Simalia oenpelliensis</i>	-	-	-	-	-	-	-	-	-	2.65	-	-	0.92	-	8.76	-	1.21	1.30	0.49	-	0.52	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-
<i>Bothrochilus boa</i>	1.38	1.92	1.71	1.69	1.58	2.44	2.91	3.38	1.53	3.58	-	2.99	4.15	1.33	-	3.84	2.26	2.35	-	2.89	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Leiopython albertsi</i>	3.04	3.58	3.38	3.35	3.24	4.10	4.57	5.04	3.19	5.24	-	4.65	5.81	-	2.99	5.50	-	-	-	-	-	-	4.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aspidites melanocephalus</i>	3.00	-	3.34	-	3.20	-	-	-	5.20	5.33	-	-	-	2.95	11.44	-	3.88	3.98	3.17	4.51	3.19	3.20	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aspidites ramsayi</i>	2.36	-	2.69	-	2.56	3.42	3.89	4.36	2.51	4.56	4.68	3.97	5.13	2.96	2.31	-	4.82	3.24	3.33	2.52	3.87	2.55	-	3.61	5.28	5.24	0.00	0.00	0.00	0.00	0.00	0.00
<i>Liasis fuscus</i>	1.62	-	1.96	1.93	1.82	2.68	3.15	3.62	-	3.82	3.95	3.23	4.39	2.22	1.57	10.06	-	2.50	2.60	1.79	3.13	1.81	1.82	-	4.50	3.86	-	0.00	0.00	0.00	0.00	0.00
<i>Liasis mackloti</i>	1.79	-	2.13	-	1.99	2.86	3.33	3.80	1.94	3.99	4.12	3.40	4.56	-	1.74	-	4.25	2.67	2.77	1.96	3.30	1.98	-	3.05	-	4.67	4.03	3.29	-	0.00	0.00	0.00
<i>Liasis olivaceus</i>	1.23	-	1.57	-	-	-	-	-	-	3.56	-	-	-	1.83	1.18	9.67	-	2.11	2.21	1.40	-	1.42	1.43	-	4.11	-	2.73	-	2.73	-	0.00	0.00
<i>Liasis papuana</i>	0.43	0.97	0.77	0.74	0.63	1.50	1.97	2.44	0.58	2.63	-	2.04	3.21	-	0.38	-	2.89	-	-	1.94	-	-	1.69	3.35	-	2.67	1.93	2.10	-	-	0.00	0.00
<i>Boa constrictor</i>	3.64	4.19	3.98	3.96	3.85	4.71	5.18	5.65	3.80	5.84	-	5.26	6.42	-	3.60	-	6.11	-	-	-	-	-	4.90	6.56	-	5.88	-	-	-	-	3.96	-

Table S14S15. Body shape space overlap tests for heterochrony (Tfh2). Pairwise tests with the null hypothesis that species overlap in shape space. Test statistics (see Materials and Methods for details) at bottom triangle, and the *P*-values of the of size-shape dissociation computed with 10,000 9,999-iterations at upper triangle. Details as in Table S12S13.

	<i>Python anchietae</i>	<i>Python bivittatus</i>	<i>Python brongersmai</i>	<i>Python curtus</i>	<i>Python molurus</i>	<i>Python regius</i>	<i>Python sebae</i>	<i>Malayopython reticulatus</i>	<i>Malayopython timoriensis</i>	<i>Antaresia childreni</i>	<i>Antaresia maculosa</i>	<i>Antaresia perthensis</i>	<i>Antaresia stimsoni</i>	<i>Morelia bredli</i>	<i>Morelia carinata</i>	<i>Morelia spilota</i>	<i>Morelia viridis</i>	<i>Simalia amethystina</i>	<i>Simalia boeleni</i>	<i>Simalia clastolepis</i>	<i>Simalia kinghorni</i>	<i>Simalia nauta</i>	<i>Simalia oenpelliensis</i>	<i>Bothrochilus boa</i>	<i>Leiopython albertsi</i>	<i>Aspidites melanocephalus</i>	<i>Aspidites ramsayi</i>	<i>Liasis fuscus</i>	<i>Liasis mackloti</i>	<i>Liasis olivaceus</i>	<i>Liasis papuana</i>	<i>Boa constrictor</i>
<i>Python anchietae</i>	-	0.00	0.01	0.00	0.334	0.00	0.07	0.00	0.03	0.00	0.07	0.01	0.01	-	0.00	0.00	0.00	0.02	0.00	0.01	-	-	0.00	0.05	0.03	0.46	0.08	0.00	0.00	0.01	0.93	
<i>Python bivittatus</i>	0.50	-	0.00	0.00	0.23	0.00	0.16	0.00	0.662	0.002	-	0.00	0.00	-	0.00	0.00	0.002	-	-	-	0.00	-	0.00	0.01	-	-	-	-	-	0.01	0.00	
<i>Python brongersmai</i>	0.39	0.81	-	0.52	0.02	0.02	0.00	0.002	0.002	0.002	0.21	0.00	0.00	0.00	0.02	0.002	0.002	0.002	0.002	0.002	0.002	0.002	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
<i>Python curtus</i>	0.28	0.70	0.58	-	0.00	0.008	0.00	0.00	0.002	0.00	-	0.00	-	-	0.00	0.002	-	-	-	-	0.00	-	0.00	0.00	-	0.002	-	-	-	0.00	0.00	
<i>Python molurus</i>	0.28	0.70	0.59	0.48	-	0.00	0.31	0.00	0.29	0.00	-	0.29	0.02	0.00	0.00	0.002	0.002	0.002	0.002	-	0.00	-	0.02	0.07	0.00	0.07	0.04	0.00	-	0.02	0.40	
<i>Python regius</i>	0.88	1.30	1.19	1.08	1.09	-	0.00	0.00	0.002	0.00	-	0.00	0.00	-	0.002	0.002	0.002	0.002	0.002	-	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00
<i>Python sebae</i>	1.46	1.88	1.76	1.65	1.66	2.26	-	0.00	0.22	0.00	-	0.00	0.00	-	0.058	0.002	0.002	0.002	0.002	0.00	-	0.00	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	
<i>Malayopython reticulatus</i>	1.81	2.23	2.12	2.01	2.01	2.61	3.18	-	0.08	0.00	0.00	0.32	0.00	-	0.676	0.002	0.002	0.15	0.16	0.00	-	-	0.00	0.43	-	0.00	0.00	0.00	-	0.21	0.00	
<i>Malayopython timoriensis</i>	0.21	0.63	0.51	0.40	0.41	1.01	1.58	1.94	-	0.002	-	0.89	0.01	-	0.126	0.002	0.002	-	-	-	-	-	0.06	0.12	-	0.00	-	0.00	-	0.00	0.03	
<i>Antaresia childreni</i>	1.91	2.33	2.21	2.11	2.11	2.71	3.28	3.64	2.03	-	0.002	0.00	0.002	-	0.002	0.002	0.002	0.002	0.002	0.00	-	-	0.00	0.002	1	0.002	0.00	0.00	-	0.002	0.00	
<i>Antaresia maculosa</i>	2.09	-	2.39	-	-	-	3.82	-	3.92	-	0.22	0.00	0.00	0.00	0.00	0.00	0.10	0.02	0.002	0.85	0.00	0.944	-	0.03	0.02	0.03	0.00	0.00	-	-	-	
<i>Antaresia perthensis</i>	1.45	1.87	1.75	1.64	1.65	2.25	2.82	3.18	1.57	3.27	3.45	-	0.11	-	0.002	0.002	0.00	0.036	0.002	0.04	-	-	0.00	1.00	-	0.096	0.01	0.002	-	0.096	0.00	
<i>Antaresia stimsoni</i>	2.23	2.65	2.53	-	2.43	3.03	3.60	3.96	2.35	4.05	4.23	3.59	-	-	0.002	0.002	0.002	0.00	0.002	0.00	-	-	0.00	0.00	-	0.00	0.00	0.002	-	0.00	0.00	
<i>Morelia bredli</i>	-	-	0.81	-	-	-	-	-	-	2.52	-	-	-	-	0.02	0.426	-	0.00	0.00	0.07	-	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	-	
<i>Morelia carinata</i>	0.05	0.47	0.36	0.25	0.25	0.85	1.42	1.78	0.18	1.88	2.06	1.42	2.20	0.48	-	0.21	0.64	0.01	0.60	0.46	0.09	0.03	-	0.00	0.10	0.064	0.00	0.144	0.03	0.02	0.102	
<i>Morelia spilota</i>	6.80	-	7.10	-	-	-	-	-	-	8.81	-	-	-	7.23	6.77	-	-	0.00	0.06	0.86	-	0.02	0.00	-	0.002	-	0.002	-	0.002	-	-	
<i>Morelia viridis</i>	2.25	2.67	2.55	2.44	2.45	3.05	3.62	3.98	2.37	4.07	-	3.61	4.39	-	2.22	-	-	0.00	-	0.00	-	-	0.00	0.00	-	0.002	-	0.002	-	0.02	0.002	
<i>Simalia amethystina</i>	0.73	-	1.04	-	0.94	-	2.11	2.46	0.86	2.56	2.74	2.10	2.88	1.16	0.70	7.45	2.90	-	0.00	0.00	0.22	0.12	0.004	0.002	-	0.00	0.00	0.00	0.00	-	-	
<i>Simalia boeleni</i>	0.95	-	1.25	-	-	2.32	2.68	-	2.77	2.96	2.31	3.09	1.38	0.92	7.67	-	-	1.60	-	0.18	0.00	0.03	0.00	0.008	-	0.00	0.00	0.00	0.00	-	-	
<i>Simalia clastolepis</i>	0.24	-	0.55	-	-	-	1.97	-	2.07	2.25	1.61	2.39	0.67	0.21	6.96	-	-	0.90	1.11	-	0.00	0.004	0.00	-	0.00	0.00	0.01	0.00	0.00	-	-	
<i>Simalia kinghorni</i>	1.36	1.78	1.66	1.56	1.56	2.16	2.73	3.09	-	3.19	3.37	2.72	3.50	-	1.33	-	3.52	2.01	2.23	1.52	-	0.12	-	0.002	-	0.00	0.00	0.00	0.00	-	0.05	-
<i>Simalia nauta</i>	-	-	0.55	-	-	-	-	-	-	2.25	-	-	0.67	0.22	6.96	-	-	0.90	1.11	0.41	1.52	-	0.00	-	0.00	0.00	0.00	0.00	0.02	-	-	
<i>Simalia oenpelliensis</i>	-	-	-	-	-	-	-	-	-	2.25	-	-	0.67	-	6.96	-	-	0.89	1.11	0.40	-	0.41	-	-	0.002	-	0.01	-	0.002	-	-	
<i>Bothrochilus boa</i>	1.16	1.58	1.46	1.35	1.36	1.96	2.53	2.89	1.28	2.98	-	2.52	3.30	-	1.13	-	3.32	1.81	2.02	-	2.43	-	-	0.00	-	0.002	-	0.002	-	0.00	0.00	
<i>Leiopython albertsi</i>	2.63	3.05	2.93	2.83	2.83	3.43	4.00	4.36	2.75	4.45	-	3.99	4.77	-	2.60	-	4.79	-	-	-	-	-	-	3.70	-	-	-	-	-	0.10	0.00	
<i>Aspidites melanocephalus</i>	2.39	-	2.69	-	2.59	-	-	-	4.22	4.40	-	-	-	2.36	9.11	-	3.04	3.26	2.55	3.67	2.55	2.55	-	-	-	0.00	0.00	0.00	-	-	-	
<i>Aspidites ramsayi</i>	1.87	-	2.17	-	2.07	2.67	3.24	3.60	1.99	3.69	3.87	3.23	4.01	2.29	1.84	-	4.03	2.52	2.73	2.03	3.14	2.03	-	2.94	4.41	4.17	-	0.00	0.00	-	0.002	0.002
<i>Liasis fuscus</i>	1.31	-	1.61	1.51	1.51	2.11	2.68	3.04	-	3.13	3.32	2.67	3.45	1.74	1.28	8.03	-	1.96	2.17	1.47	2.59	1.47	1.47	-	3.62	3.09	-	0.03	0.002	0.002	-	
<i>Liasis mackloti</i>	1.36	-	1.66	-	1.56	2.16	2.73	3.09	1.48	3.18	3.36	2.72	3.50	-	1.33	-	3.52	2.01	2.22	1.52	2.63	1.52	-	2.43	-	3.67	3.14	2.58	-	0.002	-	
<i>Liasis olivaceus</i>	0.91	-	1.21	-	-	-	-	-	-	2.91	-	-	-	1.33	0.88	7.62	-	1.56	1.77	1.07	-	1.07	1.07	-	-	3.21	-	2.13	-	-	-	
<i>Liasis papuana</i>	0.36	0.78	0.66	0.56	0.56	1.16	1.73	2.09	0.48	2.19	-	1.72	2.50	-	0.33	-	2.52	-	-	-	1.64	-	-	1.43	2.91	-	2.14	1.59	1.63	-	0.00	
<i>Boa constrictor</i>	2.89	3.31	3.19	3.09	3.09	3.69	4.26	4.62	3.01	4.71	-	4.25	5.03	-	2.86	-	5.05	-	-	-	-	-	-	3.96	5.43	-	4.67	-	-	-	3.16	-

Figure S1. Landmark and semilandmark configuration used to describe dorsal head shape in pythons. Description of numbered landmarks (large red dots) and semilandmarks (small red dots) is as follows: 1, tip of the snout; 2-3 anterior most points of the nostrils; 4-5, anterior most points of the eyes; 6-7, posterior most points of the eyes; 8-9, corners of the mouth; 10-22 and 23-35, semi-landmark curves describing the outline of the head going from the tip of the snout to the corner of the mouth for each side.

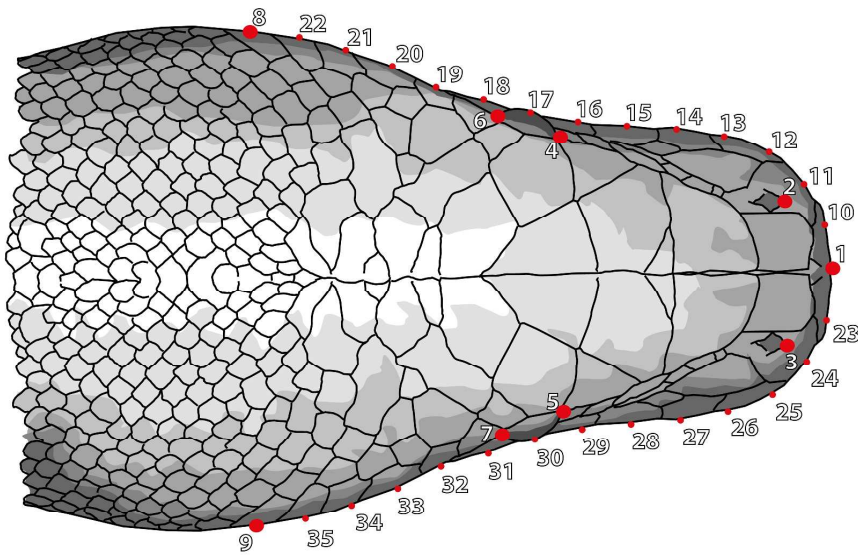
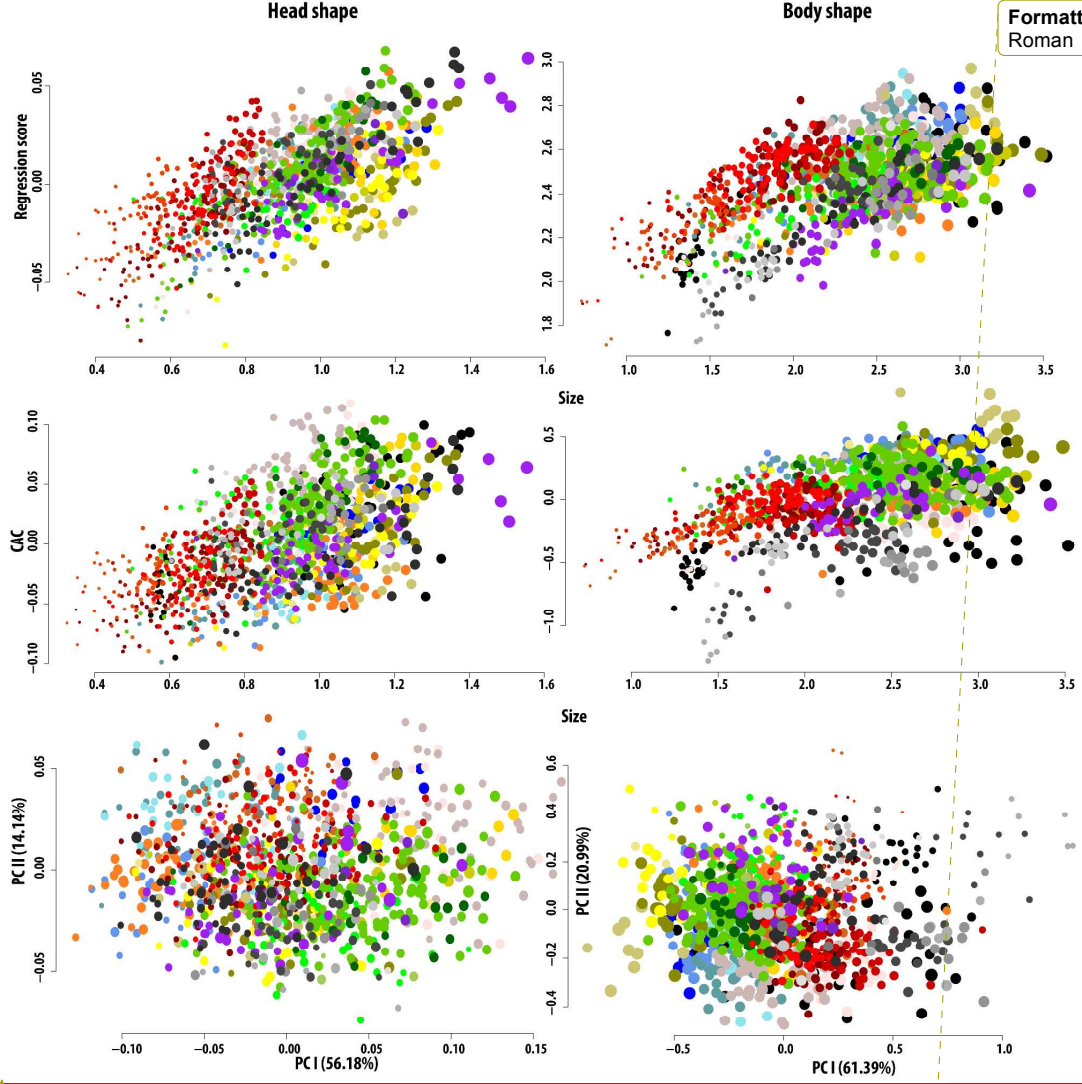


Figure S2. Regression scores (top), common allometric components (CAC; middle) and Principal Component Analysis (PCA; bottom) of python head shape (left) and body shape (right). Dots are colored according to their species and clades as in Figs. 2 and 3. Dot size is proportional to size. The x axis of size in the Regression score and CAC plots corresponds to log-transformed (centroid size) and log-transformed (size) for head and body shape, respectively. Principal component axes labels include the percentage of variance they each explain.



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Figure S3. Regression scores, CAC and PCA as described in Fig. S2 for head and body shape, separated by clade.

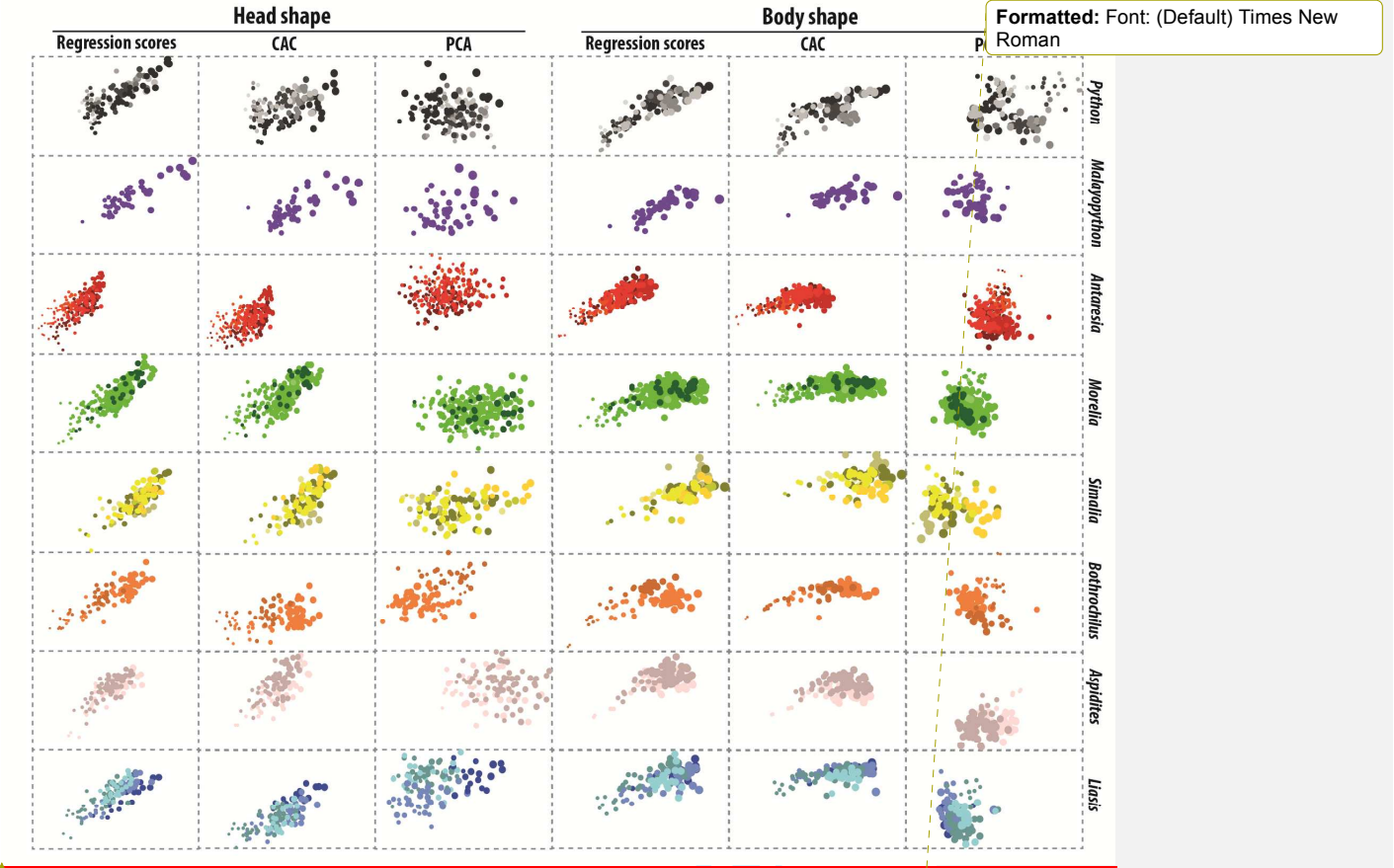


Figure S42. Slope vector lengths (the magnitude of shape change with unit of size change) for each species of python for head and body shape.

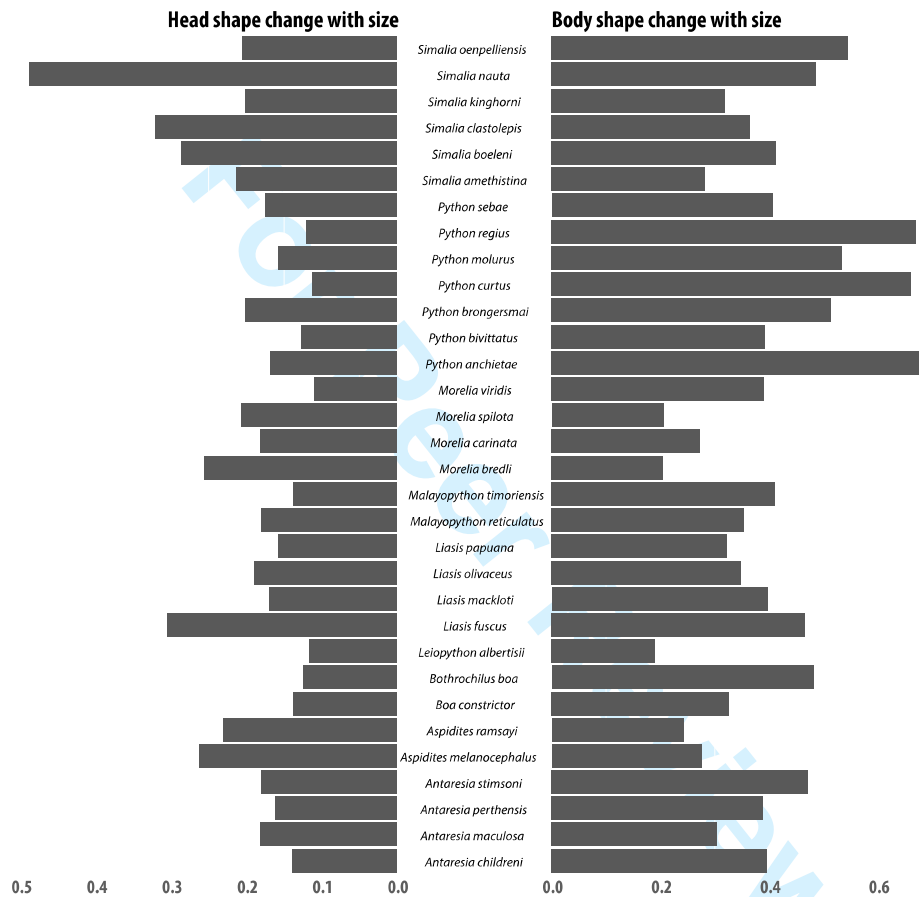


Figure S53. Maximum clade credibility time-calibrated tree of the pythons used in this study. Black circles at the nodes indicate a node supported with a posterior probability of 0.95 or higher. Blue bars at the nodes indicate the 95% highest posterior density of the divergence time estimated for that node. The scale at the bottom indicates the time frame in millions of years for the divergence of the nodes. From top to bottom, the scale indicates the geological ages, epochs and periods as a reference.

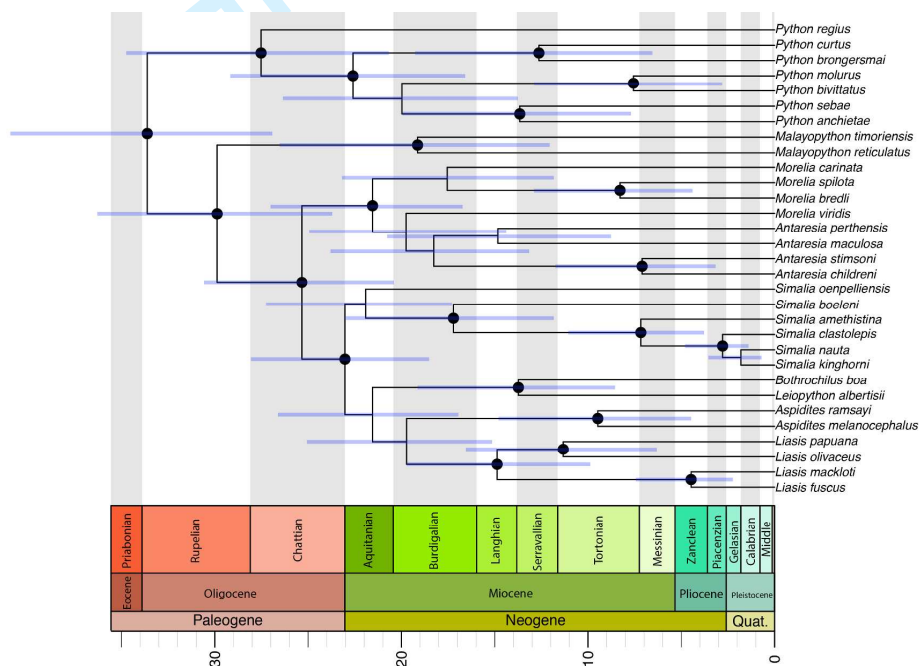
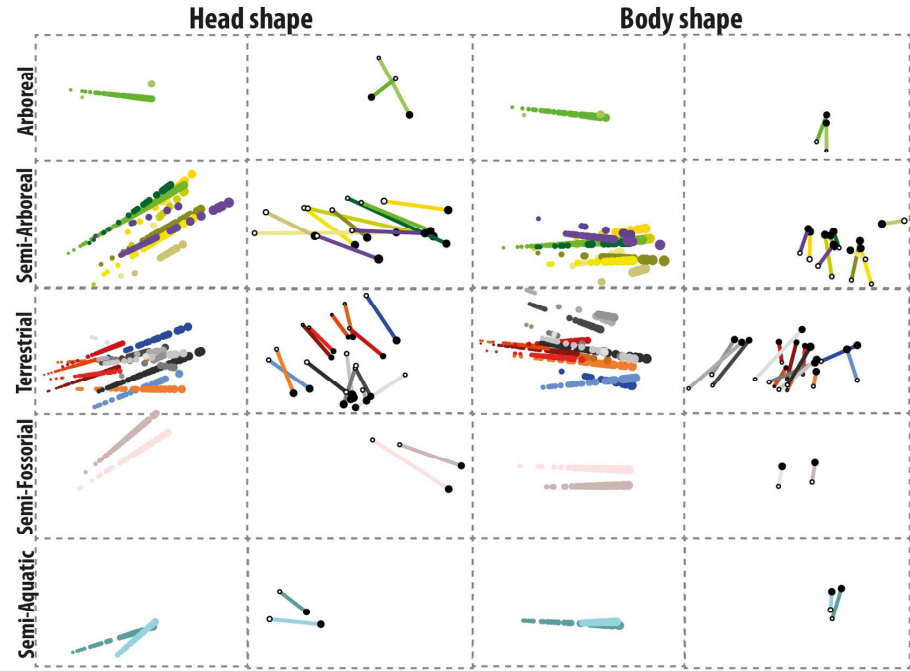


Figure S6. Ontogenetic allometric trajectories derived from the HOS (first and third columns) and PTA (second and fourth columns) tests, of head and body shape of the pythons, separated by micro-habitat choice. These are the same trajectories illustrated in Figures 2 and 3; therefore for details on the meaning of the axes and how to interpret them see the respective legends for details.



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