

Methodological challenges to study the nuclear evolutionary history of an ancient bison species

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A Masters thesis investigating the evolutionary context of *Bison priscus* at a genomic scale using advanced sequencing and bioinformatics tools. The thesis describes a workflow for the combined analysis of next generation sequencing data and genotyping microarray data. The approach addresses the gulf between the applicability of microarrays to survey modern diversity and the apparent inadequacies of the technology to produce reliable results when applied to ancient samples. The workflow includes the design of in-solution hybridisation enrichment, a computational pipeline for ancient DNA sequence data, and a method for converting this data to a format comparable with microarray data.

Student:

Oliver Wooley

Supervised:

Alan Cooper

Julien Soubrier

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