

E3TALK

May 19

14h00

FCiências.ID Amphitheatre, Ciências ULisboa

Questioning Neanderthal admixture: on models, robustness and consensus in human evolution

Genomic and ancient DNA data have transformed our understanding of human evolution and admixture across species. However, identifying and interpreting past admixture events using genetic data is complex and highly dependent on demographic models. Many studies support ancient admixture, such as between Neanderthals and *Homo sapiens*, using models that often overlook intra-continental population structure. This oversight can lead to incorrect inferences. In this study, genomic simulations under structured, admixture-free models still produced signals interpreted as Neanderthal admixture, revealing that commonly used methods may generate false positives. Additionally, published admixture models often failed to predict real genetic diversity patterns, whereas structured models performed better. Similar findings emerged in simulations involving chimpanzees and bonobos, where signals of admixture may also be misleading. These results suggest that many widely accepted hybridization events could be re-evaluated using models that incorporate realistic population structure, potentially reshaping interpretations of admixture in both humans and other species.



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