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EvoLunch

Inferring runs of homozygosity from low coverage DNA data

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The ancient DNA revolution has delivered spectacular new insight into population history of humans, and starts to do so also for other organisms. Here I present work on a novel computational method to detect long runs of homozygosity (ROH) for such data. These blocks are the direct genetic signposts of inbreeding. As such, the frequency and length of ROH blocks yields insight into recent population history and consanguinity. It is possible to identify ROH in high coverage present-day datasets, by scanning for regions that lack heterozygote markers. But this strategy frequently fails for ancient individuals: The often very low depth (<1x) makes reliable diploid genotype calls impossible for most sites. Our refined method makes use of linkage disequilibrium information from a panel of reference haplotypes under a Hidden Markov Model (HMM). It scans for long stretches of genome that can be modeled as imperfect copies from haplotypes in the reference panel. To showcase an application, we apply the method termed HAPSBURG (Haplotype Block Sharing by uninterrupted recent Genealogy) to data from ancient humans.

Wednesday, May 22, 2019 12:30pm - 01:30pm

IST Austria Campus I22 Lakeside View (I22.01)

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