

PRAVIDELNÝ SEMINÁŘ Z BIOINFORMATIKY (NDMI090)

How genomes help us understand human history

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The availability of complete human genome sequences from populations across the world has given rise to new population genetic inference methods that allow unprecedented insight into human population history. We show two methods: MSMC, explicitly modeling ancestral relationships under recombination and mutation of multiple genome sequences, and rarecoal, inferring population history and identifying fine-scale genetic ancestry from rare genetic variants.

The results suggest that the genetic separation of non-African ancestors from African Yoruban ancestors started long before 50,000 years ago and give information about human population history as recent as 2,000 years ago, including the bottleneck in the peopling of the Americas and separations within Africa, East Asia and Europe. We also show that the ancient DNA of British skeleton samples from Anglo-Saxon era are closely related to modern Dutch and Danish populations, while Iron Age samples share ancestors with multiple Northern European populations including Britain.

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