Seminar/Talk

Demographic inererence from whole genome sequence using coalescent models

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As well as carrying the functional information to build an organism, genome sequences are the product of evolution and contain information about the population history of the ancestors of the individual. In particular complete genome sequences contain rare variants that can be informative about recent history, and linkage information which is complementary to mutational information. I will talk on the one hand about models based on the sequentially Markovian coalescent model, including PSMC and derivatives, and also about models based on the rare variant part of the joint allele frequency spectrum (RareCoal with Stephan Schiffels and momi with Jack Kamm), illustrated with examples from human population history using modern and ancient samples.

Monday, December 4, 2017 03:00pm - 04:00pm

Meeting room 1st floor / Central Bldg. (I01.1OG - Zentralgebäude)

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