

Cologne Evolution Colloquium

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Molecular Basis of
Evolutionary Innovations

SFB 680

Inferring human population history and gene flow from multiple genome sequences

The availability of complete human genome sequences from populations across the world has given rise to new population genetic inference methods that explicitly model their ancestral relationship under recombination and mutation. So far, application of these methods to evolutionary history more recent than 20-30 thousand years ago and to population separations has been limited. Here we present a new method that overcomes both of these shortcomings. The Multiple Sequentially Markovian Coalescent (MSMC) analyses the observed pattern of mutations in multiple individuals, focusing on the first coalescence between any two individuals. Results from applying MSMC to genome sequences from nine populations across the world give information about human population history as recently as 2,000 years ago. They suggest that the genetic separation of non-African from African populations was a gradual process that began before 150,000 years ago and lasted for over 100,000 years, and give information about the separation of populations after the out-of-Africa event including the bottleneck in the peopling of the Americas, and within Africa, East Asia and Europe.

Wednesday, January 22, 2014, 17:00
University of Cologne, Institute for Genetics
Seminar Room 0.46

Hosted by Michael Lässig