



BiRC Seminar – open to all

Stephan Schiffels

Wellcome Trust Sanger Institute, Cambridge, United Kingdom

Title: Inferring human population history and gene flow from multiple genome sequences

Time: Thursday 12 September, 2013, 14:15 - 15:00

Place: Bioinformatics Research Centre (BiRC), Build. 1110 Aud. 223, C. F. Møllers Allé 8

Abstract:

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 recent evolutionary history after 50 thousand years ago (kya) and to population separations are very limited. Here we present a new method that overcomes both of these shortcomings. The Multiple Sequentially Markovian Coalescent (MSMC) fits local genealogical trees to the observed pattern of mutations in multiple individuals, focussing on the first coalescence among any two individuals. Results from applying MSMC to genome sequences from 9 populations from across the world suggest that the genetic separation of non-African from African populations was a gradual process that began before 150kya and lasted for over 100,000 years, and give information about the separation of populations after the out-of-Africa event including the bottleneck involved in the peopling of the Americas.

After the seminar there will be beer/soda/coffee and chips in the coffee room on the 4th floor.

<http://birc.au.dk/activities/seminar-series/>



