



## BiRC Seminar – open to all

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**Title:** Approximating Wright-Fisher models to uncover the ancestry of multiple populations  
**Time:** Friday 11 October 2013, 14:15 - 15:00  
**Venue:** Bioinformatics Research Centre (BiRC), Build. 1110 Aud. 223, C. F. Møllers Allé 8

### Abstract:

Wright-Fisher models provide a robust way of describing the evolution of genetic variation over time, and they are widely used for deriving inferences on the history of natural populations, including divergence times, migration events, mutations and selection. However, the simple formulation of the models give rise to complicated dynamics prohibiting exact computations except in the simplest situations. This has resulted in the development of a number of approximations to the different models. In this talk I will describe several commonly used approximations and discuss their suitability for different situations.

As most of the approximations are computationally expensive, the choosing among them involves a trade-off between accuracy of the approximation and feasibility of conducting the inference given limited resources. I will describe in more detail a family of mathematically convenient approximations based on Beta and Dirichlet distributions. These are used to analyze the history of closely related populations based on genetic and linguistic data.

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

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



