



## BiRC Seminar – open to all

**Anders Albrechtsen**  
Bioinformatics, Department of Biology,  
University of Copenhagen

**Title:** *Dealing with uncertainty in large scale sequencing studies - with applications for admixture inference and association studies*

**Time:** Friday 12 October, 2012, 14:15 - 15:00

**Place:** BiRC, Aud. 223, Building 1110, C. F. Møllers Allé 8

### **Abstract:**

Recent technological advances have made it possible to perform massively paralleled sequencing of whole genomes. However, the amount of sequencing required to infer the genotypes without error is still too expensive for large scale studies. Instead low coverage sequencing or targeted sequencing is performed. This strategy, while being economically efficient, presents several challenges. An intermediate step in the analysis of medium or low coverage sequencing involves working with genotype likelihoods inferred from the sequencing data. Genotypes can then be called based on this likelihood. However, calling genotypes will introduce several complications and biases in the downstream analysis.

Instead I suggest working directly on the genotype likelihoods and incorporating the uncertainty of the genotypes into the model. For inferring population structure I present a method to estimate individual ancestry from genotype likelihoods with an efficient EM algorithm that makes the method computationally feasible for whole genome sequencing 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/>



