

# *Inferring Pedigrees*

Objective: To give a presentation of about 40-90 minutes at the end of the week covering the key aspects of pedigree inference.

The questions and contents below are meant as motivators and need not be followed.

## *The Big Questions Are:*

- What are the key algorithms for calculating the likelihood of data given a pedigree?
- Which stochastic models can generate pedigrees?
- How far back in time do we find an ancestor to all present humans?
- Which are the major attempts to infer pedigrees?
- Which reconstruction principles could be applied to infer pedigrees.
- What are the practical use of inferring pedigrees?

## *Recommended literature*

[http://www2.warwick.ac.uk/fac/sci/statistics/crism/workshops/graphical\\_models/](http://www2.warwick.ac.uk/fac/sci/statistics/crism/workshops/graphical_models/)

<http://www.stats.ox.ac.uk/research/genome/grants>

<http://www.stats.ox.ac.uk/research/genome/projects/pastprojects>

Cannings, Skolnick and Thompson (1978) "Probability Functions on Complex Pedigrees" *Adv. Appl. Prob.* 10:26-61.

Elston, R.C. and Stewart, J. (1971) "A general model for the genetic analysis of pedigree data" *Human Heredity* 21: 523-543.

Gasbarra, Sillanpaa and Arjas (2005) "Backward simulation of ancestors of sampled individuals". *Theor. Pop. Biol.* 67:75-83

Hein, J.J. (2004) Human evolution: Pedigrees for all humanity. *Nature* 431:518-519

Helgason et al. (2003) A Populationwide Coalescent Analysis of Icelandic Matrilineal and Patrilineal Genealogies: Evidence for a Faster Evolutionary Rate of mtDNA Lineages than Y Chromosomes *Am. J. Hum. Genet.* 72:1370-1388,

Lauritzen, S and Sheehan, N. (2003) "Graphical Models for Genetic Analyses" *Statist. Sci.* 18, no. 4. 489-514

Lander, E.S. and Green, P. (1987) "Construction of multi-locus genetic linkage maps in humans" *PNAS* 84: 2363-2367

Rohde et al. (2004) Modelling the recent common ancestry of all living humans *Nature* 431, 562-566

Steel, M. & Hein, J. (2006) Reconstructing pedigrees: a combinatorial perspective. *Journal of Theoretical Biology*, 240(3), 360-367