

The Bioinformatics Module & Interesting Genes

These two weeks will introduce you to a series of techniques as presented by different groups. To get a more hands on experience as well, you will the first day be given a gene and must analyse in depth from a variety of angles of the course of the complete 2-week module and present your findings and background for the analysis on the very last day. Thus you must form groups and then focus on this gene from this angle. Full analysis of a gene cannot be done in 2 weeks, but you can get far. The presentation expected on Friday April 3rd, can have both background material and what you achieved in the analysis. Thus, you should have something to say whatever the outcome of the analysis. Jotun Hein, Rune Lyngsø, Adam Novak, Garrett Hellenthal (and partially Istvan Miklos) are available to assist you for the whole period. There are more sets of techniques possible than we can anticipate there will be groups formed so we must prioritize and say that certain techniques will not be tried (for instance pedigree analysis). Techniques that should be given high priority are underscored below. Some techniques are related and could possibly be done by one group (like Protein Gene Finding, RNA Gene Finding and Regulatory Signals). If any team or the whole group have qualified interest in any other gene, please tell us and we will see what we can do.

You are 10 students. We will analyze this gene with respect to four main topics and you will be able to get continuous help during the complete period, but one person will be mainly responsible for the topic and the first to be contacted. There are other facets to a gene and we could will form a 5th group pursuing this.

Genetic Mapping - Garrett Hellenthal (hellenth@stats.ox.ac.uk)

You will get a data set consisting of genotypes and phenotypes for a large set of individuals that should allow you to home in on 1 gene.

Additional options: pedigree analysis, population genetics based on the data you have,...

Protein and RNA Gene Annotation - Rune Lyngsø (lyngsoe@stats.ox.ac.uk)

Around this gene, you will define an area stretching 5 kb in both directions. To this area you will apply methods of finding RNA and protein coding genes.

Additional options: search for alternative splicing and splicing signals, binding sites for micro-RNAs,.....

Molecular Evolution and Selection around the Gene - Istvan Miklos (miklos@stats.ox.ac.uk)

Around the gene of interest you will investigate the phylogeny, the rates of evolution and strength of selection.

Additional options: positive selection and evolution of function

Regulatory Signals – Adam Novak (novak@stats.ox.ac.uk)

Around the gene of interest you will search for regulatory signals.

Additional options: describe the known signals and transcription factors in humans.

Miscellaneous analysis techniques – (contact any of us including Jotun Hein) biological background, cancer models, expression data, functional analysis/ontologies, additional knowledge of the gene, protein structure, PINs, OMICS, ...

For the days that our [group](#) is responsible for, March 23rd - 24th, 26th and April 3rd, you can see our plan on the attached plan with a little more detail. For Jotun Hein's lecture on the 23rd the appended chapter 1 from Yang: Computational Molecular Evolution is good preparatory reading. Preparatory reading for Istvan Miklos' lecture 24th is the statistical alignment paper also appended.

I hope that we will have great 2 weeks and learn a lot (teachers included)!!!