

Class 5 overview

- GWAs summary
 - Zoom in on imputation (legend explanation)
 - Zoom in on websites of NCBI and how you can find info for a gene
 - Entrez and omnibus / functional → more info via “interactions protocol” (**last class**)
 - Search in omim for multiple myeloma
 - <http://omim.org/entry/605625>
 - Check out the protein via Uniprot: <http://www.uniprot.org/uniprot/Q96EZ4>
 - Go one step back and check out the gene via ENSEMBL:
http://www.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSGO0000172927;r=11:69061605-69182494;t=ENST00000308946
 - Go one step back and obtain DNA level:
http://www.ensembl.org/Homo_sapiens/Transcript/Sequence_cDNA?db=core;g=ENSG00000172927;r=11:69061622-69064754;t=ENST00000308946
 - cDNA / splicing sites
- Connecting theory to practice: Balding tutorial:
<http://www.comp.nus.edu/~ksung/cs3225/materials/nrg1916.pdf>
 - Homework
 - How to read a GWAs paper? <http://www.genomesunzipped.org/2010/07/how-to-read-a-genome-wide-association-study.php>
- Software tools
 - Genetic analysis software alphabet
 - <http://www.scribd.com/doc/82714241/R-GWAS-Packages>: PLINK (1.9) and GenABEL
 - PLINK: see course notes ULg (non-PH homework assignment)
 - Comprehensive GenABEL tutorial that also includes tutorial about genetics package:
http://www.genabel.org/sites/default/files/html_for_import/GenABEL_tutorial_html/GenABEL-tutorial.html#x1-290005.5
 - PLATO, an alternative to PLINK
<http://gettinggeneticsdone.blogspot.be/2013/05/plato-alternative-to-plink.html>
 - Easy-going: <http://www.montefiore.ulg.ac.be/~kvansteen/GeneticEpi-UA/Class4/SNPassoc.pdf>
 - GWAtoolbox
<http://bioinformatics.oxfordjournals.org/content/early/2011/12/08/bioinformatics.btr679.full.pdf>
- Practical example in R (SNPassoc)
 - See text book “applied statistical genetics with R” and corresponding data download site
<http://people.umass.edu/foulkes/asg/data.html>

The Functional SNPs Associated with Muscle Size and Strength (FAMuSS) study was conducted to identify the genetic determinants of skeletal muscle size and strength before and after exercise training. A total of $n = 1397$ college student volunteers participated in the study, and data on 225 SNPs across multiple genes were collected. The exercise training involved students training their non-dominant arms for 12 weeks. The primary aim of

the study was to identify genes associated with muscle performance and specifically to understand associations among SNPs and normal variation in volumetric MRI (muscle, bone, subQ fat), muscle strength, response to training and clinical markers of metabolic syndrome. Primary findings are given in Thompson et al. 2004).

- QC + association signals (TA slides + manual)
- Multiple testing (TA slides)
- R – constantly on the move ...:
 - <http://www.r-bloggers.com/tag/gwas/>
 - BlueSNP: R package for highly scalable genome-wide association studies using Hadoop clusters
 - Tutorial in R for someone who has never done it:
<http://gettinggeneticsdone.blogspot.be/2009/06/pdf-tutorial-from-r-course-introduction.html>

Class 6

- Family-based testing (slides)
- A tour in FBAT

Class 7 (last class)

- Interactions
- Other omics and technologies - integration

A note on anti-aging:

- Sirtuine genes: shut down other genes to save energy when mice were put to starvation → at molecular level
- Cooling down system: internal shut down when our system gets overheated (sports, etc) to avoid heat-related selfdestruction of cells. Stanford: blood → external cooling → again in bloodstream → up to doubled performance. Knowing that exercising is good for virtually all aspects of life (muscle build-up etc), age plafond of 115 can be elevated?
- The role of nanotechnology at Stanford: little sensors put in the bloodstream in early life to detect problems before they occur → medicine intake before the disease
- Brain evolved in an environment with a limited life expectancy → so no need to remember things of 100 years ago.. (see document last year: the evolving brain)

- Preparing for the exam: list of questions