GWAS, Quality Control and Family based analysis workshop February 2016 – Matthew McQueen

Further Information and useful links

PLINK:

PLINK is a free, open-source whole genome association analysis toolset, designed to perform a range of basic, large-scale analyses in a computationally efficient manner.
The focus of **PLINK** is purely on *analysis* of genotype/phenotype data, so there is no support for steps prior to this (e.g. study design and planning, generating genotype or CNV calls from raw data). Through integration with gPLINK and Haploview, there is some support for the subsequent visualization, annotation and storage of results.
PLINK (one syllable) is being developed by Shaun Purcell at the Center for Human Genetic Research (CHGR), Massachusetts General Hospital (MGH), and the Broad Institute of Harvard & MIT, with the support of others.

http://pngu.mgh.harvard.edu/~purcell/plink/tutorial.shtml

http://pngu.mgh.harvard.edu/~purcell/plink/

https://www.cog-genomics.org/plink2

http://www.montefiore.ulg.ac.be/~kvansteen/GeneticEpi-Engineering/ac1213/QC_An%20introduction%20to%20PLINK_v2.pdf

R and R Studio:

R is a free software programming language and a software environment for statistical computing and graphics. The R language is widely used among statisticians and data miners for conducting and developing statistical software and data analysis.

R the application is installed on your computer and uses your personal computer resources to process R programming language. RStudio integrates with R as an IDE (Integrated Developmet Environment) to provide further functionality. RStudio combines a source code editor, build automation tools and a debugger.

We recommend you install both R and RStudio on your personal computer.

http://web.cs.ucla.edu/~gulzar/rstudio/

http://statistics.byu.edu/content/r-and-rstudio

http://dss.princeton.edu/training/RStudio101.pdf

https://www.r-project.org/

FBAT:

Both FBAT and PBAT provide software for implementing family-based association tests. PBAT also provides power calculations, general data analysis functions for quantitative traits, and screening procedures for multiple traits, markers, and/or models. See the FBAT User's Manual for more details.

Further Information and useful links

http://www.hsph.harvard.edu/fbat/fbat.htm

http://www.hsph.harvard.edu/fbat/FBAT_Manual_3-2014.pdf

GCTA:

GCTA (Genome-wide Complex Trait Analysis) was originally designed to estimate the proportion of phenotypic variance explained by genome- or chromosome-wide SNPs for complex traits (the GREML method), and has subsequently extended for many other analyses to better understand the genetic architecture of complex traits.

http://cnsgenomics.com/software/gcta/

http://cnsgenomics.com/software/gcta/tutorial.html

http://cnsgenomics.com/software/gcta/download.html

In case of any difficulties or questions you might have, you can approach the H3ABioNet helpdesk:
http://www.h3abionet.org/support