

Recent methods for polygenic analysis of genome-wide data

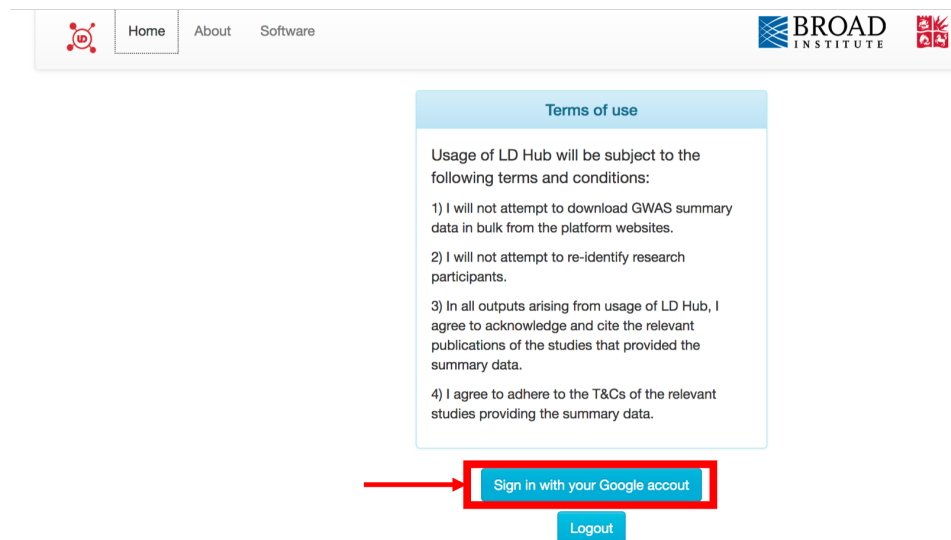
Primary objective

The primary objective of this module is to: - Estimate SNP-heritability - Calculate genetic correlations - Perform functional mapping and annotation of genetic associations

Dataset and tools

The datasets and tools that will be used in the workshop will leverage publicly available resources

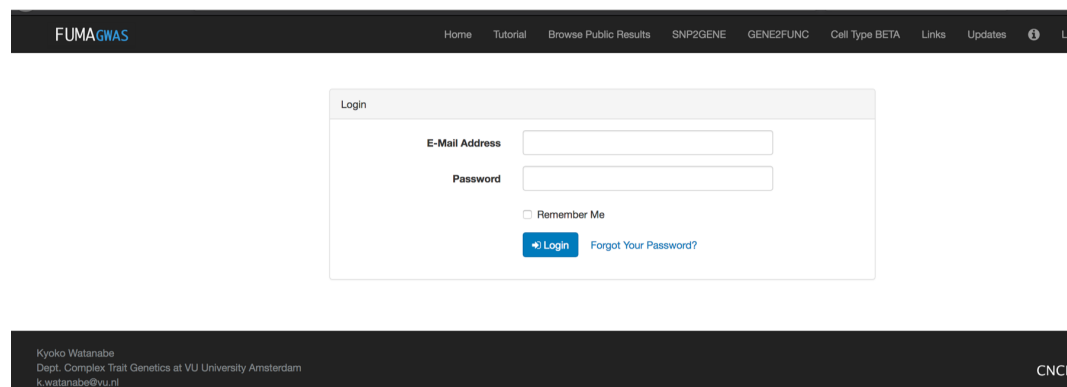
- Summary statistics (PGC, GWAS catalog):
- <https://www.med.unc.edu/pgc/results-and-downloads>
- <https://www.ebi.ac.uk/gwas/downloads/summary-statistics>
- SNP-heritability and genetic correlations (LDHub):



- <http://ldsc.broadinstitute.org/ldhub/>

You will need to login in to LDHub using your gmail account

- Functional annotation (FUMA):



- <http://fuma.ctglab.nl/login>

You will need to create an user account to use FUMA

However, if for some reason there are difficulties in doing so we have created the following account:

- account: jaxpolygenicity@gmail.com; password: jaxpolygenicity2018