Lecture 3: Introduction to the PLINK Software

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PLINK Overview

- 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:

  `pngu.mgh.harvard.edu/~purcell/plink/`

- PLINK has numerous useful features for managing and analyzing genetic data
- Data management
  - Read data in a variety of formats
  - Recode and reorder files
  - Merge two or more files
  - Extracts subsets (SNPs or individuals)
  - Flip strand of SNPs
  - Compress data in a binary file format

PLINK Overview

- Summary statistics for quality control
  - Allele, genotypes frequencies, HWE tests
  - Missing genotype rates
  - Inbreeding, IBS and IBD statistics for individuals and pairs of individuals
  - non-Mendelian transmission in family data
  - Sex checks based on X chromosome SNPs
  - Tests of non-random genotyping failure

PLINK Overview

- Basic association testing
  - Case/control
    - Standard allelic test
    - Fisher's exact test
    - Cochran-Armitage trend test
    - Mantel-Haenszel and Breslow-Day tests for stratified samples
    - Dominant/recessive and general models
    - Model comparison tests (e.g. general versus multiplicative)

PLINK Overview

- Family-based association (TDT, sibship tests)
- Quantitative traits, association and interaction
- Association conditional on one or more SNPs
- Asymptotic and empirical p-values
- Flexible clustered permutation scheme
- Analysis of genotype probability data and fractional allele counts (post-imputation)

PLINK Overview

- Multimarker predictors, haplotypic tests
  - Suite of flexible, conditional haplotype tests
  - Case/control and TDT association on the probabilistic haplotype phase
  - A set of proxy association" methods to study single SNP associations in their local haplotypic context
  - Imputation heuristic, to test untyped SNPs given a reference panel
- Copy number variant analysis
  - Joint SNP and CNV tests for common copy number variants
  - Filtering and summary procedures for segmental (rare) CNV data
  - Case/control comparison tests for global CNV properties
  - Permutation-based association procedure for identifying specific loci

PLINK Overview

- Gene-based tests of association
- Screen for epistasis
- Gene-environment interaction with continuous and dichotomous environments
- Meta-analysis
  - Automatically combine several generically-formatted summary files, for millions of SNPs

Input Files

- Genotype data is a text file
  - Pedigree file (.ped)
  - Map file (.map)
- Genotype data is a compressed binary file
  - Fam File (.fam)
  - Bim file (.bim)
  - Bed file (.bed)

Input Files

- Pedigree File - the first six columns are mandatory:
  - Family ID
  - Individual ID
  - Paternal ID
  - Maternal ID
  - Sex (1=male; 2=female; other=unknown)
  - Phenotype

Input Files

- MAP File has 4 columns:
  - chromosome (1-22, X, Y or 0 if unplaced)
  - rs# or snp identifier
  - Genetic distance (morgans)
  - Base-pair position (bp units)

Creating Binary PLINK files

- With the PLINK files `myfile.ped` and `myfile.map`, the PLINK command

  ```
  plink --file myfile --make-bed --out myfile
  ```

  generates the following files:
  - Myfile.bed
  - Myfile.bim
  - Myfile.fam

Data Management

- Inclusion/Exclusion criteria options
  - `--keep mylist.txt, --remove mylist.txt`
  - `--extract mysnps.txt, --exclude mysnps.txt`
  - `--chr 6, --from rs273744 --to rs89883`
- Other data management options
  - `--make-bed, --recode, -bmerge`
- Using files with phenotypes
  - `--pheno, --all-pheno, --mpheno`

Quality Control (QC)

- Summary statistics options:
  - minor allele frequency (MAF): --freq
  - SNP missing rate: --missing
  - Individual missing rate: --missing
  - Hardy-Weinberg: --hardy
- Inclusion/Exclusion criteria
  - MAF: --maf
  - SNP missing rate: --geno
  - Individual missing rate: --mind
  - Hardy-Weinberg: --hwe

Association Analysis with PLINK

- Basic association testing: --assoc, --qassoc
- Stratified analysis: --within myclusterfile.dat
- Covariates: –covar -- mycovfile.dat
- GxE interaction: --gxe mycovfile.dat

GWAS of Transferrin

- PLINK input files:
  - `Transferrin.bed`
  - `Transferrin.fam`
  - `Transferrin.bim`
- R Script File for Transferrin:
  - `Commands_Transferrin_Data.R`
- HELP: Use the PLINK website (very useful!)
  `pngu.mgh.harvard.edu/~purcell/plink/`

Transferrin Data: File Inspection

- Copy the transferrin PLINK files to a folder
- Use the R script to inspect files (not the .bed file!)
- Questions:
  - How many individuals are there?
  - How many SNPs are there?
  - Is the transferrin phenotype approximately normally distributed?

Transferrin Data: QC with PLINK

- Can estimate allele frequency for all SNPs with PLINK

```
./plink --bfile Transferrin --freq --out Trans_freq
```

- Calculate SNP and individual missingness with the following option:

```
--missing --out Trans_missing
```

- Fro each SNP, bbtain p-values for HWE using the following option:

```
--hardy --out Trans_hardy
```

Transferrin Data: GWAS with PLINK

- Run a GWAS analysis of Transferrin with PLINK.
- Make sure to apply some quality controls
- Command to apply QC thresholds such as MAF 0.05/ missing 0.01 / HWE 0.001 for the GWAS analysis with PLINK:

```
plink --bfile Transferrin --pheno Tr.pheno --maf 0.05
--geno 0.01 --hwe 0.001 --assoc --out
 GWAS_T_add
```

Transferrin Data: Analyzing a Subset of SNPs

- Can easily analyze a subsest of SNPs with PLINK
- The following file contains a list of SNPs that are of interest:

  `SNP_List.txt`
- Can use the following PLINK command with the "extract option to perform association testing on a subset of SNPs:

```
plink --bfile Transferrin --pheno Tr.pheno --extract
  SNP_List.txt  --assoc --out GWAS_T_add_Subset
```

- Can use the following command to perform r^2 LD calculations for all possible pairs of SNPs in the subset SNP file

```
plink --bfile Transferrin --extract SNP_List.txt --r2
  --out LD_T_Subset
```

References

- Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A.R., Bender, D., Maller, J., Sklar, P., de Bakker, P.I., Daly, M.J., et al. (2007). PLINK: A tool set for whole-genome association and population-based linkage analyses. *Am. J. Hum. Genet.* **81**, 559-575.