**2023 International Statistical Genetics Workshop**

**Day 2. Optional morning GWAS practical.**

**CHEATSHEET**

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Luke Evans & Wei Zhou

Practical originally developed by Katrina Grasby and Lucía Colodro Conde

**This cheatsheet contains the information for the GWAS practical, as well as additional information on using plink2 to perform association tests and basic functions.**

**Learning Goals:** This tutorial aims to make you familiar with genome-wide association analysis, the way in which PLINK2 works (and some of the useful options it provides!), and some tools to visualize your results.

It is important that you explore the outputs and the log files and that you understand what they mean. Please ask if you have any questions, and check the plink file formats page.

Please note, most of the options that you will be using work the same for logistic and linear regression.

*Some of the commands below are missing (indicated with XXX).* You will have to determine the correct syntax or command to run the analyses, and discuss the questions proposed.

You will find the commands and their output in Day2\_GWAS\_Practical\_CHEATSHEET.pdf.

Feel free to take a look through it during the practical, but a good strategy is to first try the commands yourself or with your group, then troubleshoot things yourself if they don't work, then ask your group, then ask others & faculty, then check the cheatsheet.

The cheatsheet has all the expected answers and figures, but the process of doing the GWAS and exploring the output is what will help you learn.

**DAY 2. GWAS TUTORIAL**

Key information can be found here:

https://www.cog-genomics.org/plink/2.0/

https://www.cog-genomics.org/plink/2.0/assoc

https://www.cog-genomics.org/plink/2.0/formats

**FIRST: Copy the files to your working directory & navigate to that directory:**

cp -r /faculty/luke/2023/gwas2/ .

cd gwas2/

**EXERCISE 1. LOGISTIC REGRESSION (BINARY TRAIT).**

**1.0. Go to the case-control folder and check the files you have there.** The phenotype is Alzheimer's Disease (AD) status.

cd casecontrol

**1.1. Run a logistic regression for the phenotype (AD status) including the principal components in file adpc.txt as covariates to correct for genetic ancestry.**

* [hint: you can find the flags and modifiers that you can include in the logistic and linear regressions on Association analysis > Regression with covariates, https://www.cog-genomics.org/plink/2.0/assoc#glm in the PLINK 2.0 website]

plink2 --bfile adclean.cc --glm sex --covar adpc.txt --out 1.1\_logistic.ad.cc --threads 4

--bfile <prefix> is the dataset filename you will use

--glm is the main tool to perform associations. Including the ‘sex’ modifier includes sex (from the fam file) as a covariate

--covar <filename> specifies the file with your covariates to use

--threads <max> This sets the number of threads that the program will use. Generally, more threads makes things faster.

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**Check the log file.** How many cases and controls were detected? How many covariates?

less -S 1.1\_logistic.ad.cc.log

less prints out only the first 10 rows of the file, using the “-S” flag prints it out only one window’s worth at a time.

There were 170 cases, 182 controls, 4 covariates detected in the covar file (not including sex, from the fam file)

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**Check the results (stored in 1.1\_logistic.ad.cc.PHENO1.glm.logistic.hybrid)** and be sure that you understand the content of each of the columns

* [hint: you can check File formats > .glm.logistic, https://www.cog-genomics.org/plink/2.0/formats#glm\_logistic, on the PLINK2.0 website]. Remember, when PLINK 1.9 uses bfiles, the effect allele is A1, which is the minor allele, and may or may not be the ALT allele. So an OR > 1 means A1 is associated with an increased risk relative to A2.

head 1.1\_logistic.ad.cc.PHENO1.glm.logistic.hybrid

head prints out only the first 10 rows of the file

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Table

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* + CHROM: Chromosome of the locus
  + POS: physical basepair position of the locus
  + ID: rsnumber of the variant
  + REF: Reference allele
  + ALT: Alternate allele
  + A1: The allele that is counted for the regression (Not necessarily ALT, but should be the minor allele)
  + OR: A1 allele’s odds ratio for the case/control phenotype
  + SE: Standard error of the allele’s beta (beta=ln(OR))
  + P: p-value of the test for this locus

**Did any SNP associations reach genome-wide significance?**

grep ADD 1.1\_logistic.ad.cc.PHENO1.glm.logistic.hybrid | awk '$13<5e-8'

One did: rs4420638, with p=1.886e-14.

What is the grep command doing here?

grep searches for a string in each row of a file. Here, it’s finding all of the “ADD” strings, which is short for ADDITIVE estimate of the allele’s effect.

It’s useful because by default PLINK writes out all of the covariate effect estimates as well (the PC1-5, SEX lines), which are good to check, but which aren’t what we’re most interested in.

So, grep ADD <file> pulls out only the SNP effect estimates.

**What if cases and controls had been coded as 1 and 0,** respectively? What could have we done to make PLINK interpret this coding appropriately?

[hint: you can check Standard data input > Phenotypes > Phenotype encoding, https://www.cog-genomics.org/plink/2.0/input#pheno, in the PLINK 2.0 website]

Plink uses 1 & 2 for controls & cases, respectively. You can change this with the --1 command

**What if sex had not been coded in the fam file, or was in both your covariate and fam files**? What could have we done to make PLINK interpret this coding appropriately?

[hint: you can check --glm modifiers in https://www.cog-genomics.org/plink/2.0/assoc#glm, in the PLINK 2.0 website]

You can tell which covariates to use by adding additional commands, such as --covar-col-num or --covar-name.

**1.2. Run a logistic regression for the case-control variable AD including the principal components as covariates and hiding the results of the covariates.**

plink2 --bfile adclean.cc --glm sex hide-covar --covar adpc.txt --out 1.2\_adclean.cc

What's the difference between the sets of results generated in 1.1 and 1.2?

--glm with the modifier “hide-covar” doesn’t print out the estimates for each of the covariates for every single locus, saving a lot of file space. The estimates are probably very nearly identical for every test, anyway.

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**1.3. Run a logistic regression for the case-control variable AD including the principal components as covariates, hiding the results of the covariates, and getting 95% Confidence intervals of odds ratios.**

[hint: you can check again https://www.cog-genomics.org/plink/2.0/assoc#glm, in the PLINK 2.0 website]

plink2 --bfile adclean.cc --glm sex hide-covar --ci 0.95 --covar adpc.txt --out 1.3\_adclean.cc --threads 4

--ci 0.95 tells plink to output the 95% CI of the estimates.

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**1.4. Run a logistic regression for the case-control variable AD including the principal components as covariates, hiding the results of the covariates, and getting the allele frequencies**.

[hint: you can check Main functions > Basic statistics > --freq or Allele frequency, https://www.cog-genomics.org/plink/1.9/basic\_stats#freq, in the PLINK 1.9 website].

plink2 --bfile adclean.cc --glm sex hide-covar --covar adpc.txt --freq --out 1.4\_adclean.cc --threads 4

--freq creates a second output, \*.afreq, which contains the frequency information.

Explore the output files and note you have an extra one, 1.4\_adclean.cc.afrq. [hint: you can check File formats > .afrq in the PLINK website]. In this one, we can see REF, ALT, and ALT\_Freq.

Graphical user interface

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**EXERCISE 2. LINEAR REGRESSION (CONTINUOUS TRAIT)**

**2.0. Go to the continuous folder and check the files you have there.** The phenotype is a transcript probe (gene expression). Pay attention to the file adclean.cont.txt.

cd ../continuous/

head adclean.cont.txt

**2.1. Run a linear regression for the continuous trait including the genetic principal components as covariates, hiding the results of the covariates, and using the --pheno option.** The advantage of using an extra file for phenotypes (and the --pheno option) is that if there were several phenotypes, it would be possible to run analyses on them at the same time (something not possible with ped or fam files). Note that when using the --pheno option, the original ped or fam files can still contain a phenotype in the phenotypc column, but it can be missing (NA/nan/-9). See Standard data input > Phenotypes, https://www.cog-genomics.org/plink/2.0/input#pheno.

plink2 --bfile adclean.cont --glm sex hide-covar --pheno adclean.cont.txt --covar adpc.txt --out 2.1\_adclean.cont --threads 4

What do you notice about the output file name? Because the phenotype file has a column name, it uses that phenotype name in the output by default.

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**2.2. Run a linear regression for the continuous trait including only PC1 as covariate, hiding the results of the covariate, using the --pheno option.**

# [hint: again, you can check the commands you can use to run logisic or linear regressions on data input > Covariates, https://www.cog-genomics.org/plink/2.0/input#pheno. For options related to how parameters are handled in other models (e.g., estimating non-additive effects), you can seehttps://www.cog-genomics.org/plink/2.0/assoc

plink2 --bfile adclean.cont --glm hide-covar --pheno adclean.cont.txt --covar adpc.txt --covar-name PC1 --out 2.2\_adclean.cont --threads 4

--covar-name <column name> allows you to specify only certain covariates out of your file. Also, this does not include sex as a covariate, because this command doesn’t have the –glm modifier ‘sex’.

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**2.3. Run a linear regression for the continuous trait including the principal components as covariates, hiding the results of the covariates, using the --pheno option, and getting 95% confidence intervals for the beta.**

plink2 --bfile adclean.cont --glm sex hide-covar --pheno adclean.cont.txt --covar adpc.txt --ci 0.95 --out 2.3\_adclean.cont --threads 4

similar to above, the –ci 0.95 command outputs the 95% CI.

What is different about these results than 2.1 results? How might you use the added information?

If you’re interested in a specific variant and its effect, the uncertainty in the effect size may be very important to know, and this is a way to get that quickly. You can also always calculate a CI of varying range yourself using a t-distribution.

A close up of a keyboard

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**2.4. Plot the results from 2.3.**

We will create three plots to explore the results. For that, we will need at least three columns: chromosome, base pair position, and p-value; having a SNP column (containing the rs number) will allow extra options in our plots. We’ll **first create a file containing this information, excluding the markers with no results**.

What is "|" doing in the next line? What does the grep command do, and why would you want to use that?

The “|” is the pipe command, which passes the standard output from the command right before it (here, awk) to the standard input of the command after it (here grep).

The grep command uses the ‘-v’ modifier so that it searches for lines WITHOUT “NA” in them. These are lines with missing estimates, and we don’t want them, so we grab all the lines that don’t have “NA” in them instead.

awk '{print $1,$2,$3,$14}' 2.3\_adclean.cont.GI\_34147330-S.glm.linear | grep -v NA > plot.adclean.cont.linear.txt

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**What’s the SNP with the lowest p-value (or top SNP)?**

sort -k4 -g plot.adclean.cont.linear.txt | head

What is the "-g" doing in the line above? Hint: use "man sort" to check the documentation of commands.

The “-g” modifier to the sort command sorts the particular column (4th, specified by -k4), as a number, even though it’s got a letter in it sometimes (using notation like 5e-8 as 0.00000005).

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**EXERCISE 3. PLOT OUT YOUR RESULTS**

**QQ and Manhattan plots.**

**Open in RStudio (https://workshop.colorado.edu/rstudio/) the script Rscript\_qqMan.R and plot the results.** Set your working directory to the folder where you have your results (you can check first what your working directory is by typing pwd in the command line). Run the script. Explore the QQ plot and the Manhattan plot. What information do you gather from these plots and the lambda value? Do you detect any anomalies?

You need to set your working directory first. This is either by specifying the path in the script or by using Session>Set Working Directory>Choose Directory in the drop-down menu at the top of RStudio.

You also need to tell it which file to use, here, “plot.adclean.cont.linear.text’.

Note that while this file does have a header column, it starts with a “#” which comments out the line and which RStudio doesn’t recognize. So, you then have to set the names of the column.

Checking the structure uses str(Data), and will output information for each column in the “Data” object.

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Graphical user interface

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**Regional plot.**

**Still in RStudio, go to the "Files" section (bottom right quadrant of the browser) and check the file plot.adclean.cont.linear.txt and the two jpg images you just created. Then go to More and then Export. The file will download to your local computer.**

You can explore association p-value results and LD patterns by uploading your results (or a genomic region of interest) to LDassoc in LDlink: https://ldlink.nci.nih.gov/?tab=ldassoc.

Upload your results using Browser (preferred: Chrome, Safari, Firefox 36+ or Internet Explorer). In real scenarios, you may want to upload only the information of a region of interest that you want to plot or only one chromosome because the upload time will be slow with very large files.

Select the columns that contain the information on Chromosome, Position, and P-Value.

LDassoc has three options for visualising regions of association: by gene, by region or by variant. We will select visualising our results by using our lowest p-value variant as the index variant (rs6050598 or chr20:25397257).

Select the CEU population (European, Utah Residents from North and West Europe) as the 1000 Genomes sub-population of interest. LDlink will calculate measures of linkage disequilibrium according to this population, which is the one that best matches the ancestry of our study population.

Leave the rest of the options as default and press Calculate.

Graphical user interface, application

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Explore the interactive plot. Is the index variant in high LD with any of the nearby variants? Remember the R2 is a measure of linkage disequilibrium or correlation of alleles for two genetic variants. Chart, scatter chart

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**If you have gotten this far with time left, you can go back to your logistic regression results and plot them:**

1.5. Plot the results from 1.4. You will need to use the commands you ran in section two to generate the intermediate files for RStudio and the interactive browser plots. Your challenge will be to adapt those commands to the right files in the right sequence, run the RStudio script again, and create the plots.