Empirical Pedigree Guide

**Copy and paste the blue code into your command shell to execute commands, but change names according to your data filenames.

1. **Getting Started:**

   A. ***Softwares to download:***

-PLINK: http://zzz.bwh.harvard.edu/plink/download.shtml

-R: https://cran.r-project.org

-SSH client: http://www.chiark.greenend.org.uk/~sgtatham/putty/download.html

-Make sure you are using genotypic and not imputed genotype data!

   B. ***Using the BASH shell:***

-To check what shell you are using type in: `echo $SHELL` ; if bash, then move onto part 2.

-If not, change to the bash shell by typing `bash`.

-You may return to your previous command shell by typing in `exit`.

2. **Filtering Data**

   C. ***Filtering SNP List:***

-Please start by creating directory /enigma/genetics and having readable and writable permissions in the folder:

To make the directory:

`mkdir /enigma/genetics`

 To change the permissions on the directory:

`chmod a+x /enigma/genetics`

Additionally: make sure that you own the directory. To check permissions:

`ls -l` # The third column should have your username for relevant files/folders.

To change ownership:

For files:

`chown username filename`

For directories:

`chown -R username filename`

-Move all PLINK genotype files (.bed, .bim, and .fam) to folder.

`mv basefilename* pathway_to/enigma/genetics`

-Copy and the paste the following lines into your bash terminal:

`Export datafileraw=yourrawdata` #yourrawdata is base filename without extension

`The pathway to the plink executable file --bfile $datafileraw --hwe 1e-6 --geno 0.05 --maf 0.01 --noweb --make-bed --out ${datafileraw}_filtered` #remember to add —nonfounders after —noweb if your dataset requires it

`export datafile=${datafileraw}_filtered`

`awk '{print $2}' base_filename.bim > base_filename.snplist.txt`

`The pathway to the plink executable file --bfile ${datafile} --extract base_filename.snplist.txt --make-bed --noweb --out local`

```
awk '{if (($5=="T" && $6=="A")||($5=="A" && $6=="T")||($5=="C" &&
$6=="G")|| ($5=="G" && $6=="C")) print $2, "ambig" ; else print
$2;}' $datafile.bim | grep -v ambig > local.snplist.txt
```

```
The pathway to the plink executable file --bfile ${datafile} --
extract base_filename.snplist.txt --make-bed --noweb --out
external
```

3. Creating KING pedigree file

-Navigate to /enigma/genetics directory

-Start SOLAR-eclipse software\

-Remember that your base_filename in this case is 'external'

1. *Regular KING pedigree file:*

-Type:

```
pedifromsnps -i base_filename -o output_filename
```

2. *KING pedigree file for each chromosome:*

-Type:

```
pedifromsnps -i base_filename -perchromo —o output_filename
```

4. Creating WAC pedigree file:

-Navigate to /enigma/genetics directory

-Start SOLAR-eclipse software

-Type:

```
pedifromsnps -i base_filename -corr # -o output_filename
```

The pound sign refers to whichever α you wish to weight with