

Measured Genetic Association (MGA) Analysis using SOLAR-Eclipse Software

Template Code with Instructions:

First, convert the plink file to a set of snp saved in the csv format using the command :

```
plink_converter -i <input PLINK base filename> -o <output base filename> -max <num SNPs>  
-bin -solar
```

* limit <num SNPs> to 5000 for optimal results!

Then, using the new genofile you've created, input:

```
load snp <filename>
```

```
snp covar optional: -nohaplos if you don't have a .haplotypes file
```

```
load pheno <filename>
```

```
Mga [if you have a separate data file : -files <gcovfile filename>] -out <output filename>
```

Example Code:

```
plink_converter -i external -o genofile -max 3000 -bin -solar
```

```
load snp genofile_0.csv
```

```
snp covar -nohaplos
```

```
load pheno AverageDTIFA_chr1_0_test.csv
```

```
trait AverageDTIFA
```

```
mga -files snp.genocov -out mga.csv
```