Example analysis

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1 Importing the data

First, load GA library

```
> library(GenABEL)
```

I will convert TPED to GenABEL RAW format:

```
> convert.snp.tped(tped="../usePrimitive/plink.tped",
+         tfam="../usePrimitive/plink.tfam",out="plink.raw")
```

```
Reading individual ids from file '../usePrimitive/plink.tfam' ...
... done.  Read 120 individual ids from file '../usePrimitive/plink.tfam'
Reading genotypes from file '../usePrimitive/plink.tped' ...
...done.  Read 500 SNPs from file '../usePrimitive/plink.tped'
Writing to file 'plink.raw' ...
... done.
```

Now imprt the data

```
> dta <- load.gwaa.data(phe="../usePrimitive/phenotypes.txt",gen="plink.raw")
```

```
ids loaded...
marker names loaded...
chromosome data loaded...
map data loaded...
allele coding data loaded...
strand data loaded...
genotype data loaded...
snp.data object created...
assignment of gwaa.data object FORCED; X-errors were not checked!
```

2 QC

3 Analysis of association