Conditional analysis

To understand whether nearby significant SNPs in our GWAS dataset represent independent signals, or are simply due to LD, try conditioning on the most significant SNP:

```
plink --bfile gwas-clean --logistic --covar gwas-mds.mds --covar-
number 2,3 --out mds-corrected-conditional --hide-covar --condition
rs16993168
```

What do you find? Are there multiple effects at the 46Mb locus?

Imputation

Copy this practical's files from */faculty/barrett/2011/imputation-practical* to a working directory and change to that directory.

Run MACH using the following command (remember that commands should be entered on the terminal as one line, even when they break across two lines in this document):

```
 mach1 -d sample.dat -p sample.ped -h hapmap.haplos -s hapmap.snps
--rounds 50 --greedy --geno
```

The README file has some tips on running MACH, and additional information can be found at:

http://www.sph.umich.edu/csg/abecasis/MACH/tour/imputation.html

How many SNPs have we imputed into this dataset?

How many have r^2 values > 0.95?

Note that this command has generated 'best guess' genotypes. You can unzip the output data using the command:

```
gunzip mach1.out.geno.gz
```

 To get more information (i.e. the genotype probabilities), try:

```
mach1 -d sample.dat -p sample.ped -h hapmap.haplos -s hapmap.snps
--rounds 50 --greedy --geno --mle --mldetails
```