

Imputation with impute2

http://mathgen.stats.ox.ac.uk/impute/impute_v2.html

Very basic use:

- -g <input file> - database to input (see format below)
- -m <map> - recombination map as 1000Genome or something like this
- -int <lower> <upper> - interval to make the imputation

Input file format

http://www.stats.ox.ac.uk/~marchini/software/gwas/file_format.html

From plink to impute format

First convert the binary files to *.ped* and *.map* if needed

<http://pngu.mgh.harvard.edu/~purcell/plink/dataman.shtml>

then you can use *gtool*,

<http://www.well.ox.ac.uk/~cfreeman/software/gwas/gtool.html>

in particular, [http://www.well.ox.ac.uk/~cfreeman/software/gwas/gtool.html#PED to GEN Conversion](http://www.well.ox.ac.uk/~cfreeman/software/gwas/gtool.html#PED%20to%20GEN%20Conversion)

```
gtool -P --ped example/example.ped --map example/example.map --og
example/out.gen --os example/out.sample
```

Before this [some awkward work](#) need to be done

[Look an example here](#)

From:
<https://cortafuegos.fundacioace.com/wiki/> - **Detritus Wiki**

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