

FAQ on postgwas functions:

General

- *Biomart normally uses the current genome assembly. All my analysis data refers to an older assembly, e.g. working on the mouse genome mm9. How can I configure biomart so that postgwas uses the older mm9 base positions and annotations?*

For some assemblies, the ensembl biomart offers archive servers (refer to the biomart's documentation). Setting the *host* element of the biomart configuration list will normally do the job. Possibly, some depending element names (attributes, filters, dataset name) might have also changed which needs to be considered. For mm9, an alternative *host* has to be specified and in addition the *mart* name has been changed:

```
myconfig <- biomartConfigs$mmusculus
myconfig$mmusculus$gene$host <- "may2012.archive.ensembl.org"
myconfig$mmusculus$gene$mart <- "ENSEMBL_MART_ENSEMBL"
myconfig$mmusculus$snp$host <- "may2012.archive.ensembl.org"
myconfig$mmusculus$snp$mart <- "ENSEMBL_MART_SNP"
```

Setting the argument *biomart.config = myconfig* in the postgwas function used should then use the mm9 configuration.

If it is not possible to change the biomart configuration appropriately, it is always feasible to supply data.frames with gene and SNP positions manually as buffer data. Running the function with *use.buffer = TRUE* will generate all buffer variables needed, which can then be customized. Refer to the corresponding documentation and examples for further information.

Snp2gene

- *Genotype data does not seem to be recognized from my ped/map files - LD computation between SNPs and genes always shows '0 snps'.*

It is necessary that chromosome names in the ped/map files match the chromosome names that are used in the configured biomart. SNPs are first mapped to biomart positions (including chromosome names) and genotypes are subsequently extracted from the ped/map files in dependence of the chromosome names.