

# GGBase – infrastructure for GGtools, genetics of gene expression

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# 1 NOTA BENE: IF STARTING ANEW, USE gQTL-Base/gQTLstats

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This package was published in the dawn of eQTL analysis. It uses somewhat idiosyncratic data structures. gQTL\* packages are more up to date.

## 2 Introduction

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The GGBase package defines infrastructure for analysis of data on the genetics of gene expression. This document is primarily of concern to developers; for information on conducting analyses in genetics of expression, please see the vignette for the GGtools package.

## 3 Primary class structure, and associated methods

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`smlSet` is used to denote “SNP matrix list” integrative container for expression plus genotype data. The `SnpMatrix` class is defined in Clayton’s `snpStats` package.

```
library(GGBase)
## Loading required package: snpStats
## Loading required package: survival
## Loading required package: Matrix
getClass("smlSet")
## Class "smlSet" [package "GGBase"]
##
## Slots:
##
## Name:          smlEnv          annotation          organism
## Class:         environment     character          character
##
## Name:          assayData       phenoData          featureData
## Class:         AssayData AnnotatedDataFrame AnnotatedDataFrame
##
## Name:          experimentData   protocolData   .__classVersion__
## Class:         MIAxE AnnotatedDataFrame       Versions
##
## Extends:
## Class "eSet", directly
## Class "VersionedBiobase", by class "eSet", distance 2
## Class "Versioned", by class "eSet", distance 3
showMethods(class="smlSet", where="package:GGBase")
## Function: [ (package base)
## x="smlSet", i="ANY", j="ANY", drop="ANY"
##
## Function: clipPCs (package GGBase)
## x="smlSet", inds2drop="numeric", center="logical"
## x="smlSet", inds2drop="numeric", center="missing"
```

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```
##  
## Function: combine (package BiocGenerics)  
## x="smlSet", y="smlSet"  
##  
## Function: exprs (package Biobase)  
## object="smlSet"  
##  
## Function: nsFilter (package genefilter)  
## eset="smlSet"  
##  
## Function: permEx (package GGBase)  
## sms="smlSet"  
##  
## Function: plot_EvG (package GGBase)  
## gsym="genesym", rsid="rsid", sms="smlSet"  
## gsym="probeId", rsid="rsid", sms="smlSet"  
##  
## Function: smList (package GGBase)  
## x="smlSet"
```

Genotype data are stored in a list in the `smlEnv` environment to diminish copying as functions are called on the `smlSet` instance.

## 4 Example data structure

Expression data were published by the Wellcome Trust GENEVAR project in 2007. Genotype data are from HapMap phase II.

```
if ("GGtools" %in% installed.packages()[,1]) {  
  library(GGtools)  
  s20 = getSS("GGtools", "20")  
  s20  
}  
## Loading required package: data.table  
## Loading required package: parallel  
## Loading required package: Homo.sapiens  
## Loading required package: AnnotationDbi  
## Loading required package: stats4  
## Loading required package: BiocGenerics  
##  
## Attaching package: 'BiocGenerics'  
## The following objects are masked from 'package:parallel':  
##  
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,  
##   clusterExport, clusterMap, parApply, parCapply, parLapply,  
##   parLapplyLB, parRapply, parSapply, parSapplyLB  
## The following objects are masked from 'package:Matrix':  
##  
##   colMeans, colSums, rowMeans, rowSums, which
```

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```
## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##   Filter, Find, Map, Position, Reduce, anyDuplicated, append,
##   as.data.frame, basename, cbind, colMeans, colSums, colnames,
##   dirname, do.call, duplicated, eval, evalq, get, grep, grepl,
##   intersect, is.unsorted, lapply, mapply, match, mget, order,
##   paste, pmax, pmax.int, pmin, pmin.int, rank, rbind, rowMeans,
##   rowSums, rownames, sapply, setdiff, sort, table, tapply, union,
##   unique, unsplit, which, which.max, which.min
## Loading required package: Biobase
## Welcome to Bioconductor
##
##   Vignettes contain introductory material; view with
##   'browseVignettes()'. To cite Bioconductor, see
##   'citation("Biobase")', and for packages 'citation("pkgname)".
## Loading required package: IRanges
## Loading required package: S4Vectors
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:data.table':
##
##   first, second
## The following object is masked from 'package:Matrix':
##
##   expand
## The following object is masked from 'package:base':
##
##   expand.grid
## Attaching package: 'IRanges'
## The following object is masked from 'package:data.table':
##
##   shift
## Loading required package: OrganismDbi
## Loading required package: GenomicFeatures
## Loading required package: GenomeInfoDb
## Loading required package: GenomicRanges
## Loading required package: GO.db
##
## Loading required package: org.Hs.eg.db
##
## Loading required package: TxDb.Hsapiens.UCSC.hg19.knownGene
## Registered S3 methods overwritten by 'ggplot2':
##   method      from
##   [.quosures  rlang
##   c.quosures  rlang
##   print.quosures rlang
## Registered S3 method overwritten by 'dplyr':
```

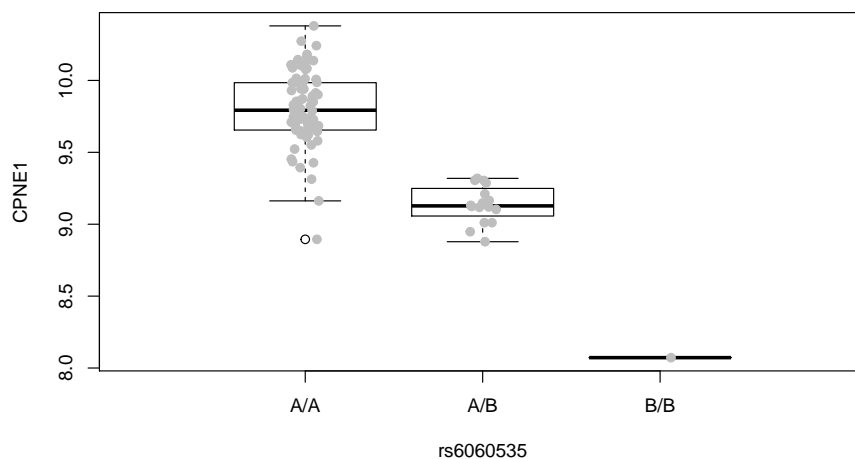
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```
## method          from
## as.data.frame.tbl_df tibble
##
## Attaching package: 'GGtools'
## The following object is masked from 'package:stats':
##
##   getCall
## SnpMatrix-based genotype set:
## number of samples: 90
## number of chromosomes present: 1
## annotation: illuminaHumanv1.db
## Expression data dims: 47293 x 90
## Total number of SNP: 119921
## Phenodata: An object of class 'AnnotatedDataFrame'
##   sampleNames: NA06985 NA06991 ... NA12892 (90 total)
##   varLabels: famid persid ... male (7 total)
##   varMetadata: labelDescription
```

## 5 Visualizing a specific gene-SNP relationship

The SNP rs6060535 was reported as an eQTL for CPNE1 by Cheung et al in a Nature paper of 2005.

```
if (exists("s20")) {
  plot_EvG(genesym("CPNE1"), rsid("rs6060535"), s20)
} else plot(1) # pdf must exist...
##
```



## 6 Genotype representations

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The `Snpmatrix` class of the `snpStats` package is used to represent genotypes. Imputed genotypes and their uncertainties can be represented in this scheme, but the example does not depict this.

```
if (exists("s20")) {
  # raw bytes
  as(smlist(s20)[[1]], "matrix")[1:5,1:5]
  # generic calls
  as(smlist(s20)[[1]], "character")[1:5,1:5]
  # risk allele (alphabetically later nucleotide) counts
  as(smlist(s20)[[1]], "numeric")[1:5,1:5]
}
##          rs4814683 rs6076506 rs6139074 rs1418258 rs7274499
## NA06985          2          2          2          2          2
## NA06991          1          2          1          1          2
## NA06993          0          2          0          0          2
## NA06994          0          2          0          0          2
## NA07000          2          2          2          2          2
```

## 7 Reducing memory footprint of integrative data structures

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When millions of genotypes are recorded, it can be cumbersome to work with all simultaneously in memory, and it is seldom scientifically relevant to do so. Thus a packaging protocol has been established in conjunction with the `getSS` function to allow chromosome-at-a-time loading of genotype data in conjunction with expression data.

To deploy the packaging protocol, use the `externalize` function on a “one-time” full `smlSet` representation of the data, or mimic the behavior of this function by creating a new package folder structure and populating the `inst/parts` with `rda` files representing a partition (usually by chromosome) of the genotype `Snpmatrix` instances.