

# GGBase: infrastructure for genetics of gene expression

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## 1 Introduction

Data representations for genetics of gene expression in humans must be as efficient as possible. Up to Bioconductor 2.1, integrative genomics experiments could be represented by `racExSet` instances as defined in package `GGtools`. Genotypes were represented as integers.

For Bioconductor 2.2, we have access to the `snpMatrix` package of D. Clayton, and we have introduced the `smlSet` class to represent genetics of gene expression studies with lists of `snp.matrix` instances, along with ordinary representations of expression data.

## 2 Primary class structure, and associated methods

```
> library(GGBase)
> 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	.___classVersion__
Class:	MIAME	Versions

```
Extends:
```

```
Class "eSet", directly
```

Class "VersionedBiobase", by class "eSet", distance 2

Class "Versioned", by class "eSet", distance 3

```
> library(GGtools)
```

```
> showMethods(class = "smlSet", where = "package:GGBase")
```

Function: [ (package base)

x="smlSet", i="ANY", j="ANY", drop="ANY"

Function: combine (package Biobase)

x="smlSet", y="smlSet"

Function: exprs (package Biobase)

object="smlSet"

Function: getAlleles (package GGBase)

x="smlSet", rs="rsid"

Function: getSnpsLocs (package GGBase)

x="smlSet", c="chrnum"

x="smlSet", c="missing"

Function: plot\_EvG (package GGBase)

gsym="genesym", rsid="rsid", sms="smlSet"

gsym="probeId", rsid="rsid", sms="smlSet"

Function: plot\_EvG2 (package GGBase)

gsym="genesym", rsid1="rsid", rsid2="rsid", sms="smlSet"

gsym="probeId", rsid1="rsid", rsid2="rsid", sms="smlSet"

Function: show (package methods)

object="smlSet"

Function: smlEnv (package GGBase)

x="smlSet"

Function: smList (package GGBase)

x="smlSet"

Function: snpNames (package GGBase)

x="smlSet", c="chrnum"

x="smlSet", c="missing"

```
Function: snps (package GGBase)
x="smlSet", chr="chrnum"
```

```
> showMethods(class = "smlSet", where = "package:GGtools")
```

```
Function: [ (package base)
x="smlSet", i="ANY", j="ANY", drop="ANY"
```

```
Function: gwSnpTests (package GGtools)
sym="formula", sms="smlSet", cnum="cnumOrMissing", cs="ANY"
sym="formula", sms="smlSet", cnum="snpdepth", cs="ANY"
sym="formula", sms="smlSet", cnum="snpdepth", cs="chunksize"
```

```
Function: hbTests (package GGtools)
fmla="genesym", sms="smlSet", cnum="chrnum", rsid="numeric", rad="numeric"
```

```
Function: residTests (package GGtools)
fit="cwSnpScreenResult", sms="smlSet", litfmla="formula", rsnum="missing"
```

### 3 Example data structure

```
> data(hmceuB36.2021)
> hmceuB36.2021
```

```
snp.matrix-based genotype set:
number of samples: 90
number of chromosomes present: 2
annotation: illuminaHumanv1.db
Expression data dims: 47293 x 90
Phenodata: An object of class "AnnotatedDataFrame"
  sampleNames: NA06985, NA06991, ..., NA12892 (90 total)
  varLabels and varMetadata description:
    famid: hapmap family id
    persid: hapmap person id
    ...: ...
    male: logical TRUE if male
    (7 total)
```

### 4 SNP location infrastructure

see the newSNPloc vignette

## 5 Conclusion

The concepts discussed above define the bulk of the tools supporting the `gwSnpTests` method of GGtools. Consult the vignette of GGtools for more information.