

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   protocolData       .__classVersion__
Class:         MIAME 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: coerce (package methods)  
from="smlSet", to="ExpressionSet"
```

```
Function: combine (package Biobase)  
x="smlSet", y="smlSet"
```

```
Function: exprs (package Biobase)  
object="smlSet"
```

```
Function: getAlleles (package GGBase)  
x="smlSet", rs="rsid"
```

```
Function: getSnps (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"
```

```
Function: updateObject (package Biobase)  
object="smlSet"
```

3 Example data structure

```
> data(smlSet.example)  
> smlSet.example
```

```
snp.matrix-based genotype set:  
number of samples: 10  
number of chromosomes present: 1  
annotation: illuminaHumanv1.db  
Expression data dims: 100 x 10  
Phenodata: An object of class "AnnotatedDataFrame"  
  sampleNames: NA06985, NA06991, ..., NA07048 (10 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.