

Package ‘GGdata’

April 20, 2016

Title all 90 hapmap CEU samples, 47K expression, 4mm SNP

Description data exemplars dealing with hapmap SNP reports, GWAS, etc.

Version 1.8.0

Author VJ Carey <stvjc@channing.harvard.edu>

Maintainer VJ Carey <stvjc@channing.harvard.edu>

biocViews ExperimentData, HapMap, Genome, SequencingData,
MicroarrayData, SNPData

Depends R (>= 2.12.0), methods, Biobase (>= 2.5.5), GGBase, snpStats,
illuminaHumanv1.db, AnnotationDbi

Enhances GGtools

LazyLoad yes

License LGPL

NeedsCompilation no

R topics documented:

hmceuB36 1

Index 3

hmceuB36 *representations of HapMap snp data + expression data*

Description

representations of HapMap snp data + expression data

Usage

```
# getSS("GGdata", "20") # for example, to get full expression, + genotypes  
# on chr20
```

Format

ExpressionSet and SnpMatrix instances to be combined using `getSS`

Details

Instances of class `smlSet` are created from two basic sources.

First, the expression data for 90 CEU families in CEPH were obtained from SANGER GENEVAR project.

Second, data on forward non-redundant SNPs in these individuals the HapMap build 36 ftp site in march 2008. Full provenance information still to be supplied.

Value

instances of class `smlSet`

Note

As of March 2011 the `smlSet` is no longer serialized. Instead, use `getSS("GGdata", [chrs])` to create an `smlSet` with all probes and selected chromosomes. There is an instance of `ExpressionSet-class` named `ex` in the data folder of this package that will be united with genotype data using `getSS`.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References

Cheung VG., Spielman RS., Ewens KG., Weber TM., Morley M & Burdick JT.: *Mapping determinants of human gene expression by regional and whole genome association.* Nature, 437: 1365-1369, 2005

Examples

```
library(GGtools)
hmceuB36 = getSS("GGdata", c("20")) # just 1 chromosome
exprs(hmceuB36)[1:4,1:4]
as(smlList(hmceuB36)[[1]][1:4,1:4], "character")
library(GGtools)
library(illuminaHumanv1.db)
cptag = get("CPNE1", revmap(illuminaHumanv1SYMBOL))
tt = eqtlTests(hmceuB36[probeId(cptag),], ~male)
topFeats(probeId(cptag), mgr=tt, ffind=1)
```

Index

*Topic **packages**

hmceuB36, [1](#)

ex (hmceuB36), [1](#)

getSS, [2](#)

hmceuB36, [1](#)

hmceuB36-package (hmceuB36), [1](#)

sm1Set, [2](#)