Package ‘GGdata’

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Title  all 90 hapmap CEU samples, 47K expression, 4mm SNP
Description data exemplars dealing with hapmap SNP reports, GWAS, etc.
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biocViews ExperimentData, HapMap, Genome, SequencingData,
MicroarrayData, SNPData
Depends R (>= 2.12.0), methods, Biobase (>= 2.5.5), GGBase, snpStats,
iluminaHumanv1.db, AnnotationDbi
Enhances GGtools
LazyLoad yes
License LGPL.
NeedsCompilation no

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  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)

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References


Examples

```r
library(GGtools)
hmceuB36 = getSS("GGdata", c("20")) # just 1 chromosome
eqtl(hmceuB36)
eqtl(hmceuB36)[1:4,1:4]
as(smList(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), mg=tt, ffind=1)
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