

Package ‘GeuvadisTranscriptExpr’

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Type Package

Title Data package with transcript expression and bi-allelic genotypes from the GEUVADIS project

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Date 2021-11-21

Description Provides transcript expression and bi-allelic genotypes corresponding to the chromosome 19 for CEU individuals from the GEUVADIS project, Lappalainen et al.

Depends R (>= 3.3.0)

License GPL (>= 3)

LazyData true

biocViews Homo_sapiens_Data, SNPData, Genome, RNASeqData, SequencingData, ExpressionData

VignetteBuilder knitr

Suggests limma, rtracklayer, GenomicRanges, Rsamtools, VariantAnnotation, tools, BiocStyle, knitr, testthat

NeedsCompilation no

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`counts`*Sample data for sQTL analysis*

Description

Subsets of raw data available in this package and saved as Rdata objects for faster loading.

Usage

`counts``gene_ranges``genotypes``snp_ranges`

Format

`counts` is a data frame with subset of counts from `TrQuantCount_CEU_chr19.tsv`

`gene_ranges` is a `GRanges` object containing subset of gene coordinates from `genes_chr19.bed`

`genotypes` is a data frame with subset of genotypes from `genotypes_CEU_chr19.tsv`

`snp_ranges` is a `Granges` object containing subset of SNP coordinates from `genotypes_CEU_chr19.tsv`

For all the details on how these data sets were produced, see examples.

Value

`counts`, `gene_ranges`, `genotypes`, `snp_ranges`

Source

Lappalainen T, Sammeth M, Friedlander MR, et al. Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*. 2013;501(7468):506-11

Examples

```
library(rtracklayer)
data_dir <- system.file("extdata", package = "GeuvadisTranscriptExpr")

gene_id_subset <- readLines(file.path(data_dir, "gene_id_subset.txt"))
snp_id_subset <- readLines(file.path(data_dir, "snp_id_subset.txt"))

# Load gene ranges with names!
gene_ranges <- import(file.path(data_dir, "genes_chr19.bed"))
names(gene_ranges) <- mcols(gene_ranges)$name

gene_ranges <- gene_ranges[gene_id_subset, ]
```

```
# Load transcript counts
counts <- read.table(file.path(data_dir, "TrQuantCount_CEU_chr19.tsv"),
                    header = TRUE, sep = "\t", as.is = TRUE)

counts <- counts[counts$Gene_Symbol %in% gene_id_subset, ]

# Load genotypes
genotypes <- read.table(file.path(data_dir, "genotypes_CEU_chr19.tsv"),
                       header = TRUE, sep = "\t", as.is = TRUE)

genotypes <- genotypes[genotypes$snpId %in% snp_id_subset, ]

# Create SNP ranges with names!
snp_ranges <- GRanges(Rle(genotypes$chr), IRanges(genotypes$start,
                                                  genotypes$end))
names(snp_ranges) <- genotypes$snpId
```

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* **datasets**

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