

Package ‘GeuvadisTranscriptExpr’

August 28, 2025

Type Package

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

Version 1.37.1

Date 2025-06-27

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

Author Malgorzata Nowicka [aut, cre]

Maintainer Malgorzata Nowicka <gosia.nowicka@uzh.ch>

git_url <https://git.bioconductor.org/packages/GeuvadisTranscriptExpr>

git_branch devel

git_last_commit bd75e6a

git_last_commit_date 2025-06-27

Repository Bioconductor 3.22

Date/Publication 2025-08-28

Contents

counts	2
Index	4

`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
```

Index

* **datasets**

counts, [2](#)

counts, [2](#)

gene_ranges (counts), [2](#)

genotypes (counts), [2](#)

snp_ranges (counts), [2](#)