Package ‘supersigs’

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Description Generate SuperSigs (supervised mutational signatures) from single nucleotide variants in the cancer genome. Functions included in the package allow the user to learn supervised mutational signatures from their data and apply them to new data. The methodology is based on the one described in Afsari (2021, ELife).

biocViews FeatureExtraction, Classification, Regression, Sequencing, WholeGenome, SomaticMutation

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dataset of mutations
Example dataset of mutations

Description

A dataset containing a list of mutations and other necessary attributes

Usage

example_dt

Format

A data frame with 10 rows and 5 columns:

- sample_id  ID of the patient
- age  age of the patient
- chromosome  chromosomal position of the mutation
- position  position of the mutation
- ref  original nucleotide
- alt  mutated nucleotide
get_signature

Function to obtain a SuperSig

Description

Generate a tissue-specific SuperSig for a given dataset of mutations and exposure factor. Returns the SuperSig and a classification model trained with the SuperSig.

Usage

get_signature(data, factor, wgs = FALSE)

Arguments

data: a data frame of mutations containing columns for sample_id, age, IndVar, and the 96 trinucleotide mutations (see vignette for details)
factor: the factor/exposure (e.g. "age", "smoking"). If the factor = "age", the SuperSig is computed using counts. Otherwise, rates (counts/age) are used.
wgs: logical value indicating whether sequencing data is whole-genome (wgs = TRUE) or whole-exome (wgs = FALSE)

Value

get_signature returns an object of class SuperSig

Examples

head(example_dt) # use example data from package
input_dt <- make_matrix(example_dt) # convert to correct format
input_dt$IndVar <- c(1, 1, 1, 0, 0) # add IndVar column
get_signature(data = input_dt, factor = "Age") # get SuperSig

make_matrix

Function to transform mutations into "matrix" format

Description

Transform a data frame of mutations in long format into a data frame of trinucleotide mutations with flanking bases in a wide matrix format.

Usage

make_matrix(data, genome = "hg19")
Arguments

data a data frame of mutations in VCF format (see vignette for details)
genome the reference genome used ("hg19" or "hg38")

Value

make_matrix returns a data frame of mutations, one row per sample

Examples

head(example_dt) # use example data from package
input_dt <- make_matrix(example_dt) # convert to correct format
head(input_dt)

partial_signature Function to remove the contribution of a SuperSig

Description

Remove the contribution of a SuperSig from the data and return the data.

Usage

partial_signature(data, object)

Arguments

data a data frame of mutations containing columns for sample_id, age, IndVar, and the 96 trinucleotide mutations (see vignette for details)
object an object of class SuperSig

Value

predict_signature returns the original data frame with the contribution of a supervised signature removed

Examples

head(example_dt) # use example data from package
input_dt <- make_matrix(example_dt) # convert to correct format
input_dt$IndVar <- c(1, 1, 1, 0, 0) # add IndVar column
supersig <- get_signature(data = input_dt, factor = "Age") # get SuperSig
partial_signature(data = input_dt, object = supersig)
predict_signature

Function to predict using SuperSig object

Description

Using a generated SuperSig, predict on a new dataset and return predicted probabilities for each observation.

Usage

predict_signature(object, newdata, factor)

Arguments

object      an object of class SuperSig
newdata     a data frame of mutations containing columns for sample_id, age, IndVar, and the 96 trinucleotide mutations (see vignette for details)
factor      the factor/exposure (e.g. "age", "smoking")

Value

predict_signature returns the original data frame with additional columns for the feature counts and classification score

Examples

head(example_dt) # use example data from package
input_dt <- make_matrix(example_dt) # convert to correct format
input_dt$IndVar <- c(1, 1, 1, 0, 0) # add IndVar column
out <- get_signature(data = input_dt, factor = "Age") # get SuperSig
newdata <- predict_signature(out, newdata = input_dt, factor = "age")
suppressPackageStartupMessages(library(dplyr))
head(newdata %>% select(score))

process_vcf

Function to transform VCF object into "matrix" format

Description

Transform a VCF object into a data frame of trinucleotide mutations with flanking bases in a wide matrix format. The function assumes that the VCF object contains only one sample and that each row in rowRanges represents an observed mutation in the sample.

Usage

process_vcf(vcf)
Arguments

vcf  a VCF object (from VariantAnnotation package)

Value

process_vcf returns a data frame of mutations, one row per mutation

Examples

# Use example vcf from VariantAnnotation
suppressPackageStartupMessages({library(VariantAnnotation)})
fl <- system.file("extdata", "chr22.vcf.gz", package="VariantAnnotation")
vcf <- VariantAnnotation::readVcf(fl, "hg19")

# Subset to first sample
vcf <- vcf[, 1]
# Subset to row positions with homozygous or heterozygous alt
positions <- geno(vcf)$GT != "0|0"
vcf <- vcf[positions[, 1],]
colData(vcf)$age <- 50  # Add patient age to colData (optional)

# Run function
dt <- process_vcf(vcf)
head(dt)

simplify_signature  Function to simplify signature representation into interpretable labels for visualization purposes

Description

Take a signature representation from SuperSig and group trinucleotides within each feature into interpretable labels, with optional IUPAC labeling from IUPAC_CODE_MAP in the Biostrings package

Usage

simplify_signature(object, iupac)

Arguments

object  an object of class SuperSig
iupac   logical value indicating whether to use IUPAC labels (iupac = TRUE) or not (iupac = FALSE)
SuperSig-class

Value

simplify_signature returns a vector of simplified features and their difference in mean mean rates between exposed and unexposed (or average rate if the factor is "age")

Examples

head(example_dt) # use example data from package
input_dt <- make_matrix(example_dt) # convert to correct format
input_dt$IndVar <- c(1, 1, 1, 0, 0) # add IndVar column
supersig <- get_signature(data = input_dt, factor = "Smoking")
simplify_signature(object = supersig, iupac = FALSE)
simplify_signature(object = supersig, iupac = TRUE)

SuperSig-class

An S4 class for SuperSig

Description

An S4 class for SuperSig

Slots

Signature data frame of features and their difference in mean rates between exposed and unexposed (or the average rate if the factor is "age")

Features list of features that comprise the signature and their representation in terms of the fundamental (trinucleotide) mutations

AUC length-one numeric vector of the apparent AUC (i.e. not cross-validated)

Model list of a glm class for trained logistic regression model

supersig_ls Trained SuperSigs from TCGA

Description

A list containing 67 SuperSigs

Usage

supersig_ls

Format

A named list with 67 elements, each of which is a ‘SuperSig’
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