Package 'SureTypeSCR'

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Title Interface to python based package SureTypeSC via reticulate

Description SureTypeSCR is the implementation of algorithm for regenotyping of single cell data coming from Illumina BeadArrays without genome studio.

Version 0.99.0

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Suggests testthat

Depends R (>= 3.5.0), reticulate, knitr, BiocStyle

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License Artistic-2.0

biocViews Software, GenotypingArray,SingleCell

VignetteBuilder knitr

SystemRequirements python (>= 2.7), sklearn, numpy, pandas, SureTypeSC, IlluminaBeadArrayFiles

NeedsCompilation no

R topics documented:

`allele_freq` *The frequency function is to calculate the allele frequency over all the samples*

Description

The frequency function is to calculate the allele frequency over all the samples

Usage

```
allele_freq(df,th=0)
```

Arguments

`df`	the pandas dataframe from GenomeStudio or scbasic function
`th`	the threshold

Value

The frequency values of all samples

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- allele_freq(df,th=0.2)
```

apply_thresh *To apply threshold over all samples on GenCall score*

Description

To apply threshold over all samples on GenCall score

Usage

```
apply_thresh(df,th)
```

Arguments

df	the Data object from create_from_frame function
th	the threshold

Value

Data object only with applied threshold

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

df <- create_from_frame(df)

df <- apply_thresh(df,0.01)
```

calculate_ma *To calculate m and a features*

Description

To calculate m and a features

Usage

```
calculate_ma(df)
```

Arguments

df	the Data object from create_from_frame function

Value

Data object with adding m and a features

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

df <- create_from_frame(df)

dfs <- calculate_ma(df)
```

---

callrate *The callrate function is to calculate the allele frequency over all the samples*

Description

The callrate function is to calculate the allele frequency over all the samples

Usage

```
callrate(df,th=0)
```

Arguments

df	the pandas dataframe from GenomeStudio or scbasic function
th	the threshold

Value

The callrate values of all samples

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- callrate(df,th=0.2)
```

`callrate_chr` *The callrate function is to calculate the allele frequency over all the samples of one specific chromosome*

Description

The callrate function is to calculate the allele frequency over all the samples of one specific chromosome

Usage

```
callrate_chr(df,chr_name,th=0)
```

Arguments

`df`	the pandas dataframe from GenomeStudio or scbasic function
`chr_name`	the name of the selected chromsome
`th`	the threshold

Value

The callrate values of all samples of one specific chromosome

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)
```

```
# The Random Forest classifier
call <- callrate_chr(df,'1',th=0.2)
```

`create_from_frame` *convert pandas dataframe to Data object*

Description

Convert pandas dataframe to Data object and rearrange the index level

Usage

```
create_from_frame(df)
```

Arguments

`df`	genotyping pandas dataframe from scbasic function

Value

Data object with index rearrangement (multi-leve index)

Examples

```
gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

# get genotyping data from gtc files and meta file
df <- scbasic(manifest_path,cluster_path,samplesheet)


# create Data object and rearrange the index
df <- create_from_frame(df)
```

locus_cluster *To do intensity aggregation at a specific locus*

Description

To do intensity aggregation at a specific locus

Usage

```
locus_cluster(df,locus)
```

Arguments

df	the pandas dataframe from GenomeStudio or scbasic function
locus	the name of the locus

Value

the intensity of one locus

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- locus_cluster(df,'rs3128117')
```

locus_ma *To do m and a aggregation at a specific locus*

Description

To do m and a aggregation at a specific locus

Usage

```
locus_ma(df,locus)
```

Arguments

df	the pandas dataframe from GenomeStudio or scbasic function
locus	the name of the locus

Value

the m and a of one locus

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- locus_ma(df,'rs3128117')
```

---

pca_chr *To apply principle component annalysis on frequency dataframe of samples of one chromosome*

Description

To apply principle component annalysis on frequency dataframe of samples

Usage

```
pca_chr(df,chr_name,th=0,n=2)
```

Arguments

df	the pandas dataframe from GenomeStudio or scbasic function
chr_name	the name of the specific chromosome
th	the threshold
n	n is the number of components

Value

Component values

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- pca_chr(df,'X')
```

---

pca_samples *To apply principle component annalysis on frequency dataframe of samples*

Description

To apply principle component annalysis on frequency dataframe of samples

Usage

```
pca_samples(df,th=0)
```

Arguments

df	the pandas dataframe from GenomeStudio or scbasic function
th	the threshold

Value

Component values

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- pca_samples(df,th=0.2)
```

restrict_chrom *To choose certain chromosomes with Data object*

Description

To choose certain chromosomes with Data object

Usage

```
restrict_chrom(df,chrom)
```

Arguments

df	the Data object from create_from_frame function
chrom	the list of selected chromosomes

Value

Data object only with certain chromosomes

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

df <- create_from_frame(df)

df <- restrict_chrom(df,c('1','2'))
```

sample_ma *To do m and a aggregation at a specific chromosome of a specific sample*

Description

To do m and a at a specific chromosome of a specific sample

Usage

```
sample_ma(df,sample_name,chr_name)
```

Arguments

df	the pandas dataframe from GenomeStudio or scbasic function
sample_name	the name of the sample
chr_name	the name of the chromosome

Value

the m and a a of specific chromosome of a specific sample

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)

# The Random Forest classifier
call <- sample_ma(df,'Kit4_4mos_SC21','1')
```

scbasic *Function to process raw gtc data and meta data without genomestudio*

Description

Function to process raw gtc data and meta data without genomestudio

Usage

```
scbasic(bpm,egt,samplesheet)
```

Arguments

bpm	a pathname to manifest file
egt	a pathname to cluster file
samplesheet	a pathname to samplesheet file

Value

pandas data frame of genotyping data

Examples

```
gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

# get genotyping data from gtc files and meta file
df <- scbasic(manifest_path,cluster_path,samplesheet)

#/Users/apple/anaconda3/envs/gtc2/lib/python2.7/site-packages/sklearn/ensemble/weight_boosting.py:29:
#DeprecationWarning: numpy.core.umath_tests is an internal NumPy module and should not be imported.
#It will be removed in a future NumPy release.
  #from numpy.core.umath_tests import inner1d
#Reading cluster file
#Reading sample file
#Number of samples: 2
#Reading manifest file
#Initializing genotype data
#Generating
#9968648019_R06C01
#9968648019_R06C02
#Finish parsing
```

---

scEls *mediate access to python modules*

Description

mediate access to python modules

Usage

```
scEls()
```

Value

list of (S3) "python.builtin.module"

Note

Returns a list with elements sc (SureTypeSC), pd (pandas)each referring to python modules.

Examples

```
els = scEls()

els

##$sc
##Module(SureTypeSC)

##$pd
##Module(pandas)
```

`scload` *Load Random Forest classifier or Gaussian Discrinimate Analysis*

Description

Load Random Forest classifier or Gaussian Discrinimate Analysis

Usage

```
scload(filename)
```

Arguments

`filename`	a pathname to an classifier

Value

instance of a classifier

Examples

```
clf_rf_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')
clf_gda_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')

# The Random Forest classifier
clf_rf <- scload(clf_rf_path)

# The Gaussian Discriminate Analysis classifier
clf_gda <- scload(clf_gda_path)
```

scpredict *Predictions from Random Forest classifier or Gaussian Discriminant Analysis*

Description

Predictions from Random Forest classifier or Gaussian Discriminant Analysis

Usage

```
scpredict(clf,test,clftype='rf')
```

Arguments

clf	classifier load by using scload
test	Data object including m and a feature
clftype	The type of classifier (rf: Random Forest; gda: Gaussian Discriminant Analysis; rf-gda: the cascade of Random Forest and Gaussian Discriminant Analysis)

Value

The prediction Data object.

The predicted items might include:

rf_ratio:1_pred: Random Forest prediction (binary)

rf_ratio:1_prob: Random Forest Score for the positive class

gda_ratio:1_prob: Gaussian Discriminant Analysis score for the positive class

gda_ratio:1_pred: Gaussian Disciminant Analysis prediction (binary)

rf-gda_ratio:1_prob: combined 2-layer RF and GDA - probability score for the positive class

rf-gda_ratio:1_pred: binary prediction of RF-GDA

Examples

```
gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')
clf_rf_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')
clf_gda_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')



# The Random Forest classifier
clf_rf <- scload(clf_rf_path)

# The Gaussian Disciminant Analysis
```

```
clf_gda <- scload(clf_gda_path)

# get genotyping data from gtc files and meta file
df <- scbasic(manifest_path,cluster_path,samplesheet)

# create Data object and rearrange the index
dfs <- create_from_frame(df)

# extract the chromosomes 1 and 2
dfs <- restrict_chrom(dfs,c('1','2'))

# mask the Gencall score lower than 0.01
dfs <- apply_thresh(dfs,0.01)

# calculate the m and a feature
dfs <- calculate_ma(dfs)

# prediction by Random Forest
result_rf <- scpredict(clf_rf,dfs,clftype='rf')

# prediction by Guassian Discriminate Analysis
result_gda <- scpredict(clf_gda,dfs,clftype='gda')
```

---

scsave *Save the predictions from different classifiers*

Description

Save the predictions from different classifiers

Usage

```
# save different mdoes based on the full prediction table
scsave(result,filename,header=TRUE,clftype='rf',threshold=0.15,all=FALSE)
```

Arguments

result	The predicted result
filename	The path where the result will be saved
header	the index
clftype	classifier type
threshold	the threshold of gencall score
all	if the users want to save the full table or not

Value

txt file of the results

Examples

```
gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')
clf_rf_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')
clf_gda_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')


# The Random Forest classifier
clf_rf = scload(clf_rf_path)

# The Gaussian Disciminant Analysis
clf_gda = scload(clf_gda_path)

# get genotyping data from gtc files and meta file
df <- scbasic(manifest_path,cluster_path,samplesheet)

# create Data object and rearrange the index
dfs <- create_from_frame(df)


#original shape (294602, 15)
#shape after operation (294602, 12)



# extract the chromosomes 1 and 2
dfs <- restrict_chrom(dfs,c('1','2'))

# mask the Gencall score lower than 0.01
dfs <- apply_thresh(dfs,0.01)

# calculate the m and a feature
dfs <- calculate_ma(dfs)

# prediction by Random Forest
result_rf <- scpredict(clf_rf,dfs,clftype='rf')

# prediction by Guassian Discriminate Analysis
result_gda <- scpredict(clf_gda,dfs,clftype='gda')

# Train the rf-gda classifier
trainer <- scTrain(result_gda,clfname='gda')

# The prediction from the cascade of Random Forest and Gaussian Discriminate Analysis
result_end <- scpredict(trainer,result_gda,clftype='rf-gda')

# Save the complete prediction table
scsave(result_end,'fulltable.txt',clftype='rf',header=TRUE,threshold=0.15,all=TRUE)

# recall mode
scsave(result_end,'fulltable.txt',clftype='rf',threshold=0.15,header=TRUE,all=FALSE)
```

scTrain *Train Gaussian Discriminate Analysis by using the output of predicitons of Random Forest*

Description

Train Gaussian Discriminate Analysis by using the output of predicitons of Random Forest

Usage

```
scTrain(trainingdata, clfname='gda')
```

Arguments

trainingdata	Data object, the training data of scTrain
clfname	The classifier type

Value

instance of a classifier

Examples

```
gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')
clf_rf_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')
clf_gda_path = system.file('files/clf_30trees_7228_ratio1_lightweight.clf',package='SureTypeSCR')



# The Random Forest classifier
clf_rf <- scload(clf_rf_path)

# The Gaussian Disciminant Analysis
clf_gda <- scload(clf_gda_path)

 # get genotyping data from gtc files and meta file
df <- scbasic(manifest_path,cluster_path,samplesheet)

# create Data object and rearrange the index
dfs <- create_from_frame(df)

# extract the chromosomes 1 and 2
dfs <- restrict_chrom(dfs,c('1','2'))

# mask the Gencall score lower than 0.01
dfs <- apply_thresh(dfs,0.01)

# calculate the m and a feature
```

```
dfs <- calculate_ma(dfs)

# prediction by Random Forest
result_rf <- scpredict(clf_rf,dfs,clftype='rf')

# prediction by Guassian Discriminate Analysis
result_gda <- scpredict(clf_gda,dfs,clftype='gda')

# Train the rf-gda classifier
trainer <- scTrain(result_rf,clfname='gda')

# The prediction from the cascade of Random Forest and Gaussian Discriminate Analysis
result_end <- scpredict(trainer,result_gda,clftype='rf-gda')
```

`sc_allele_freq` *This function is to calculate the allele frequency over all the samples*

Description

The callrate function is to calculate the allele frequency over all the samples

Usage

```
sc_allele_freq(df,alg,threshold)
```

Arguments

`df`	Data object
`alg`	algorithm
`threshold`	the threshold

Value

The callrate values of all samples

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)
```

```
# create Data object and rearrange the index
df <- create_from_frame(df)

# The Random Forest classifier
call <- sc_allele_freq(df,'score',0.2)
```

`sc_callrate` *The callrate function is to calculate the allele frequency over all the samples*

Description

The callrate function is to calculate the allele frequency rate over all the samples

Usage

```
sc_callrate(df,alg,threshold)
```

Arguments

`df`	Data object
`alg`	algorithm
`threshold`	the threshold

Value

The callrate values of all samples

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)


# create Data object and rearrange the index
df <- create_from_frame(df)

# The Random Forest classifier
call <- sc_callrate(df,'score',0.2)
```

sc_callrate_chr *The callrate function is to calculate the allele frequency of all the samples of one chromosome*

Description

The callrate function is to calculate the allele frequency rate over all the samples

Usage

```
sc_callrate_chr(df,alg,threshold,chrr)
```

Arguments

df	Data object
alg	algorithm
threshold	the threshold
chrr	the name of chromosome

Value

The callrate values of all samples of one chromosome

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)


# create Data object and rearrange the index
df <- create_from_frame(df)

# The Random Forest classifier
call <- sc_callrate_chr(df,'score',0.2,'21')
```

`sc_chr_freq` *This function is to calculate the allele frequency over all the samples of one chromosome*

Description

The callrate function is to calculate the allele frequency over all the samples of one chromosome

Usage

```
sc_chr_freq(df,alg,threshold,chrr)
```

Arguments

`df`	Data object
`alg`	algorithm
`threshold`	the threshold
`chrr`	the name of chromosome

Value

The callrate values of all samples

Examples

```
# parsing file from gtc raw files

gtc_path = system.file("files/GTCs",package='SureTypeSCR')
cluster_path = system.file('files/HumanKaryomap-12v1_A.egt',package='SureTypeSCR')
manifest_path = system.file('files/HumanKaryomap-12v1_A.bpm',package='SureTypeSCR')
samplesheet = system.file('files/Samplesheetr.csv',package='SureTypeSCR')

df <- scbasic(manifest_path,cluster_path,samplesheet)


# create Data object and rearrange the index
df <- create_from_frame(df)

# The Random Forest classifier
call <- sc_chr_freq(df,'score',0.2,'21')
```

Index