

Package ‘scMitoTracing’

January 15, 2022

Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

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Suggests knitr,
rmarkdown

VignetteBuilder knitr

Depends R (>= 2.10)

LazyData true

R topics documented:

AddDatatoplot_clustering	2
AddDatatoplot_clustering,mitoTracing-method	2
AddDist	3
AddDist,mitoTracing-method	3
AddTree	4
AddTree,mitoTracing-method	4
CountVperCell	5
Create_mitoTracing	5
CW_mgatk.read	6
Datatoplots-class	7
DepthSummary	7
DistObjects-class	8
GTSummary	8
Make_matrix	9
Make_matrix,mitoTracing-method	9
Make_tree	10
Make_tree,mitoTracing-method	10
mitoTracing-class	11
MutationProfile.bulk	11
plot_depth	12

plot_variant	12
SeuratLSIClustering	13
SeuratLSIClustering, mitoTracing-method	13
show, mitoTracing-method	14
TREE-class	14
Vfilter_v3	15

Index	16
--------------	-----------

AddDatatoplot_clustering

AddDatatoplot_clustering This prepare the clonal clustering data to plot

Description

AddDatatoplot_clustering This prepare the clonal clustering data to plot

Usage

```
AddDatatoplot_clustering(object, ...)
```

Arguments

object mitoTracin class

AddDatatoplot_clustering, mitoTracing-method

AddDatatoplot_clustering This prepare the clonal clustering data to plot

Description

AddDatatoplot_clustering This prepare the clonal clustering data to plot

Usage

```
## S4 method for signature 'mitoTracing'
AddDatatoplot_clustering(object)
```

Arguments

object mitoTracin class

Value

mitoTracing class

AddDist	<i>AddDist This add Jaccard, Dice, Jaccard3W distance and stored in DistObjects</i>
---------	---

Description

AddDist This add Jaccard, Dice, Jaccard3W distance and stored in DistObjects

Usage

```
AddDist(object, ...)
```

Arguments

object	mitoTracin class
--------	------------------

AddDist, mitoTracing-method
<i>AddDist This add Jaccard, Dice, Jaccard3W distance and stored in DistObjects</i>

Description

AddDist This add Jaccard, Dice, Jaccard3W distance and stored in DistObjects

Usage

```
## S4 method for signature 'mitoTracing'  
AddDist(object)
```

Arguments

object	mitoTracin class
--------	------------------

Value

mitoTracing class

AddTree

Add_Tree Optional, if a phylogentic tree object phylo is already available, can be directly added to the mitoTracing

Description

Add_Tree Optional, if a phylogentic tree object phylo is already available, can be directly added to the mitoTracing

Usage

```
AddTree(object, phylo, ...)
```

Arguments

object	mitoTracin class
phylo	phyogenetic tree object

AddTree, mitoTracing-method

Add_Tree Optional, if a phylogentic tree object phylo is already available, can be directly added to the mitoTracing class in slot TREE

Description

Add_Tree Optional, if a phylogentic tree object phylo is already available, can be directly added to the mitoTracing class in slot TREE

Usage

```
## S4 method for signature 'mitoTracing'
AddTree(object, phylo, record = "")
```

Arguments

object	mitoTracin class
phylo	phyogenetic tree object

Value

mitoTracing class

CountVperCell	<i>Internal function in plot_variant</i>
---------------	--

Description

Internal function in plot_variant

Usage

```
CountVperCell(x, name, CellN)
```

Arguments

x	CellVar.Sum\$VN
name	c
CellN	nrow(CellVar.Sum)

Examples

```
CountVperCell(CellVar.Sum$VN,c,CellN=nrow(CellVar.Sum))
```

Create_mitoTracing	<i>Create_mitoTracing</i>
--------------------	---------------------------

Description

This function is to create mitoTracing with basic information

Usage

```
Create_mitoTracing(
  GTsummary_list,
  depth_list,
  feature.list_list,
  meta_list,
  labels,
  thr = "VerySensitive",
  qualifiedCellCut = 10,
  OnlyHetero = T,
  VAFcut = 1,
  Cellcut = 2,
  maxctscut = 2
)
```

Arguments

GTsummary_list	simply put GTSummary (Generated by CW_mgatk.read) into list, this allows merging multiple dataset this way.
depth_list	simply put depth(Generated by DepthSummary) into list, this allows merging multiple dataset this way.
feature.list_list	simply put feature.list(Generated by Vfilter_v3) into list, this allows merging multiple dataset this way.
labels	a vector of labels for the samples.
thr	One of the following "Total", "VerySensitive", "Sensitive", "Specific"
qualifiedCellCut	The minimum median mitochondrial coverage for a qualified cell, default is 10
OnlyHetero	If only consider the heteroplasmy variants, default is T
VAFCut	only use variants with VAF smaller than VAFcut. Default is 1. We can use smaller value to constrain into only using rare variants
Cellcut	only use variants with at least cellcut cells carry
maxctscut	only use variants with at least in one cell with at least maxctscut variant fragments

Value

mitoTracing class

CW_mgatk.read	<i>Function to read in mitoV outputs</i>
---------------	--

Description

This function allows you to read raw data from XX/final folder, the output from mitoV

Usage

```
CW_mgatk.read(path, Processed = F)
```

Arguments

path	The XX/final folder, the output from mitoV
Processed	Boolean variable (Default F), if true directly readRDS("VariantsGTSummary.RDS") or, generate and saveout "VariantsGTSummary.RDS"

Value

this returns depth which is a list of 4 df (Total/VerySensitive/Sensitive/Specific), each is a genotype summary

Examples

```
WD<-"/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/SecondaryAnalysis/Donor01_CD34_1.VariantsGTSummary"
DN1CD34_1.VariantsGTSummary<-CW_mgatk.read(WD,Processed =T)
```

Datatoplots-class *An intermediate S4 class Datatoplots*

Description

An intermediate S4 class Datatoplots

Slots

clustering dataframe that store the data to plot

DepthSummary *Function to summarize the depth (Total that passed Q30)*

Description

This function allows you to summarize the depth

Usage

```
DepthSummary(path, CellSubset = NA, cellSubSetName = NA)
```

Arguments

path	The XX/final folder, the output from mitoV
CellSubset	A vector of ATAC cell names for subsetting, default is NA
cellSubSetName	a string to name this Subset, should explain with the CellSubset
Processed	Boolean variable(Default T), if true directly readRDS("depth.RDS") or, generate and saveout "depth.RDS"

Value

this returns depth which is a list of 4 list(Total/VerySensitive/Sensitive/Specific), each contains 2 df, summarize mito coverage by Pos/Cell

Examples

```
WD<-"/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/SecondaryAnalysis/Donor01_CD34_1"
DN1CD34_1.depth<-DepthSummary(WD,Processed = T)
```

DistObjects-class	<i>An intermediate S4 class Datatoplots</i>
-------------------	---

Description

An intermediate S4 class Datatoplots

Slots

jaccard distance object dist: Jaccard distance

Dice distance object dist: Dice distance

jaccard3W distance object dist: jaccard3W

GTSummary	<i>Function to generate GTS summary</i>
-----------	---

Description

This function allows you to summarize the meta data for each genotyped variant

Usage

```
GTSummary(RawGenotypes, filterN = T)
```

Arguments

RawGenotypes Well-named "RawGenotypes.Sensitive.StrandBalance" file in function CW_mgatk.read

filterN Boolean variable, if true filter out the variant with "N"

Value

Genotypes.summary a dataframe that summarize several metrics for each genotype

Examples

Usually used inside of function CW_mgatk.read

Make_matrix	<i>Make_matrix This will make the matixies of Cell VS mitochondrial variants and return mitoTracing Results stored in Cts.Mtx and Cts.Mtx.bi</i>
-------------	--

Description

Make_matrix This will make the matixies of Cell VS mitochondrial variants and return mitoTracing Results stored in Cts.Mtx and Cts.Mtx.bi

Usage

```
Make_matrix(object)
```

Arguments

object	mitoTracin class
--------	------------------

Make_matrix, mitoTracing-method	<i>Make_matrix This will make the matixies of Cell VS mitochondrial variants and return mitoTracing Results stored in Cts.Mtx and Cts.Mtx.bi</i>
---------------------------------	--

Description

Make_matrix This will make the matixies of Cell VS mitochondrial variants and return mitoTracing Results stored in Cts.Mtx and Cts.Mtx.bi

Usage

```
## S4 method for signature 'mitoTracing'
Make_matrix(object)
```

Arguments

object	mitoTracin class
--------	------------------

Value

mitoTracin class

Make_tree	<i>Make_tree This will generate a basic phylogenetic tree</i>
-----------	---

Description

Make_tree This will generate a basic phylogenetic tree

Usage

```
Make_tree(object, d = "jaccard", algorithm = "upgma", onlyreturntree = F, ...)
```

Arguments

object	mitoTracin class
d	"jaccard" or "Dice" or "jaccard3W"
algorithm	the algorithm used to build the tree, choose from "nj" and "upgma"

Make_tree, mitoTracing-method	<i>Make_tree This will generate a basic phylogenetic tree</i>
-------------------------------	---

Description

Make_tree This will generate a basic phylogenetic tree

Usage

```
## S4 method for signature 'mitoTracing'
Make_tree(object, d, algorithm, onlyreturntree = F)
```

Arguments

object	mitoTracin class
d	"jaccard" or "Dice" or "jaccard3W"
algorithm	the algorithm used to build the tree, choose from "nj" and "upgma"

Value

mitoTracin class

mitoTracing-class *Major mitoTracing class that store clonal-resolved multi-omics*

Description

Major mitoTracing class that store clonal-resolved multi-omics

Slots

GTsummary.filtered The Mitochondrial genotype data frame
 CellMeta Store meta data for each cell type
 V.filtered.list a list of data frame of variant metrics, VAF, cellIN, etc (each for different stringency),
 UniqueV A character showing the number of usable variant
 Cts.Mtx A sparse matrix cell-mitoVariants, store the variant count
 Cts.Mtx.bi A sparse matrix cell-mitoVariants, The variant count has been binarized into 0 and 1
 para A character showing the parameter of this object
 Seurat Seurat object storing the clonal clustering results
 DataToplotList The customized class of Datatoplots: A list of dataframe for further plotting
 DistObjects The customized class that stores the cell-cell distances
 TREE The customized class that wraps phylogenetic tree

MutationProfile.bulk
 Function to plot bulk level mutation signatures

Description

This function allows you to plot the mito mutation signatures

Usage

```
MutationProfile.bulk(cell_variants)
```

Arguments

cell_variants
 a vector of variants formatted as c('93_A_G'103_G_A'146_T_C')

Value

p from ggplot2

Examples

```
MutationProfile.bulk(DN1CD34_1.Variants.feature.lst[[name]]$Variants
```

plot_depth	<i>Function to plot the mito depth summary</i>
------------	--

Description

This function allows you to plot both position-wise and cell-wise mito depth summary

Usage

```
plot_depth(depth = DN1CD34_1.depth, name = "", w = 10, h = 3)
```

Arguments

depth	The .depth file by function DepthSummary
name	The plot name shown on top
w	the Width of the plot, default=10
h	the height of the plot default=3

Value

directly out put the plot

Examples

```
plot_depth(DN1CD34_1.depth$Total, "Total")
```

plot_variant	<i>Function to plot variant metrics</i>
--------------	---

Description

This function allows you to plot the mito mutation metrics For each category(stringency), p1: Variant allele frequency(VAF); p2: Heteroplasmy histogram p3: CellN(Number of caells that carry the variants) VS maxcts(The number of variant counts in the highest cell) p4: Histogram to show the distribution of the number of variant per cell

Usage

```
plot_variant(
  GTSummary,
  feature.list,
  depth,
  cat = c("Total", "VerySensitive", "Sensitive", "Specific"),
  p4xlim = 50,
  QualifyCellCut = 10
)
```

Arguments

GTSummary	The GTSummary file read in by function CW_mgatk.read
feature.list	The variant feature list generated by Vfilter_v3
depth	The .depth file by function DepthSummary
cat	The category(or the striengency to be plotted), default is c("Total","VerySensitive","Sensitive","Specifi
p4xlim	the p4 xlim(number of variant per cell), default is 50
QualifyCellCut	median coverage for qualified cells, default is 10

Value

no returns, directly plot

Examples

```
plot_variant(DN1CD34_1.VariantsGTSummary,DN1CD34_1.Variants.feature.lst,depth=DN1CD34_1.d
```

```
SeuratLSIClustering
```

SeuratLSIClustering This will use the mito variants for Seurat clustering (LSI based)

Description

SeuratLSIClustering This will use the mito variants for Seurat clustering (LSI based)

Usage

```
SeuratLSIClustering(object, ...)
```

Arguments

object	mitoTracin class
--------	------------------

```
SeuratLSIClustering,mitoTracing-method
```

SeuratLSIClustering This will use the mito variants for Seurat clustering (LSI based)

Description

SeuratLSIClustering This will use the mito variants for Seurat clustering (LSI based)

Usage

```
## S4 method for signature 'mitoTracing'
SeuratLSIClustering(object, binary = T, res = 0.3)
```

Arguments

binary	Default is tree, to make use of the binary matrix
res	Default os 0.3, the resolution of the clustering
mitoTracing	class

Value

mitoTracing class

show, mitoTracing-method
show This will show the basics of mitoTracin class

Description

show This will show the basics of mitoTracin class

Usage

```
## S4 method for signature 'mitoTracing'
show(object)
```

Arguments

object	mitoTracin class
--------	------------------

Value

print out basics

TREE-class *An intermediate S4 class Tree that store tree info*

Description

An intermediate S4 class Tree that store tree info

Slots

phylo the phylo tree class from ape package
treedata treedata class from tidytree
records character to store annotations

Vfilter_v3

Function to filter variants

Description

This function allows you to filter variants

Usage

```
Vfilter_v3(
  InputSummary,
  depth,
  Rmvhomo = F,
  Min_Cells = 2,
  Max_Count_perCell = 2,
  QualifyCellCut = 10
)
```

Arguments

InputSummary	The GTSummary file read in by function CW_mgatk.read
depth	The .depth file by function DepthSummary
Rmvhomo	Boolean (Default F) If true, remove the homozygous variants
Min_Cells	Default 2, A qualified variant needs the minimum number of cells that have this variant
Max_Count_perCell	Default 2, A qualified variant needs to show at least 2 counts in one cell
QualifyCellCut	Default 10, Minimum depth for a qualified cell

Value

this returns feature.list

Examples

```
DN1CD34_1.Variants.feature.lst<-Vfilter_v3(InputSummary=DN1CD34_1.VariantsGTSummary,depth
```

Index

AddDatatoplot_clustering, [2](#)
AddDatatoplot_clustering, mitoTracing-method,
[2](#)
AddDist, [3](#)
AddDist, mitoTracing-method, [3](#)
AddTree, [4](#)
AddTree, mitoTracing-method, [4](#)

CountVperCell, [5](#)
Create_mitoTracing, [5](#)
CW_mgatk.read, [6](#)

Datatoplots (*Datatoplots-class*), [7](#)
Datatoplots-class, [7](#)
DepthSummary, [7](#)
DistObjects (*DistObjects-class*), [8](#)
DistObjects-class, [8](#)

GTSummary, [8](#)

Make_matrix, [9](#)
Make_matrix, mitoTracing-method,
[9](#)
Make_tree, [10](#)
Make_tree, mitoTracing-method, [10](#)
mitoTracing (*mitoTracing-class*),
[11](#)
mitoTracing-class, [11](#)
MutationProfile.bulk, [11](#)

plot_depth, [12](#)
plot_variant, [12](#)

SeuratLSIClustering, [13](#)
SeuratLSIClustering, mitoTracing-method,
[13](#)
show, mitoTracing-method, [14](#)

TREE (*TREE-class*), [14](#)
TREE-class, [14](#)

Vfilter_v3, [15](#)