Package 'sitePath'

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Type Package

Title Phylogeny-based sequence clustering with site polymorphism

Version 1.21.0

Description Using site polymorphism is one of the ways to cluster DNA/protein sequences but it is possible for the sequences with the same polymorphism on a single site to be genetically distant. This package is aimed at clustering sequences using site polymorphism and their corresponding phylogenetic trees. By considering their location on the tree, only the structurally adjacent sequences will be clustered. However, the adjacent sequences may not necessarily have the same polymorphism. So a branch-and-bound like algorithm is used to minimize the entropy representing the purity of site polymorphism of each cluster.

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Contents

allSitesName *Retrieve position of all the sites*

Description

The function is a way to get position of the resulting sites from SNPsites, fixationSites and parallelSites. The numbering is consistent with what's being set by setSiteNumbering

Usage

```
allSitesName(x, ...)

## S3 method for class 'SNPsites'
allSitesName(x, ...)

## S3 method for class 'sitesMinEntropy'
allSitesName(x, ...)

## S3 method for class 'fixationSites'
allSitesName(x, ...)

## S3 method for class 'parallelSites'
allSitesName(x, ...)

## S3 method for class 'paraFixSites'
allSitesName(x, type = c("paraFix", "fixation", "parallel"), ...)
```

Arguments

x	The object containing the sites from analysis
...	Other arguments
type	Return fixation or parallel sites

Value

An integer vector for sites position

Examples

```
data(zikv_tree)
msaPath <- system.file('extdata', 'ZIKV.fasta', package = 'sitePath')
tree <- addMSA(zikv_tree, msaPath = msaPath, msaFormat = 'fasta')
snp <- SNPsites(tree)
allSitesName(snp)
```

`as.data.frame.fixationSites` *Convert results to Data Frame*

Description

Convert return of functions in `sitePath` package to a `data.frame` so can be better worked with. The group name for each tip is the same as `groupTips`.

A `fixationSites` object will output the mutation name of the fixation and the cluster name before and after the mutation.

An `SNPsites` object will output the tip name with the SNP and its position.

An `parallelSites` object will output the tip name with the group name and mutation info.

Usage

```
## S3 method for class 'fixationSites'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class 'SNPsites'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class 'parallelSites'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

`x`	The object to be converted to `data.frame`.
`row.names`	Unimplemented.
`optional`	Unimplemented.
`...`	Other arguments.

Value

A `data.frame` object.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
fixations <- fixationSites(lineagePath(tree))
as.data.frame(fixations)
```

extractSite *Extract tips for a single site*

Description

The functions in sitePath usually include the results on more than one site. The function extractSite can be used to extract the predicted result on a single site.

Usage

```
extractSite(x, site, ...)

## S3 method for class 'fixationSites'
extractSite(x, site, ...)
```

Arguments

x	A fixationSites or a parallelSites object. More type will be supported in the later version.
site	A site included in the result.
...	Other arguments

Value

The predicted result of a single site

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
mutations <- fixationSites(lineagePath(tree))
extractSite(mutations, 139)
```

extractTips *Extract grouped tips for a single site*

Description

The result of fixationSites and sitePath contains all the possible sites with fixation mutation. The function extractTips retrieves the name of the tips involved in the fixation.

For lineagePath, the function extractTips groups all the tree tips according to the amino acid/nucleotide of the site.

For parallelSites and sitePara object, the function extractTips retrieve all the tips with parallel mutation.

Usage

```
extractTips(x, ...)

## S3 method for class 'lineagePath'
extractTips(x, site, ...)

## S3 method for class 'sitesMinEntropy'
extractTips(x, site, ...)

## S3 method for class 'fixationSites'
extractTips(x, site, select = 1, ...)

## S3 method for class 'sitePath'
extractTips(x, select = 1, ...)

## S3 method for class 'parallelSites'
extractTips(x, site, ...)

## S3 method for class 'sitePara'
extractTips(x, ...)
```

Arguments

x	A `fixationSites` or a `sitePath` object.
...	Other arguments
site	A site predicted to experience fixation.
select	For a site, there theoretically might be more than one fixation on different lineages. You may use this argument to extract for a specific fixation of a site. The default is the first fixation of the site.

Value

Tree tips grouped as `list`

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
mutations <- fixationSites(lineagePath(tree))
extractTips(mutations, 139)
```

fixationIndels *Fixation indels prediction*

Description

The fixation of insertions of deletions.

Usage

```
fixationIndels(x, ...)

## S3 method for class 'sitesMinEntropy'
fixationIndels(x, ...)
```

Arguments

x	The return from sitesMinEntropy function.
...	Other arguments.

Value

A fixationIndels object.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
fixationIndels(sitesMinEntropy(tree))
```

fixationPath *Accumulation of fixed mutation as a tree*

Description

The tips are clustered according to the fixation sites. The transition of fixation sites will be plotted as a phylogenetic tree. The length of each branch represents the number of fixation mutation between two clusters. The name of the tree tips indicate the number of sequences in the cluster.

Usage

```
fixationPath(x, ...)

## S3 method for class 'sitesMinEntropy'
fixationPath(x, minEffectiveSize = NULL, ...)

## S3 method for class 'fixationSites'
fixationPath(x, minEffectiveSize = NULL, ...)
```

Arguments

x	The return from fixationSites function.
...	Further arguments passed to or from other methods.
minEffectiveSize	The minimum size for a tip cluster.

Value

An fixationPath object

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
paths <- lineagePath(tree)
mutations <- fixationSites(paths)
fixationPath(mutations)
```

---

fixationSites *Fixation sites prediction*

Description

After finding the lineagePath of a phylogenetic tree, fixationSites uses the result to find those sites that show fixation on some, if not all, of the lineages. The number of tips before and after the fixation mutation is expected to be more than minEffectiveSize. Also, the fixation will be skipped if the amino acid/nucleotide is gap or ambiguous character. A lineage has to have at least one fixation mutation to be reported.

Usage

```
fixationSites(paths, ...)

## S3 method for class 'lineagePath'
fixationSites(
  paths,
  minEffectiveSize = NULL,
  searchDepth = 1,
  method = c("compare", "insert", "delete"),
  ...
)

## S3 method for class 'sitesMinEntropy'
fixationSites(paths, ...)

## S3 method for class 'paraFixSites'
fixationSites(paths, ...)
```

Arguments

paths	A lineagePath object returned from lineagePath function.
...	further arguments passed to or from other methods.
minEffectiveSize	The minimum number of tips in a group.
searchDepth	The function uses heuristic search but the termination of the search cannot be intrinsically decided. searchDepth is needed to tell the search when to stop.
method	The strategy for predicting the fixation. The basic approach is entropy minimization and can be achieved by adding or removing fixation point, or by comparing the two.

Value

A fixationSites object.

See Also

as.data.frame.fixationSites

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
fixationSites(lineagePath(tree))
```

---

groupTips *The grouping of tree tips*

Description

The tips between divergent nodes or fixation mutations on the lineages are each gathered as group.

Usage

```
groupTips(tree, ...)

## S3 method for class 'phyMSAmatched'
groupTips(
  tree,
  similarity = NULL,
  simMatrix = NULL,
  forbidTrivial = TRUE,
  tipnames = TRUE,
  ...
)
```

```
## S3 method for class 'lineagePath'
groupTips(tree, tipnames = TRUE, ...)

## S3 method for class 'sitesMinEntropy'
groupTips(tree, tipnames = TRUE, ...)

## S3 method for class 'fixationSites'
groupTips(tree, tipnames = TRUE, ...)

## S3 method for class 'fixationPath'
groupTips(tree, tipnames = TRUE, ...)
```

Arguments

tree	The return from addMSA, lineagePath, sitesMinEntropy or other functions.
...	Other arguments.
similarity	This decides how minor SNPs are to remove. If provided as fraction between 0 and 1, then the minimum number of SNP will be total tips times similariy. If provided as integer greater than 1, the minimum number will be similariy. The default similariy is 0.05 for lineagePath.
simMatrix	Deprecated and will not have effect.
forbidTrivial	Does not allow trivial trimming.
tipnames	If return tips as integer or tip names.

Value

groupTips returns grouping of tips.

Examples

```
data(zikv_tree)
data(zikv_align)
tree <- addMSA(zikv_tree, alignment = zikv_align)
groupTips(tree)
```

---

h3n2_align *Multiple sequence alignment of H3N2's HA protein*

Description

The raw protein sequences were downloaded from NCBI database and aligned using MAFFT (https://mafft.cbrc.jp/alignment/software/).

h3n2_align_reduced is a truncated version of h3n2_align

Usage

```
data(h3n2_align)

data(h3n2_align_reduced)
```

Format

an alignment object

an alignment object

---

h3n2_tree *Phylogenetic tree of H3N2's HA protein*

Description

Tree was built from h3n2_align using RAxML (http://www.exelixis-lab.org/) with default settings.

h3n2_tree_reduced is a truncated version of h3n2_tree

Usage

```
data(h3n2_tree)

data(h3n2_tree_reduced)
```

Format

a phylo object

a phylo object

---

lineagePath *Resolving lineage paths using SNP*

Description

lineagePath finds the lineages of a phylogenetic tree providing the corresponding sequence alignment. This is done by finding 'major SNPs' which usually accumulate along the evolutionary pathways.

sneakPeek is intended to plot 'similarity' (actually the least percentage of 'major SNP') as a threshold against number of output lineagePath. This plot is intended to give user a rough view about how many lineages they could expect from the 'similarity' threshold in the function lineagePath. The number of lineagePath is preferably not be too many or too few. The result excludes where the number of lineagePath is greater than number of tips divided by 20 or user-defined maxPath. The zero lineagePath result will also be excluded.

When used on the return of sneakPeek, a lineagePath with the closest similarity will be retrieved from the returned value.

similarity has no effect when using on paraFixSites object

Usage

```
lineagePath(tree, similarity, ...)

## S3 method for class 'phylo'
lineagePath(
  tree,
  similarity = NULL,
  alignment = NULL,
  seqType = c("AA", "DNA", "RNA"),
  reference = NULL,
  gapChar = "-",
  minSkipSize = NULL,
  ...
)

## S3 method for class 'treedata'
lineagePath(tree, ...)

## S3 method for class 'phyMSAmatched'
lineagePath(
  tree,
  similarity = NULL,
  simMatrix = NULL,
  forbidTrivial = TRUE,
  ...
)

sneakPeek(tree, step = 9, maxPath = NULL, minPath = 0, makePlot = TRUE)

## S3 method for class 'sneakPeekedPaths'
lineagePath(tree, similarity, ...)

## S3 method for class 'paraFixSites'
lineagePath(tree, similarity = NULL, ...)
```

Arguments

tree	The return from addMSA or sneakPeek function.
similarity	The parameter for identifying phylogenetic pathway using SNP. If provided as fraction between 0 and 1, then the minimum number of SNP will be total tips times Nmin. If provided as integer greater than 1, the minimum number will be Nmin.
...	Other arguments.

alignment	An alignment object. This commonly can be from sequence parsing function in the seqinr package. Sequence names in the alignment should include all tip.label in the tree
seqType	The type of the sequence in the alignment file. The default is "AA" for amino acid. The other options are "DNA" and "RNA".
reference	Name of reference for site numbering. The name has to be one of the sequences' name. The default uses the intrinsic alignment numbering
gapChar	The character to indicate gap. The numbering will skip the gapChar for the reference sequence.
minSkipSize	The minimum number of tips to have gap or ambiguous amino acid/nucleotide for a site to be ignored in other analysis. This will not affect the numbering. The default is 0.8.
simMatrix	Deprecated and will not have effect.
forbidTrivial	Does not allow trivial trimming.
step	the 'similarity' window for calculating and plotting. To better see the impact of threshold on path number. The default is 10.
maxPath	maximum number of path to return show in the plot. The number of path in the raw tree can be far greater than trimmed tree. To better see the impact of threshold on path number. This is preferably specified. The default is one 20th of tree tip number.
minPath	minimum number of path to return show in the plot. To better see the impact of threshold on path number. The default is 1.
makePlot	Whether make a plot when return.

Value

Lineage path represent by node number.

sneakPeek return the similarity threhold against number of lineagePath. There will be a simple dot plot between threshold and path number if makePlot is TRUE.

Examples

```
data('zikv_tree')
data('zikv_align')
tree <- addMSA(zikv_tree, alignment = zikv_align)
lineagePath(tree)
sneakPeek(tree, step = 3)
x <- sneakPeek(tree, step = 3)
lineagePath(x, similarity = 0.05)
```

paraFixSites *The fixation sites with mutation on parallel lineage*

Description

The operation between the results of `fixationSites` and `parallelSites`.

Usage

```
paraFixSites(x, ...)

## S3 method for class 'phylo'
paraFixSites(
  x,
  alignment = NULL,
  seqType = c("AA", "DNA", "RNA"),
  Nmin = NULL,
  reference = NULL,
  gapChar = "-",
  minSkipSize = NULL,
  ...
)

## S3 method for class 'treedata'
paraFixSites(x, ...)

## S3 method for class 'lineagePath'
paraFixSites(
  x,
  minEffectiveSize = NULL,
  searchDepth = 1,
  method = c("compare", "insert", "delete"),
  ...
)

## S3 method for class 'sitesMinEntropy'
paraFixSites(
  x,
  category = c("intersect", "union", "parallelOnly", "fixationOnly"),
  minSNP = NULL,
  mutMode = c("all", "exact", "pre", "post"),
  ...
)
```

Arguments

x	A `lineagePath` object returned from `lineagePath` function.

`...`	further arguments passed to or from other methods.
`alignment`	An `alignment` object. This commonly can be from sequence parsing function in the `seqinr` package. Sequence names in the alignment should include all `tip.label` in the tree
`seqType`	The type of the sequence in the alignment file. The default is "AA" for amino acid. The other options are "DNA" and "RNA".
`Nmin`	The parameter for identifying phylogenetic pathway using SNP. If provided as fraction between 0 and 1, then the minimum number of SNP will be total tips times `Nmin`. If provided as integer greater than 1, the minimum number will be `Nmin`.
`reference`	Name of reference for site numbering. The name has to be one of the sequences' name. The default uses the intrinsic alignment numbering
`gapChar`	The character to indicate gap. The numbering will skip the `gapChar` for the reference sequence.
`minSkipSize`	The minimum number of tips to have gap or ambiguous amino acid/nucleotide for a site to be ignored in other analysis. This will not affect the numbering. The default is 0.8.
`minEffectiveSize`	The minimum number of tips in a group.
`searchDepth`	The function uses heuristic search but the termination of the search cannot be intrinsically decided. `searchDepth` is needed to tell the search when to stop.
`method`	The strategy for predicting the fixation. The basic approach is entropy minimization and can be achieved by adding or removing fixation point, or by comparing the two.
`category`	Could be `parallelOnly`, `fixationOnly`, `intersect` or `union`.
`minSNP`	The minimum number of mutations to be qualified as parallel on at least two lineages. The default is 1.
`mutMode`	The strategy for finding parallel site. The default `all` is to consider any mutation regardless of the amino acid/nucleotide before and after mutation; Or `exact` to force mutation to be the same; Or `pre`/`post` to select the site having amino acid/nucleotide before/after mutation.

Value

A `paraFixSites` object.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
paraFixSites(zikv_tree_reduced, alignment = zikv_align_reduced)
```

`parallelSites` *Mutation across multiple phylogenetic lineages*

Description

A site may have mutated on parallel lineages. Mutation can occur on the same site across the phylogenetic lineages solved by `lineagePath`. The site will be considered mutated in parallel if the mutation occurs on the non-overlap part of more than two lineages. The amino acid/nucleotide before and after the mutation can be allowed different on different lineages or only the exact same mutations are considered.

Usage

```
parallelSites(x, ...)

## S3 method for class 'lineagePath'
parallelSites(
  x,
  minSNP = NULL,
  mutMode = c("all", "exact", "pre", "post"),
  ...
)

## S3 method for class 'sitesMinEntropy'
parallelSites(
  x,
  minSNP = NULL,
  mutMode = c("all", "exact", "pre", "post"),
  ...
)

## S3 method for class 'paraFixSites'
parallelSites(x, ...)
```

Arguments

`x`	A `lineagePath` or a `sitesMinEntropy` object.
`...`	The arguments in `sitesMinEntropy`.
`minSNP`	The minimum number of mutations to be qualified as parallel on at least two lineages. The default is 1.
`mutMode`	The strategy for finding parallel site. The default `all` is to consider any mutation regardless of the amino acid/nucleotide before and after mutation; Or `exact` to force mutation to be the same; Or `pre`/`post` to select the site having amino acid/nucleotide before/after mutation.

Value

A parallelSites object

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
paths <- lineagePath(tree)
x <- sitesMinEntropy(paths)
parallelSites(x)
```

---

phyMSAmatched *Add matching sequence alignment to the tree*

Description

addMSA wraps read.alignment function in seqinr package and helps match names in tree and sequence alignment. Either provide the file path to an alignment file and its format or an alignment object from the return of read.alignment function. If both the file path and alignment object are given, the function will use the sequence in the alignment file.

Usage

```
addMSA(tree, ...)

## S3 method for class 'phylo'
addMSA(
  tree,
  msaPath = "",
  msaFormat = c("fasta", "clustal", "phylip", "mase", "msf"),
  alignment = NULL,
  seqType = c("AA", "DNA", "RNA"),
  ...
)

## S3 method for class 'treedata'
addMSA(tree, ...)
```

Arguments

tree	A phylo object. This commonly can be from tree parsing function in ape or ggtree. All the tip.label should be found in the sequence alignment. The tree is supposed to be fully resolved (bifurcated) and will be resolved by multi2di if is.binary gives FALSE.
...	Other arguments.
msaPath	The file path to the multiple sequence alignment file.

msaFormat	The format of the multiple sequence alignment file. The internal uses the read.alignment from seqinr package to parse the sequence alignment. The default is "fasta" and it also accepts "clustal", "phylip", "mase", "msf".
alignment	An alignment object. This commonly can be from sequence parsing function in the seqinr package. Sequence names in the alignment should include all tip.label in the tree
seqType	The type of the sequence in the alignment file. The default is "AA" for amino acid. The other options are "DNA" and "RNA".

Value

Since 1.5.12, the function returns a phyMSAmatched object to avoid S3 methods used on phylo (better encapsulation).

See Also

read.alignment

Examples

```
data(zikv_tree)
msaPath <- system.file('extdata', 'ZIKV.fasta', package = 'sitePath')
addMSA(zikv_tree, msaPath = msaPath, msaFormat = 'fasta')
```

---

plot.phyMSAmatched *Visualize the results*

Description

The plot function to visualize the return of functions in the package. The underlying function applies ggplot2. The function name plot is used to keep the compatibility with previous versions, but they do not behave like the generic plot function since 1.5.4.

A phyMSAmatched object will be plotted as a tree diagram.

A lineagePath object will be plotted as a tree diagram and paths are black solid line while the trimmed nodes and tips will use gray dashed line.

A parallelSites object will be plotted as original phylogenetic tree marked with parallel mutations attached as dot plot.

A fixationSites object will be plotted as original phylogenetic tree marked with fixation substitutions.

A sitePath object can be extracted by using extractSite on the return of fixationSites.

A fixationIndels object will be plotted as original phylogenetic tree marked with indel fixation.

A fixationPath object will be plotted as a phylo object. The tips are clustered according to the fixation sites. The transition of fixation sites will be plotted as a phylogenetic tree. The length of each branch represents the number of fixation mutation between two clusters.

Usage

```
## S3 method for class 'phyMSAmatched'
plot(x, y = TRUE, ...)

## S3 method for class 'lineagePath'
plot(x, y = TRUE, showTips = FALSE, ...)

## S3 method for class 'parallelSites'
plot(x, y = TRUE, ...)

## S3 method for class 'fixationSites'
plot(x, y = TRUE, tipsGrouping = NULL, ...)

## S3 method for class 'sitePath'
plot(x, y = NULL, select = NULL, showTips = FALSE, ...)

## S3 method for class 'fixationIndels'
plot(x, y = TRUE, ...)

## S3 method for class 'fixationPath'
plot(x, y = TRUE, ...)
```

Arguments

x	The object to plot.
y	Whether to show the fixation mutation between clusters. For `lineagePath` object and `sitePath` object, it is deprecated and no longer have effect since 1.5.4.
...	Other arguments. Since 1.5.4, the function uses `ggtree` as the base function to make plots so the arguments in `plot.phylo` will no longer work.
showTips	Whether to plot the tip labels. The default is `FALSE`.
tipsGrouping	A `list` to hold the grouping of tips for how the tree will be colored.
select	For a `sitePath` object, it can have result on more than one evolution pathway. This is to select which path to plot. The default is `NULL` which will plot all the paths. It is the same as `select` in `plotSingleSite`.

Value

A ggplot object to make the plot.

Examples

```
data(zikv_tree)
data(zikv_align)
tree <- addMSA(zikv_tree, alignment = zikv_align)
plot(tree)
paths <- lineagePath(tree)
plot(paths)
parallel <- parallelSites(paths)
```

```
plot(parallel)
fixations <- fixationSites(paths)
plot(fixations)
sp <- extractSite(fixations, 139)
plot(sp)
x <- fixationPath(fixations)
plot(x)
```

`plotFixationSites` *Plot the result of fixation sites*

Description

Visualize the results of `paraFixSites`

Usage

```
plotFixationSites(x, ...)

## S3 method for class 'fixationSites'
plotFixationSites(x, site = NULL, ...)

## S3 method for class 'paraFixSites'
plotFixationSites(x, site = NULL, ...)
```

Arguments

`x`	return from `paraFixSites`
`...`	further arguments passed to or from other methods.
`site`	the number of the site according to `setSiteNumbering`. If not provided, all sites will be plotted as labels on the tree

Value

A `ggplot` object.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
paraFix <- paraFixSites(zikv_tree_reduced, alignment = zikv_align_reduced)
plotFixationSites(paraFix)
```

plotMutSites *Plot tree and mutation sites*

Description

The mutated sites for each tip in a phylogenetic tree will be represented as colored dots positioned by their site number.

Usage

```
plotMutSites(x, ...)

## S3 method for class 'SNPsites'
plotMutSites(x, showTips = FALSE, ...)

## S3 method for class 'lineagePath'
plotMutSites(x, ...)

## S3 method for class 'parallelSites'
plotMutSites(x, ...)

## S3 method for class 'fixationSites'
plotMutSites(x, ...)

## S3 method for class 'paraFixSites'
plotMutSites(
  x,
  widthRatio = 0.75,
  fontSize = 3.88,
  dotSize = 1,
  lineSize = 0.5,
  ...
)
```

Arguments

x	An SNPsites object.
...	Other arguments
showTips	Whether to plot the tip labels. The default is FALSE.
widthRatio	The width ratio between tree plot and SNP plot
fontSize	The font size of the mutation label in tree plot
dotSize	The dot size of SNP in SNP plot
lineSize	The background line size in SNP plot

Value

A tree plot with SNP as dots for each tip.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
plotMutSites(SNPsites(tree))
```

---

plotParallelSites *Plot the result of fixation sites*

Description

Visualize the results of paraFixSites

Usage

```
plotParallelSites(x, ...)

## S3 method for class 'parallelSites'
plotParallelSites(x, site = NULL, ...)

## S3 method for class 'paraFixSites'
plotParallelSites(x, site = NULL, ...)
```

Arguments

x	return from paraFixSites
...	further arguments passed to or from other methods.
site	the number of the site according to setSiteNumbering

Value

A ggplot object.

Examples

```
data(zikv_tree)
data(zikv_align)
paraFix <- paraFixSites(zikv_tree, alignment = zikv_align)
plotParallelSites(paraFix)
```

plotSingleSite *Color the tree by a single site*

Description

Plot and color the tree according to amino acid/nucleotide of the selected site. The color scheme depends on the seqType set in addMSA function.

For lineagePath, the tree will be colored according to the amino acid of the site. The color scheme tries to assign distinguishable color for each amino acid.

For parallelSites, the tree will be colored according to the amino acid of the site if the mutation is not fixed.

For fixationSites, it will color the ancestral tips in red, descendant tips in blue and excluded tips in grey.

Usage

```
plotSingleSite(x, site, ...)

## S3 method for class 'lineagePath'
plotSingleSite(x, site, showPath = TRUE, showTips = FALSE, ...)

## S3 method for class 'sitesMinEntropy'
plotSingleSite(x, site, ...)

## S3 method for class 'parallelSites'
plotSingleSite(x, site, showPath = TRUE, ...)

## S3 method for class 'fixationSites'
plotSingleSite(x, site, select = NULL, ...)
```

Arguments

x	The object to plot.
site	For lineagePath, it can be any site within sequence length. For fixationSites and parallelSites, it is restrained to a predicted fixation site. The numbering is consistent with the reference defined by setSiteNumbering.
...	Other arguments. Since 1.5.4, the function uses ggtree as the base function to make plots so the arguments in plot.phylo will no longer work.
showPath	If plot the lineage result from lineagePath. The default is TRUE.
showTips	Whether to plot the tip labels. The default is FALSE.
select	Select which fixation path in to plot. The default is NULL which will plot all the fixations.

Value

Since 1.5.4, the function returns a ggplot object so on longer behaviors like the generic `plot` function.

See Also

`plot.sitePath`

Examples

```
data(zikv_tree)
data(zikv_align)
tree <- addMSA(zikv_tree, alignment = zikv_align)
paths <- lineagePath(tree)
plotSingleSite(paths, 139)
fixations <- fixationSites(paths)
plotSingleSite(fixations, 139)
```

---

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

ape `as.phylo`, `read.tree`

seqinr `read.alignment`

tidytree `as.treedata`

---

sars2_align *Multiple sequence alignment of SARS-CoV-2 genome CDS*

Description

The raw sequences were downloaded from GISAID database (https://www.gisaid.org/) and aligned using MAFFT (https://mafft.cbrc.jp/alignment/software/) with default settings.

Usage

```
data(sars2_align)
```

Format

an `alignment` object

sars2_tree *Phylogenetic tree of SARS-CoV-2 genome CDS*

Description

Tree was built from sars2_align using RAxML (http://www.exelixis-lab.org/) with default settings. The tip EPI_ISL_402125 was used as the outgroup to root the tree.

Usage

```
data(sars2_tree)
```

Format

a phylo object

setSiteNumbering *Set site numbering to the reference sequence*

Description

A reference sequence can be used to define a global site numbering scheme for multiple sequence alignment. The gap in the reference sequence will be skipped for the numbering. Also, the site that is gap or amino acid/nucleotide for too many tips will be ignored but won't affect numbering.

Usage

```
setSiteNumbering(x, reference, gapChar, ...)

## S3 method for class 'phyMSAmatched'
setSiteNumbering(x, reference = NULL, gapChar = "-", minSkipSize = NULL, ...)
```

Arguments

x	The object to set site numbering. It could be a phyMSAmatched or a lineagePath object.
reference	Name of reference for site numbering. The name has to be one of the sequences' name. The default uses the intrinsic alignment numbering
gapChar	The character to indicate gap. The numbering will skip the gapChar for the reference sequence.
...	Further arguments passed to or from other methods.
minSkipSize	The minimum number of tips to have gap or ambiguous amino acid/nucleotide for a site to be ignored in other analysis. This will not affect the numbering. The default is 0.8.

Value

The input x with numbering mapped to reference.

Examples

```
data(zikv_tree)
msaPath <- system.file('extdata', 'ZIKV.fasta', package = 'sitePath')
tree <- addMSA(zikv_tree, msaPath = msaPath, msaFormat = 'fasta')
setSiteNumbering(tree)
```

---

similarityMatrix *Similarity between sequences*

Description

Get similarity between aligned sequences with gap ignored.

Usage

```
similarityMatrix(tree)
```

Arguments

tree	The return from addMSA function.

Value

A diagonal matrix of similarity between sequences.

Examples

```
data(zikv_tree)
data(zikv_align)
tree <- addMSA(zikv_tree, alignment = zikv_align)
simMatrix <- similarityMatrix(tree)
```

sitePath-deprecated *Deprecated functions in package 'sitePath'*

Description

These functions are provided for compatibility with older versions of 'sitePath' only, and will be defunct at the next release.

Details

The following functions are deprecated and will be made defunct; use the replacement indicated below:

- multiFixationSites: `fixationSites`

sitesMinEntropy *Fixation sites prediction*

Description

After finding the `lineagePath` of a phylogenetic tree, `sitesMinEntropy` perform entropy minimization on every site of the sequence to group the tips according to amino acid/nucleotide.

Usage

```
sitesMinEntropy(x, ...)

## S3 method for class 'lineagePath'
sitesMinEntropy(
  x,
  minEffectiveSize = NULL,
  searchDepth = 1,
  method = c("compare", "insert", "delete"),
  ...
)
```

Arguments

`x`	A `lineagePath` object returned from `lineagePath` function.
`...`	further arguments passed to or from other methods.
`minEffectiveSize`	The minimum number of tips in a group.
`searchDepth`	The function uses heuristic search but the termination of the search cannot be intrinsically decided. `searchDepth` is needed to tell the search when to stop.
`method`	The strategy for predicting the fixation. The basic approach is entropy minimization and can be achieved by adding or removing fixation point, or by comparing the two.

Value

A `sitesMinEntropy` object.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
sitesMinEntropy(lineagePath(tree))
```

`SNPsites` *Finding sites with variation*

Description

Single nucleotide polymorphism (SNP) in the whole package refers to variation of amino acid. `SNPsite` will try to find SNP in the multiple sequence alignment. A reference sequence and gap character may be specified to number the site.

Usage

```
SNPsites(tree, ...)

## S3 method for class 'phyMSAmatched'
SNPsites(tree, minSNP = NULL, ...)
```

Arguments

`tree`	A `phyMSAmatched` object.
`...`	Other arguments
`minSNP`	Minimum number of a mutation to be a SNP. The default is 10th of the total tree tips.

Value

A `SNPsites` object.

Examples

```
data(zikv_tree_reduced)
data(zikv_align_reduced)
tree <- addMSA(zikv_tree_reduced, alignment = zikv_align_reduced)
SNPsites(tree)
```

zikv_align *Multiple sequence alignment of Zika virus polyprotein*

Description

The raw protein sequences were downloaded from ViPR database (https://www.viprbrc.org/) and aligned using MAFFT (https://mafft.cbrc.jp/alignment/software/). with default settings.

zikv_align_reduced is a truncated version of zikv_align

Usage

```
data(zikv_align)

data(zikv_align_reduced)
```

Format

an alignment object

an alignment object

zikv_tree *Phylogenetic tree of Zika virus polyprotein*

Description

Tree was built from zikv_align using RAxML (http://www.exelixis-lab.org/) with default settings. The tip ANK57896 was used as outgroup to root the tree.

zikv_tree_reduced is a truncated version of zikv_tree

Usage

```
data(zikv_tree)

data(zikv_tree_reduced)
```

Format

a phylo object

a phylo object

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