

Package ‘fastreeR’

June 30, 2022

Type Package

Title Phylogenetic, Distance and Other Calculations on VCF and Fasta Files

Version 1.0.0

biocViews Phylogenetics, Metagenomics, Clustering

Description Calculate distances, build phylogenetic trees or perform hierarchical clustering between the samples of a VCF or FASTA file. Functions are implemented in Java and called via rJava. Parallel implementation that operates directly on the VCF or FASTA file for fast execution.

License GPL-3

Encoding UTF-8

Language en-US

LazyData false

Depends R (>= 4.2)

Imports ape, data.table, dynamicTreeCut, methods, R.utils, rJava, stats, stringr, utils

SystemRequirements Java (>= 8)

RoxygenNote 7.1.2

URL <https://github.com/gkanogiannis/fastreeR>,
<https://github.com/gkanogiannis/BioInfoJava-Utills>

BugReports <https://github.com/gkanogiannis/fastreeR/issues>

Suggests BiocFileCache, BiocStyle, graphics, knitr, memuse, rmarkdown, spelling, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

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

git_branch RELEASE_3_15

git_last_commit a27d336

git_last_commit_date 2022-04-26

Date/Publication 2022-06-30

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dist2clusters	<i>Perform Hierarchical Clustering and tree pruning on a distance matrix</i>
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Description

Performs Hierarchical Clustering on a distance matrix (i.e. calculated with [vcf2dist](#) or [fasta2dist](#)) and generates a phylogenetic tree with agglomerative Neighbor Joining method (complete linkage) (as in [dist2tree](#)). The phylogenetic tree is then pruned with [cutreeDynamic](#) to get clusters (as in [tree2clusters](#)).

Usage

```
dist2clusters(inputDist, cutHeight = NULL, minClusterSize = 1, extra = TRUE)
```

Arguments

inputDist	Input distances file location (generated with vcf2dist or fasta2dist). File can be gzip compressed. Or a dist distances object.
cutHeight	Define at which height to cut tree. Default automatically defined.
minClusterSize	Minimum size of clusters. Default 1.
extra	Boolean whether to use extra parameters for the cutreeDynamic .

Value

A list of :

- **character** vector of the generated phylogenetic tree in Newick format
- **character** vector of the clusters. Each row contains data for a cluster, separated by space. The id of the cluster, the size of the cluster (number of elements) and the names of its elements, Cluster id 0 contains all the objects not assigned to a cluster (singletons). Example clusters output :

```
0 3 Sample1 Sample2 Sample3
1 3 Sample4 Sample5 Sample6
2 2 Sample7 Sample8
3 2 Sample9 Sample0
```

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utills>

Examples

```
my.clust <- dist2clusters(  
  inputDist =  
    system.file("extdata", "samples.vcf.dist.gz", package = "fastreeR")  
)
```

dist2tree

Generate phylogenetic tree from samples of a distance matrix

Description

Performs Hierarchical Clustering on a distance matrix (i.e. calculated with [vcf2dist](#) or [fasta2dist](#)) and generates a phylogenetic tree with agglomerative Neighbor Joining method (complete linkage).

Usage

```
dist2tree(inputDist)
```

Arguments

inputDist Input distances file location (generated with [vcf2dist](#) or [fasta2dist](#)). File can be gzip compressed. Or a [dist](#) distances object.

Value

A `character` vector of the generated phylogenetic tree in Newick format.

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utills>

Examples

```
my.tree <- dist2tree(  
  inputDist =  
    system.file("extdata", "samples.vcf.dist.gz", package = "fastreeR")  
)
```

fasta2dist

Calculate distances between sequences of a FASTA file

Description

This function calculates a `d2_S` type dissimilarity measurement between the `n` sequences (which can represent samples) of a FASTA file. See [doi:10.1186/s1285901611863](https://doi.org/10.1186/s1285901611863) for more details.

Usage

```
fasta2dist(  
  ...,  
  outputFile = NULL,  
  threads = 2,  
  kmer = 6,  
  normalize = FALSE,  
  compress = TRUE  
)
```

Arguments

...	Input fasta files locations (uncompressed or gzip compressed).
outputFile	Output distances file location.
threads	Number of java threads to use.
kmer	Kmer length to use for analyzing fasta sequences.
normalize	Normalize on sequences length.
compress	Compress output (adds .gz extension).

Value

A `dist` distances object of the calculation.

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utills>

Examples

```
my.dist <- fasta2dist(  
  inputfile = system.file("extdata", "samples.fasta.gz",  
    package = "fastreeR"  
  )  
)
```

tree2clusters	<i>Perform Hierarchical Clustering and tree pruning on a phylogenetic tree</i>
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Description

The phylogenetic tree is pruned with `cutreeDynamic` to get clusters.

Usage

```
tree2clusters(  
  treeStr,  
  treeDistances = NULL,  
  treeLabels = NULL,  
  cutHeight = NULL,  
  minClusterSize = 1,  
  extra = TRUE  
)
```

Arguments

treeStr	A <code>character</code> vector of a phylogenetic tree in Newick format
treeDistances	codenumeric <code>matrix</code> of distances, that were used to generate the tree. If <code>NULL</code> , it will be inferred from tree branch lengths.
treeLabels	A <code>character</code> vector of tree leaf labels.
cutHeight	Define at which height to cut tree. Default automatically defined.
minClusterSize	Minimum size of clusters. Default 1.
extra	Boolean whether to use extra parameters for the <code>cutreeDynamic</code> .

Value

- **character** vector of the clusters. Each row contains data for a cluster, separated by space. The id of the cluster, the size of the cluster (number of elements) and the names of its elements, Cluster id 0 contains all the objects not assigned to a cluster (singletons). Example clusters output :

```

0 3 Sample1 Sample2 Sample3
1 3 Sample4 Sample5 Sample6
2 2 Sample7 Sample8
3 2 Sample9 Sample0

```

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utills>

Examples

```

my.clust <- tree2clusters(
  treeStr = dist2tree(
    inputDist = system.file("extdata", "samples.vcf.dist.gz",
      package = "fastreeR"
    )
  )
)

```

vcf2clusters	<i>Perform Hierarchical Clustering and tree pruning on samples of VCF file</i>
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Description

Performs Hierarchical Clustering on a distance matrix calculated as in [vcf2dist](#) and generates a phylogenetic tree with agglomerative Neighbor Joining method (complete linkage) (as in [dist2tree](#)). The phylogenetic tree is then pruned with [cutreeDynamic](#) to get clusters (as in [tree2clusters](#)).

Usage

```

vcf2clusters(
  inputFile,
  threads = 2,
  ignoreMissing = FALSE,
  onlyHets = FALSE,
  ignoreHets = FALSE,

```

```

    cutHeight = NULL,
    minClusterSize = 1,
    extra = TRUE
)

```

Arguments

inputFile	Input vcf file location (uncompressed or gzip compressed).
threads	Number of java threads to use.
ignoreMissing	Ignore variants with missing data (./. or . .)
onlyHets	Only calculate on variants with heterozygous calls.
ignoreHets	Only calculate on variants with homozygous calls.
cutHeight	Define at which height to cut tree. Default automatically defined.
minClusterSize	Minimum size of clusters. Default 1.
extra	Boolean whether to use extra parameters for the cutreeDynamic .

Details

Biallelic or multiallelic (maximum 7 alternate alleles) SNP and/or INDEL variants are considered, phased or not. Some VCF encoding examples are:

- heterozygous variants : 1/0 or 0/1 or 0/2 or 1|0 or 0|1 or 0|2
- homozygous to the reference allele variants : 0/0 or 0|0
- homozygous to the first alternate allele variants : 1/1 or 1|1

If there are n samples and m variants, an $n \times n$ zero-diagonal symmetric distance matrix is calculated. The calculated cosine type distance $(1 - \text{cosine_similarity})/2$ is in the range $[0,1]$ where value 0 means completely identical samples (cosine is 1), value 0.5 means perpendicular samples (cosine is 0) and value 1 means completely opposite samples (cosine is -1).

The calculation is performed by a Java back-end implementation, that supports multi-core CPU utilization and can be demanding in terms of memory resources. By default a JVM is launched with a maximum memory allocation of 512 MB. When this amount is not sufficient, the user needs to reserve additional memory resources, before loading the package, by updating the value of the `java.parameters` option. For example in order to allocate 4GB of RAM, the user needs to issue `options(java.parameters="-Xmx4g")` before `library(fastreeR)`.

Value

A list of :

- `dist` distances object.
- `character` vector of the generated phylogenetic tree in Newick format
- `character` vector of the clusters. Each row contains data for a cluster, separated by space. The id of the cluster, the size of the cluster (number of elements) and the names of its elements, Cluster id 0 contains all the objects not assigned to a cluster (singletons). Example clusters output :

```
0 3 Sample1 Sample2 Sample3
1 3 Sample4 Sample5 Sample6
2 2 Sample7 Sample8
3 2 Sample9 Sample0
```

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utills>

Examples

```
my.clust <- vcf2clusters(
  inputFile = system.file("extdata", "samples.vcf.gz",
    package = "fastreeR"
  )
)
```

vcf2dist

Calculate distances between samples of a VCF file

Description

This function calculates a cosine type dissimilarity measurement between the n samples of a VCF file.

Usage

```
vcf2dist(
  inputFile,
  outputFile = NULL,
  threads = 2,
  ignoreMissing = FALSE,
  onlyHets = FALSE,
  ignoreHets = FALSE,
  compress = FALSE
)
```

Arguments

inputFile	Input vcf file location (uncompressed or gzip compressed).
outputFile	Output distances file location.
threads	Number of java threads to use.

ignoreMissing	Ignore variants with missing data (./. or . .)
onlyHets	Only calculate on variants with heterozygous calls.
ignoreHets	Only calculate on variants with homozygous calls.
compress	Compress output (adds .gz extension).

Details

Biallelic or multiallelic (maximum 7 alternate alleles) SNP and/or INDEL variants are considered, phased or not. Some VCF encoding examples are:

- heterozygous variants : 1/0 or 0/1 or 0/2 or 1|0 or 0|1 or 0|2
- homozygous to the reference allele variants : 0/0 or 0|0
- homozygous to the first alternate allele variants : 1/1 or 1|1

If there are n samples and m variants, an $n \times n$ zero-diagonal symmetric distance matrix is calculated. The calculated cosine type distance $(1 - \text{cosine_similarity})/2$ is in the range $[0,1]$ where value 0 means completely identical samples (cosine is 1), value 0.5 means perpendicular samples (cosine is 0) and value 1 means completely opposite samples (cosine is -1).

The calculation is performed by a Java backend implementation, that supports multi-core CPU utilization and can be demanding in terms of memory resources. By default a JVM is launched with a maximum memory allocation of 512 MB. When this amount is not sufficient, the user needs to reserve additional memory resources, before loading the package, by updating the value of the `java.parameters` option. For example in order to allocate 4GB of RAM, the user needs to issue `options(java.parameters="-Xmx4g")` before `library(fastreeR)`.

Output file, if provided, will contain $n+1$ lines. The first line contains the number n of samples and number m of variants, separated by space. Each of the subsequent n lines contains $n+1$ values, separated by space. The first value of each line is a sample name and the rest n values are the calculated distances of this sample to all the samples. Example output file of the distances of 3 samples calculated from 1000 variants:

```
3 1000
Sample1 0.0 0.5 0.2
Sample2 0.5 0.0 0.9
Sample3 0.2 0.9 0.0
```

Value

A `dist` distances object of the calculation.

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utils>

Examples

```
my.dist <- vcf2dist(  
  inputFile = system.file("extdata", "samples.vcf.gz",  
    package = "fastreeR"  
  )  
)
```

vcf2istats

Calculate various per sample statistics from a VCF file

Description

Only biallelic SNPs are considered. For each sample, the following statistics are calculated :

- INDIV : Sample name
- N_SITES : Total number of SNPs
- N_HET : Number of SNPs with heterozygous call (0/1 or 0|1 or 1/0 or 1|0)
- N_ALT : Number of SNPs with alternate homozygous call (1/1 or 1|1)
- N_REF : Number of SNPs with reference homozygous call (0/0 or 0|0)
- N_MISS : Number of SNPs with missing call (./. or .|.)
- P_HET : Percentage of heterozygous calls
- P_ALT : Percentage of alternate homozygous calls
- P_REF : Percentage of reference homozygous calls
- P_MISS : Percentage of missing calls (missing rate)

Usage

```
vcf2istats(inputFile, outputFile = NULL)
```

Arguments

inputFile	Input vcf file location (uncompressed or gzip compressed).
outputFile	Output samples statistics file location.

Value

A [data.frame](#) of sample statistics.

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utils>

Examples

```
my.istats <- vcf2istats(  
  inputFile =  
    system.file("extdata", "samples.vcf.gz", package = "fasttreeR")  
)
```

vcf2tree

Generate phylogenetic tree from samples of a VCF file

Description

This function calculates a distance matrix between the samples of a VCF file as in [vcf2dist](#) and performs Hierarchical Clustering on this distance matrix as in [dist2tree](#). A phylogenetic tree is calculated with agglomerative Neighbor Joining method (complete linkage).

Usage

```
vcf2tree(  
  inputFile,  
  threads = 2,  
  ignoreMissing = FALSE,  
  onlyHets = FALSE,  
  ignoreHets = FALSE  
)
```

Arguments

inputFile	Input vcf file location (uncompressed or gzip compressed).
threads	Number of java threads to use.
ignoreMissing	Ignore variants with missing data (./. or . .)
onlyHets	Only calculate on variants with heterozygous calls.
ignoreHets	Only calculate on variants with homozygous calls.

Details

Biallelic or multiallelic (maximum 7 alternate alleles) SNP and/or INDEL variants are considered, phased or not. Some VCF encoding examples are:

- heterozygous variants : 1/0 or 0/1 or 0/2 or 1|0 or 0|1 or 0|2
- homozygous to the reference allele variants : 0/0 or 0|0
- homozygous to the first alternate allele variants : 1/1 or 1|1

If there are n samples and m variants, an $n \times n$ zero-diagonal symmetric distance matrix is calculated. The calculated cosine type distance $(1 - \text{cosine_similarity})/2$ is in the range $[0,1]$ where value 0 means completely identical samples (cosine is 1), value 0.5 means perpendicular samples (cosine is 0) and value 1 means completely opposite samples (cosine is -1).

The calculation is performed by a Java backend implementation, that supports multi-core CPU utilization and can be demanding in terms of memory resources. By default a JVM is launched with a maximum memory allocation of 512 MB. When this amount is not sufficient, the user needs to reserve additional memory resources, before loading the package, by updating the value of the `java.parameters` option. For example in order to allocate 4GB of RAM, the user needs to issue `options(java.parameters="-Xmx4g")` before `library(fastreeR)`.

Value

A `character` vector of the generated phylogenetic tree in Newick format.

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

Java implementation: <https://github.com/gkanogiannis/BioInfoJava-Utils>

Examples

```
my.tree <- vcf2tree(  
  inputFile = system.file("extdata", "samples.vcf.gz",  
    package = "fastreeR"  
  )  
)
```

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