Package: phruta (via r-universe)

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Type Package

Title Phylogenetic Reconstruction and Time-dating

Version 0.1.3

URL <https://docs.ropensci.org/phruta/index.html>,
<https://github.com/ropensci/phruta>,
<https://ropensci.github.io/phruta/>

BugReports <https://github.com/ropensci/phruta/issues>

Description The phruta R package is designed to simplify the basic
phylogenetic pipeline. Specifically, all code is run within the
same program and data from intermediate steps are saved in
independent folders. Furthermore, all code is run within the
same environment which increases the reproducibility of your
analysis. phruta retrieves gene sequences, combines newly
downloaded and local gene sequences, and performs sequence
alignments.

Encoding UTF-8

LazyData true

Depends R (>= 3.5.0)

Imports rgbif, pbapply, rentrez, taxize, ips, ape, geiger, methods,
DECIPHER, reutils, foreach, doParallel, doSNOW, Biostrings,
msa, odseq, XML, Rogue

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Repository https://ropensci.r-universe.dev

RemoteUrl https://github.com/ropensci/phruta

RemoteRef main

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Contents

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acc.table.retrieve   *Retrieve accession numbers and titles for a given combination of species and genes in genbank*

Description

Retrieve accession numbers and titles for complex searches conducted in genbank. Note that this function depends on `acc.retrieve` as it actually uses `expand.grid` to find all the relevant organism/gene combinations in genbank.

Usage

```
acc.table.retrieve(
  clades = NULL,
  species = NULL,
  genes = NULL,
  speciesLevel = NULL,
  npar = 2,
  nSearchesBatch = 499
)
```

Arguments

clades	A vector of clade names (character). Note that this can either be the name of a clade (e.g. Apis) or the code in NCBI (e.g. txid7459).
species	A vector of species names (logical). Note that this can either be the name of a clade (e.g. Apis) or the code in NCBI (e.g. txid7459).
genes	A vector of gene names (character; optional).
speciesLevel	Whether the result should be a species-level dataset (logical).
npar	Number of parallel searches (the default is probably the best option).
nSearchesBatch	Number of searches per batch

Value

This function returns an object of class data.frame that includes the following columns. First, Species with the species name listed in GenBank. Second, Ti including the title of the accession in GenBank. Third, Acc listing the accession number. Fourth, gene including the name of the target gene.

Examples

```
## Not run:
acc.table.retrieve(
 clades  = c('Felis', 'Vulpes', 'Phoca'),
 species = 'Manis_pentadactyla' ,
 genes   = c("A2AB","ADORA3","ADRB2","APOB",
             "APP","ATP7","BCHE","BDNF",
             "BMI1","BRCA1","BRCA2","CNR1",
             "COI","CREM","CYTB","DMP1",
             "EDG1","ENAM","FBN1","GHR",
             "IRBP","ND1","ND2","PLCB4",
             "PNOC","RAG1a","RAG1b","RAG2",
             "TTN","TYR1","VWF"),
 speciesLevel = FALSE
)

## End(Not run)
```

---

gene.sampling.retrieve

Retrieve the distribution of genes for given organism in genbank

---

Description

This function retrieves the gene names for given organism in genbank. This function is useful to explore the genes that are widely sampled for a given taxon in genbank. However, note that the performance of gene.sampling.retrieve is entirely dependant on the quality of submissions to genbank. For instance, if most of the sequences in genbank (nucleotide) don't have information on

the sequenced region, this function won't provide reliable estimates of the sampling frequency of each gene in the database. We recommend using this function with caution, and only when there is no additional information on the genes that are widely sampled for the target group(s) of interest.

Usage

```
gene.sampling.retrieve(
  organism,
  speciesSampling = TRUE,
  npar = 2,
  nSearchesBatch = 499
)
```

Arguments

organism   A vector of taxonomic groups (character).

speciesSampling
                Whether the results should be at the species-level (logical).

npar   Number of simultaneous searches (character; optional). The default 2 is gener-
                ally fast enough and does not exceed the maximum number of connections to
                genbank.

nSearchesBatch Number of searches per batch

Value

This function returns a data.frame that comprises the following columns. First, Gene, includ-
ing the name of the relevant gene sampled in the target taxonomic groups. Second, Sampled in N
species includes the number of species where the gene is sampled among the target taxa. Third,
PercentOfSampledSpecies indicates the percentage of species where the gene is sampled (assum-
ing GeneBank's taxonomic backbone).

Examples

```
## Not run:
test.spp <- gene.sampling.retrieve(organism = "Puma", speciesSampling = TRUE)
test.pop <- gene.sampling.retrieve(organism = "Puma", speciesSampling = FALSE)

## End(Not run)
```

---

sq.add   *Add local sequences to previously downloaded sequences*

Description

This function adds sequences located in a particular folder (default is `"0.AdditionalSequences"`) to fasta files in another folder (default is `"0.Sequences"`). Files must be in FASTA format and names of the files should perfectly match the ones in the previously downloaded folder (e.g. `"0.Sequences"`). This function creates a third new folder `"0.0.OriginalDownloaded"` containing the originally downloaded sequences. The sequences in the `"0.Sequences"` folder get replaced with the combined ones. Note that new sequences can be added even for just a fraction of the originally downloaded genes.

Usage

```
sq.add(folderDownloaded = "0.Sequences", folderNew = "0.AdditionalSequences")
```

Arguments

folderDownloaded

> Name of the folder with downloaded sequences.

folderNew   Name of the folder with local sequences.

Value

None

Examples

```
## Not run:
sq.add(folderDownloaded = "0.Sequences",
        folderNew = "0.AdditionalSequences")

## End(Not run)
```

---

sq.aln   *Align sequences*

Description

Perform multiple sequence alignment on all the fasta files saved in a given folder. Alignment is conducted using `"BiocManager::install("DECIPHER")"`. Note that this function first optimizes the direction of the sequences, then aligns using `"BDECIPHER"`, and finally masks the resulting alignment (optionally but does it per default). The masking step includes removing common gaps across all the species and removing highly ambiguous positions. The resulting aligned sequences are stored to a new folder `"2.Alignments"`.'

Usage

```
sq.aln(
  folder = "1.CuratedSequences",
  FilePatterns = "renamed",
  sqs.object = NULL,
  mask = TRUE,
  maxFractionGapsSpecies = 0.01,
  ...
)
```

Arguments

`folder`	Name of the folder where the sequences to align are stored (character).
`FilePatterns`	A string that is common to all the target files in the relevant folder (character). Note that this argument can be set to `"NULL"` if no specific pattern wants to be analyzed.
`sqs.object`	A list of sequences generated from sq.curate. Only use if you're not interested in download sequences locally.
`mask`	Removes ambiguous sites (Logical, TRUE or FALSE).
`maxFractionGapsSpecies`	
	Maximum fraction of gaps per species (when masked)
`...`	Arguments passed to `"DECIPHER::AlignSeqs"`.

Value

This function will return an object of class `list` including the original and renamed sequence alignments. Optionally, this object will also include the masked alignments.

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  kingdom = "animals", folder = "0.Sequences"
)
sq.aln(folder = "1.CuratedSequences")

## End(Not run)
```

---

sq.curate   *Curate sequences from genbank*

Description

After downloading sequences from genbank, this function curates sequences based on taxonomic information. Note that this function provides two summary datasets. First, the accession numbers. Second, the taxonomic information for each species in the database. The taxonomy strictly follows the gbif taxonomic backbone. The resulting files are saved to `"1.CuratedSequences"`. The resulting files also have the most recent curated taxonomy following the gbif (or selected database) taxonomic backbone.

Usage

```
sq.curate(
  filterTaxonomicCriteria = NULL,
  mergeGeneFiles = NULL,
  database = "gbif",
  kingdom = NULL,
  folder = "0.Sequences",
  sqs.object = NULL,
  removeOutliers = TRUE,
  minSeqs = 5,
  threshold = 0.05,
  ranks = c("kingdom", "phylum", "class", "order", "family", "genus", "species")
)
```

Arguments

filterTaxonomicCriteria

A single string of terms (delimited using "|") listing all the strings that could be used to identify the species that should be in the dataset (character).

mergeGeneFiles A named list, with each element being a character vector indicating the names of the files in `"0.Sequences"` that need to be combined into a single fasta file. For instance, you can use this argument to combine CO1 and COI.

database   A name of a database with taxonomic information. Although 'gbif' is faster, it only has information for animals and plants. Other databases follow taxize::classification.

kingdom   Optional and only used when database='gbif'. Two possible options: "animals" or "plants."

folder   The name of the folder where the original sequences are located (character).

sqs.object   A list of sequences generated from `sq.retrieve.indirect`. Only use if you're not interested in download sequences locally.

removeOutliers Whether `odseq:odseq` should be used to remove outliers

minSeqs   minimum number of sequences per locus

threshold	Relative to odseq::odseq. Only important if removeOutliers = TRUE
ranks	The taxonomic ranks used to examine the taxonomy of the species in the 0.Sequences folder.

Value

This function will return an object of class list with the following elements. First, the curated sequences with original names. Second, the curated sequences with species-level names. Third, the accession numbers table. Fourth, a summary of taxonomic information for all the species sampled in the files.

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  database = "gbif", kingdom = "animals",
  folder = "0.Sequences"
)

## End(Not run)
```

---

sq.partitionfinderv1   *Run Partitionfinder v.1*

Description

This function runs partitionfinder v1 within phruta. For now, all analyses are based on genes. Please note that you need at least two gene regions to run partitionfinder.

Usage

```
sq.partitionfinderv1(
  folderAlignments = "2.Alignments",
  FilePatterns = "Masked",
  folderPartitionFinder = "2.1.PartitionFinderv1",
  models = "all",
  run = TRUE
)
```

Arguments

folderAlignments
> Name of the folder where the sequences to align are stored (character).

FilePatterns   A string that is common to all the target files in the relevant folder (character).
Note that this argument can be set to "NULL" if no specific pattern wants to be
analyzed.

folderPartitionFinder
> Name of the new folder where the output files are stored (string).

models   Models to run in partitionfinder (string).

run   Run partitionfinder?

Value

None

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  kingdom = "animals", folder = "0.Sequences"
)
sq.aln(folder = "1.CuratedSequences")
sq.partitionfinderv1(
  folderAlignments = "2.Alignments",
  FilePatterns = "Masked",
  models = "all"
)

## End(Not run)
```

---

sq.retrieve.direct   *Retrieve sequences from genbank*

Description

Downloads sequences from genbank (nucleotide database) for particular taxa and genes into a folder
called "0.Sequences".

Usage

```
sq.retrieve.direct(
  clades = NULL,
  species = NULL,
  genes = NULL,
  db = "itis",
  maxseqs = 1,
  maxlength = 5000
)
```

Arguments

clades	A vector listing taxonomic groups of interest (character).
species	A vector listing additional species interest (character). This argument can be used to define additional target species in the ingroup or species to be sampled in the outgroup (character).
genes	A vector listing gene names of interest (character).
db	Follows db in `taxize::downsteam`. Choose from `itis`, `gbif`, `ncbi`, `worms`, or `bold`.
maxseqs	Maximum number of sequences to retrieve per search (taxa + gene) (numeric).
maxlength	Maximum length of the gene sequence (numeric).

Value

None

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)

## End(Not run)
```

---

sq.retrieve.indirect	*Retrieve sequences from genbank based on a dataset of accession numbers*

Description

Downloads sequences from genbank (nucleotide database) for particular taxa and genes into a folder called "0.Sequences".

Usage

```
sq.retrieve.indirect(acc.table, download.sqs = FALSE)
```

Arguments

acc.table   An accession table, ideally generated using `acc.table.retrieve`. The data.frame
                   must have the Species, Acc, and gene column names.

download.sqs   Logical indicating whether sequences should be downloaded locally or returned
                   as a list.

Value

None

Examples

```
## Not run:
acc.table.retrieve(
 clades  = c('Felis', 'Vulpes', 'Phoca'),
 species = 'Manis_pentadactyla' ,
 genes   = c("A2AB","ADORA3","ADRB2","APOB",
             "APP","ATP7","BCHE","BDNF",
             "BMI1","BRCA1","BRCA2","CNR1",
             "COI","CREM","CYTB","DMP1",
             "EDG1","ENAM","FBN1","GHR",
             "IRBP","ND1","ND2","PLCB4",
             "PNOC","RAG1a","RAG1b","RAG2",
             "TTN","TYR1","VWF"),
 speciesLevel=TRUE
)

sq.retrieve.indirect(test)


## End(Not run)
```

---

tree.constraint   *Tree inference under RAxML*

Description

Performs tree inference under "RAxML" for aligned fasta sequences in a given folder (default is
"2.Alignments").

Usage

```
tree.constraint(
  taxonomy_folder = "1.CuratedSequences",
  targetColumns = c("kingdom", "phylum", "class", "order", "family", "genus",
    "species_names"),
  Topology = "((ingroup), outgroup);",
  outgroup = NULL
)
```

Arguments

taxonomy_folder

Name of the folder where the 1.Taxonomy file is stored.

targetColumns   Where to find "RAxML" or how to run it from the console? (string).

Topology   A string summarizing the desired topological constraint in newick format.

outgroup   Optional and only required when the topology argument is not "((ingroup), out-group);".

Value

None

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  kingdom = "animals", folder = "0.Sequences"
)

tree.constraint(
  taxonomy_folder = "1.CuratedSequences",
  targetColumns = c("kingdom", "phylum", "class", "order", "family",
  "genus", "species_names"),
  Topology = "((ingroup), outgroup);",
  outgroup = "Manis_pentadactyla"
)
tree.constraint(
  taxonomy_folder = "1.CuratedSequences",
  targetColumns = c("kingdom", "phylum", "class", "order", "family",
  "genus", "species_names"),
  Topology = "((Felis), (Phoca));"
)

## End(Not run)
```

---

tree.dating   *Tree dating under treePL or*

Description

Performs tree dating under "treePL" or "PATHd-8" based on secondary calibrations. Note that "treePL" or "PATHd-8" must be installed in your PATH. How to install "PATHd-8" in mac "https://gist.github.com/cro and "treePL" can be installed using homebrew (brew install brewsci/bio/treepl). Thanks to Brian O'Meara and Jonathan Chang, respectively.

Usage

```
tree.dating(
  taxonomyFolder = "1.CuratedSequences",
  phylogenyFolder = "3.Phylogeny",
  ...
)
```

Arguments

taxonomyFolder   Name of the folder where "1.Taxonomy.csv", created duing the "sq.curate" step, is stored (character).

phylogenyFolder

Name of the folder where "RAxML_bipartitions.phruta", created duing the "tree.raxml" step, is stored (character).

...   Arguments passed to "geiger::congruify.phylo".

Value

None

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  kingdom = "animals", folder = "0.Sequences"
)
sq.aln(folder = "1.CuratedSequences")
tree.raxml(
  folder = "2.Alignments", FilePatterns = "Masked",
  raxml_exec = "raxmlHPC", Bootstrap = 100,
  outgroup = "Manis_pentadactyla"
```

```
)
tree.dating(
  taxonomyFolder = "1.CuratedSequences",
  phylogenyFolder = "3.Phylogeny", scale = "treePL"
)

## End(Not run)
```

---

tree.raxml   *Tree inference under RAxML*

Description

Performs tree inference under "RAxML" for aligned fasta sequences in a given folder (default is
"2.Alignments"). Note that you need at least two gene regions to run a partitioned analysis.

Usage

```
tree.raxml(
  folder = "2.Alignments",
  FilePatterns = "Masked_",
  raxml_exec = "raxmlHPC",
  Bootstrap = 100,
  outgroup,
  partitioned = FALSE,
  ...
)
```

Arguments

folder	Name of the folder where the sequences to align are stored (character).
FilePatterns	A string that is common to all the target files in the relevant folder (character). Note that this argument can be set to "NULL" if no specific pattern wants to be analized.
raxml_exec	Where to find "RAxML" or how to run it from the console? (string).
Bootstrap	Number of bootstrap replicates (numeric).
outgroup	A single string of comma-separated tip labels to be used as outgroup in "RAxML" See "RAxML" documentation for more details (character).
partitioned	Whether analyses should be partitioned by gene (Logical).
...	Arguments passed to "ips::raxml".

Value

None

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  kingdom = "animals", folder = "0.Sequences"
)
sq.aln(folder = "1.CuratedSequences")
tree.raxml(
  folder = "2.Alignments", FilePatterns = "Masked",
  raxml_exec = "raxmlHPC", Bootstrap = 100,
  outgroup = "Manis_pentadactyla"
)

## End(Not run)
```

---

tree.roguetaxa	*RogueNaRok within phruta*

Description

Implements the RogueNaRok algorithm for rogue taxon identification within phruta

Usage

```
tree.roguetaxa(folder = "3.Phylogeny", ...)
```

Arguments

folder	Name of the folder where the sequences to align are stored (character).
...	Arguments passed to "Rogue::RogueTaxa".

Value

None

Examples

```
## Not run:
sq.retrieve.direct(
  clades = c("Felis", "Vulpes", "Phoca"),
  species = "Manis_pentadactyla",
  genes = c("ADORA3", "CYTB")
)
sq.curate(
```

```
  filterTaxonomicCriteria = "Felis|Vulpes|Phoca|Manis",
  kingdom = "animals", folder = "0.Sequences"
)
sq.aln(folder = "1.CuratedSequences")
tree.raxml(
  folder = "2.Alignments", FilePatterns = "Masked",
  raxml_exec = "raxmlHPC", Bootstrap = 100,
  outgroup = "Manis_pentadactyla"
)
tree.roguetaxa(folder = "3.Phylogeny")

## End(Not run)
```

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