

# Package ‘BoSSA’

January 20, 2025

**Type** Package  
**Title** A Bunch of Structure and Sequence Analysis  
**Version** 3.7  
**Date** 2020-10-16  
**Author** Pierre Lefeuvre  
**Maintainer** Pierre Lefeuvre <pierre.lefeuvre@cirad.fr>  
**Depends** R (>= 3.3.0)  
**Imports** ape, RSQLite, jsonlite, phangorn, plotrix  
**Suggests** prettydoc, knitr, rmarkdown, XML, rentrez, http  
**VignetteBuilder** knitr  
**Description** Reads and plots phylogenetic placements.  
**License** GPL  
**NeedsCompilation** no  
**Repository** CRAN  
**Date/Publication** 2020-10-20 07:20:05 UTC

## Contents

BoSSA-package . . . . .	2
circular_tree . . . . .	3
plot.pplace . . . . .	4
pplace . . . . .	6
pplace_to_matrix . . . . .	6
pplace_to_table . . . . .	8
pplace_to_taxonomy . . . . .	9
print.pplace . . . . .	9
print.protdb . . . . .	10
read_jplace . . . . .	11
read_protdb . . . . .	12
read_sqlite . . . . .	13
refpkg . . . . .	14
sub_pplace . . . . .	15
write_jplace . . . . .	17

---

BoSSA-package                      *A Bunch of Structure and Sequence Analysis*

---

## Description

Reads and plots phylogenetic placements.

## Details

The DESCRIPTION file:

```

Package:      BoSSA
Type:         Package
Title:        A Bunch of Structure and Sequence Analysis
Version:      3.7
Date:         2020-10-16
Author:       Pierre Lefeuvre
Maintainer:   Pierre Lefeuvre <pierre.lefeuvre@cirad.fr>
Depends:      R (>= 3.3.0)
Imports:      ape, RSQLite, jsonlite, phangorn, plotrix
Suggests:    prettydoc, knitr, rmarkdown, XML, rentrez, httr
VignetteBuilder: knitr
Description:  Reads and plots phylogenetic placements.
License:      GPL

```

Index of help topics:

```

BoSSA-package      A Bunch of Structure and Sequence Analysis
circular_tree      Plot an inside-out circular tree
plot.pplace        Plot a pplace or jplace object
pplace             A placement object as obtained with the
                  read_sqlite function
pplace_to_matrix   Pplace to contingency matrix
pplace_to_table    Merge the multiclass and the placement table of
                  pplace object
pplace_to_taxonomy Convert a pplace object to a taxonomy table
print.pplace       Compact display of pplace and jplace objects
print.protdb       Compact display of protdb object
read_jplace        Read a jplace file
read_protdb        Read Protein Data Bank (PDB) file
read_sqlite        Read a pplacer/guppy sqlite file
refpkg            Summary data and plots for reference packages
sub_pplace         Subsets a pplace object
write_jplace       Write a jplace or pplace object to the disk

```

BoSSA contains functions to read and plot phylogenetic placement files obtained using softwares such as pplacer, guppy, EPA and RAPPAS.

**Author(s)**

Pierre Lefeuvre Maintainer: Pierre Lefeuvre <pierre.lefeuvre@cirad.fr>

**References**

- pplacer and guppy <http://matsen.fhcrc.org/pplacer/> <http://matsen.github.io/pplacer/> - EPA <https://sco.hits.org/exelixis/web/software/epa/index.html> - RAPPAS <https://github.com/benclaff/RAPPAS> - Common file format <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0031009>

---

circular_tree	<i>Plot an inside-out circular tree</i>
---------------	---

---

**Description**

Plot a tree in a circular manner with the tips pointing inward

**Usage**

```
circular_tree(phy,ratio=0.5,def=1000,pos_out=FALSE,tip_labels=TRUE,cex_tips=0.5)
```

**Arguments**

phy	a class phylo object
ratio	the ratio of the tree size compared to the plot size
def	the def parameter controls the granularity of the curves
pos_out	a matrix with the x and y coordinates of the branches extremities (i.e. nodes and tips) is outputed when set to TRUE
tip_labels	whether or not the tiplabels should be plotted
cex_tips	the size of the tiplabels

**Details**

The function plot a tree in a circular manner. Note that the tree will produce a correct output only if there is no topology modifications after reading the original tree using the ape read.tree function.

**Value**

a plot

**Author(s)**

pierre lefeuvre

**Examples**

```
library(ape)

test_tree <- rtree(20)

circular_tree(test_tree)
```

---

plot.pplace                      *Plot a pplace or jplace object*

---

**Description**

Plot the tree and placements from a pplace or a jplace object

**Usage**

```
## S3 method for class 'pplace'
plot(x,type="precise",simplify=FALSE,
     main="",N=NULL,transfo=NULL,legend=TRUE,stl=FALSE,
     asb=FALSE,edge.width=1,max_width=10,cex.number=0.5,
     cex.text=0.8,transp=80,add=FALSE,color=NULL,discrete_col=FALSE,
     pch=16,run_id=NULL, ...)
```

**Arguments**

x	A pplace or jplace object
type	The type of plotting desired with either, "precise", "color", "fattree" or "number". For each option, placement sizes represent the multiplication of the N value with the placement ML ratio.
simplify	If set to TRUE, only plot the best position for each placement. default is FALSE.
main	An optionnal title to plot along the tree
N	An optionnal vector of the weight of each placement. Must be of the same length and order as placements in the multiclass table. Note that the placement mass (potentially) available from the original files are imported into R but aren't use in the analysis. The N parameter should be used instead.
transfo	An optionnal function to transform the placement size when type set to "precise". Beware that it is also applied to the legend so that it does not anymore correspond to the placement size but to the transform dot size
legend	Plot a legend. Not available for type "number" or "fattree"
stl	Show tip labels
asb	Add scale bar
edge.width	The tree edge width
max_width	The maximum edge width when type is set to "fattree"

cex.number	Control the size of the text when type is set to "number"
cex.text	Control the size of the main
transp	Control the transparency of the placement when type is "precise" and the transparency of the branch without placement when type is set to "color". Encoded in hexadecimal scale (i.e. range from "00" to "FF")
add	Add placement to an existing plot when type is set to precise. Default is FALSE. If it was drawn, the legend won't be updated. Beware to use the same value for the "transfo" option in each plot. Dots color scale won't be accurate when using the "add" option. It is highly recommended to use a single color.
color	The colors used for pendant branch length scale when type is set to "precise". Default is a color ramp with "blue", "green", "yellow" and "red"
discrete_col	Discretise the color scale for pendant branch length
pch	The dot style used for placements when type is set to "precise"
run_id	A vector of run_id to subset
...	Further arguments passed to or from other methods.

**Author(s)**

pierre lefeuvre

**Examples**

```

data(pplace)

### number type
plot(pplace,type="number",main="number")

### color type without and with legend
plot(pplace,type="color",main="color without legend",legend=FALSE)
plot(pplace,type="color",main="color with legend",legend=TRUE)

### fattree type
plot(pplace,type="fattree",main="fattree")

### precise type
plot(pplace,type="precise",main="precise vanilla")
plot(pplace,type="precise",simplify=TRUE,main="precise simplify")

# using the read number information encoded here in the name (if available)
Npplace <- sample(1:100,nrow(pplace$multiclass),replace=TRUE)
# in the following exemple, the dots are too large...
plot(pplace,type="precise",main="precise N",legend=TRUE,N=Npplace,simplify=TRUE)

# using the transfo option to modify dot sizes
# note that placements sizes inferior to 1 won't
# behave properly with log10 as a transformation function.
# In this case, you rather use simplify (all the placement
# will corresponds to at least one sequence).
# Beware that when using the transfo option,

```

```
# the legend does not anymore correspond to the actual placement
# size but to the transform placement size
# (i.e. the transform function applied to the dot size).
# we will use the the log10 function
plot(pplace,type="precise",main="precise log10",
     legend=TRUE,N=Npplace,transfo=log10)
# or without simplify, you can use a custom function
# as transfo that will produce positive sized dots
plot(pplace,type="precise",main="precise custom"
     ,legend=TRUE,N=Npplace,transfo=function(X){log10(X+1)})
```

---

pplace

*A placement object as obtained with the read\_sqlite function*


---

### Description

A placement object as obtained with the read\_sqlite function. In this example, a set of 100 sequence reads are placed over a 16S phylogeny. This example is a subset of those available for download at <http://fhcrc.github.io/microbiome-demo/>

### Usage

```
data("pplace")
```

### References

<http://fhcrc.github.io/microbiome-demo/>

### Examples

```
data(pplace)
str(pplace)
```

---

pplace\_to\_matrix

*Pplace to contingency matrix*


---

### Description

Convert the pplace object into a contingency matrix OTUs / sample

### Usage

```
pplace_to_matrix(pplace, sample_info, N = NULL, tax_name = FALSE
,run_id=NULL,round_type=NULL)
```

**Arguments**

pplace	A pplace object
sample_info	A vector or list specifying the association between placement (in the multiclass table) and sample. In the case of a list, multiple sample can be associated with a single placement.
N	An optionnal vector or list with a number of occurrence (or weight) associated to each placed sequence. If "sample_info" is a list, "N" must also be a list. Note that the placement mass (potentially) available from the original files are imported into R but aren't use in the analysis. The N parameter should be used instead.
tax_name	Either the tax ids (when set to FALSE, default) or the tax names (when set to TRUE) are used as column names. The tax names are obtained form the "taxo" table of the pplace object.
run_id	A vector of run_id to subset
round_type	The name of the rounding fonction to apply to the product of the number of individuals classified in a given category and the likelihood ratio of this classification. Should be set to NULL (no rounding) or one of "trunc", "round", "ceiling" or "floor".

**Value**

A contingency matrix with OTUs / species in rows and samples in columns.

**Author(s)**

pierre lefeuvre

**Examples**

```
data(pplace)

### simple example
pplace_to_matrix(pplace,c(rep("sample1",27),rep("sample2",50),rep("sample3",23)))

### using the N option to specify the number of sequence each placement represents
Npplace <- sample(1:20,100,replace=TRUE)
pplace_to_matrix(pplace,c(rep("sample1",27),rep("sample2",50),rep("sample3",23)),N=Npplace)

### with tax_name=TRUE
pplace_to_matrix(pplace,c(rep("sample1",27),rep("sample2",50),rep("sample3",23)),tax_name=TRUE)
```

---

pplace\_to\_table      *Merge the multiclass and the placement table of pplace object*

---

**Description**

Merge the multiclass and the placement table of pplace object

**Usage**

```
pplace_to_table(pplace, type = "full", run_id=NULL)
```

**Arguments**

pplace	a pplace object
type	the placement type to consider
run_id	A vector of run_id to subset

**Details**

For the type argument, either "full" or "best" are accepted. Whereas for the "full" type, all the placements are considered, only the best placement for each sequence is considered for the "best" type.

**Value**

a data frame with the same column names as the multiclass and placements tables

**Author(s)**

pierre lefeuvre

**Examples**

```
data(pplace)

### with every placement
pplace_to_table(pplace)

### keeping only the best placement for each sequence
pplace_to_table(pplace, type="best")
```



---

pplace\_to\_taxonomy      *Convert a pplace object to a taxonomy table*

---

### Description

Convert a pplace object to a taxonomy table

### Usage

```
pplace_to_taxonomy(pplace, taxonomy,
rank=c("phylum", "class", "order", "family", "genus", "species"),
type="all", tax_name=TRUE, run_id=NULL)
```

### Arguments

pplace	A pplace object
taxonomy	The taxonomy table as obtained using the refseq fonction with type set to taxonomy
rank	The desired rank for the taxonomy table
type	Wether all the possible classification available in the multiclass table are outputed (type="all") or only the best (type="best")
tax_name	Wether to use taxonomy names (default) or tax_id number
run_id	A vector of run_id to subset

### Value

A matrix with taxonomic ranks for each sequence

### Author(s)

pierre lefeuvre

---

print.pplace      *Compact display of pplace and jplace objects*

---

### Description

Compact display of pplace and jplace objects

### Usage

```
## S3 method for class 'pplace'
print(x, ...)
```

**Arguments**

x                    a pplace or jplace object  
...                   further arguments passed to or from other methods

**Author(s)**

pierre lefeuvre

**Examples**

```
data(pplace)  
print(pplace)
```

---

print.protdb                    *Compact display of protdb object*

---

**Description**

Function to print the header section of the protdb object.

**Usage**

```
## S3 method for class 'protdb'  
print(x, ...)
```

**Arguments**

x                    a protdb class object  
...                   further arguments passed to or from other methods

**Author(s)**

pierre lefeuvre

**Examples**

```
pdb_file <- system.file("extdata", "1L2M.pdb", package = "BoSSA")  
pdb <- read_protdb(pdb_file)  
print(pdb)
```

---

read_jplace	<i>Read a jplace file</i>
-------------	---------------------------

---

**Description**

Read a jplace file

**Usage**

```
read_jplace(jplace_file, full = TRUE)
```

**Arguments**

jplace_file	A jplace file name
full	If set to FALSE, only the tree is read from the jplace file

**Details**

When the jplace or sqlite files are imported into R, the node numbering available in the original file is converted to the class "phylo" numbering. The class phylo is defined in the "ape" package.

**Value**

A list with

arbre	The tree in class "phylo" over which placements are performed
placement	The placement table
multiclass	The multiclass table
run	The command line used to obtain the jplace file

**Author(s)**

pierre lefeuvre

**See Also**

read\_sqlite

---

read_protodb	<i>Read Protein Data Bank (PDB) file</i>
--------------	--

---

**Description**

Read Protein Data Bank (PDB) file

**Usage**

```
read_protodb(X)
```

**Arguments**

X                    The path/name of a pdb file.

**Value**

The output is a list of objects

header	The header of the pdb file
compound	A data frame summarizing the CMPND part of the pdb file. This include the molecule ID, the molecule name and the chain ID
atom	A data frame with the atom type, the amino acid, the amino acid number, the chain and the euclidian X, Y, Z coordinates of the atoms
sequence	A list with the numbering of the amino acid and the amino acid sequence for each chain

**Author(s)**

pierre lefeuvre

**References**

<http://www.rcsb.org/pdb/home/home.do>

**Examples**

```
pdb_file <- system.file("extdata", "1L2M.pdb", package = "BoSSA")
pdb <- read_protodb(pdb_file)
pdb
```

---

read_sqlite	<i>Read a pplacer/guppy sqlite file</i>
-------------	---

---

**Description**

Read a pplacer/guppy sqlite file

**Usage**

```
read_sqlite(sqlite_file, jplace_file=gsub("sqlite$", "jplace", sqlite_file),
rank="species")
```

**Arguments**

sqlite_file	A pplacer/guppy sqlite path/file name
jplace_file	An optionnal jplace file name. By default, the sqlite file name with the suffix changed from "sqlite" to jplace" is used. If different, the jplace path/name must be specified.
rank	The desired taxonomic assignation rank to extract. default is "species".

**Details**

As the tree informations are not available in the sqlite file, the jplace file is also required. When the jplace or sqlite files are import into R, the node numbering available in the original file is converted to the class "phylo" numbering.

**Value**

A list with

runs	The command line used to obtained the sqlite file
taxa	The taxonomic information table
multiclass	The multiclass table
placement_positions	A data frame with the posiotn of each placement in the reference tree
arbre	The tree in class "phylo" over wich placements are performed
edge_key	A matrix with correspondance of node numbering between the original tree in the jplace file and the class phylo tree of the "arbre" component
original_tree	The tree string from the jplace file

For details on the other components (i.e. "placements", "placement\_classifications", "placement\_evidence", "placement\_median\_identities", "placement\_names", "placement\_nbc", "placements", "ranks" and "sqlite\_sequence", please, refer to [http://erick.matsen.org/pplacer/generated\\_rst/guppy\\_classify.html](http://erick.matsen.org/pplacer/generated_rst/guppy_classify.html))

**Author(s)**

pierre lefeuvre

## References

[http://erick.matsen.org/pplacer/generated\\_rst/guppy\\_classify.html](http://erick.matsen.org/pplacer/generated_rst/guppy_classify.html)

## Examples

```
### the path to the sqlite and jplace files
sqlite_file <- system.file("extdata", "example.sqlite", package = "BoSSA")
jplace_file <- system.file("extdata", "example.jplace", package = "BoSSA")
jplace <- read_sqlite(sqlite_file, jplace_file)
```

---

refpkg

*Summary data and plots for reference packages*

---

## Description

Summary data and plots for reference packages

## Usage

```
refpkg(refpkg_path, type="summary", rank_tree="species",
rank_pie=c("phylum", "class", "order", "family", "genus"),
scale_pie=TRUE, alpha_order=TRUE, cex.text=0.7,
cex.legend=1, asb=TRUE, rotate_label=TRUE,
out_krona="for_krona.txt", text2krona=NULL)
```

## Arguments

refpkg_path	The path of the reference package directory
type	The type of summary to perform with "summary", "taxonomy", "info", "tree", "pie" or "krona" available
rank_tree	The desired rank for tree coloring
rank_pie	The ranks to be plot for the taxonomy pie chart
scale_pie	Whether or not to take into account the number of sequences available within the reference package for the pie chart
alpha_order	Whether or not the color should follow taxa alphabetic order when type set to "tree"
cex.text	The tip labels cex parameter when type is set to "tree" and the text cex parameter when type is set to "pie"
cex.legend	The size of the legend when type set to "tree"
asb	Add a scale bar on the tree
rotate_label	Rotates the pie slice labels
out_krona	The name of the output file when type is set to "krona".
text2krona	The full path to the krona "ImportText.pl" script when KronaTools is installed and you wish to directly produce the html krona file.

**Value**

A summary print on screen when type set to "summary". A data frame when type set to "taxonomy" or "info". A file written to the disk when type is set to "krona". A plot otherwise.

**Author(s)**

pierre lefeuvre

**References**

<https://github.com/marbl/Krona/wiki/KronaTools> <http://fhcrc.github.io/taxtastic/>

**Examples**

```
refpkg_path <- paste(find.package("BoSSA"), "/extdata/example.refpkg", sep="")

### summary
refpkg(refpkg_path)

### taxonomy
taxonomy <- refpkg(refpkg_path, type="taxonomy")
head(taxonomy)

### info
refpkg(refpkg_path, type="info")

### tree
refpkg(refpkg_path, type="tree", rank_tree="order", cex.text=0.5)

### pie
refpkg(refpkg_path, type="pie", rank_pie=c("class", "order", "family"), cex.text=0.6)

### krona
# it will produce a flat text file
# this file can be use as input for the the "ImportText.pl" krona script
# see https://github.com/marbl/Krona/wiki/KronaTools for more details on krona
## Not run:
refpkg(refpkg_path, type="krona", out_krona="for_krona.txt")

## End(Not run)
```

---

sub\_pplace

*Subsets a pplace object*


---

**Description**

Subsets a pplace or jplace object based on the placement\_id, the name of the placement or a regular expression of the name of the placement

**Usage**

```
sub_pplace(x, placement_id = NULL, ech_id = NULL, ech_regexp = NULL, run_id = NULL)
```

**Arguments**

x	The pplace or jplace object to subset
placement_id	A vector of the placement_id to subset
ech_id	A vector of the names of the placement to subset
ech_regexp	A regular expression of the name of the placement to subset
run_id	A vector of run_id to subset

**Details**

When using placement\_id, the subset is performed based on the placement\_id column of the multiclass, placements, placement\_positions, placement\_names, placement\_classifications, placement\_evidence, placement\_median\_identities and placement\_nbc data frames. When using ech\_id and ech\_regexp, the subset is performed from the multiclass\$name column. When using run\_id, the subset is performed based on the placements\$run\_id column.

**Value**

A pplace object

**Author(s)**

pierre lefeuvre

**Examples**

```
data(pplace)

### subsetting using placement ids. Here placements 1 to 5
sub1 <- sub_pplace(pplace,placement_id=1:5)
sub1

### subsetting using sequenes ids
id <- c("GWZHISEQ01:514:HMCLFBCXX:2:1108:1739:60356_90",
"GWZHISEQ01:514:HMCLFBCXX:2:1114:13665:31277_80")
sub2 <- sub_pplace(pplace,ech_id=id)
sub2

### subsetting using a regular expression of sequence ids
sub3 <- sub_pplace(pplace,ech_regexp="^HWI")
sub3
```



---

write_jplace	<i>Write a jplace or pplace object to the disk</i>
--------------	--

---

**Description**

Write a jplace or pplace object to the disk in the jplace JSON format

**Usage**

```
write_jplace(x,outfile)
```

**Arguments**

x	A pplace or jplace object
outfile	The name of the output file

**Note**

Note that the placement mass (potentially) available from the original files are imported into R but aren't use in the analysis. Anyway, the write\_jplace function takes into account possible weight/mass information available in the the "nm" column of the multiclass table for jplace objects and in the "mass" column from the placement\_names table for the pplace objects. The values in these column can be edited before writing the jplace file if one want to use distinct mass/weight in downstream analysis (e.g. using the guppy program functionalities).

**Author(s)**

pierre lefeuvre

**Examples**

```
data(pplace)
## Not run:
write_jplace(pplace,"test.jplace")

## End(Not run)
```

# Index

BoSSA (BoSSA-package), [2](#)  
BoSSA-package, [2](#)

[circular\\_tree](#), [3](#)

[plot.jplace](#) ([plot.pplace](#)), [4](#)  
[plot.pplace](#), [4](#)  
[pplace](#), [6](#)  
[pplace\\_to\\_matrix](#), [6](#)  
[pplace\\_to\\_table](#), [8](#)  
[pplace\\_to\\_taxonomy](#), [9](#)  
[print.jplace](#) ([print.pplace](#)), [9](#)  
[print.pplace](#), [9](#)  
[print.protdb](#), [10](#)

[read\\_jplace](#), [11](#)  
[read\\_protdb](#), [12](#)  
[read\\_sqlite](#), [13](#)  
[refpkg](#), [14](#)

[sub\\_pplace](#), [15](#)

[write\\_jplace](#), [17](#)