

# Taxonomic classification using **pplacer**, *clst*, and *clstutils*

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## 1 Introduction

This vignette assumes that you have already created a reference package, and have used it to run **pplacer** against an alignment of reference sequences. For instruction on performing the above operations, see the documentation for **pplacer** here: <http://matsen.fhcrc.org/pplacer/>

## 2 Input files

The following input is required (file names defined as variables in parentheses):

1. a reference package (**refpkg**)
2. a **pplacer** file created using the same reference package (**placefile**)
3. a file providing distances between nodes in the reference tree (**distfile**)

Note that **distfile** is generated from **placefile** using **placeutil** (distributed with **pplacer**).

```
> library(clstutils)
> expand <- function(fname){
+   orig.dir <- getwd()
+   destdir <- tempdir()
+   setwd(destdir)
+   archive <- system.file('extdata', 'vaginal_16s.refpkg.tar.bz2', package='clstutils')
+   system(sprintf('tar --no-same-owner -xjf "%s"', archive))
+   setwd(orig.dir)
+   file.path(destdir, fname)
+ }
> refpkg <- expand('vaginal_16s.refpkg')
> placefile <- system.file('extdata', 'merged.json', package='clstutils')
> distfile <- system.file('extdata', 'merged.distmat.bz2', package='clstutils')
```

### 3 Reading the input

Classification requires a matrix representation of distances between “objects” being classified, in this case sequences in a phylogenetic tree. `treeDists` returns a list containing matrix representations of distances between internal and terminal edges (`$dists` and `$paths`), and `$dmat`, a square matrix of distances between terminal edges.

```
> treedists <- treeDists(distfile=distfile, placefile=placefile)
```

We also need a description of the taxonomy of the reference sequences. This is read from the reference package using `taxonomyFromRefpkg`. The `seqnames` argument ensures that the output is arranged in an order compatible with `treedists`. We indicate that the most specific rank that we want to consider is “species” using `lowest_rank`.

```
> taxdata <- taxonomyFromRefpkg(refpkg, seqnames=rownames(treedists$dmat), lowest_rank='species')
```

### 4 Classification of a single sequence

Given the distances and taxonomic information describing the reference tree, the only additional data required to perform classification is the position of a sequence placed onto a tree. At a minimum, this consists of a `data.frame` with columns `at`, `edge`, and `branch`. This data will be used to generate a vector of branch lengths between the query sequence and each of the reference sequences on the tree.

```
> placetab <- data.frame(at=49, edge=5.14909e-07, branch=5.14909e-07)
```

The function `classifyPlacements` is a wrapper around `clst::classifyIter`. The output is a `data.frame` describing the taxonomic assignment, along with a description of the confidence of the classification. See the man page for `clst::classify` for details on the output.

```
> cdata <- classifyPlacements(taxdata, treedists, placetab)
```

```
> cdata
```

	tax_id	tax_name	rank	below	above	score	match	min	median	max
1	2702	Gardnerella vaginalis	species	10	0	0.95	1	0	0.06	0.1
	d	at								
1	0.16	49								