

# Package ‘speedytax’

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**Title** Rapidly Import Classifier Results into 'phyloseq'

**Version** 1.0.4

**Description** Import classification results from the 'RDP Classifier' (Ribosomal Database Project), 'USEARCH syntax,' 'vsearch syntax' and the 'QIIME2' (Quantitative Insights into Microbial Ecology) classifiers into 'phyloseq' tax\_table objects.

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**Imports** dplyr, phyloseq, Rcpp, stringr, tibble, tidyr

**Encoding** UTF-8

**RoxygenNote** 7.3.1

**LinkingTo** Rcpp

**NeedsCompilation** yes

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**Repository** CRAN

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`import_qiime2_tax_table`*Import QIIME2 Classification Table*

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## Description

Import taxonomy results exported from the QIIME2 Bayesian classifiers

## Usage

```
import_qiime2_tax_table(in_file)
```

## Arguments

`in_file`            A tab-delimited classification table output by QIIME2

## Details

This function expects up to 7 ranks (Domain, Phylum, Class, Order, Family, Genus and Species) but determines the number actually in the file.

Depending on how the QIIME2 classifier is built, the ranks in the Taxon field of the classification result may be separated by a semicolon or by a semicolon plus a space. This function correctly parses the Taxon field in both cases.

## Value

A phyloseq `tax_table` object

## References

Bolyen E, Rideout JR, Dillon MR, Bokulich NA, *et al.* 2019. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat Biotechnol* 37:852-857.

## Examples

```
## Example with ranks in Taxon field separated by semicolon plus a space.
taxonomy_file <- system.file("extdata", "qiime2_table.tsv", package = "speedytax")
example_tax_table <- import_qiime2_tax_table(in_file = taxonomy_file)
example_tax_table
## Example with ranks in Taxon field separated by semicolon only.
taxonomy_file <- system.file("extdata", "qiime2_table_a.tsv", package = "speedytax")
example_tax_table <- import_qiime2_tax_table(in_file = taxonomy_file)
example_tax_table
```

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import\_rdp\_tax\_table *Import RDP Classifier Taxonomy Table*

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### Description

Imports fixed rank taxonomy files created with the RDP Classifier

### Usage

```
import_rdp_tax_table(in_file, confidence)
```

### Arguments

in_file	A fix-rank tab-delimited text file output by the RDP Classifier
confidence	The confidence level for filtering the taxonomy

### Details

The RDP Classifier must be given the option `-f fixrank` (or `--format fixrank`) in order for this importer to work correctly.

A confidence value of 0.8 for is recommended for full-length 16S rRNA gene sequences and a value of 0.5 is recommended for shorter amplicons.

### Value

A phyloseq `tax_table` object

### References

Wang Q, Garrity GM, Tiedje JM, Cole JR. 2007. Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Appl Environ Microbiol* 73:5261-5267.

### Examples

```
taxonomy_file <- system.file("extdata", "rdp_table.tsv", package = "speedytax")
example_tax_table <- import_rdp_tax_table(in_file = taxonomy_file)
example_tax_table
```

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`import_sintax_tax_table`*Import SINTAX Taxonomy Table*

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**Description**

Imports taxonomy files created with USEARCH and vsearch sintax commands

**Usage**

```
import_sintax_tax_table(in_file, confidence)
```

**Arguments**

<code>in_file</code>	A fix-rank tab-delimited text file output by SINTAX
<code>confidence</code>	The confidence level for filtering the taxonomy (0.8 by default)

**Details**

This function works with both vsearch and USEARCH sintax results.

A confidence value of 0.8 is recommended for full-length 16S rRNA gene sequences and a value of 0.5 is recommended for shorter amplicons.

**Value**

A phyloseq `tax_table` object

**References**

Rognes T, Flouri T, Nichols B, Quince C, Mahé F. (2016) VSEARCH: a versatile open source tool for metagenomics. PeerJ 4:e2584. doi: 10.7717/peerj.2584

Edgar RC (2016) SINTAX: a simple non-Bayesian taxonomy classifier for 16S and ITS sequences. bioRxiv. doi:10.1101/074161

**Examples**

```
# With a vsearch sintax result
taxonomy_file <- system.file("extdata", "vsearch_sintax_table.tsv", package = "speedytax")
example_tax_table <- import_sintax_tax_table(in_file = taxonomy_file)
example_tax_table
# With a USEARCH sintax result
taxonomy_file <- system.file("extdata", "usearch_sintax_table.tsv", package = "speedytax")
example_tax_table <- import_sintax_tax_table(in_file = taxonomy_file)
example_tax_table
```

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read_tax_example	<i>Get path to example taxonomy files</i>
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**Description**

Access the files in speedyseq's inst/extdata sub-directory

**Usage**

```
read_tax_example(file = NULL)
```

**Arguments**

file                   Name of file to return.

**Value**

Returns the full path to the requested file from the package sub-directory inst/extdata if it exists, or a list of the files in the directory if no file is specified.

**Examples**

```
read_tax_example()  
read_tax_example("rdp_table.tsv")
```

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simple_cap	<i>Simple Capitalization</i>
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**Description**

Simple Capitalization

**Usage**

```
simple_cap(x)
```

**Arguments**

x                      A string or vector of strings

**Value**

The string with every word capitalized

**Examples**

```
simple_cap("an old dog learning new tricks")
```

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