

# Package ‘TaxSEA’

June 16, 2025

**Type** Package

**Title** Taxon Set Enrichment Analysis

**Version** 1.0.0

**Description** TaxSEA is an R package for Taxon Set Enrichment Analysis, which utilises a Kolmogorov-Smirnov test analyses to investigate differential abundance analysis output for whether there are alternations in a-priori defined sets of taxa from five previously published databases (BugSigDB, MiMeDB, GutMGene, mBodyMap and GMRepoV2). TaxSEA takes as input a list of taxonomic identifiers (e.g. species names, NCBI IDs etc.) and a rank (E.g. fold change, correlation coefficient). TaxSEA be applied to any microbiota taxonomic profiling technology (array-based, 16S rRNA gene sequencing, shotgun metagenomics & metatranscriptomics etc.) and enables researchers to rapidly contextualize their findings within the broader literature to accelerate interpretation of results.

**License** GPL-3

**Encoding** UTF-8

**LazyData** false

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**biocViews** Microbiome, Metagenomics, Sequencing, GeneSetEnrichment, RNASeq

**URL** <https://github.com/feargalr/taxsea>

**BugReports** <https://github.com/feargalr/taxsea/issues>

**Depends** R (>= 4.5.0)

**Suggests** BiocStyle, bugsigdbr, fgsea, knitr, rmarkdown, testthat

**Imports** stats, utils

**Config/testthat/edition** 3

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|--------------------|-------------------------------------------------------------|
| get_ncbi_taxon_ids | <i>Retrieve NCBI Taxonomy IDs for a list of taxon names</i> |
|--------------------|-------------------------------------------------------------|

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Description

This function takes a vector of taxon names and returns a vector of NCBI taxonomy IDs by querying the NCBI Entrez API.

Usage

```
get_ncbi_taxon_ids(taxon_names)
```

Arguments

taxon\_names      A character vector of taxon names

Value

A character vector of NCBI taxonomy IDs corresponding to the input taxon names

Examples

```
taxon_names <- c("Escherichia coli", "Staphylococcus aureus")  
taxon_ids <- get_ncbi_taxon_ids(taxon_names)
```

---

`get_taxon_sets`*Retrieve Taxon Sets from TaxSEA Library*

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**Description**

Retrieve from the TaxSEA database which taxon sets (metabolite producers and disease signatures) contain a taxon of interest.

**Usage**

```
get_taxon_sets(taxon_to_fetch = taxon)
```

**Arguments**

`taxon_to_fetch` The taxon to search for in the TaxSEA database.

**Value**

A character vector containing the names of taxonomic sets where the specified taxon is present.

**Examples**

```
# Retrieve sets for Bifidobacterium longum
get_taxon_sets(taxon="Bifidobacterium_longum")
```

---

`NCBI_ids`*NCBI IDs Dataset*

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**Description**

A dataset for mapping NCBI IDs to species/genus names. This named vector allows for lookup of NCBI IDs associated with species or genus names.

**Usage**

```
NCBI_ids
```

**Format**

A named vector where:

**names** NCBI IDs

**values** Species or genus names

**Source**

NCBI

**Examples**

```
data(NCBI_ids)
# Can look up either with or without spaces
NCBI_ids["Bifidobacterium_breve"]
NCBI_ids["Bifidobacterium breve"]
```

TaxSEA

*TaxSEA: Taxon Set Enrichment Analysis***Description**

TaxSEA enables rapid annotation of changes by testing for enrichment of pre-defined taxon sets.

**Usage**

```
TaxSEA(
  taxon_ranks,
  lookup_missing = FALSE,
  min_set_size = 5,
  max_set_size = 100,
  custom_db = NULL
)
```

**Arguments**

|                |                                                                                       |
|----------------|---------------------------------------------------------------------------------------|
| taxon_ranks    | A named vector of log2 fold changes between control and test groups.                  |
| lookup_missing | Logical indicating whether to fetch missing NCBI IDs. Default is FALSE.               |
| min_set_size   | Minimum size of taxon sets to include in the analysis. Default is 5.                  |
| max_set_size   | Maximum size of taxon sets to include in the analysis. Default is 100.                |
| custom_db      | A user-provided list of taxon sets. If NULL (default), the built-in database is used. |

**Value**

A list of data frames with taxon set enrichment results.

**See Also**

- <https://doi.org/10.1093/nar/gkac868> for MiMeDB
- <https://doi.org/10.1093/nar/gkab1019> for GMrepo
- <https://doi.org/10.1093/nar/gkab786> for gutMGene
- <https://doi.org/10.1038/s41587-023-01872-y> for BugSigDB

Examples

```
data("TaxSEA_test_data")
taxsea_results <- TaxSEA(TaxSEA_test_data)
```

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|           |                                                                                                                                              |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------|
| TaxSEA_db | <i>TaxSEA Database A dataset containing taxon sets. Each item in the list is a taxon set, and each member within a taxon set is a taxon.</i> |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------|

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Description

TaxSEA Database A dataset containing taxon sets. Each item in the list is a taxon set, and each member within a taxon set is a taxon.

Usage

```
TaxSEA_db
```

Format

A list of vectors. Each vector contains character strings representing taxa.

Source

See READ ME.

Examples

```
data(TaxSEA_db)
all_sets <- names(TaxSEA_db)
GABA_producers<-TaxSEA_db[["MiMeDB_producers_of_GABA"]]
```

---

|                  |                         |
|------------------|-------------------------|
| TaxSEA_test_data | <i>TaxSEA Test Data</i> |
|------------------|-------------------------|

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Description

A dataset containing taxon ranks and taxon IDs.

Usage

```
TaxSEA_test_data
```

**Format**

A data frame with two columns:

**rank** Character vector representing taxon ranks

**id** Character vector representing taxon IDs

**Source**

See READ ME.

**Examples**

```
data(TaxSEA_test_data)
test_results <- TaxSEA(TaxSEA_test_data)
```

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