Taxa and metacoder: R packages for parsing, visualization, and manipulation of taxonomic data

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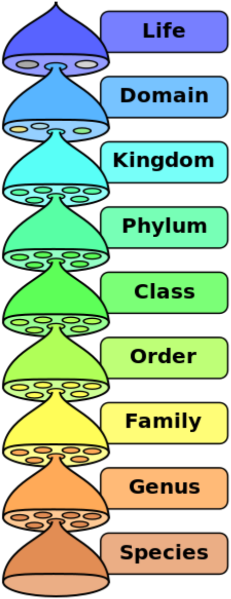
The challenges of taxonomic data



- Taxonomic data is hierarchical
- Associated with tabular data
- Can be names, classifications, or IDs
- Many different taxonomic systems
- Many different data formats
- Hierarchical visualization is difficult

Sources of taxonomic data

DNA sequence databases

NCBI National Center for Biotechnology Information

unite

green genes
16S rRNA gene database and workbench compatible with ARB
greengenes.lbl.gov

Species occurrence databases

GBIF
Global Biodiversity Information Facility

iNaturalist.org

ATLAS OF LIVING AUSTRALIA
sharing biodiversity knowledge

Museum records

Smithsonian

北京自然博物馆
Beijing Museum of Natural History

NATURAL HISTORY MUSEUM

Sources of taxonomic data: DNA sequences

NCBI Genbank

AC073210.8 Homo sapiens BAC clone RP11-460N20 from 7, complete sequence

UNITE

SH099456.05FU_FJ357315_refs k__Fungi;p__Ascomycota;c__Dothideomycetes
;o__Pleosporales;f__Pleosporaceae;g__Embellisia;s__Embellisia_planifunda

RDP

S000448483 Sparassis crispa; MBUH-PIRJO&ILKKA94-1587/ss5
Lineage=Root;rootrank ;Fungi;domain;Basidiomycota;phylum;Agaricomycetes;
class;Polyporales;order ;Sparassidaceae;family;Sparassis;genus

SILVA

GCVF01000431.1.2369
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales
;Alcanivoraceae;Alcanivorax;Thalassiosira rotula

Sources of taxonomic data: Occurrence records

Global Biodiversity Information Facility : Archea database

```r
readr::read_tsv("datasets/gbif_archea.csv")[4:8]
```

```
# A tibble: 19,013 x 5
   kingdom phylum        class        order             family
   <chr>   <chr>         <chr>        <chr>             <chr>
 1 Archaea Euryarchaeota Halobacteria Halobacteriales   Halobacteriaceae
 2 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 3 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 4 Archaea Crenarchaeota Thermoprotei Desulfurococcales Desulfurococcaceae
 5 Archaea Crenarchaeota Thermoprotei Desulfurococcales Pyrodictiaceae
 6 Archaea Crenarchaeota Thermoprotei Thermoproteales   Thermoproteaceae
 7 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 8 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 9 Archaea Euryarchaeota Halobacteria Halobacteriales   Halobacteriaceae
10 Archaea Euryarchaeota Halobacteria Halobacteriales   Halobacteriaceae
# ... with 19,003 more rows
```

Sources of taxonomic data: Museum records

Smithsonian Museum of Natural History: Mammal database

```r
readr::read_csv("datasets/SNMNH.csv")[9]
```

```
# A tibble: 5,000 x 1
   `Name Hierarchy`
   <chr>
 1 Abditomys latidens : Muridae : Rodentia : Mammalia : Chordata
 2 Abrawayaomys ruschii : Cricetidae : Rodentia : Mammalia : Chordata
 3 Abrawayaomys ruschii : Cricetidae : Rodentia : Mammalia : Chordata
 4 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 5 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 6 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 7 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 8 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 9 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
10 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
# ... with 4,990 more rows
```

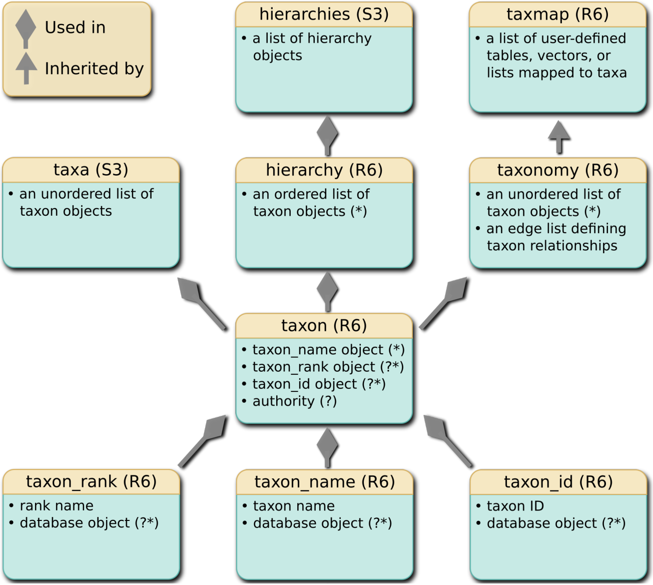
The `taxa` package

build passing | codecov 87% | repo status WIP | downloads 311/month | CRAN 0.2.1

The `taxa` package is designed to be a solid foundation for using taxonomic data in R.

- R6 classes to hold taxa, taxonomies, and associated data
- Flexible parsers to convert raw data to these classes
- Dplyr-inspired functions to manipulate these classes
- Functions to get data associated with each taxon in a taxonomy

Classes defined by `taxa`: Relationships



hierarchies (S3)
- a list of hierarchy objects

taxmap (R6)
- a list of user-defined tables, vectors, or lists mapped to taxa

taxa (S3)
- an unordered list of taxon objects

hierarchy (R6)
- an ordered list of taxon objects (*)

taxonomy (R6)
- an unordered list of taxon objects (*)
- an edge list defining taxon relationships

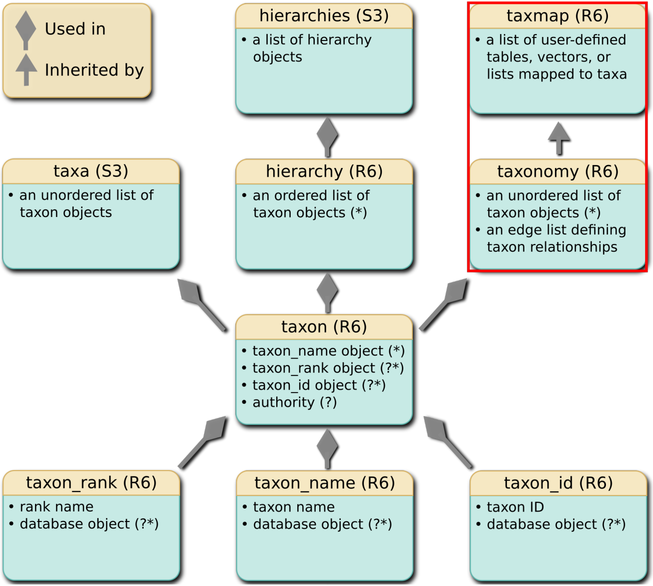
taxon (R6)
- taxon_name object (*)
- taxon_rank object (?*)
- taxon_id object (?*)
- authority (?)

taxon_rank (R6)
- rank name
- database object (?*)

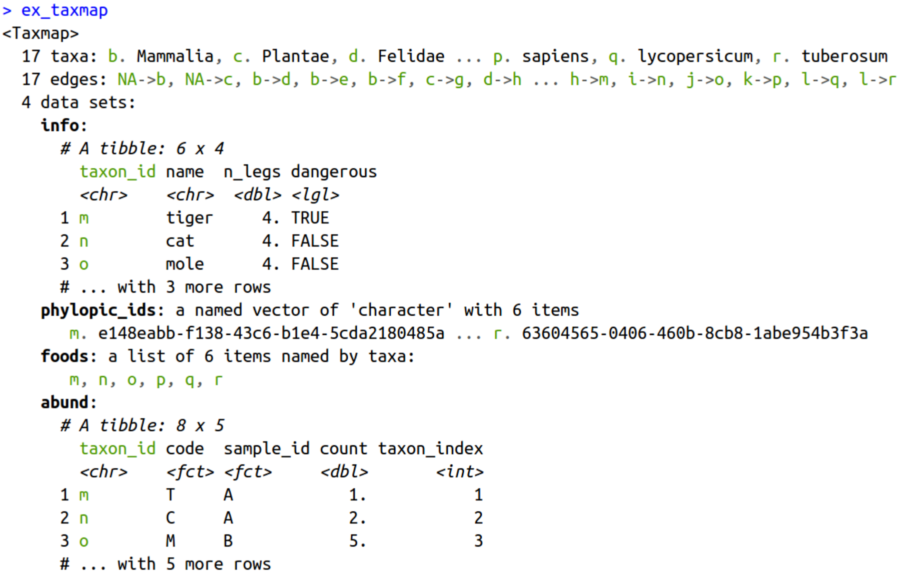
taxon_name (R6)
- taxon name
- database object (?*)

taxon_id (R6)
- taxon ID
- database object (?*)

Classes defined by `taxa`: Relationships



Classes defined by `taxa`: The `taxmap` class



```
> ex_taxmap
<Taxmap>
  17 taxa: b. Mammalia, c. Plantae, d. Felidae ... p. sapiens, q. lycopersicum, r. tuberosum
  17 edges: NA->b, NA->c, b->d, b->e, b->f, c->g, d->h ... h->m, i->n, j->o, k->p, l->q, l->r
  4 data sets:
    info:
      # A tibble: 6 x 4
        taxon_id name  n_legs dangerous
        <chr>    <chr>  <dbl> <lgl>
      1 m        tiger     4. TRUE
      2 n        cat       4. FALSE
      3 o        mole      4. FALSE
      # ... with 3 more rows
    phylopic_ids: a named vector of 'character' with 6 items
       m. e148eabb-f138-43c6-b1e4-5cda2180485a ... r. 63604565-0406-460b-8cb8-1abe954b3f3a
    foods: a list of 6 items named by taxa:
       m, n, o, p, q, r
    abund:
      # A tibble: 8 x 5
        taxon_id code  sample_id count taxon_index
        <chr>    <fct> <fct>     <dbl>       <int>
      1 m        T     A            1.           1
      2 n        C     A            2.           2
      3 o        M     B            5.           3
      # ... with 5 more rows
```

Parsing

		Input data format		
		Simple	Embedded	Raw string
		> print(data) [1] "**input_1**" "**input_2**" [3] "**input_3**"	> print(data) x input y 1 a **input_1** 100 2 b **input_2** 200 3 c **input_3** 300	> print(data) [1] ">id:a-tax:**input_1**" [2] ">id:b-tax:**input_2**" [3] ">id:c-tax:**input_3**"
Input type	Classification Primates;Hominidae;Homo;sapiens	> print(data) [1] "Primates;Hominidae;Hom... [2] "Primates;Haplorhini;Cr... > **parse_tax_data**(data, class_sep = ";")	> print(data) x class y 1 a Primates;Hominidae;... 100 2 b Primates;Haplorhini... 200 > **parse_tax_data**(data, class_cols = "class", class_sep = ";")	> print(data) [1] ">id:a-tax:Primates;Hom..." [2] ">id:b-tax:Primates;Hap..." > **extract_tax_data**(data, regex = ">id:(.+)-tax:(.+)", key = c("info", "class"), class_sep = ";")
	Taxon ID 9606	> print(data) [1] "9606" "100937" ... > **lookup_tax_data**(data, type = "taxon_id")	> print(data) x id y 1 a 9606 100 2 b 100937 200 > **lookup_tax_data**(data, type = "taxon_id", column = "id")	> print(data) [1] ">id:a-tax:9606" [2] ">id:b-tax:100937" > **extract_tax_data**(data, regex = ">id:(.+)-tax:(.+)", key = c("info", "taxon_id"), database = "ncbi")
	Taxon name Homo sapiens	> print(data) [1] "Homo sapiens" [2] "Primates" ... > **lookup_tax_data**(data, type = "taxon_name")	> print(data) x name y 1 a Homo sapiens 100 2 b Primates 200 > **lookup_tax_data**(data, type = "taxon_name", column = "name")	> print(data) [1] ">id:a-tax:Homo sapiens" [2] ">id:b-tax:Primates" > **extract_tax_data**(data, regex = ">id:(.+)-tax:(.+)", key = c("info","taxon_name"), database = "ncbi")
	Sequence ID AC073210	> print(data) [1] "AC073210" "KC312885" ... > **lookup_tax_data**(data, type = "seq_id")	> print(data) x ncbi_id y 1 a AC073210 100 2 b KC312885 200 > **lookup_tax_data**(data, type = "seq_id", column = "ncbi_id")	> print(data) [1] ">id:a-tax:AC073210" [2] ">id:b-tax:KC312885" > **extract_tax_data**(data, regex = ">id:(.+)-tax:(.+)", key = c("info","seq_id"), database = "ncbi")

Parsing: vectors of classifications

```r
x <- c("Mammalia;Theria;Metatheria;Diprotodontia;Macropodiformes",
       "Mammalia;Theria;Eutheria;Primates;Haplorrhini;Simiiformes")

parse_tax_data(x, class_sep = ";")
```

```
<Taxmap>
  9 taxa: b. Mammalia, c. Theria ... j. Simiiformes
  9 edges: NA->b, b->c, c->d, c->e, d->f, e->g, f->h, g->i, i->j
  1 data sets:
    tax_data: a named vector of 'character' with 2 items
       h. Mammalia;Theria;[truncated] ... j. Mammalia;Theria;[truncated]
  0 functions:
```

Parsing: vectors of names

```r
x <- c("Homo sapiens", "Macropus", "Chordata")

lookup_tax_data(x, type = "taxon_name", database = "ncbi")
```

```
<Taxmap>
  35 taxa: 131567. cellular organisms ... 9606. Homo sapiens
  35 edges: NA->131567, 131567->2759 ... 207598->9605, 9605->9606
  2 data sets:
    tax_data:
      # A tibble: 35 x 4
        taxon_id ncbi_name          ncbi_rank    ncbi_id
        <chr>    <chr>              <chr>        <chr>
      1 131567   cellular organisms no rank      131567
      2 2759     Eukaryota          superkingdom 2759
      3 33154    Opisthokonta       no rank      33154
      # ... with 32 more rows
    query_data: a named vector of 'character' with 3 items
       9606. Homo sapiens, 9312. Macropus, 7711. Chordata
  0 functions:
```

Parsing: vectors of taxon IDs

```r
x <- c("9606", "207598", "7711") # NCBI taxon IDs

lookup_tax_data(x, type = "taxon_id", database = "ncbi")
```

```
<Taxmap>
  31 taxa: 131567. cellular organisms ... 9606. Homo sapiens
  31 edges: NA->131567, 131567->2759 ... 207598->9605, 9605->9606
  2 data sets:
    tax_data:
      # A tibble: 31 x 4
        taxon_id ncbi_name          ncbi_rank    ncbi_id
        <chr>    <chr>              <chr>        <chr>
      1 131567   cellular organisms no rank      131567
      2 2759     Eukaryota          superkingdom 2759
      3 33154    Opisthokonta       no rank      33154
      # ... with 28 more rows
    query_data: a named vector of 'character' with 3 items
       9606. 9606, 207598. 207598, 7711. 7711
  0 functions:
```

Parsing: vectors of sequence IDs

```r
x <- c("AC073210", "MG014608", "AE006468") # NCBI sequence IDs

lookup_tax_data(x, type = "seq_id", database = "ncbi")
```

```
<Taxmap>
  46 taxa: 131567. cellular organisms ... 9606. Homo sapiens
  46 edges: NA->131567, 131567->2759 ... 207598->9605, 9605->9606
  2 data sets:
    tax_data:
      # A tibble: 46 x 4
        taxon_id ncbi_name          ncbi_rank    ncbi_id
        <chr>    <chr>              <chr>        <chr>
      1 131567   cellular organisms no rank      131567
      2 2759     Eukaryota          superkingdom 2759
      3 33154    Opisthokonta       no rank      33154
      # ... with 43 more rows
    query_data: a named vector of 'character' with 3 items
       9606. AC073210, 9316. MG014608, 99287. AE006468
  0 functions:
```

Parsing: tables

Global Biodiversity Information Facility : Archea database

```
readr::read_tsv("datasets/gbif_archea.csv")[4:8]
```

```
# A tibble: 19,013 x 5
   kingdom phylum        class        order             family
   <chr>   <chr>         <chr>        <chr>             <chr>
 1 Archaea Euryarchaeota Halobacteria Halobacteriales   Halobacteriaceae
 2 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 3 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 4 Archaea Crenarchaeota Thermoprotei Desulfurococcales Desulfurococcaceae
 5 Archaea Crenarchaeota Thermoprotei Desulfurococcales Pyrodictiaceae
 6 Archaea Crenarchaeota Thermoprotei Thermoproteales   Thermoproteaceae
 7 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 8 Archaea Euryarchaeota Thermococci  Thermococcales    Thermococcaceae
 9 Archaea Euryarchaeota Halobacteria Halobacteriales   Halobacteriaceae
10 Archaea Euryarchaeota Halobacteria Halobacteriales   Halobacteriaceae
# ... with 19,003 more rows
```

Parsing: tables

```r
x = readr::read_tsv("datasets/gbif_archea.csv")

parse_tax_data(x, class_cols = 4:8)
```

```
<Taxmap>
  95 taxa: ab. Archaea, ac. Euryarchaeota ... dr. Methermicoccaceae
  95 edges: NA->ab, ab->ac, ab->ad ... aw->dp, at->dq, ax->dr
  1 data sets:
    tax_data:
      # A tibble: 19,013 x 45
        taxon_id  gbifid datasetkey occurrenceid kingdom phylum class
        <chr>      <int> <chr>      <chr>        <chr>   <chr>  <chr>
      1 br        1.84e9 3c6e7390-~ D7C42A39-3A~ Archaea Eurya~ Halo~
      2 bs        1.83e9 863efcc4-~ <NA>         Archaea Eurya~ Ther~
      3 bs        1.83e9 863efcc4-~ <NA>         Archaea Eurya~ Ther~
      # ... with 1.901e+04 more rows, and 38 more variables:
      #   order <chr>, family <chr>, genus <chr>, species <chr>,
      #   infraspecificepithet <chr>, taxonrank <chr>,
      #   scientificname <chr>, countrycode <chr>, locality <chr>,
      #   publishingorgkey <chr>, ...
  0 functions:
```

Parsing: tables

Smithsonian Museum of Natural History: Mammal database

```r
readr::read_csv("datasets/SNMNH.csv")[9]
```

```
# A tibble: 5,000 x 1
   `Name Hierarchy`
   <chr>
 1 Abditomys latidens : Muridae : Rodentia : Mammalia : Chordata
 2 Abrawayaomys ruschii : Cricetidae : Rodentia : Mammalia : Chordata
 3 Abrawayaomys ruschii : Cricetidae : Rodentia : Mammalia : Chordata
 4 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 5 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 6 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 7 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 8 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
 9 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
10 Abrocoma bennettii bennettii : Abrocomidae : Rodentia : Mammalia : Chordata
# ... with 4,990 more rows
```

Parsing: tables

```
x = readr::read_csv("datasets/SNMNH.csv")

parse_tax_data(x, class_cols = "Name Hierarchy",
               class_sep = " : ", class_reversed = TRUE)
```

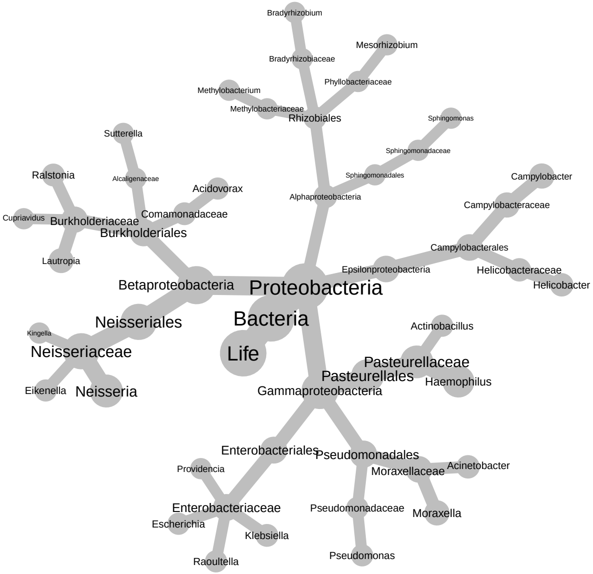
```
<Taxmap>
  141 taxa: ab. Chordata ... fl. Allactaga williamsi
  141 edges: NA->ab, ab->ac, ac->ad ... ay->fj, ay->fk, ay->fl
  1 data sets:
    tax_data:
      # A tibble: 5,000 x 53
        taxon_id Museum `Museum Abbreviation` `Catalog Number`
        <chr>    <chr>  <chr>                 <chr>
      1 az       <NA>   USNM                  357244
      2 ba       <NA>   USNM                  552416
      3 ba       <NA>   USNM                  <NA>
      # ... with 4,997 more rows, and 49 more variables: `Special
      #   Collections` <chr>, `Kind of Object` <chr>, `Specimen
      #   Count` <int>, `Current Identification` <chr>, `Other
      #   Identifications` <chr>, `Name Hierarchy` <chr>,
      #   Order <chr>, Family <chr>, `Type Status` <chr>, `Type
      #   Citations` <chr>, ...
  0 functions:
```

Parsing: complex strings (NCBI Genbank)

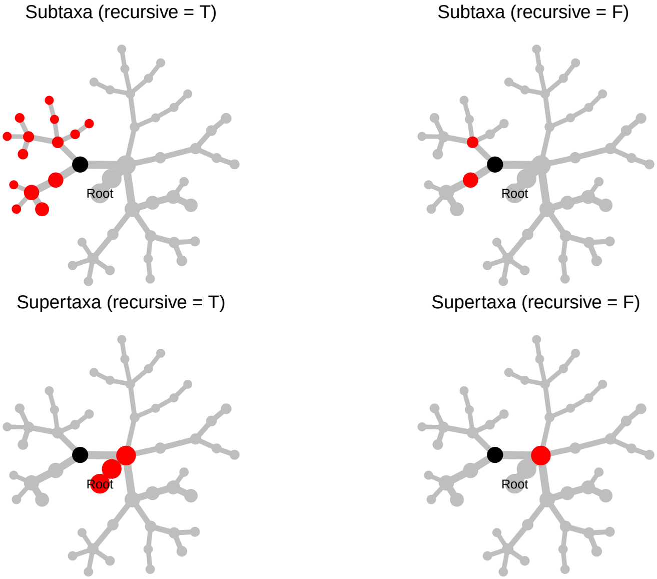
```
x = c("AC073210.8 Homo sapiens BAC clone RP11-460N20 from 7, complete sequence"
      "AE006468.2 Salmonella enterica subsp. enterica serovar Typhimurium",
      "MG014608.1 Macropus fuliginosus Csf1r gene, enhancer")

extract_tax_data(x, database = "ncbi", regex = "([A-Z0-9.]+) (.+)",
                 key = c(my_ncbi_id = "seq_id", my_desc = "info"))
```

```
<Taxmap>
  46 taxa: 131567. cellular organisms ... 9606. Homo sapiens
  46 edges: NA->131567, 131567->2759 ... 207598->9605, 9605->9606
  2 data sets:
    tax_data:
      # A tibble: 46 x 4
        taxon_id ncbi_name          ncbi_rank    ncbi_id
        <chr>    <chr>              <chr>        <chr>
      1 131567   cellular organisms no rank      131567
      2 2759     Eukaryota          superkingdom 2759
      3 33154    Opisthokonta       no rank      33154
      # ... with 43 more rows
    query_data:
      # A tibble: 3 x 4
        taxon_id my_ncbi_id my_desc              input
        <chr>    <chr>      <chr>                <chr>
      1 9606     AC073210.8 Homo sapiens BAC cl~ AC073210.8 Homo sap~
      2 99287    AE006468.2 Salmonella enterica~ AE006468.2 Salmonel~
```

Taxonomy terminology



Taxonomy terminology: subtaxa and supertaxa

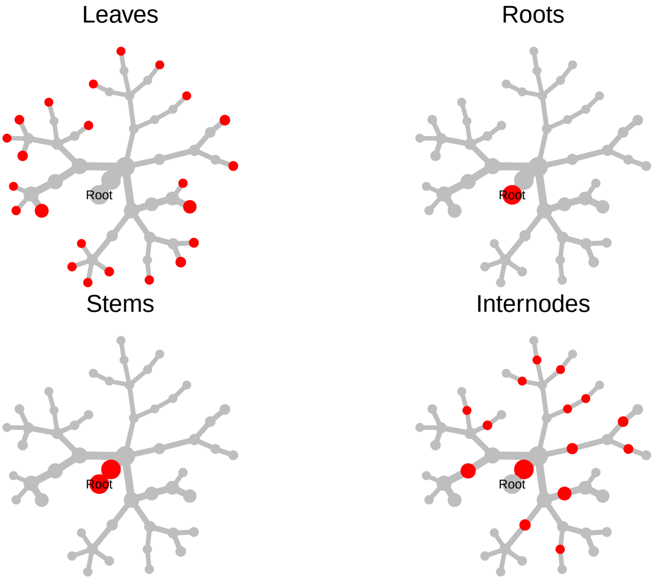

Subtaxa (recursive = T)

Subtaxa (recursive = F)

Supertaxa (recursive = T)

Supertaxa (recursive = F)

Taxonomy terminology: parts of a tree



Leaves

Roots

Stems

Internodes

Manipulating

Here is the example object that will be used:

```
print(obj)
```

```
<Taxmap>
  17 taxa: b. Mammalia, c. Plantae ... q. lycopersicum, r. tuberosum
  17 edges: NA->b, NA->c, b->d, b->e ... j->o, k->p, l->q, l->r
  3 data sets:
    info:
      # A tibble: 6 x 4
        taxon_id name  n_legs dangerous
        <chr>    <chr>  <dbl> <lgl>
      1 m        tiger     4. TRUE
      2 n        cat       4. FALSE
      3 o        mole      4. FALSE
      # ... with 3 more rows
    phylopic_ids: a named vector of 'character' with 6 items
       m. e148eabb-f138-43[truncated] ... r. 63604565-0406-46[truncated]
    foods: a list of 6 items named by taxa:
       m, n, o, p, q, r
  1 functions:
    reaction
```

Manipulating: Subsetting the taxonomy

Subset taxonomy and data to one taxon:

```r
filter_taxa(obj, taxon_names == "Plantae", subtaxa = TRUE)
```

```
<Taxmap>
  5 taxa: c. Plantae, g. Solanaceae, l. Solanum, q. lycopersicum, r. tuberosum
  5 edges: NA->c, c->g, g->l, l->q, l->r
  3 data sets:
    info:
      # A tibble: 2 x 4
        taxon_id name   n_legs dangerous
        <chr>    <chr>   <dbl> <lgl>
      1 q        tomato     0. FALSE
      2 r        potato     0. FALSE
    phylopic_ids: a named vector of 'character' with 2 items
       q. b6400f39-345a-47[truncated] ... r. 63604565-0406-46[truncated]
    foods: a list of 2 items named by taxa:
       q, r
  1 functions:
    reaction
```

Manipulating: Subsetting the taxonomy

Subset taxonomy to one rank:

```
filter_taxa(obj, taxon_ranks == "family", supertaxa = TRUE)
```

```
<Taxmap>
  6 taxa: b. Mammalia, c. Plantae ... f. Hominidae, g. Solanaceae
  6 edges: NA->b, NA->c, b->d, b->e, b->f, c->g
  3 data sets:
    info:
      # A tibble: 6 x 4
        taxon_id name  n_legs dangerous
        <chr>    <chr>  <dbl> <lgl>
      1 d        tiger     4. TRUE
      2 d        cat       4. FALSE
      3 e        mole      4. FALSE
      # ... with 3 more rows
    phylopic_ids: a named vector of 'character' with 6 items
       d. e148eabb-f138-43[truncated] ... g. 63604565-0406-46[truncated]
    foods: a list of 6 items named by taxa:
       d, d, e, f, g, g
  1 functions:
    reaction
```

Manipulating: Subsetting user data

Subset data and remove any taxa not in subset:

```
filter_obs(obj, "info", n_legs == 4, drop_taxa = TRUE)
```

```
<Taxmap>
  9 taxa: b. Mammalia, d. Felidae ... n. catus, o. typhlops
  9 edges: NA->b, b->d, b->e, d->h, d->i, e->j, h->m, i->n, j->o
  3 data sets:
    info:
      # A tibble: 3 x 4
        taxon_id name  n_legs dangerous
        <chr>    <chr>  <dbl> <lgl>
      1 m        tiger     4. TRUE
      2 n        cat       4. FALSE
      3 o        mole      4. FALSE
    phylopic_ids: a named vector of 'character' with 3 items
       m. e148eabb-f138-43[truncated] ... o. 11b783d5-af1c-4f[truncated]
    foods: a list of 3 items named by taxa:
       m, n, o
  1 functions:
    reaction
```

Manipulating: Adding user data

Add a column to a dataset:

```
mutate_obs(obj, "info", bipedal = n_legs == 2)
```

```
<Taxmap>
  17 taxa: b. Mammalia, c. Plantae ... q. lycopersicum, r. tuberosum
  17 edges: NA->b, NA->c, b->d, b->e ... j->o, k->p, l->q, l->r
  3 data sets:
    info:
      # A tibble: 6 x 5
        taxon_id name  n_legs dangerous bipedal
        <chr>    <chr>  <dbl> <lgl>     <lgl>
      1 m        tiger     4. TRUE      FALSE
      2 n        cat       4. FALSE     FALSE
      3 o        mole      4. FALSE     FALSE
      # ... with 3 more rows
    phylopic_ids: a named vector of 'character' with 6 items
       m. e148eabb-f138-43[truncated] ... r. 63604565-0406-46[truncated]
    foods: a list of 6 items named by taxa:
       m, n, o, p, q, r
  1 functions:
    reaction
```

Manipulating: Adding user data

Add a new dataset:

```
mutate_obs(obj, "new_data", n_obs)
```

```
<Taxmap>
  17 taxa: b. Mammalia, c. Plantae ... q. lycopersicum, r. tuberosum
  17 edges: NA->b, NA->c, b->d, b->e ... j->o, k->p, l->q, l->r
  4 data sets:
    info:
      # A tibble: 6 x 4
        taxon_id name  n_legs dangerous
        <chr>    <chr>  <dbl> <lgl>
      1 m        tiger     4. TRUE
      2 n        cat       4. FALSE
      3 o        mole      4. FALSE
      # ... with 3 more rows
    phylopic_ids: a named vector of 'character' with 6 items
       m. e148eabb-f138-43[truncated] ... r. 63604565-0406-46[truncated]
    foods: a list of 6 items named by taxa:
       m, n, o, p, q, r
    new_data: a named vector of 'numeric' with 17 items
       b. 4, c. 2, d. 2, e. 1, f. 1 ... n. 1, o. 1, p. 1, q. 1, r. 1
  1 functions:
    reaction
```

Manipulating: values accessible to NSE

The following can be used in manipulation functions as if they were independent variables:

- Functions that return per-taxon information
- User-defined table columns
- User-defined vectors and lists
- User-defined functions

```
unname(all_names(obj))
```

```
 [1] "taxon_names"     "taxon_ids"       "taxon_indexes"   "classifications"
 [5] "n_supertaxa"     "n_supertaxa_1"   "n_subtaxa"       "n_subtaxa_1"    
 [9] "n_leaves"        "n_leaves_1"      "taxon_ranks"     "is_root"        
[13] "is_stem"         "is_branch"       "is_leaf"         "is_internode"   
[17] "n_obs"           "n_obs_1"         "name"            "n_legs"         
[21] "dangerous"       "phylopic_ids"    "foods"           "reaction"       
```

Taxon attributes

There are a set of functions for transforming the hierarchical information in a taxonomy into per-taxon information named by taxon IDs.

Ranks, names, and IDs

`taxon_names`, `taxon_ranks`, `taxon_ids`

Parts of the tree

`branches`, `internodes`, `leaves`, `roots`, `stems`, `supertaxa`, `subtaxa`

Numbers of supertaxa/subtaxa/data

`n_supertaxa`, `n_subtaxa`, `n_obs`, `n_supertaxa_1`, `n_subtaxa_1`, `n_obs_1`

Taxon attributes: Ranks, names, and IDs

These are derived from the list of taxon objects.

```r
taxon_names(ex_taxmap) %>% head
```

```
             b              c              d              e              f 
    "Mammalia"      "Plantae"      "Felidae" "Notoryctidae"    "Hominidae" 
             g 
  "Solanaceae" 
```

```r
taxon_ranks(ex_taxmap) %>% head
```

```
        b         c         d         e         f         g 
  "class" "kingdom"  "family"  "family"  "family"  "family" 
```

```r
taxon_ids(ex_taxmap) %>% head
```

```
  b   c   d   e   f   g 
"b" "c" "d" "e" "f" "g" 
```

Taxon attributes: Parts of the tree

These return a list of vectors named by taxon IDs.

```r
subtaxa(ex_taxmap, value = "taxon_names")[1:3]
```

```
$b
             d              h              m              i              n 
     "Felidae"     "Panthera"       "tigris"        "Felis"        "catus" 
             e              j              o              f              k 
"Notoryctidae"   "Notoryctes"     "typhlops"    "Hominidae"         "homo" 
             p 
     "sapiens" 

$c
             g              l              q              r 
  "Solanaceae"      "Solanum" "lycopersicum"    "tuberosum" 

$d
         h          m          i          n 
"Panthera"   "tigris"    "Felis"    "catus" 
```

Taxon attributes: Parts of the tree

These return a list of vectors named by taxon IDs.

```
subtaxa(ex_taxmap, value = "taxon_names", recursive = FALSE)[1:3]
```

```
$b
             d              e              f 
     "Felidae" "Notoryctidae"    "Hominidae" 

$c
           g 
"Solanaceae" 

$d
         h          i 
"Panthera"    "Felis" 
```

Taxon attributes: Parts of the tree

Any value accessible to NSE can be returned, including user-defined data.

```
subtaxa(ex_taxmap, value = "taxon_ranks", recursive = FALSE)[1:3]
```

```
$b
       d        e        f 
"family" "family" "family" 

$c
       g 
"family" 

$d
      h       i 
"genus" "genus" 
```

Taxon attributes: Parts of the tree

There are a set that return logical vectors for filtering.

```r
is_leaf(ex_taxmap)
```

```
    b     c     d     e     f     g     h     i     j     k     l     m     n 
FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE 
    o     p     q     r 
 TRUE  TRUE  TRUE  TRUE 
```

```r
is_root(ex_taxmap)
```

```
    b     c     d     e     f     g     h     i     j     k     l     m     n 
 TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE 
    o     p     q     r 
FALSE FALSE FALSE FALSE 
```

Taxon attributes: counts

These return counts of things per taxon.

```
n_subtaxa(ex_taxmap)
```

```
 b  c  d  e  f  g  h  i  j  k  l  m  n  o  p  q  r 
11  4  4  2  2  3  1  1  1  1  2  0  0  0  0  0  0 
```

```
n_supertaxa(ex_taxmap)
```

```
b c d e f g h i j k l m n o p q r 
0 0 1 1 1 1 2 2 2 2 2 3 3 3 3 3 3 
```

```
n_obs(ex_taxmap, "info")
```

```
b c d e f g h i j k l m n o p q r 
4 2 2 1 1 2 1 1 1 1 2 1 1 1 1 1 1 
```

```
n_obs(ex_taxmap, "abund")
```

```
b c d e f g h i j k l m n o p q r 
8 0 4 2 2 0 2 2 2 2 0 2 2 2 2 0 0 
```

Taxon attributes: counts

The *_1 variants return non-recursive counts.

```r
n_subtaxa_1(ex_taxmap)
```

```
b c d e f g h i j k l m n o p q r
3 1 2 1 1 1 1 1 1 1 2 0 0 0 0 0 0
```

```r
n_supertaxa_1(ex_taxmap)
```

```
b c d e f g h i j k l m n o p q r
0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```r
n_obs_1(ex_taxmap, "info")
```

```
b c d e f g h i j k l m n o p q r
0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1
```

```r
n_obs_1(ex_taxmap, "abund")
```

```
b c d e f g h i j k l m n o p q r
0 0 0 0 0 0 0 0 0 0 0 2 2 2 2 0 0
```

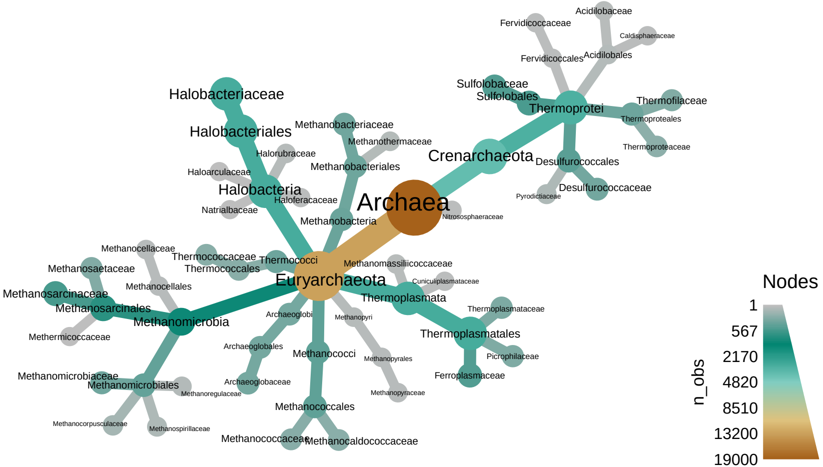
Compatiblity with other packages

`taxa` is still being developed, but we hope it will become a foundation for an ecosystem of R packages that use taxonomic data.

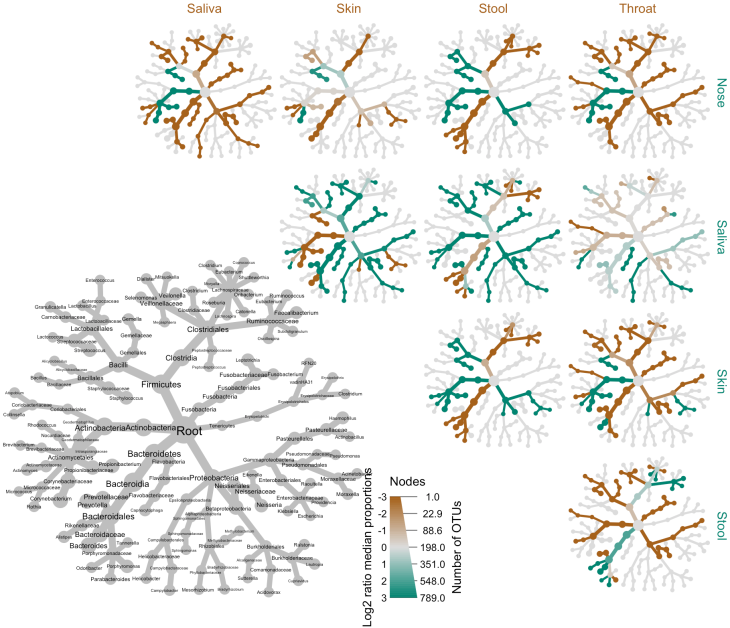
- Flexible parsers can read most formats
- Working on making ‘taxize‘ compatible with ‘taxa‘
- Fully compatible with ‘metacoder‘

Metacoder: visulization of taxonomic data

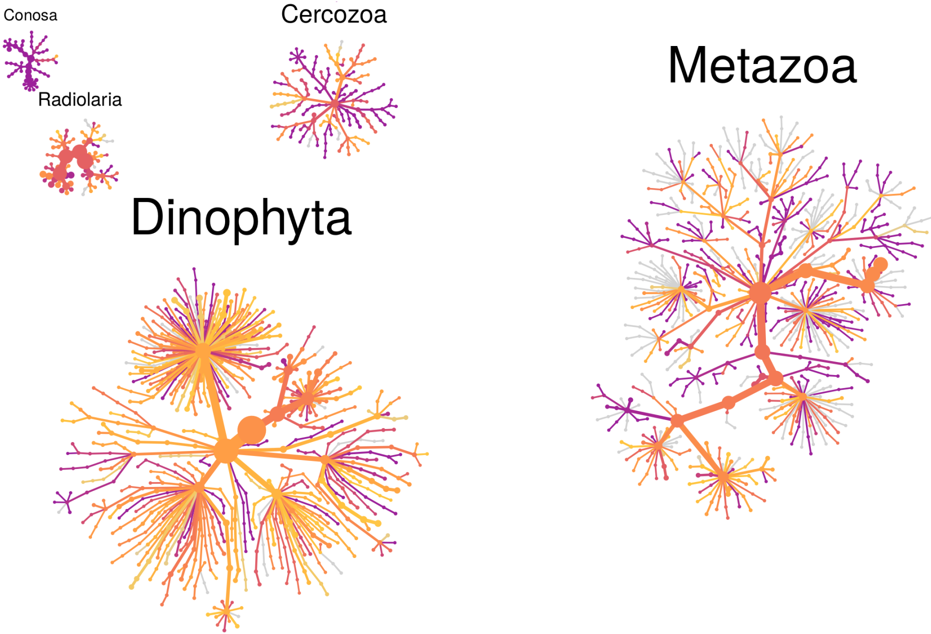
```
readr::read_tsv("datasets/gbif_archea.csv") %>%
  parse_tax_data(class_cols = 4:8) %>%
  filter_taxa(taxon_names != "") %>%
  heat_tree(node_label = taxon_names, node_color = n_obs,
            node_size = n_obs, layout = "da")
```



Metacoder: visulization of taxonomic data



Metacoder: visulization of taxonomic data



Thanks for listening!

Questions?