taxa: An R package for taxonomic data

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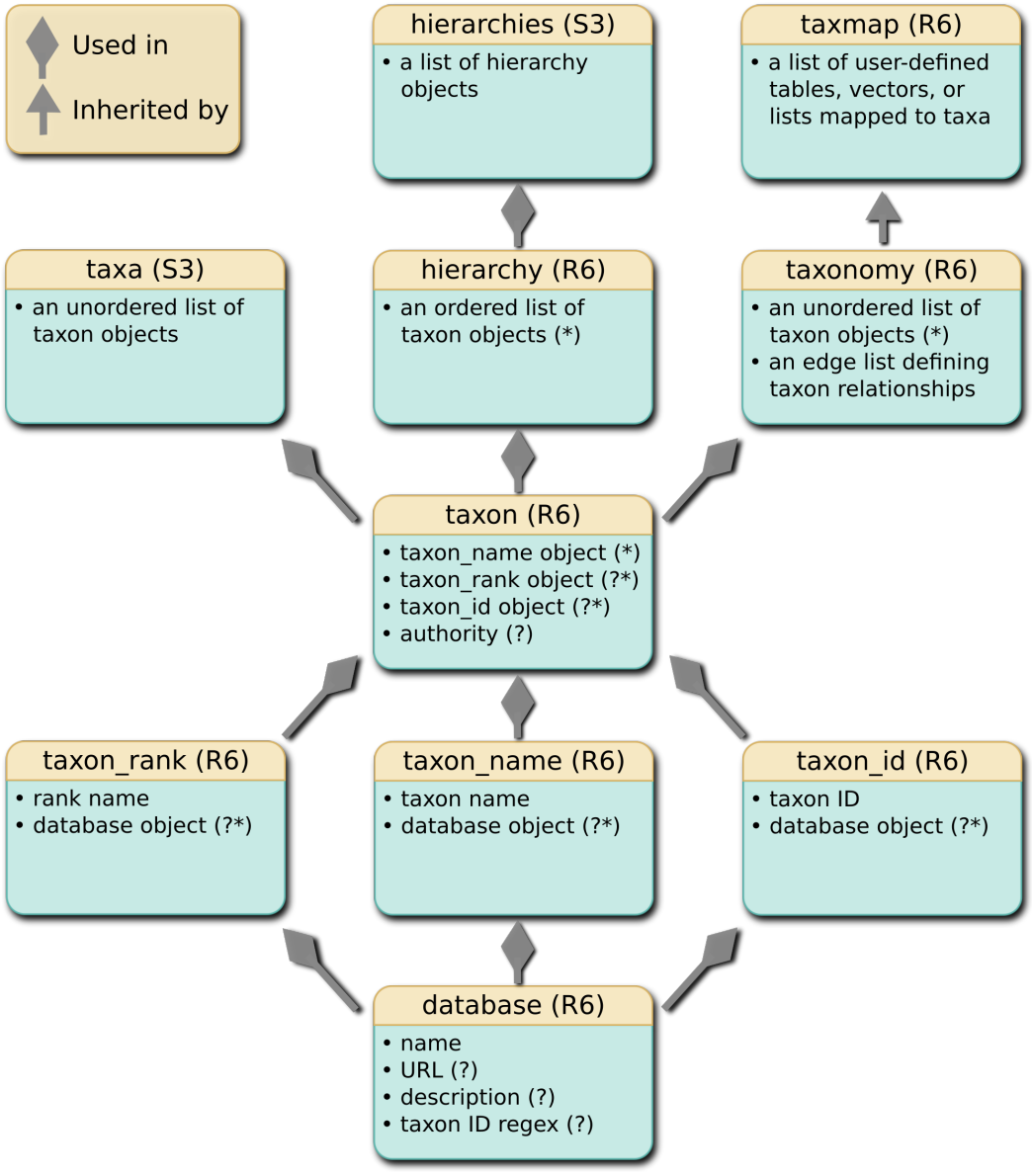
The challenges of taxonomic data

- Taxonomic data is hierarchical
- It is often associated with other data
- "Taxa" can be names, classifications of names, or IDs
- Each source of taxonomic data formats things differently

Database	FASTA sequence header format
UNITE	Lachnum_sp|JQ347180|SH189775.06FU|reps|k__Fungi;p__Ascomycota;c__Leotiomycetes;o__Helotial…
Genbank	gi|626414534|ref|NR_119473.1| Lysurus cruciatus MA Fungi 26792 ITS region; from TYPE mater…
PR2	10-044.1.1773|Eukaryota|Stramenopiles|Stramenopiles_X|Oomycota|Oomycota_X|Oomycota_XX|Oomy…
RDP	S001191995 uncultured archaeon; LCDARCH35 Lineage=Root;rootrank;Archaea;domain;“Euryarchaeo…
ITS1	AF455489_ITS1_GB|Lecanicillium aphanocladii|132584| ITS1 located by Genbank annotation, 18…

What taxa provides

- Classes to hold taxa, taxonomies, and associated data
- Flexible parsers to convert raw data to these classes
- Dplyr-inspired functions to manipulate these classes
- A flexible base for other packages to use



taxmap: user-defined data mapped to a taxonomy

```
> ex_taxmap
<Taxmap>
  17 taxa: b. Mammalia, c. Plantae, d. Felidae ... q. lycopersicum, r. tuberosum
  17 edges: NA->b, NA->c, b->d, b->e, b->f, c->g ... 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-f138-43[truncated] ... r. 63604565-0406-46[truncated]
    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
  1 functions:
    reaction
```

Reading data from diverse formats

Input data format

Input type

	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"`

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")`

Dplyr-like manipulation of taxonomic data

Subset taxonomy and data to one taxon:

```
filter_taxa(x, taxon_names == "Plantae", subtaxa = TRUE)
```

Subset taxonomy to one rank:

```
filter_taxa(x, taxon_ranks == "genus", supertaxa = TRUE)
```

Subset data and remove any taxa not in subset:

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

Add a column to a dataset:

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