

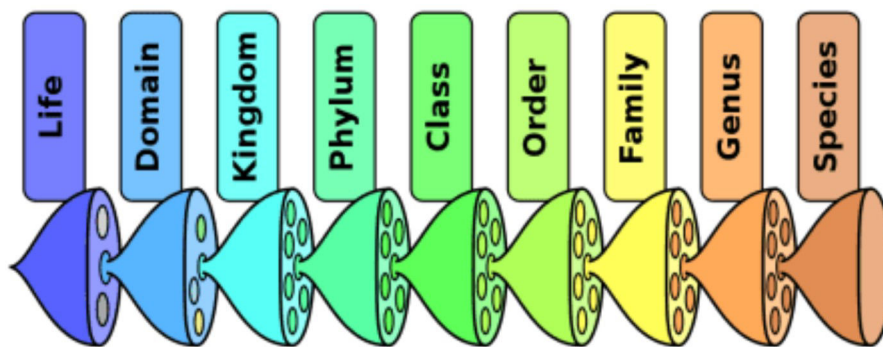
Taxonomic Rank

The [Linnaean Taxonomy](#) is a hierarchical classification system for organisms devised by Carl Linnaeus. An organism is assigned to the following levels in the hierarchy (in increasing order of granularity):

- domain
- kingdom
- phylum
- class
- order
- family
- genus and
- species.

The relative level of a group of organisms in this hierarchy determines its [taxonomic rank](#).

💡 The Linnaean Taxonomy was developed way before the idea of evolution arose. As a consequence, despite being a useful framework for classifying organisms, it does not take into account evolutionary relationships.



Taxonomic ranks. Image from [Wikipedia](#).

Let's take a look at the classification data in the `{hagr}` package.

```
library(hagr)
```

Linnaean Taxonomic Levels

We'll start at the top level, domain.

```
age %>% count(domain, sort = TRUE)
# A tibble: 1 x 2
  domain      n
1 Eukarya 4219
```

There's only one domain, [Eukarya](#), present. So we don't have any information on *Bacteria* or *Archaea* (single-celled organisms).

If we dig down one level then we find that the *Eukarya* domain consists of three kingdoms: *Animalia*, *Fungi* and *Plantae*. There's actually a fourth kingdom in *Eukarya*, *Protista*, however there's no data for it in `age`.

```
age %>% count(kingdom, sort = TRUE)
# A tibble: 3 x 2
  kingdom      n
```

```
1 Animalia  4215
2 Fungi       3
3 Plantae     1
```

It's clear that *Animalia* is the dominant kingdom, so let's focus on that exclusively.

```
animalia <- age %>% filter(kingdom == "Animalia")
```

The next level in the hierarchy is phylum.

```
animalia %>% count(phylum, sort = TRUE)
# A tibble: 7 x 2
  phylum      n
```

```
1 Chordata      4200
2 Arthropoda     8
3 Echinodermata  2
4 Porifera       2
5 Cnidaria       1
6 Mollusca       1
7 Nematoda       1
```

It appears that *Chordata* is the dominant phylum in the data, so let's further narrow our attention.

```
chordata <- animalia %>% filter(phylum == "Chordata")
```

Now let's drill all the way down to genus.

```
chordata %>% count(class, order, family, genus, sort = TRUE)
# A tibble: 2,035 x 5
  class      order      family      genus      n
1 Teleostei  Scorpaeniformes  Scorpaenidae  Sebastes    49
2 Teleostei  Perciformes     Percidae     Etheostoma  35
3 Aves       Passeriformes   Parulidae    Setophaga   23
4 Teleostei  Cypriniformes   Cyprinidae   Notropis    23
5 Mammalia   Chiroptera      Vespertilionidae  Myotis     21
6 Reptilia   Squamata        Viperidae     Crotalus    19
7 Teleostei  Perciformes     Lutjanidae    Lutjanus    18
8 Aves       Psittaciformes  Psittacidae   Amazona     17
9 Chondrichthyes  Carcharhiniformes  Carcharhinidae  Carcharhinus  17
10 Aves      Falconiformes   Falconidae    Falco       15
# ... with 2,025 more rows
```

Adding in species takes you to the most granular level in the hierarchy.

```
chordata %>% select(class, order, family, genus, species, common_name)
# A tibble: 4,200 x 6
  class      order family      genus  species  common_name
1 Amphibia Anura  Bombinatoridae Bombina  bombina  Firebelly toad
```

```

2 Amphibia Anura Bombinatoridae Bombina orientalis Oriental firebelly
toad
3 Amphibia Anura Bombinatoridae Bombina variegata Yellow-bellied
toad
4 Amphibia Anura Bufonidae Anaxyrus americanus American toad
5 Amphibia Anura Bufonidae Anaxyrus boreas Western toad
6 Amphibia Anura Bufonidae Anaxyrus canorus Yosemite toad
7 Amphibia Anura Bufonidae Anaxyrus cognatus Great plains toad
8 Amphibia Anura Bufonidae Anaxyrus debilis Green toad
9 Amphibia Anura Bufonidae Anaxyrus hemiophrys Canadian toad
10 Amphibia Anura Bufonidae Anaxyrus punctatus Red-spotted toad
# ... with 4,190 more rows

```

💡 The combination of genus and species gives the **binomial scientific name** for organisms. For example, the Killer Whale is *Orcinus orca*.

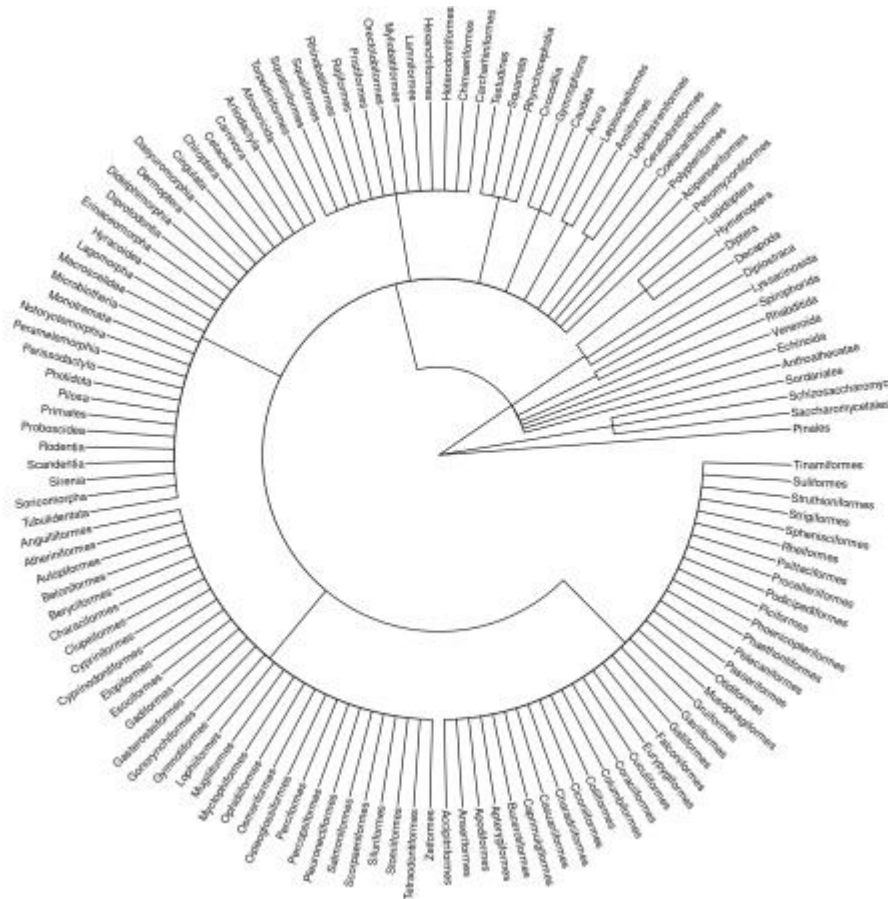
```

age %>%
  filter(str_detect(common_name, "^(Killer|Blue|Sperm) whale$")) %>%
  select(class:common_name)
# A tibble: 3 x 6
  class      order      family      genus      species
common_name
1 Mammalia Cetacea Balaenopteridae Balaenoptera musculus Blue
whale
2 Mammalia Cetacea Delphinidae Orcinus orca Killer
whale
3 Mammalia Cetacea Physeteridae Physeter macrocephalus Sperm
whale

```

Growing a Tree

We'll use `{ggtree}` to construct a phylogenetic tree from *domain* down to *order*.



The dominance of the *Chordata* phylum in the data is readily apparent! It'd be nice to include more levels in this tree, but it gets very big and rather messy.

There's such a wealth of cool information in this dataset. Really indebted to the the [Human Ageing Genomic Resources](#) project for putting it together and generously sharing it.