Programming in R Workshop

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Load packages

Load `purrr`, `tidyverse` and `dplyr` packages.

```
library(purrr)
library(tidyverse)
library(conflicted)
library(dplyr)
```

Load the Eukaryotes dataset - only have to run this once to get the data

```
eukaryotes <- read_tsv(
  file = "ftp://ftp.ncbi.nlm.nih.gov/genomes/GENOME_REPORTS/eukaryotes.txt",
  na = c("", "na", "-")
)

# Reformat dataset headers
names_new <- names(eukaryotes) |>
  str_replace_all("[#%()]", "") |>
  str_replace_all("[ /]", "_") |>
  str_to_lower()
```

```r
eukaryotes <- eukaryotes |>
  set_names(names_new)

# Save tibble
write_tsv(eukaryotes, "eukaryotes.tsv")
```

Load the saved dataset

```r
eukaryotes <- read_tsv("https://raw.githubusercontent.com/swuyts/purrr_tutorial/master/data/e
```

```
Rows: 11508 Columns: 19
-- Column specification --------------------------------------------------------
Delimiter: "\t"
chr  (10): organism_name, bioproject_accession, group, subgroup, assembly_ac...
dbl   (7): taxid, bioproject_id, size_mb, gc, scaffolds, genes, proteins
date  (2): release_date, modify_date

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

How many different organisms are there in our dataset?

```r
eukaryotes |>
  pull(organism_name) |>
  n_distinct()
```

```
[1] 6111
```

Subset dataframe by selecting variables for the analysis:

```r
eukaryotes_subset <- eukaryotes |>
     select(organism_name, group, subgroup)
```

Using `n_distinct` to each variable of eukaryotes_subset

```r
map(eukaryotes_subset, n_distinct)
```

```
$organism_name
[1] 6111

$group
[1] 5

$subgroup
[1] 19
```

```
eukaryotes_subset |>
  map(n_distinct)
```

```
$organism_name
[1] 6111

$group
[1] 5

$subgroup
[1] 19
```

Nested Tibbles

Split the eukaryotes dataset according to groups defined in the group variable:

```
eukaryotes |> pull(group) |> unique()
```

```
[1] "Other"    "Protists" "Plants"   "Fungi"    "Animals"
```

```
eukaryotes_nested <- eukaryotes |>
  group_by(group) |>
  nest()

eukaryotes_nested
```

```
# A tibble: 5 x 2
# Groups:   group [5]
  group    data
  <chr>    <list>
```

```
1 Other    <tibble [51 x 18]>
2 Protists <tibble [888 x 18]>
3 Plants   <tibble [1,304 x 18]>
4 Fungi    <tibble [6,064 x 18]>
5 Animals  <tibble [3,201 x 18]>
```

Split the "eukaryotes_nested" into 5 smaller dataframes.

```
eukaryotes_nested |> pull(data)
```

```
[[1]]
# A tibble: 51 x 18
   organism_name       taxid bioproject_accession bioproject_id subgroup size_mb
   <chr>               <dbl> <chr>                        <dbl> <chr>      <dbl>
 1 Pyropia yezoensis    2788 PRJNA589917                589917 Other      108.
 2 Thalassiosira pse~ 296543 PRJNA191                       191 Other       32.4
 3 Guillardia theta ~ 905079 PRJNA53577                   53577 Other       87.1
 4 Cyanidioschyzon m~ 280699 PRJNA10792                   10792 Other       16.5
 5 Galdieria sulphur~ 130081 PRJNA13023                   13023 Other       13.7
 6 Phaeodactylum tri~ 556484 PRJNA13152                   13152 Other       27.5
 7 Bigelowiella nata~ 753081 PRJNA47111                   47111 Other       91.4
 8 Ectocarpus silicu~   2880 PRJEA42625                   42625 Other      196.
 9 Thalassiosira oce~ 159749 PRJNA36595                   36595 Other       92.2
10 Fragilariopsis cy~ 635003 PRJNA32761                   32761 Other       80.5
# i 41 more rows
# i 12 more variables: gc <dbl>, assembly_accession <chr>, replicons <chr>,
#   wgs <chr>, scaffolds <dbl>, genes <dbl>, proteins <dbl>,
#   release_date <date>, modify_date <date>, status <chr>, center <chr>,
#   biosample_accession <chr>

[[2]]
# A tibble: 888 x 18
   organism_name       taxid bioproject_accession bioproject_id subgroup size_mb
   <chr>               <dbl> <chr>                        <dbl> <chr>      <dbl>
 1 Emiliania huxleyi~ 280463 PRJNA77753                   77753 Other P~  168.
 2 Leishmania major ~ 347515 PRJNA10724                   10724 Kinetop~   32.9
 3 Trypanosoma bruce~ 679716 PRJEA40697                   40697 Kinetop~   22.1
 4 Trypanosoma cruzi    5693 PRJNA11755                   11755 Kinetop~   89.9
 5 Entamoeba histoly~ 294381 PRJNA142                       142 Other P~   20.8
 6 Giardia intestina~   5741 PRJNA561185                561185 Other P~   11.5
 7 Eimeria tenella      5802 PRJEB4863                  224694 Apicomp~   51.9
 8 Cryptosporidium p~ 353152 PRJNA144                       144 Apicomp~    9.10
```

```
 9 Toxoplasma gondii~ 508771 PRJNA28893                  28893 Apicomp~   65.7
10 Plasmodium berghei   5821 PRJEB11993                 305111 Apicomp~   18.8
# i 878 more rows
# i 12 more variables: gc <dbl>, assembly_accession <chr>, replicons <chr>,
#   wgs <chr>, scaffolds <dbl>, genes <dbl>, proteins <dbl>,
#   release_date <date>, modify_date <date>, status <chr>, center <chr>,
#   biosample_accession <chr>

[[3]]
# A tibble: 1,304 x 18
   organism_name       taxid bioproject_accession bioproject_id subgroup size_mb
   <chr>               <dbl> <chr>                        <dbl> <chr>      <dbl>
 1 Arabidopsis thali~   3702 PRJNA10719                   10719 Land Pl~    120.
 2 Glycine max          3847 PRJNA19861                   19861 Land Pl~    979.
 3 Medicago truncatu~   3880 PRJNA10791                   10791 Land Pl~    413.
 4 Solanum lycopersi~   4081 PRJNA119                       119 Land Pl~    828.
 5 Hordeum vulgare s~ 112509 PRJEB34217                  576847 Land Pl~   4341.
 6 Oryza sativa Japo~  39947 PRJNA12269                   12269 Land Pl~    374.
 7 Triticum aestivum    4565 PRJNA392179                 392179 Land Pl~  15419.
 8 Zea mays             4577 PRJNA10769                   10769 Land Pl~   2135.
 9 Coffea arabica      13443 PRJNA506972                  506972 Land Pl~   1094.
10 Lotus japonicus     34305 PRJDA28941                   28941 Land Pl~    394.
# i 1,294 more rows
# i 12 more variables: gc <dbl>, assembly_accession <chr>, replicons <chr>,
#   wgs <chr>, scaffolds <dbl>, genes <dbl>, proteins <dbl>,
#   release_date <date>, modify_date <date>, status <chr>, center <chr>,
#   biosample_accession <chr>

[[4]]
# A tibble: 6,064 x 18
   organism_name       taxid bioproject_accession bioproject_id subgroup size_mb
   <chr>               <dbl> <chr>                        <dbl> <chr>      <dbl>
 1 Pneumocystis cari~ 1.41e6 PRJNA223511                 223511 Ascomyc~    7.66
 2 Schizosaccharomyc~ 4.90e3 PRJNA13836                   13836 Ascomyc~   12.6
 3 Saccharomyces cer~ 5.59e5 PRJNA43747                   43747 Ascomyc~   12.2
 4 Aspergillus nidul~ 2.27e5 PRJNA130                       130 Ascomyc~   30.3
 5 Aspergillus fumig~ 3.31e5 PRJNA131                       131 Ascomyc~   29.4
 6 Neurospora crassa~ 3.67e5 PRJNA13841                   13841 Ascomyc~   41.1
 7 Phanerochaete chr~ 5.31e3 PRJNA343563                 343563 Basidio~   39.2
 8 Candida albicans ~ 2.38e5 PRJNA10701                   10701 Ascomyc~   14.3
 9 Encephalitozoon c~ 2.85e5 PRJNA13833                   13833 Other F~    2.50
10 Aspergillus terre~ 3.42e5 PRJNA15631                   15631 Ascomyc~   29.4
# i 6,054 more rows
```

```
# i 12 more variables: gc <dbl>, assembly_accession <chr>, replicons <chr>,
#   wgs <chr>, scaffolds <dbl>, genes <dbl>, proteins <dbl>,
#   release_date <date>, modify_date <date>, status <chr>, center <chr>,
#   biosample_accession <chr>

[[5]]
# A tibble: 3,201 x 18
   organism_name       taxid bioproject_accession bioproject_id subgroup size_mb
   <chr>               <dbl> <chr>                        <dbl> <chr>      <dbl>
 1 Caenorhabditis br~   6238 PRJNA10731                   10731 Roundwo~   108.
 2 Caenorhabditis el~   6239 PRJNA13758                   13758 Roundwo~   100.
 3 Brugia malayi        6279 PRJNA10729                   10729 Roundwo~    93.7
 4 Aedes aegypti        7159 PRJNA392114                 392114 Insects   1279.
 5 Aedes albopictus     7160 PRJNA552090                 552090 Insects   2538.
 6 Anopheles gambiae~ 180454 PRJNA1438                     1438 Insects    265.
 7 Drosophila melano~   7227 PRJNA13669                   13669 Insects    144.
 8 Apis mellifera       7460 PRJNA477511                 477511 Insects    225.
 9 Ciona intestinalis   7719 PRJDA65419                   65419 Other A~   115.
10 Danio rerio          7955 PRJNA11776                   11776 Fishes    1679.
# i 3,191 more rows
# i 12 more variables: gc <dbl>, assembly_accession <chr>, replicons <chr>,
#   wgs <chr>, scaffolds <dbl>, genes <dbl>, proteins <dbl>,
#   release_date <date>, modify_date <date>, status <chr>, center <chr>,
#   biosample_accession <chr>
```

Combine nested tibbles and map

Count number of rows for each sub data frames

```
map(eukaryotes_nested$data, nrow)
```

```
[[1]]
[1] 51

[[2]]
[1] 888

[[3]]
[1] 1304

[[4]]
```

```
[1] 6064

[[5]]
[1] 3201
```

Create a new column using `mutate()`

```
eukaryotes_nested |>
  mutate(n_row = map_int(data, nrow))
```

```
# A tibble: 5 x 3
# Groups:   group [5]
  group    data                  n_row
  <chr>    <list>                <int>
1 Other    <tibble [51 x 18]>       51
2 Protists <tibble [888 x 18]>     888
3 Plants   <tibble [1,304 x 18]>  1304
4 Fungi    <tibble [6,064 x 18]>  6064
5 Animals  <tibble [3,201 x 18]>  3201
```

How many different organisms are there per group ?

There are two different ways:

```
# Define a custom function
n_distinct_organisms <- function(data) {

  data |>
    pull(organism_name) |>
    n_distinct()

}

# Define a custom function as a formula
# .x is the notation for the object that is given as an input to this function.
n_distinct_organisms2 <- ~ .x |>
  pull(organism_name) |>
  n_distinct()
```

Apply the function to our nested data:

```
eukaryotes_nested |>
  mutate(n_organisms = map_dbl(data,
                               n_distinct_organisms
                     ),
         n_organisms2 = map_dbl(data,
                               n_distinct_organisms2
                     )
         )
```

```
# A tibble: 5 x 4
# Groups:   group [5]
  group    data                  n_organisms n_organisms2
  <chr>    <list>                      <dbl>        <dbl>
1 Other    <tibble [51 x 18]>             35           35
2 Protists <tibble [888 x 18]>           490          490
3 Plants   <tibble [1,304 x 18]>         673          673
4 Fungi    <tibble [6,064 x 18]>        2926         2926
5 Animals  <tibble [3,201 x 18]>        1987         1987
```

We can define the functions on the fly:

```
eukaryotes_nested |>
  mutate(n_organisms = map_dbl(data,
                               ~ .x |> pull(organism_name) |> n_distinct()),
         n_centers = map_dbl(data,
                             ~ .x |> pull(center) |> n_distinct()),
         n_subgroups = map_dbl(data,
                               ~ .x |> pull(subgroup) |>  n_distinct()))
```

```
# A tibble: 5 x 5
# Groups:   group [5]
  group    data                  n_organisms n_centers n_subgroups
  <chr>    <list>                      <dbl>     <dbl>       <dbl>
1 Other    <tibble [51 x 18]>             35        34           1
2 Protists <tibble [888 x 18]>           490       265           3
3 Plants   <tibble [1,304 x 18]>         673       492           3
4 Fungi    <tibble [6,064 x 18]>        2926       950           3
5 Animals  <tibble [3,201 x 18]>        1987       769           9
```

pmap and walk2 functions

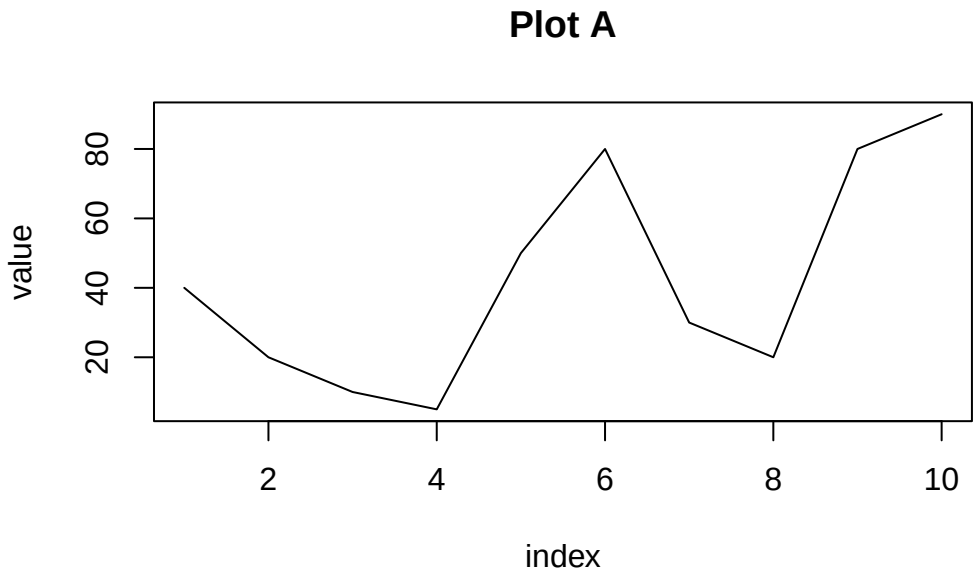
We will explain by the following example for `pmap`:

```
df <- data.frame(
  x = c("ATTTTACTGGGAGGGAA", "TATTTTTTAAAGGGCCC", "GCGCGCCCCAAATTATAGGC", "TGCCACATTTTATCCGC
  pattern = c("A", "T", "G", "C"),
  replacement = c("a", "t", "g", "c"),
  stringsAsFactors = FALSE
  )

pmap(df, gsub)
```

```
[[1]]
[1] "aTTTTaCTGGGaGGGaa"

[[2]]
[1] "tAttttttAAAGGGCCC"

[[3]]
[1] "gCgCgCCCCAAATTATAggC"

[[4]]
[1] "TGccAcATTTTATccGcGcA"
```

Example for `walk2`:

```
df1 <- data.frame(
  index = c(1,2,3,4,5,6,7,8,9,10,1,2,3,4,5,6,7,8,9,10),
  value = c(40,20,10,5,50,80,30,20,80,90,33,21,56,66,43,89,66,80,30,10),
  category = c("A","A","A","A","A","A","A","A","A","A","B","B","B","B","B","B","B","B","B","
)

df1 %>%
  split(.$category) %>%
  .[order(names(.))] %>%
  walk2(paste('Plot', names(.)),
        ~plot(value ~ index, data = .x, type = "l", main = .y))
```


Plot A
value
20
40
60
80
2
4
6
8
10
index


Plot B
value
20
40
60
80
2
4
6
8
10
index