

23 OCTOBER 2018

Herman Teirlinck, 01.72 - Kaat Tilley

```
> say("Welcome to the coding club!", "turkey")
Welcome to the coding club!
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           '. -=-' ;,}.<u>_</u>.}
            `-,_ _.'` '-._}
```

jgs `|||

.=='=,

> library(cowsay)

LOOPS

Install the package suite:

```
install.packages("tidyverse")
install.packages("rgbif")
```

Load the package suite:

```
library(tidyverse)
library(rgbif)
```

Old skool...

```
For Loop
for (variable in sequence){
   Do something
              Example
for (i in 1:4){
   i < -i + 10
   print(j)
```

New kids:

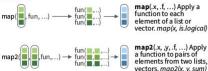
purrr

Apply functions with purrr:: cheat sheet



Apply Functions

Map functions apply a function iteratively to each element of a list





pmap(.l, .f, ...) Apply a function to groups of elements from list of lists, vectors. pmap(list(x, y, z), sum, na.rm = TRUE)



Imap(x, .f, ...) Apply function to each list-element of a list or vector. imap(x, .f, ...) Apply .f to each element of a list or vector and its index.

OUTPUT

map(), map2(), pmap(), imap and invoke map each return a list. Use a suffixed version to return the results as a specific type of flat vector, e.g. map2_chr, pmap_lgl, etc.

Use walk, walk2, and pwalk to trigger side effects. Each return its input invisibly.

function returns map chr character vector double (numeric) vector map_dbl data frame (column bind) data frame (row bind) map int integer vector logical vector walk triggers side effects, returns the input invisibly

~ .x .v becomes

function(.x, .y) .x .y, e.g.

 $map2(l, p, \sim x + y)$ becomes

map2(l, p, function(l, p) l + p)

SHORTCUTS - within a purrr function:

"name" becomes function(x) x[["name"]]. e.g. map(l, "a") extracts a from each element of /

~ .x becomes function(x) x. e.g. $map(1. \sim 2 + x)$ becomes map(l, function(x) 2 + x)

~ ..1 ..2 etc becomes function(..1, ..2, etc) ..1 ..2 etc, e.g. pmap(list(a, b, c), ~ ..3 + ..1 - ..2) becomes pmap(list(a, b, c), function(a, b, c) c + a - b

Work with Lists

FILTER LISTS



pluck(.x, ..., .default=NULL) Select an element by name or index. pluck(x."b") .or its attribute with attr getter. pluck(x,"b",attr getter("n"))



keep(.x, .p, ...) Select elements that pass a logical test. keep(x, is.na) discard(.x, .p, ...) Select elements that do not pass a



logical test. discard(x, is.na) compact(.x. .p = identity) Drop empty elements. compact(x)



head_while(.x,.p,...) Return head elements until one does not pass. Also tail while. head while(x, is.character)

RESHAPE LISTS



flatten(.x) Remove a level of indexes from a list. Also flatten chr. flatten dbl. flatten dfc, flatten dfr, flatten_int, flatten_lgl. flatten(x)



transpose(.l. .names = NULL) Transposes the index order in a multi-level list. transpose(x)

→ func(■, ■)

SUMMARISE LISTS



every(.x, .p, ...) Do all elements pass a test? every(x, is,character) elements pass a test?



some(x, is,character) has element(.x..v) Does a list contain an element? has element(x. "foo")

some(.x..p....) Do some



.p) Find first element to pass. detect(x, is.character) detect_index(.x, .f, ..., .right = FALSE, .p) Find index of first element to pass.

detect(.x, .f, ..., .right=FALSE,



detect index(x, is,character) vec depth(x) Return depth (number of levels of indexes). vec_depth(x)

JOIN (TO) LISTS



append(x, values, after = length(x)) Add to end of list. append(x, list(d = 1))



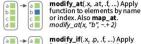
prepend(x, values, before = 1) Add to start of list. prepend(x, list(d=1))splice(...) Combine objects into a list, storing S3 objects

as sub-lists. splice(x, y, "foo")

TRANSFORM LISTS



modify(.x, .f, ...) Apply function to each element, Also map, map chr. map dbl. map dfc, map dfr, map int. map lgl. modify(x, ~, +2)



modify_if(.x, .p, .f, ...) Apply function to elements that pass a test. Also map_if. modify if(x, is.numeric, ~.+2)

modify at(.x. .at, .f. ...) Apply

modify_depth(.x,.depth,.f,...) Apply function to each element at a given level of a list. modify_depth(x, 1, ~.+ 2)

WORK WITH LISTS



array_tree(array, margin = NULL) Turn array into list. Also array branch. array tree(x, margin = 3)

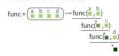


cross2(.x, .y, .filter = NULL) All combinations of .x and .y. Also cross, cross3, cross_df. cross2(1:3, 4:6)



set_names(x, nm = x) Set the names of a vector/list directly or with a function. set_names(x, c("p", "q", "r")) set_names(x, tolower)

Reduce Lists



reduce(.x..f.....init) Apply function recursively to each element of a list or vector. Also reduce_right, reduce2, reduce2_right. reduce(x, sum)

accumulate(.x, .f, ..., .init) Reduce but also return intermediate results. Also func(m, m)→ m accumulate_right. accumulate(x, sum)

Modify function behavior quietly() Modify

compose() Compose multiple functions.

lift() Change the type of input a function takes. Also lift_dl, lift_dv, lift_ld, lift_lv, lift_vd, lift_vl.

rerun() Rerun expression n times. negate() Negate a predicate function (a pipe friendly!)

partial() Create a version of a function that has some args preset to values.

safely() Modify func to return list of results and errors

output, messages, warnings. possibly() Modify function to return default value

function to return

list of results.

whenever an error occurs (instead of error).



Share your snippets and solutions during the coding session:

Go to https://hackmd.io/jwSucdiFQDCcIFSbHgLCCg and post your code in between backticks:

```
For example:
```

```
library(tidyverse)
my_data <- ...</pre>
```



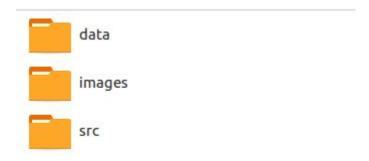
We defined a number of challenges. If you were able to achieve a challenge, add a to r laptop screen.

The objective is that everyone achieves

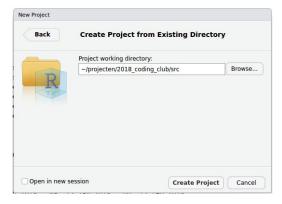


- Someone has more than you? **Ask for help!**
- Someone has less than you? **Provide help!**

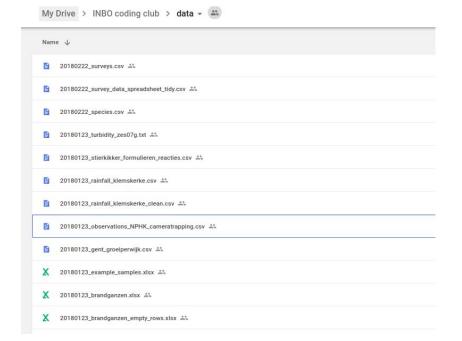
- Download coding club material and work locally, **not in sync** with the Google drive



- Create new Rstudio project in the /STC folder



- Download coding club material and work locally, not in sync with the Google drive
- Create new Rstudio project in the **src** folder...
- Use relative paths to data files!
- > library(readr)
- > read_csv2("../data/20180123_gent_groeiperwijk.csv")



For this coding club:

20180222 species.csv

```
20180522_gent_groeiperwijk_tidy.csv
```

```
for (variable in sequence){
  Do something
```

This code makes and saves a plot of the demographic evolution of Ghent's districts for year 2000.

}

```
library(readr)
groei gent df <- read csv("../data/20180522 gent groeiperwijk tidy.csv")</pre>
year plot <- groei gent df %>% filter(year == 2000) %>%
  ggplot(aes(x = wijk, y = growth)) + geom bar(stat = "identity") +
  coord flip()
ggsave(file.path("..", "images", "district evol 2000.png"), year plot)
```

How to do the same for all years from 2000 to 2003 using a for loop?





Apply function name_backbone() to a vector/list of taxa (animals in the example below).

name backbone (): lookup names in the GBIF backbone taxonomy.

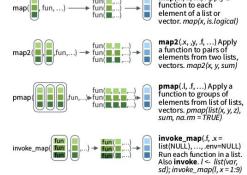
```
library (rqbif)
```

```
name backbone ("Branta", rank = "GENUS")
name backbone ("Sus", rank = "GENUS")
animals <- c("Branta", "Sus")</pre>
```

Can you get the result as a data.frame using purrr package as well?

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Use walk, walk2, and

pwalk to trigger side effects. Each return its

input invisibly.

	map	list
	map_chr	character vector
	map_dbl	double (numeric) vecto
	map_dfc	data frame (column bir
	map_dfr	data frame (row bind)
	map_int	integer vector
	map_lgl	logical vector

triggers side effects, returns the input invisibly



Apply function name backbone () to all scientific names of the species data (genus + species) and add the results (multiple columns) to original data frame df species

```
df species <- read csv("../data/20180222 species.csv")</pre>
df species %>%
    mutate(scientific name = str c(genus, species,
                                           sep = "")
```

. . .

```
# A tibble: 55 x 27
   usageKey scientificName canonicalName rank status confidence matchType kingdom phylum order family genus species
      <int> <chr>
                             <chr>
                                                                                   <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
                                             <chr> <chr>
                                                                 <int> <chr>
1 2491757 Amphispiza bi... Amphispiza b... SPEC... ACCEP...
                                                                     98 EXACT
                                                                                    Animal... Chord... Pass... Ember... Amph... Amphis...
2 2437568 Ammospermophi... Ammospermoph... SPEC... ACCEP...
                                                                     96 FUZZY
                                                                                    Animal... Chord... Rode... Sciur... Ammo... Ammosp...
3 2491123 Ammodramus sa... Ammodramus s... SPEC... ACCEP...
                                                                     98 EXACT
                                                                                    Animal... Chord... Pass... Ember... Ammo... Ammodr...
    2444480 Crotalus scut... Crotalus scu... SPEC... ACCEP...
                                                                     92 FUZZY
                                                                                    Animal... Chord... Squa... Viper... Crot... Crotal...
   8071886 Cnemidophorus... Cnemidophoru... SPEC... SYNON...
                                                                     97 EXACT
                                                                                    Animal... Chord... Squa... Teiid... Aspi... Aspido...
10 5227544 Cnemidophorus... Cnemidophoru... SPEC... SYNON...
                                                                     98 EXACT
                                                                                    Animal... Chord... Squa... Teiid... Aspi... Aspido...
# ... with 45 more rows, and 14 more variables: kingdomKevint>, phylumKey <int>, classKey <int>, orderKey <int>,
    familyKey <int>, genusKey <int>, speciesKey <int>, synonym <lql>, class <chr>, acceptedUsageKey <int>,
    species id <chr>, genus <chr>, species1 <chr>, taxa <chr>
```

Apply Functions

Map functions apply a function iteratively to each element of a list



map2(.x, ,y, .f, ...) Apply a function to pairs of elements from two lists vectors. map2(x, y, sum)

map(.x, .f, ...) Apply a function to each element of a list or



pmap(.l, .f, ...) Apply a function to groups of elements from list of lists vectors. pmap(list(x, v, z), sum. na.rm = TRUE)



list(NULL), ..., .env=NULL) Run each function in a list Also invoke. I <- list(var, sd); $invoke_map(l, x = 1:9)$

Imap(.x, .f, ...) Apply function to each list-element of a list or vector. imap(.x, .f, ...) Apply .f to each element of a list or vector and its index

OUTPUT

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Use walk, walk2, and pwalk to trigger side effects. Each return its input invisibly.

function	returns
map	list
map_chr	character vector
map_dbl	double (numeric) vector
map_dfc	data frame (column bind)
map_dfr	data frame (row bind)
map_int	integer vector
map_lgl	logical vector
walk	triggers side effects, returns
	map_chr map_dbl map_dfc map_dfr map_int map_lgl

the input invisibly



Go to https://hackmd.io/jwSucdiFQDCcIFSbHgLCCg...



Zaal: Herman Teirlinck - 01.71 - Frans Breziers

Datum: 2018-11-29, van 10:00 tot 12:00

(registration announced via DG_useR@inbo.be)