Functional programming in R

2023-04-06

purrr: A functional programming toolkit for R

Complete and consistent set of tools for working with functions and vectors

Problems we want to solve:

1. Making code clear
2. Making code safe
3. Working iteratively with lists and data frames

Lists, vectors, and data.frames (or tibbles)

```
1 c(char = "hello", num = 1)
```

```
   char      num
"hello"      "1"
```

lists can contain any object

```
1 list(char = "hello", num = 1, fun = mean)
```

```
$char
[1] "hello"

$num
[1] 1

$fun
function (x, ...)
UseMethod("mean")
<bytecode: 0x12e9afd48>
<environment: namespace:base>
```

Your Turn 1

```
measurements <- list(
  blood_glucose = rnorm(10, mean = 140, sd = 10),
  age = rnorm(5, mean = 40, sd = 5),
  heartrate = rnorm(20, mean = 80, sd = 15)
)
```

There are two ways to subset lists: dollar signs and brackets. Try to subset `blood_glucose` from `measurements` using these approaches.

Are they different? What about `measurements[["blood_glucose"]]`?

Your Turn 1

```
1 measurements["blood_glucose"]
```

```
$blood_glucose
 [1] 127.9293 142.7743 150.8444 116.5430 144.2912 145.0606
134.2526 134.5337
 [9] 134.3555 131.0996
```

```
1 measurements$blood_glucose
```

```
 [1] 127.9293 142.7743 150.8444 116.5430 144.2912 145.0606
134.2526 134.5337
 [9] 134.3555 131.0996
```

```
1 measurements[["blood_glucose"]]
```

```
 [1] 127.9293 142.7743 150.8444 116.5430 144.2912 145.0606
134.2526 134.5337
 [9] 134.3555 131.0996
```

data frames are lists

```r
x <- list(char = "hello", num = 1)
as.data.frame(x)
```

```
  char num
1 hello   1
```

data frames are lists

```
1 library(gapminder)
2 head(gapminder$pop)
```

```
[1]  8425333  9240934 10267083 11537966 13079460 14880372
```

data frames are lists

```
gapminder[1:6, "pop"]
```

```
# A tibble: 6 × 1
       pop
     <int>
1  8425333
2  9240934
3 10267083
4 11537966
5 13079460
6 14880372
```

data frames are lists

```
1 head(gapminder[["pop"]])
```

```
[1]  8425333  9240934 10267083 11537966 13079460 14880372
```

programming with functions

functions are objects, too

```
1  f <- mean
2  f
```

```
function (x, ...)
UseMethod("mean")
<bytecode: 0x12e9afd48>
<environment: namespace:base>
```

```
1  identical(mean, f)
```

```
[1] TRUE
```

programming with functions

source code of a function

```
1 mean
```

```
function (x, ...)
UseMethod("mean")
<bytecode: 0x12e9afd48>
<environment: namespace:base>
```

```
1 sd
```

```
function (x, na.rm = FALSE)
sqrt(var(if (is.vector(x) || is.factor(x)) x else as.double(x),
    na.rm = na.rm))
<bytecode: 0x118f1ec88>
<environment: namespace:stats>
```

dplyr::across()

use within **mutate()** or **summarize()** to apply function(s) to a **selection** *of* **columns!**

EXAMPLE:

```
df %>%
group_by(species) %>%
summarize(
  across(where(is.numeric), mean)
)
```

species	mass_g	age_yr	range_sqmi
pika	163	2.4	0.46
marmot	1509	3.0	0.87
marmot	2417	5.6	0.62

@allison_horst

Art by Allison Horst

mutate(across())

```
mutate(
  <DATA>,
  across(c(<VARIABLES>), list(<NAMES> = <FUNCTIONS>))
)
```

mutate(across())

```
mutate(
  diamonds,
  across(c("carat", "depth"), mean)
)
```

```
# A tibble: 53,940 × 10
   carat cut       color clarity depth table price     x     y
   <dbl> <ord>     <ord> <ord>   <dbl> <dbl> <int> <dbl> <dbl>
 1 0.798 Ideal     E     SI2      61.7    55   326  3.95  3.98
 2 0.798 Premium   E     SI1      61.7    61   326  3.89  3.84
 3 0.798 Good      E     VS1      61.7    65   327  4.05  4.07
 4 0.798 Premium   I     VS2      61.7    58   334  4.2   4.23
 5 0.798 Good      J     SI2      61.7    58   335  4.34  4.35
 6 0.798 Very G…   J     VVS2     61.7    57   336  3.94  3.96
 7 0.798 Very G…   I     VVS1     61.7    57   336  3.95  3.98
 8 0.798 Very G…   H     SI1      61.7    55   337  4.07  4.11
 9 0.798 Fair      E     VS2      61.7    61   337  3.87  3.78
10 0.798 Very G…   H     VS1      61.7    61   338  4     4.05
# … with 53,930
```

mutate(across())

```
mutate(
  diamonds,
  across(c("carat", "depth"), list(mean = mean, sd = sd))
)
```

```
# A tibble: 53,940 × 14
   carat cut       color clarity depth table price     x     y
   <dbl> <ord>     <ord> <ord>   <dbl> <dbl> <int> <dbl> <dbl>
 1  0.23 Ideal     E     SI2      61.5    55   326  3.95  3.98
 2  0.21 Premium   E     SI1      59.8    61   326  3.89  3.84
 3  0.23 Good      E     VS1      56.9    65   327  4.05  4.07
 4  0.29 Premium   I     VS2      62.4    58   334  4.2   4.23
 5  0.31 Good      J     SI2      63.3    58   335  4.34  4.35
 6  0.24 Very G…   J     VVS2     62.8    57   336  3.94  3.96
 7  0.24 Very G…   I     VVS1     62.3    57   336  3.95  3.98
 8  0.26 Very G…   H     SI1      61.9    55   337  4.07  4.11
 9  0.22 Fair      E     VS2      65.1    61   337  3.87  3.78
10  0.23 Very G…   H     VS1      59.4    61   338  4     4.05
# … with 53,930
```

mutate(across(where()))

```
mutate(
  gapminder,
  across(where(is.numeric), median)
)
```

```
# A tibble: 1,704 × 6
   country     continent  year lifeExp      pop gdpPercap
   <fct>       <fct>     <dbl>   <dbl>    <dbl>     <dbl>
 1 Afghanistan Asia       1980.    60.7 7023596.     3532.
 2 Afghanistan Asia       1980.    60.7 7023596.     3532.
 3 Afghanistan Asia       1980.    60.7 7023596.     3532.
 4 Afghanistan Asia       1980.    60.7 7023596.     3532.
 5 Afghanistan Asia       1980.    60.7 7023596.     3532.
 6 Afghanistan Asia       1980.    60.7 7023596.     3532.
 7 Afghanistan Asia       1980.    60.7 7023596.     3532.
 8 Afghanistan Asia       1980.    60.7 7023596.     3532.
 9 Afghanistan Asia       1980.    60.7 7023596.     3532.
10 Afghanistan Asia       1980.    60.7 7023596.     3532.
# … with 1,694
```

Review: `tidyselect`

Workhorse for `dplyr::select()`, `dplyr::pull()`, and `tidyr::pivot_` functions

`starts_with()`, `ends_with()`, `contains()`, `matches()`, etc.

Review: tidyselect

```
1 # column names contain a word
2 select(diabetes, ends_with("ht"))
```

```
# A tibble: 403 × 2
   height weight
    <dbl>  <dbl>
 1     62    121
 2     64    218
 3     61    256
 4     67    119
 5     68    183
 6     71    190
 7     69    191
 8     59    170
 9     69    166
10     63    202
# ℹ 393 more rows
```

```
1 # regular expression
2 select(diabetes, matches("\\d"))
```

```
# A tibble: 403 × 4
   bp.1s bp.1d bp.2s bp.2d
   <dbl> <dbl> <dbl> <dbl>
 1   118    59    NA    NA
 2   112    68    NA    NA
 3   190    92   185    92
 4   110    50    NA    NA
 5   138    80    NA    NA
 6   132    86    NA    NA
 7   161   112   161   112
 8    NA    NA    NA    NA
 9   160    80   128    86
10   108    72    NA    NA
# ℹ 393 more rows
```

mutate(across()) & summarise()

```
gapminder |>
  group_by(continent) |>
  summarise(
    across(
      c("lifeExp", "gdpPercap"),
      list(med = median,  iqr = IQR)
  ))
```

```
# A tibble: 5 × 5
  continent lifeExp_med lifeExp_iqr gdpPercap_med
  <fct>           <dbl>       <dbl>          <dbl>
1 Africa           47.8       12.0           1192.
2 Americas         67.0       13.3           5466.
3 Asia             61.8       18.1           2647.
4 Europe           72.2        5.88         12082.
5 Oceania          73.7        6.35         17983.
# ℹ 1 more variable: gdpPercap_iqr <dbl>
```

`mutate(across())` & `summarise()`

Control output names with `.names` argument

```
1 gapminder |>
2   group_by(continent) |>
3   summarise(
4     across(
5       c("lifeExp", "gdpPercap"),
6       list(med = median, iqr = IQR),
7       .names = "{.fn}_{.col}"
8     ))
```

```
# A tibble: 5 × 5
  continent med_lifeExp iqr_lifeExp med_gdpPercap
  <fct>           <dbl>       <dbl>         <dbl>
1 Africa           47.8       12.0          1192.
2 Americas         67.0       13.3          5466.
3 Asia             61.8       18.1          2647.
4 Europe           72.2        5.88        12082.
5 Oceania          73.7        6.35        17983.
# ℹ 1 more variable: iqr_gdpPercap <dbl>
```

Your Turn 2

Use `starts_with()` from `tidyselect()` to calculate the average `bp` columns in `diabetes`, grouped by `gender`. Give the new columns the name pattern `column_function`, e.g. `bp.1s_mean`.

hint: `{.fn}` will give you the function name, and `{.col}` will give you the column name

Your Turn 2

```
diabetes |>
  group_by(gender) |>
  summarise(
    across(
      starts_with("bp"),
      mean,
      na.rm = TRUE,
      .names = "{.col}_{.fn}"
    ))
```

```
# A tibble: 2 × 5
  gender bp.1s_1 bp.1d_1 bp.2s_1 bp.2d_1
  <chr>    <dbl>   <dbl>   <dbl>   <dbl>
1 female    136.    82.5    153.    91.8
2 male      138.    84.5    151.    93.5
```

vectorized functions don’t work on lists

```
1  sum(rnorm(10))
```

```
[1] -7.198318
```

vectorized functions don’t work on lists

```
1  sum(list(x = rnorm(10), y = rnorm(10), z = rnorm(10)))
```

```
Error in sum(list(x = rnorm(10), y = rnorm(10), z = rnorm(10))):
invalid 'type' (list) of argument
```

`map(.x, .f)`

`.x`: a vector, list, or data frame

`.f`: a function

Returns a list

Using `map()`

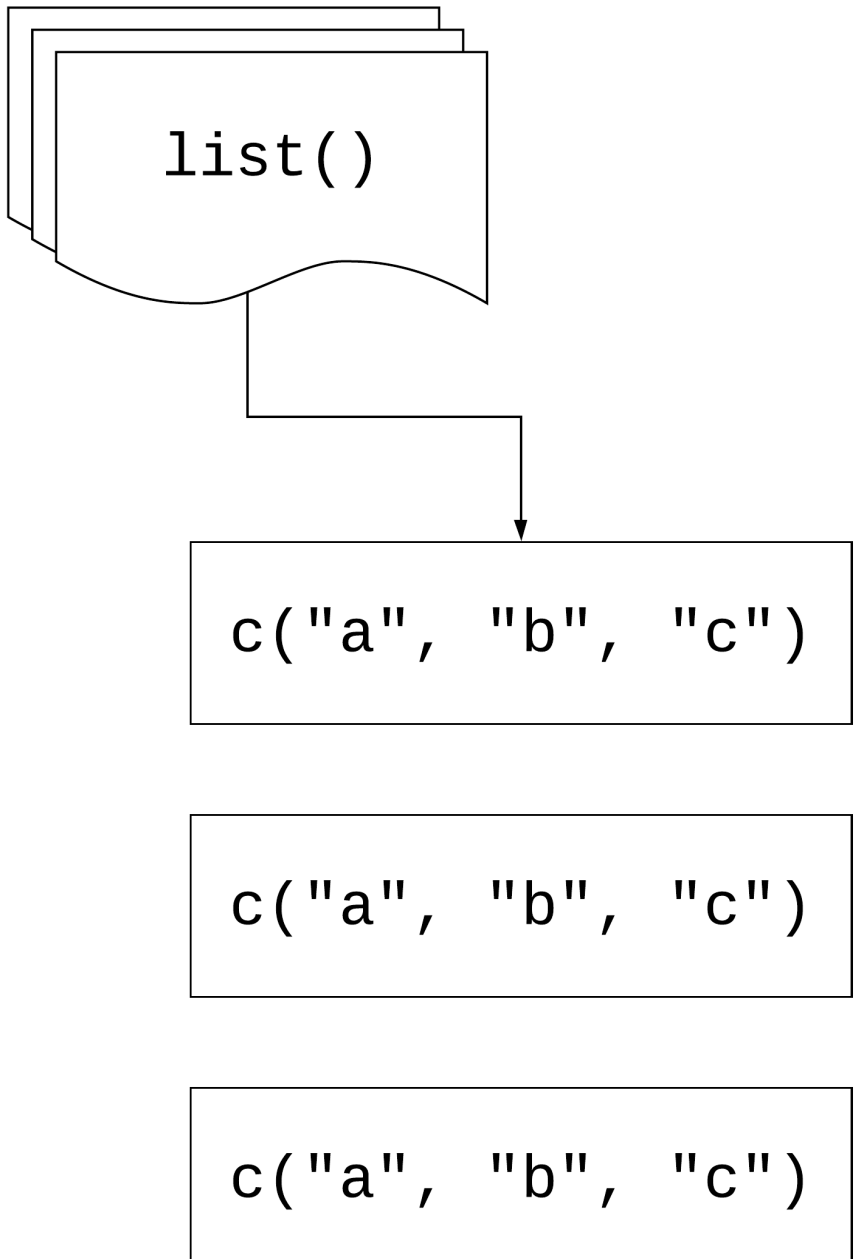
```r
library(purrr)
measurements <- list(
  blood_glucose = rnorm(10, mean = 140, sd = 10),
  age = rnorm(5, mean = 40, sd = 5),
  heartrate = rnorm(20, mean = 80, sd = 15)
)

map(measurements, mean)
```

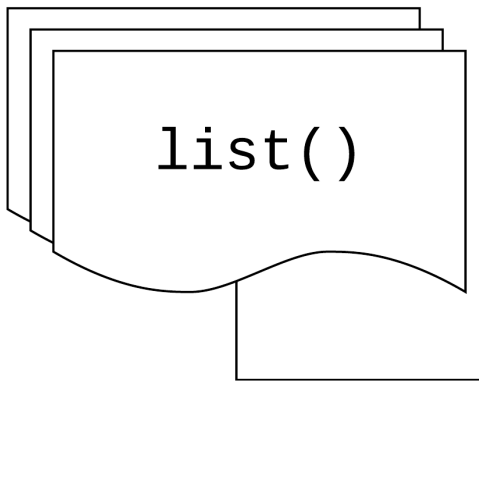
```
$blood_glucose
[1] 136.6299

$age
[1] 39.45875

$heartrate
[1] 83.01965
```


list()
c("a", "b", "c")
c("a", "b", "c")
c("a", "b", "c")

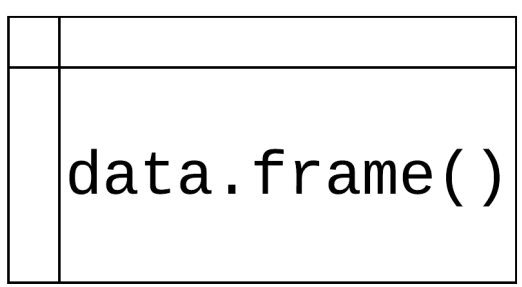
```
map( list() , .f)
```



```
.f( c("a", "b", "c") )
.f( c("a", "b", "c") )
.f( c("a", "b", "c") )
```

map(c("a", "b", "c") , .f)

map( , .f)

map( , .f)

Your Turn 3

Read the code in the first chunk and predict what will happen

Run the code in the first chunk. What does it return?

```
list(
  blood_glucose = sum(measurements$blood_glucose),
  age = sum(measurements$age),
  heartrate = sum(measurements$heartrate)
)
```

Now, use `map()` to create the same output.

Your Turn 3

```
1  map(measurements, sum)
```

```
$blood_glucose
[1] 1366.299

$age
[1] 197.2938

$heartrate
[1] 1660.393
```

using `map()` with data frames

```
1 library(dplyr)
2 gapminder |>
3   select(where(is.numeric)) |>
4   map(sd)
```

```
$year
[1] 17.26533

$lifeExp
[1] 12.91711

$pop
[1] 106157897

$gdpPercap
[1] 9857.455
```

Your Turn 4

Pass diabetes to `map()` and map using `class()`. What are these results telling you?

Your Turn 4

```
1 head(
2   map(diabetes, class),
3   3
4 )
```

```
$id
[1] "numeric"

$chol
[1] "numeric"

$stab.glu
[1] "numeric"
```

Review: writing functions

```
library(readxl)
weird_data1 <- read_excel(
  "data/weird_data1.xlsx",
  col_names = c("id", "x", "y", "z"),
  skip = 5
)
```

Review: writing functionss

```
library(readxl)
weird_data1 <- read_excel(
  "data/weird_data1.xlsx",
  col_names = c("id", "x", "y", "z"),
  skip = 5
)

weird_data2 <- read_excel(
  "data/weird_data1.xlsx",
  col_names = c("id", "x", "y", "z"),
  skip = 5
)

weird_data1 <- read_excel(
  "data/weird_data3.xlsx",
  col_names = c("id", "x", "y", "z"),
  skip = 5
)
```

Review: writing functionss

```
library(readxl)
weird_data1 <- read_excel(
  "data/weird_data1.xlsx",
  sheet = 2,
  col_names = c("id", "x", "y", "z"),
  skip = 6
)

weird_data2 <- read_excel(
  "data/weird_data1.xlsx",
  col_names = c("id", "x", "y", "z"),
  skip = 5
)

weird_data1 <- read_excel(
  "data/weird_data3.xlsx",
  col_names = c("id", "x", "y", "z"),
  skip = 5
)
```

Review: writing functions

```
library(readxl)
read_weird_excel <- function(path) {
  read_excel(
    path,
    sheet = 2,
    col_names = c("id", "x", "y", "z"),
    skip = 6
  )
}

weird_data1 <- read_weird_excel("data/weird_data1")
weird_data2 <- read_weird_excel("data/weird_data2")
weird_data3 <- read_weird_excel("data/weird_data3")
```

If you copy and paste your *code* three times, it's time to write a function

If you copy and paste your *function* three times, it's (*probably*) time to iterate

Iterating with functions

```
files <- c(
  "data/weird_data1.xlsx",
  "data/weird_data2.xlsx",
  "data/weird_data3.xlsx"
)

weird_data <- map(files, read_weird_excel) |>
  bind_rows()
```

Your Turn 5

Write a function that returns the mean and standard deviation of a numeric vector.

Give the function a name

Find the mean and SD of `x`

Map your function to `measurements`

Your Turn 5

```
mean_sd <- function(x) {
  x_mean <- mean(x)
  x_sd <- sd(x)
  tibble(mean = x_mean, sd = x_sd)
}

map(measurements, mean_sd)
```

Your Turn 5

```
$blood_glucose
# A tibble: 1 × 2
   mean    sd
  <dbl> <dbl>
1  137.  6.84

$age
# A tibble: 1 × 2
   mean    sd
  <dbl> <dbl>
1  39.5  3.84

$heartrate
# A tibble: 1 × 2
```

Three ways to pass functions to `map()`

1. pass directly to `map()`
2. use an anonymous function
3. use a lambda (`\()` or `~`)

```r
map(
    .x,
    mean,
    na.rm = TRUE
)
```

```r
map(
   .x,
   function(.x) mean(.x, na.rm = TRUE)
)
```

```r
map(
    .x,
    \(.x) mean(.x, na.rm = TRUE)
)
```

```r
map(
    .x,
    ~ mean(.x, na.rm = TRUE)
)
```

```r
map(
  gapminder,
  \(.x) length(unique(.x))
)
```

```
$country
[1] 142

$continent
[1] 5

$year
[1] 12

$lifeExp
[1] 1626

$pop
```

Returning types

map	returns
`map()`	list
`map_chr()`	character vector
`map_dbl()`	double vector (numeric)
`map_int()`	integer vector
`map_lgl()`	logical vector
`map_dfc()`	data frame (by column)
`map_dfr()`	data frame (by row)

Iterating with functions: revisited

```
files <- c(
  "data/weird_data1.xlsx",
  "data/weird_data2.xlsx",
  "data/weird_data3.xlsx"
)

weird_data <- map(files, read_weird_excel) |>
  bind_rows()
```

Iterating with functions: revisited

```
files <- c("data/weird_data1.xlsx", "data/weird_data2.xlsx", "da
weird_data <- map_dfr(files, read_weird_excel)
```

Returning types

```
1 map_int(gapminder, \(.x) length(unique(.x)))
```

```
country continent      year   lifeExp       pop gdpPercap
    142         5        12      1626      1704      1704
```

Your Turn 6

Do the same as #4 above but return a vector instead of a list.

Your Turn 6

```
1  map_chr(diabetes, class)
```

```
        id       chol    stab.glu        hdl      ratio      glyhb
 "numeric"  "numeric"  "numeric"  "numeric"  "numeric"  "numeric"
  location        age     gender     height     weight      frame
"character"  "numeric" "character"  "numeric"  "numeric" "character"
      bp.1s      bp.1d      bp.2s      bp.2d      waist        hip
 "numeric"  "numeric"  "numeric"  "numeric"  "numeric"  "numeric"
  time.ppn
 "numeric"
```

Your Turn 7

Check `diabetes` for any missing data.

Using the `\(.x) .f(.x)` shorthand, check each column for any missing values using `is.na()` and `any()`

Return a logical vector. Are any columns missing data? What happens if you don't include `any()`? Why?

Try counting the number of missing, returning an integer vector

Your Turn 7

```
1  map_lgl(diabetes, \(.x) any(is.na(.x)))
```

```
     id    chol stab.glu     hdl   ratio   glyhb location     age
  FALSE    TRUE    FALSE    TRUE    TRUE    TRUE    FALSE   FALSE
 gender  height   weight   frame   bp.1s   bp.1d   bp.2s   bp.2d
  FALSE    TRUE     TRUE    TRUE    TRUE    TRUE    TRUE    TRUE
  waist     hip time.ppn
   TRUE    TRUE     TRUE
```

Your Turn 7

```
1  map_int(diabetes, \(.x) sum(is.na(.x)))
```

```
      id     chol stab.glu      hdl    ratio    glyhb location      age
       0        1        0        1        1       13        0        0
  gender   height   weight    frame    bp.1s    bp.1d    bp.2s    bp.2d
       0        5        1       12        5        5      262      262
   waist      hip time.ppn
       2        2        3
```

group_map()

Apply a function across a grouping variable and return a list of grouped tibbles

```
library(broom)
diabetes |>
  group_by(gender) |>
  group_map(\(.x, ...) tidy(lm(weight ~ height, data = .x)))
```

group_map()

```
[[1]]
# A tibble: 2 × 5
  term        estimate std.error statistic   p.value
  <chr>          <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept)   -73.8      59.2      -1.25 0.214
2 height          3.90      0.928     4.20 0.0000383

[[2]]
# A tibble: 2 × 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)   -49.7      68.9      -0.722 0.471
2 height          3.35      0.995     3.37  0.000945
```

group_modify()

Apply a function across grouped tibbles and return grouped tibbles

```
diabetes |>
  group_by(gender) |>
  group_modify(\(.x, ...) tidy(lm(weight ~ height, data = .x)))
```

```
# A tibble: 4 × 6
# Groups:   gender [2]
  gender term        estimate std.error statistic   p.value
  <chr>  <chr>          <dbl>     <dbl>     <dbl>     <dbl>
1 female (Intercept)   -73.8      59.2     -1.25   0.214
2 female height          3.90      0.928    4.20   0.0000383
3 male   (Intercept)   -49.7      68.9     -0.722  0.471
4 male   height          3.35      0.995    3.37   0.000945
```

Your Turn 8

Fill in the model_lm function to model chol (the outcome) with ratio and pass the .data argument to lm()

Group `diabetes` by `location`

Use `group_modify()` with `model_lm`

Your Turn 8

```
model_lm <- function(.data, ...) {
  mdl <- lm(chol ~ ratio, data = .data)
  # get model statistics
  glance(mdl)
}

diabetes |>
  group_by(location) |>
  group_modify(model_lm)
```

Your Turn 8

```
# A tibble: 2 × 13
# Groups:   location [2]
  location  r.squared adj.r.squared sigma statistic  p.value
  <chr>         <dbl>         <dbl> <dbl>     <dbl>    <dbl>
1 Buckingh…     0.252         0.248  38.8      66.4 4.11e-14
2 Louisa        0.204         0.201  39.4      51.7 1.26e-11
# ℹ 7 more variables: df <dbl>, logLik <dbl>, AIC <dbl>,
#   BIC <dbl>, deviance <dbl>, df.residual <int>, …
```

`map2(.x, .y, .f)`

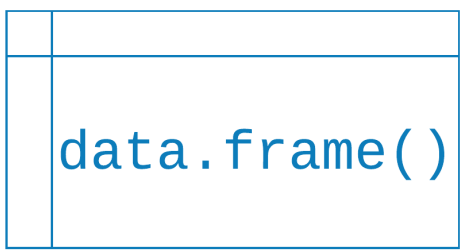
`.x`, `.y`: a vector, list, or data frame

`.f`: a function that takes *two* arguments

Returns a list

```
map2(
```

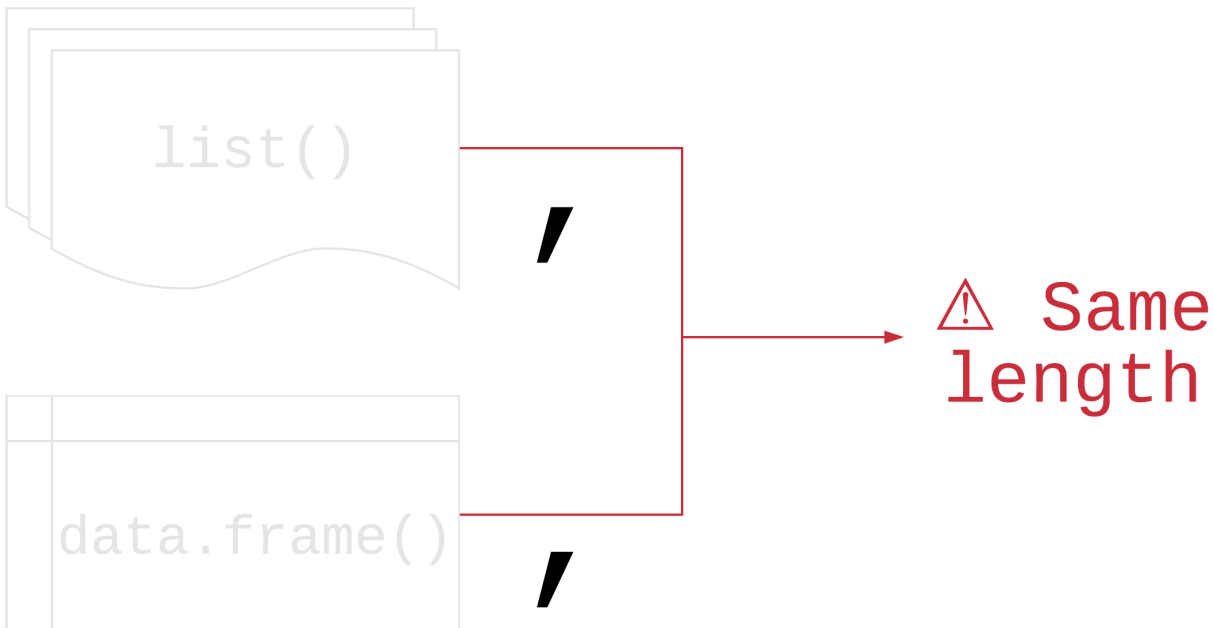
,



,

```
  .f
)
```

```
map2(
```




```
  .f
)
```

map2()

```
means <- c(-3, 4, 2, 2.3)
sds <- c(.3, 4, 2, 1)

map2_dbl(means, sds, rnorm, n = 1)
```

```
[1] -3.0587804  1.4037210 -0.2195345  3.1492742
```

Your Turn 9

Split the gapminder dataset into a list by country using the `split()` function

Create a list of models using `map()`. For the first argument, pass gapminder_countries. For the second, use the `\()` notation to write a model with `lm()`. Use `lifeExp` on the left hand side of the formula and `year` on the second. Pass `.x` to the data argument.

Use `map2()` to take the models list and the data set list and map them to `predict()`. Since we're not adding new arguments, you don't need to use `\()`.

Your Turn 9

```
gapminder_countries <- split(gapminder, gapminder$country)
models <- map(
  gapminder_countries,
  \(.x) lm(lifeExp ~ year, data = .x)
)
preds <- map2(models, gapminder_countries, predict)
head(preds, 3)
```

Your Turn 9

```
$Afghanistan
       1        2        3        4        5        6        7        8
29.90729 31.28394 32.66058 34.03722 35.41387 36.79051 38.16716 39.54380
       9       10       11       12
40.92044 42.29709 43.67373 45.05037

$Albania
       1        2        3        4        5        6        7        8
59.22913 60.90254 62.57596 64.24938 65.92279 67.59621 69.26962 70.94304
       9       10       11       12
72.61646 74.28987 75.96329 77.63671

$Algeria
       1        2        3        4        5        6        7        8
43.37497 46.22137 49.06777 51.91417 54.76057 57.60697 60.45337 63.29976
       9       10       11       12
66.14616 68.99256 71.83896 74.68536
```

input 1	input 2	returns
`map()`	`map2()`	list
`map_chr()`	`map2_chr()`	character vector
`map_dbl()`	`map2_dbl()`	double vector (numeric)
`map_int()`	`map2_int()`	integer vector
`map_lgl()`	`map2_lgl()`	logical vector
`map_dfc()`	`map2_dfc()`	data frame (by column)
`map_dfr()`	`map2_dfr()`	data frame (by row)

Other mapping functions

`pmap()` and friends: take n lists or data frame with argument names

`walk()` and friends: for side effects like plotting; returns input invisibly

`imap()` and friends: includes counter `i`

`map_if()`, `map_at()`: Apply only to certain elements

input 1	input 2	input n	returns
`map()`	`map2()`	`pmap()`	list
`map_chr()`	`map2_chr()`	`pmap_chr()`	character vector
`map_dbl()`	`map2_dbl()`	`pmap_dbl()`	double vector (numeric)
`map_int()`	`map2_int()`	`pmap_int()`	integer vector
`map_lgl()`	`map2_lgl()`	`pmap_lgl()`	logical vector
`map_dfc()`	`map2_dfc()`	`pmap_dfc()`	data frame (by column)
`map_dfr()`	`map2_dfr()`	`pmap_dfr()`	data frame (by row)
`walk()`	`walk2()`	`pwalk()`	input (side effects!)

group_walk()

Use group_walk() for side effects across groups

```
# fs helps us work with files
library(fs)
temp <- "temporary_folder"
dir_create(temp)
gapminder |>
  group_by(continent) |>
  group_walk(
    \(.x, .key) write_csv(
      .x,
      file = path(temp,  paste0(.key$continent, ".xlsx"))
    )
  )
```

group_walk()

```
temporary_folder
├── Africa.xlsx
├── Americas.xlsx
├── Asia.xlsx
├── Europe.xlsx
└── Oceania.xlsx
```

Your turn 10

Create a new directory using the fs package. Call it "figures".

Write a function to plot a line plot of a given variable in gapminder over time, faceted by continent. Then, save the plot (how do you save a ggplot?). For the file name, paste together the folder, name of the variable, and extension so it follows the pattern `"folder/variable_name.png"`

Create a character vector that has the three variables we'll plot: "lifeExp", "pop", and "gdpPercap".

Use `walk()` to save a plot for each of the variables

Your turn 10

```
dir_create("figures")

ggsave_gapminder <- function(variable) {
  p <- ggplot(
    gapminder,
    aes(x = year, y = {{ variable }}, color = country)
  ) +
    geom_line() +
    scale_color_manual(values = country_colors) +
    facet_wrap(~ continent) +
    theme(legend.position = "none")

  ggsave(
    filename = paste0("figures/", variable, ".png"),
    plot = p,
    dpi = 320
  )
}
```

Your turn 10

```
vars <- c("lifeExp", "pop", "gdpPercap")
walk(vars, ggsave_gapminder)
```

Base R

base R	purrr
`lapply()`	`map()`
`vapply()`	`map_*()`
`sapply()`	?
`x[] <- lapply()`	`map_dfc()`
`mapply()`	`map2()`,`pmap()`

Benefits of purrr

1. Consistent
2. Type-safe

Loops vs functional programming

```
1 x <- rnorm(10)
2 y <- map(x, mean)
```

Loops vs functional programming

```
x <- rnorm(10)
y <- vector("list", length(x))
for (i in seq_along(x)) {
  y[[i]] <- mean(x[[i]])
}
```

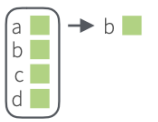
Of course someone has to write loops. It doesn't have to be you.

—Jenny Bryan

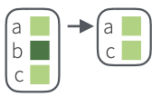
Working with lists and nested data

Work with Lists

FILTER LISTS

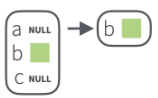


pluck(.x, ..., .default=NULL) Select an element by name or index, *pluck(x,"b")* ,or its attribute with **attr_getter**. *pluck(x,"b",attr_getter("n"))*

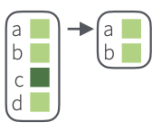


keep(.x, .p, …) Select elements that pass a logical test. *keep(x, is.na)*

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

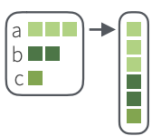


compact(.x, .p = identity) Drop empty elements. *compact(x)*

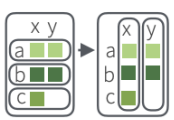


head_while(.x, .p, …) Return head elements until one does not pass. Also **tail_while**. *head_while(x, is.character)*

RESHAPE LISTS



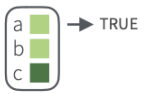
flatten(.x) Remove a level of indexes from a list. Also **flatten_chr**, **flatten_dbl**, **flatten_dfc**, **flatten_dfr**, **flatten_int**, **flatten_lgl**. *flatten(x)*



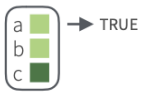
transpose(.l, .names = NULL) Transposes the index order in a multi-level list. *transpose(x)*

SUMMARISE LISTS

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



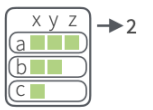
some(.x, .p, …) Do some elements pass a test? *some(x, is.character)*



has_element(.x, .y) Does a list contain an element? *has_element(x, "foo")*

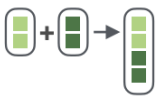
detect(.x, .f, ..., .right=FALSE, .p) Find first element to pass. *detect(x, is.character)*

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

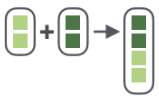


vec_depth(x) Return depth (number of levels of indexes). *vec_depth(x)*

JOIN (TO) LISTS



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

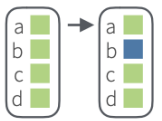


prepend(x, values, before = 1) Add to start of list. *prepend(x, list(d = 1))*

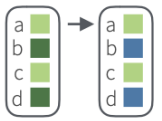
splice(…) Combine objects into a list, storing S3 objects as sub-lists. *splice(x, y, "foo")*

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_at(.x, .at, .f, ...) Apply function to elements by name or index. Also **map_at**. *modify_at(x, "b", ~.+2)*



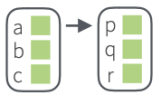
modify_if(.x, .p, .f, ...) Apply function to elements that pass a test. Also **map_if**. *modify_if(x, is.numeric,~.+2)*

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)*

Working with lists and nested data

Nested Data

A **nested data frame** stores individual tables within the cells of a larger, organizing table.

nested data frame

Species	data
setosa	<tibble [50 x 4]>
versicolor	<tibble [50 x 4]>
virginica	<tibble [50 x 4]>

n_iris

"cell" contents

Sepal.L	Sepal.W	Petal.L	Petal.W
5.1	3.5	1.4	0.2
4.9	3.0	1.4	0.2
4.7	3.2	1.3	0.2
4.6	3.1	1.5	0.2
5.0	3.6	1.4	0.2

n_iris$data[[1]]

Sepal.L	Sepal.W	Petal.L	Petal.W
7.0	3.2	4.7	1.4
6.4	3.2	4.5	1.5
6.9	3.1	4.9	1.5
5.5	2.3	4.0	1.3
6.5	2.8	4.6	1.5

n_iris$data[[2]]

Sepal.L	Sepal.W	Petal.L	Petal.W
6.3	3.3	6.0	2.5
5.8	2.7	5.1	1.9
7.1	3.0	5.9	2.1
6.3	2.9	5.6	1.8
6.5	3.0	5.8	2.2

n_iris$data[[3]]

Use a nested data frame to:

- preserve relationships between observations and subsets of data
- manipulate many sub-tables at once with the **purrr** functions **map()**, **map2()**, or **pmap()**.

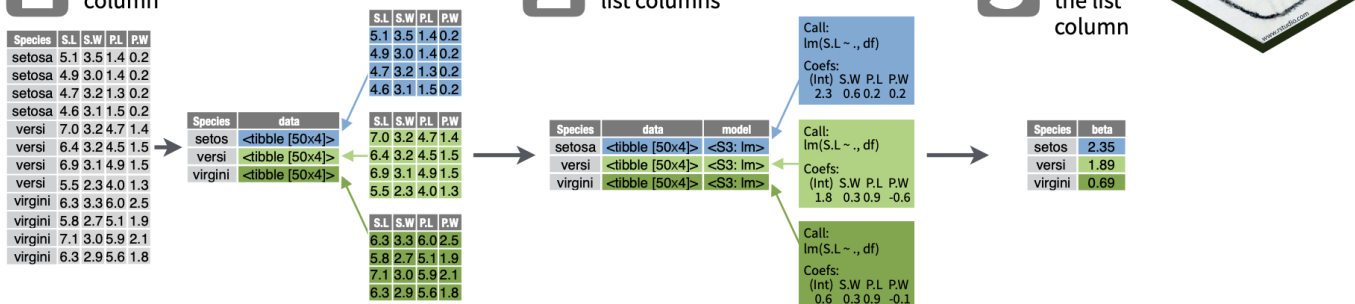
List Column Workflow

Nested data frames use a **list column**, a list that is stored as a column vector of a data frame. A typical **workflow** for list columns:

1 **Make** a list column

2 **Work with** list columns

3 **Simplify** the list column




```
n_iris <- iris %>%
  group_by(Species) %>%
  nest()
```

```
mod_fun <- function(df)
  lm(Sepal.Length ~ ., data = df)

m_iris <- n_iris %>%
  mutate(model = map(data, mod_fun))
```

```
b_fun <- function(mod)
  coefficients(mod)[[1]]

m_iris %>% transmute(Species,
  beta = map_dbl(model, b_fun))
```

1. MAKE A LIST COLUMN - You can create list columns with functions in the **tibble** and **dplyr** packages, as well as **tidyr**'s nest()

tibble::**tribble(**…**)** tibble::**tibble(**…**)** dplyr::**mutate(**.data, …**)** Also **transmute()**

Adverbs: Modify function behavior

Modify function behavior

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.

quietly() Modify function to return list of results, output, messages, warnings.

possibly() Modify function to return default value whenever an error occurs (instead of error).

Resources

Jenny Bryan's purrr tutorial: A detailed introduction to purrr. Free online.

R for Data Science, 2nd ed.: A comprehensive but friendly introduction to the tidyverse. Free online.

Posit Primers: Free interactive courses in the Tidyverse