

purrr for biostatisticians



with examples

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purrr



www.rstudio.com

let's get started

purrr package

purrr enhances R's functional programming toolkit (read: the apply family of functions) by providing a complete and consistent set of tools for working with functions and vectors

best place to start is the family of `map()` functions which allow you to replace many for loops* with code that is more succinct and easier to read

`map()` functions transform their input by applying a function to each element and returning a vector the same length as the input

[*] And much much more

base::apply vs purrr::map

base apply is to *Sister Act* as
purrr map is to _____ ?

base::apply vs purrr::map

base apply is to *Sister Act* as

purrr map is to *Sister Act 2: Back in the Habit*, the sequel to a great film that is better than the first!



base::apply

- first argument to `lapply()` is the data; the first argument to `mapply()` is the function
- no consistent way to pass additional arguments; most use `...`, `mapply()` uses `MoreArgs`, and some require you to create a new anonymous function
- output from `*apply()` is not consistent

base::apply

- first argument to `lapply()` is the data; the first argument to `mapply()` is the function
- no consistent way to pass additional arguments; most use `...`, `mapply()` uses `MoreArgs`, and some require you to create a new anonymous function
- output from `*apply()` is not consistent
- `v-`, `s-`, and `mapply()` use `USE.NAMES = FALSE` to suppress names in output; `lapply()` does not have this argument



purrr::map

- the `map*()` family has greater consistency among functions
- `map()`, `map2()`, and `pmap()` inputs are the same and allow for flexible input
- consistent methods for passing additional arguments

purrr::map

- the `map*()` family has greater consistency among functions
- `map()`, `map2()`, and `pmap()` inputs are the same and allow for flexible input
- consistent methods for passing additional arguments

- the output from the map family of functions is predictable and easily modified



use cases

1. subgroup analyses
2. sensitivity analyses
3. reading all files in a folder
4. bootstrap analyses
5. other purrr package functions

usage

```
map(.x, .f, ...)
```

.x A list or atomic vector

.f A function or formula

 If a function, it is used as is

 If a formula (e.g. `~ .x +2`), it is converted to a function

 - For a single argument function, use ``.`, ``.x``, or ``.1``

... Additional arguments passed on to the mapped function

usage

```
map(.x, .f, ...)
```

`.x` A list or atomic vector

`.f` A function or formula

 If a function, it is used as is

 If a formula (e.g. `~ .x + 2`), it is converted to a function

 - For a single argument function, use ``.`, ``.x``, or ``.1``

`...` Additional arguments passed on to the mapped function

```
a = list(1:3, 4:6, 7:9)
```

```
map(a, sum)
```

```
## [[1]]
```

```
## [1] 6
```

```
##
```

```
## [[2]]
```

```
## [1] 15
```

```
##
```

```
## [[3]]
```

```
## [1] 24
```

usage

pass a function name to `map()`

additional function arguments can be passed as well

```
a = list(1:3, 4:6, 7:9)
map(a, sum)
map(a, sum, na.rm = FALSE)
```

usage

pass a function name to `map()`

additional function arguments can be passed as well

```
a = list(1:3, 4:6, 7:9)
map(a, sum)
map(a, sum, na.rm = FALSE)
```

create a new function with `function(x)`

```
map(a, function(x) sum(x))
```

usage

pass a function name to `map()`

additional function arguments can be passed as well

```
a = list(1:3, 4:6, 7:9)
map(a, sum)
map(a, sum, na.rm = FALSE)
```

create a new function with `function(x)`

```
map(a, function(x) sum(x))
```

use the "~" shortcut to create a function (*my preferred method*)

```
map(a, ~sum(.))
map(a, ~sum(.x))
map(a, ~sum(..1))
```


usage

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

.x, .y A list or atomic vector

.l A list of vectors

.f A function or formula

If a function, it is used as is

If a formula (e.g. `~ .x + 2`), it is converted to a function

- For two arguments use `.x` and `.y`, or `..1` and `..2`

- For more arguments, use `..1`, `..2`, `..3`, etc.

... Additional arguments passed on to the mapped function

```
a = list(1:3, 4:6, 7:9)
b = list(9:7, 6:4, 3:1)
map2(a, b, ~sum(c(.x, .y)))
```

```
## [[1]]
## [1] 30
##
## [[2]]
## [1] 30
##
## [[3]]
## [1] 30
```

```
pmap(list(a, b), ~sum(c(.x, .y)))
```

```
## [[1]]
## [1] 30
##
## [[2]]
## [1] 30
##
## [[3]]
## [1] 30
```

```
a = list(1:3, 4:6, 7:9)
b = list(9:7, 6:4, 3:1)
map2(a, b, ~sum(c(..1, ..2)))
```

```
## [[1]]
## [1] 30
##
## [[2]]
## [1] 30
##
## [[3]]
## [1] 30
```

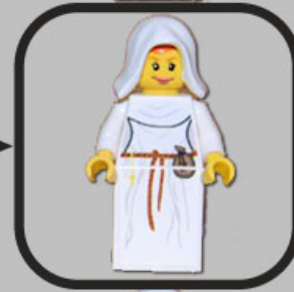
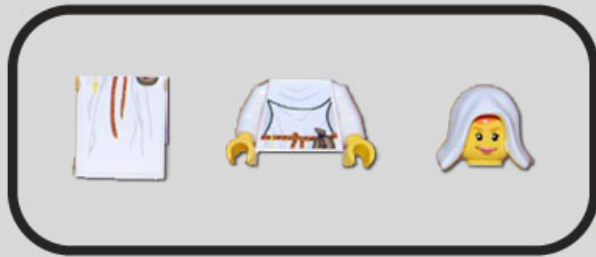
```
pmap(list(a, b), ~sum(c(..1, ..2)))
```

```
## [[1]]
## [1] 30
##
## [[2]]
## [1] 30
##
## [[3]]
## [1] 30
```

pmap (.l, embody)



pmap (.l, embody)



trial dataset

```
library(biostatR)
trial %>%
  fmt_table1(by = "trt", missing = "no") %>%
  add_n()
```

Variable	N	Drug	Placebo
		N = 107	N = 93
Age, yrs	192	47 (39, 58)	46 (36, 54)
Marker Level, ng/mL	192	0.61 (0.22, 1.20)	0.72 (0.22, 1.63)
T Stage	200		
T1		25 (23%)	26 (28%)
T2		26 (24%)	23 (25%)
T3		29 (27%)	13 (14%)
T4		27 (25%)	31 (33%)
Grade	200		
I		38 (36%)	29 (31%)
II		34 (32%)	24 (26%)
III		35 (33%)	40 (43%)
Tumor Response	191	52 (51%)	30 (33%)

USE CASES

1. *subgroup analyses*
2. sensitivity analyses
3. read all files in a folder
4. bootstrap analyses
5. other purrr package functions

subgroup analysis

tidyr::nest + purrr::map

```
trial %>%  
  group_by(grade) %>%  
  nest()
```

```
## # A tibble: 3 x 2  
##   grade data  
##   <fct> <list>  
## 1 I     <tibble [67 x 5]>  
## 2 III   <tibble [75 x 5]>  
## 3 II    <tibble [58 x 5]>
```

subgroup analysis

tidyr::nest + purrr::map

```
trial %>%  
  group_by(grade) %>%  
  nest()
```

```
## # A tibble: 3 x 2  
##   grade data  
##   <fct> <list>  
## 1 I     <tibble [67 x 5]>  
## 2 III   <tibble [75 x 5]>  
## 3 II    <tibble [58 x 5]>
```

tibbles

- share the same structure as data frames
- possible to have a list column
- this means you can put any object in a tibble!
- keep related objects together in a row, no matter object complexity

subgroup analysis

tidyr::nest + dplyr::mutate + purrr::map

```
trial %>%  
  group_by(grade) %>%  
  nest() %>%  
  mutate(  
    cross_tab = map(data, ~ table(.x[["response"]], .x[["trt"]]))  
  )
```

```
## # A tibble: 3 x 3  
##   grade data                cross_tab  
##   <fct> <list>                <list>  
## 1 I     <tibble [67 x 5]> <S3: table>  
## 2 III   <tibble [75 x 5]> <S3: table>  
## 3 II    <tibble [58 x 5]> <S3: table>
```

subgroup analysis

tibbles can store complex objects

the `cross_tab` column is just a list of table objects

```
## [[1]]  
##  
##      Drug Placebo  
##    0     14      17  
##    1     20      10  
##  
## [[2]]  
##  
##      Drug Placebo  
##    0     17      25  
##    1     17      14  
##  
## [[3]]  
##  
##      Drug Placebo  
##    0     18      18  
##    1     15       6
```

subgroup analysis

tidyr::nest + dplyr::mutate + purrr::map

```
trial %>%  
  group_by(grade) %>%  
  nest() %>%  
  mutate(  
    cross_tab = map(data, ~ table(.x[["response"]], .x[["trt"]])),  
    chi_sq = map(cross_tab, ~ chisq.test(.)),  
    p_value = map(chi_sq, ~ ..1[["p.value"]])  
  )
```

```
## # A tibble: 3 x 5  
##   grade data          cross_tab  chi_sq    p_value  
##   <fct> <list>          <list>    <list>    <list>  
## 1 I    <tibble [67 x 5]> <S3: table> <S3: htest> <dbl [1]>  
## 2 III  <tibble [75 x 5]> <S3: table> <S3: htest> <dbl [1]>  
## 3 II   <tibble [58 x 5]> <S3: table> <S3: htest> <dbl [1]>
```

subgroup analysis

tidyr::nest + dplyr::mutate + purrr::map

```
trial %>%  
  group_by(grade) %>%  
  nest() %>%  
  mutate(  
    cross_tab = map(data, ~ table(.x[["response"]], .x[["trt"]])),  
    chi_sq = map(cross_tab, ~ chisq.test(.)),  
    p_value = map(chi_sq, ~ ..1[["p.value"]])  
  )
```

```
## # A tibble: 3 x 5  
##   grade data          cross_tab  chi_sq    p_value  
##   <fct> <list>          <list>    <list>    <list>  
## 1 I    <tibble [67 x 5]> <S3: table> <S3: htest> <dbl [1]>  
## 2 III  <tibble [75 x 5]> <S3: table> <S3: htest> <dbl [1]>  
## 3 II   <tibble [58 x 5]> <S3: table> <S3: htest> <dbl [1]>
```

we want the p-values, not a list of p-values!

subgroup analysis

tidyr::nest + dplyr::mutate + purrr::map_dbl

```
trial %>%  
  group_by(grade) %>%  
  nest() %>%  
  mutate(  
    cross_tab = map(data, ~ table(.x[["response"]], .x[["trt"]])),  
    chi_sq = map(cross_tab, ~ chisq.test(.)),  
    p_value = map_dbl(chi_sq, ~ ..1[["p.value"]])  
  )
```

```
## # A tibble: 3 x 5  
##   grade data          cross_tab  chi_sq    p_value  
##   <fct> <list>          <list>    <list>    <dbl>  
## 1 I    <tibble [67 x 5]> <S3: table> <S3: htest> 0.152  
## 2 III  <tibble [75 x 5]> <S3: table> <S3: htest> 0.328  
## 3 II   <tibble [58 x 5]> <S3: table> <S3: htest> 0.193
```

output types

the default output of `map()` is a list

we can coerce the output type with `map_*()`

function	output type
<code>map()</code>	list
<code>map_dbl()</code>	double
<code>map_int()</code>	integer
<code>map_lgl()</code>	logical
<code>map_dfr()</code>	tibble (bind_rows)
<code>map_df()</code>	tibble (bind_cols)

when using the `map_*()` functions, `map()` runs as it typically would with the added step of coercing the output at the end

tip: make sure your code works with `map()` before adding `map_*()`

use cases

1. subgroup analyses
2. *sensitivity analyses*
3. read all files in a folder
4. bootstrap analyses
5. other purrr package functions

sensitivity analyses

run your analysis among

- all patients (TRUE)
- excluding low grade patients (grade != 'I')

```
tibble(  
  cohort = c("TRUE", "grade != 'I'")  
) %>%  
kable(format = "html")
```

cohort

TRUE

grade != 'I'

sensitivity analyses

run your analysis among

- all patients (TRUE)
- excluding low grade patients (grade != 'I')

```
tibble(  
  cohort = c("TRUE", "grade != 'I'")  
) %>%  
mutate(  
  data = map(cohort, ~ trial %>% filter_(.x)),  
  p_value = map_dbl(  
    data,  
    ~ table(.x[["response"]], .x[["trt"]]) %>%  
      chisq.test() %>%  
      pluck("p.value")  
  )  
)
```

sensitivity analyses

```
tibble(  
  cohort = c("TRUE", "grade != 'I'")  
) %>%  
mutate(  
  data = map(cohort, ~ trial %>% filter_(.x)),  
  p_value = map_dbl(  
    data,  
    ~ table(.x[["response"]], .x[["trt"]]) %>%  
      chisq.test() %>%  
      pluck("p.value")  
  )  
)
```

```
## # A tibble: 2 x 3  
##   cohort      data      p_value  
##   <chr>      <list>    <dbl>  
## 1 TRUE      <tibble [200 x 6]> 0.0172  
## 2 grade != 'I' <tibble [133 x 6]> 0.0922
```

sensitivity analyses

you can also save figures in a tibble

```
tibble(  
  cohort = c("TRUE", "grade != 'I'")  
) %>%  
mutate(  
  data = map(cohort, ~ trial %>% filter_(.x)),  
  ggplt = map(  
    data,  
    ~ ggplot(.x, aes(x = age, y = marker)) +  
      geom_point()  
  )  
)
```

```
## # A tibble: 2 x 3  
##   cohort      data      ggplt  
##   <chr>      <list>    <list>  
## 1 TRUE      <tibble [200 x 6]> <S3: gg>  
## 2 grade != 'I' <tibble [133 x 6]> <S3: gg>
```

use cases

1. subgroup analyses
2. sensitivity analyses
3. *read all files in a folder*
4. bootstrap analyses
5. other purrr package functions

read files

store vector of the files you want to import

```
file_list = list.files(pattern = "*.csv", recursive = TRUE)
```

read files

store vector of the files you want to import

```
file_list = list.files(pattern = "*.csv", recursive = TRUE)
```

use `map()` to read the files

returns a list where each element is a tibble

```
map(file_list, read_csv)
```

```
## [[1]]  
## # A tibble: 1 x 1  
##   var1  
##   <chr>  
## 1 hello darkness  
##  
## [[2]]  
## # A tibble: 1 x 1  
##   var1  
##   <chr>  
## 1 my old friend
```

read files

append each of the data sets with the `map_dfr()` function

after files have been imported, `bind_rows()` will create one final tibble

```
map_dfr(file_list, read_csv)
```

read files

append each of the data sets with the `map_dfr()` function

after files have been imported, `bind_rows()` will create one final tibble

```
map_dfr(file_list, read_csv)
```

include an identifier with a piped `mutate()`

```
map_dfr(file_list, ~read_csv(.x) %>% mutate(file = .x))
```

```
## # A tibble: 2 x 2
##   var1          file
##   <chr>         <chr>
## 1 hello darkness csv_files/file1.csv
## 2 my old friend  csv_files/file2.csv
```


USE CASES

1. subgroup analyses
2. sensitivity analyses
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4. *bootstrap analyses*
5. other purrr package functions

bootstrap analyses

use bootstrap re-sampling to estimate the difference in response rate by treatment

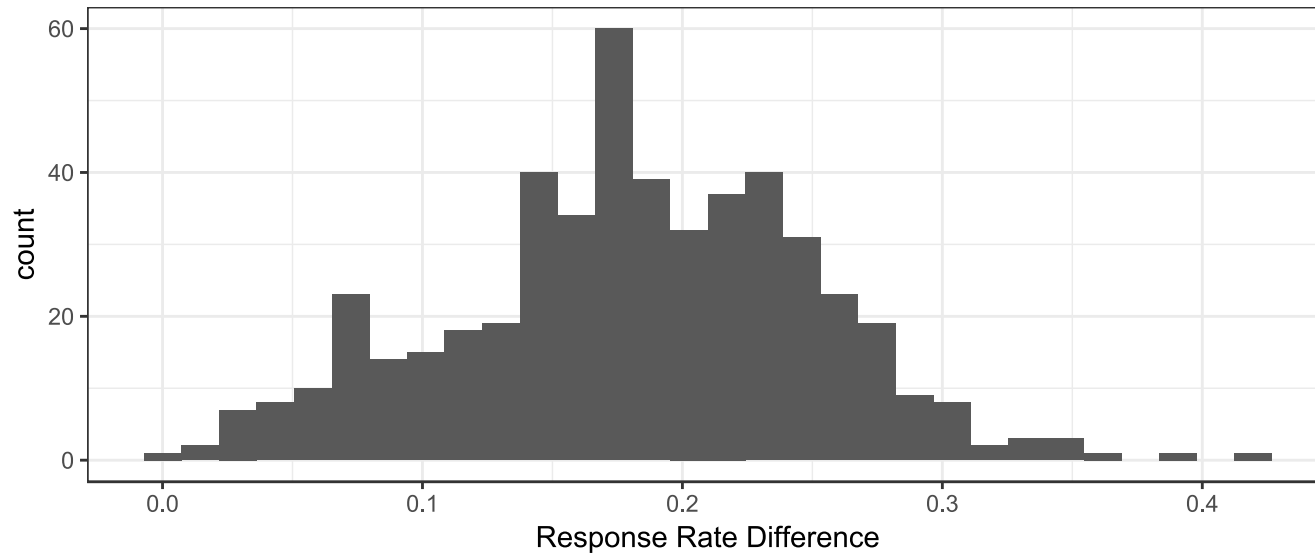
we'll use 500 re-sampled data sets to estimate the standard deviation of the response rate difference

assuming normality of the response rate difference, construct a 95% confidence interval for the difference

```
# create function to calculate risk difference
risk_diff <- function(data) {
  mean(data$response[data$trt == "Drug"], na.rm = TRUE) -
    mean(data$response[data$trt == "Placebo"], na.rm = TRUE)
}
```

bootstrap analyses

```
# resample dataset 500 times and calculate risk difference
risk_diff_boot <- map_dbl(
  1:500,
  ~ trial %>%
    slice(sample.int(n(), replace = TRUE)) %>%
    risk_diff()
)
```



bootstrap analyses

bootstrap confidence interval 18% (95% CI 4.6%, 32%)

bootstrap analyses

bootstrap confidence interval 18% (95% CI 4.6%, 32%)

Wald confidence interval 18% (95% CI 4.1%, 31%) **Success!**



use cases

1. subgroup analyses
2. sensitivity analyses
3. read all files in a folder
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5. *other purrr package functions*

other purrr functions

- `modify()`
- `imap()`
- `map_depth()`
- `keep()` and `discard()`
- `pluck()` and `chuck()`
- `cross_df()`
- `possibly()`, `safely()`, and `quietly()`
- `negate()`



Yes, Lauren Hill was in *Sister Act 2*!

modify()

unlike `map()` and its variants which always return a fixed object type (list for `map()`, integer vector for `map_int()`, etc), the `modify()` family always returns the same type as the input object

```
modify(c("hello", "world"), ~ .x)
```

```
## [1] "hello" "world"
```

```
modify(1:3, ~ .x)
```

```
## [1] 1 2 3
```


imap()

`imap(x, ...)` is short hand for `map2(x, names(x), ...)` if `x` has names, or `map2(x, 1:length(x), ...)` if it does not

```
trial %>% select(age, marker) %>%  
  imap(~ glue::glue("{.y}: {mean(.x, na.rm = TRUE)}"))
```

```
## $age  
## age: 46.859375  
##  
## $marker  
## marker: 0.928015625
```

imap()

`imap(x, ...)` is short hand for `map2(x, names(x), ...)` if `x` has names, or `map2(x, 1:length(x), ...)` if it does not

```
trial %>% select(age, marker) %>%  
  imap(~ glue::glue("{.y}: {mean(.x, na.rm = TRUE)}"))
```

```
## $age  
## age: 46.859375  
##  
## $marker  
## marker: 0.928015625
```

```
trial %>% select(age, marker) %>%  
  map2(., names(.), ~ glue::glue("{.y}: {mean(.x, na.rm = TRUE)}"))
```

```
## $age  
## age: 46.859375  
##  
## $marker  
## marker: 0.928015625
```

map_depth()

`map_depth(.x, .depth, .f, ...)` recursively traverses nested vectors and map a function at a certain depth

- `map_depth(x, 0, fun)` is equivalent to `fun(x)`.
- `map_depth(x, 1, fun)` is equivalent to `map(x, fun)`
- `map_depth(x, 2, fun)` is equivalent to `map(x, ~ map(., fun))`

keep() and discard()

keep or discard elements of a list or vector

```
1:10 %>%  
  keep(~. < 5)
```

```
## [1] 1 2 3 4
```

```
1:10 %>%  
  discard(~.x >= 5)
```

```
## [1] 1 2 3 4
```

pluck()

pluck is similar to "[[" and selects a single element from a list or vector

use position or name to select item

pluck is easier to read when used with the pipe (%>%)

```
lm(mpg ~ vs, mtcars) %>%  
  pluck("coefficients")
```

```
## (Intercept)          vs  
##    16.616667    7.940476
```

cross_df()

like `expand.grid()` without the factors...ahhhh!

```
list(  
  outcome = c("mets", "death"),  
  cohort = c("tpsa > 0", "tpsa > 1")  
) %>%  
  cross_df()
```

```
## # A tibble: 4 x 2  
##   outcome cohort  
##   <chr>    <chr>  
## 1 mets    tpsa > 0  
## 2 death   tpsa > 0  
## 3 mets    tpsa > 1  
## 4 death   tpsa > 1
```

check out `cross()`, `cross2()`, `cross3()`

they are similar, but return lists rather than a tibble

possibly(), safely(), and quietly()

these functions wrap functions

instead of generating side effects through printed output, messages, warnings, and errors, they return enhanced output

safely() wrapped function returns a list with components `result` and `error`

quietly() wrapped function instead returns a list with components `result`, `output`, `messages` and `warnings`

possibly() wrapped function uses a default value (otherwise) whenever an error occurs

similar to `try()` and `tryCatch()`

negate()

negates a predicate function

a predicate function returns TRUE and FALSE, e.g. `is.anything()`

returns a *function*, not the same as `!` operator

good for piping

```
d = c(5, NA, 1, NA, 2, NA)
```

```
d %>% negate(is.na)()
```

```
## [1] TRUE FALSE TRUE FALSE TRUE FALSE
```

```
d %>% {!is.na(.)}
```

```
## [1] TRUE FALSE TRUE FALSE TRUE FALSE
```


done! questions?



▶ slides at danielsjoberg.com/purrr-for-biostatisticians

🔄 source code at github.com/ddsjoberg/purrr-for-biostatisticians