purrr for biostatisticians

⚔

with examples

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February, 19 2019

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!**

www.impawards.com

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

Hadley Wickhamm on www.stackoverflow.com

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), if 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), if 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

```r
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), if 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
```

```r
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
```

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

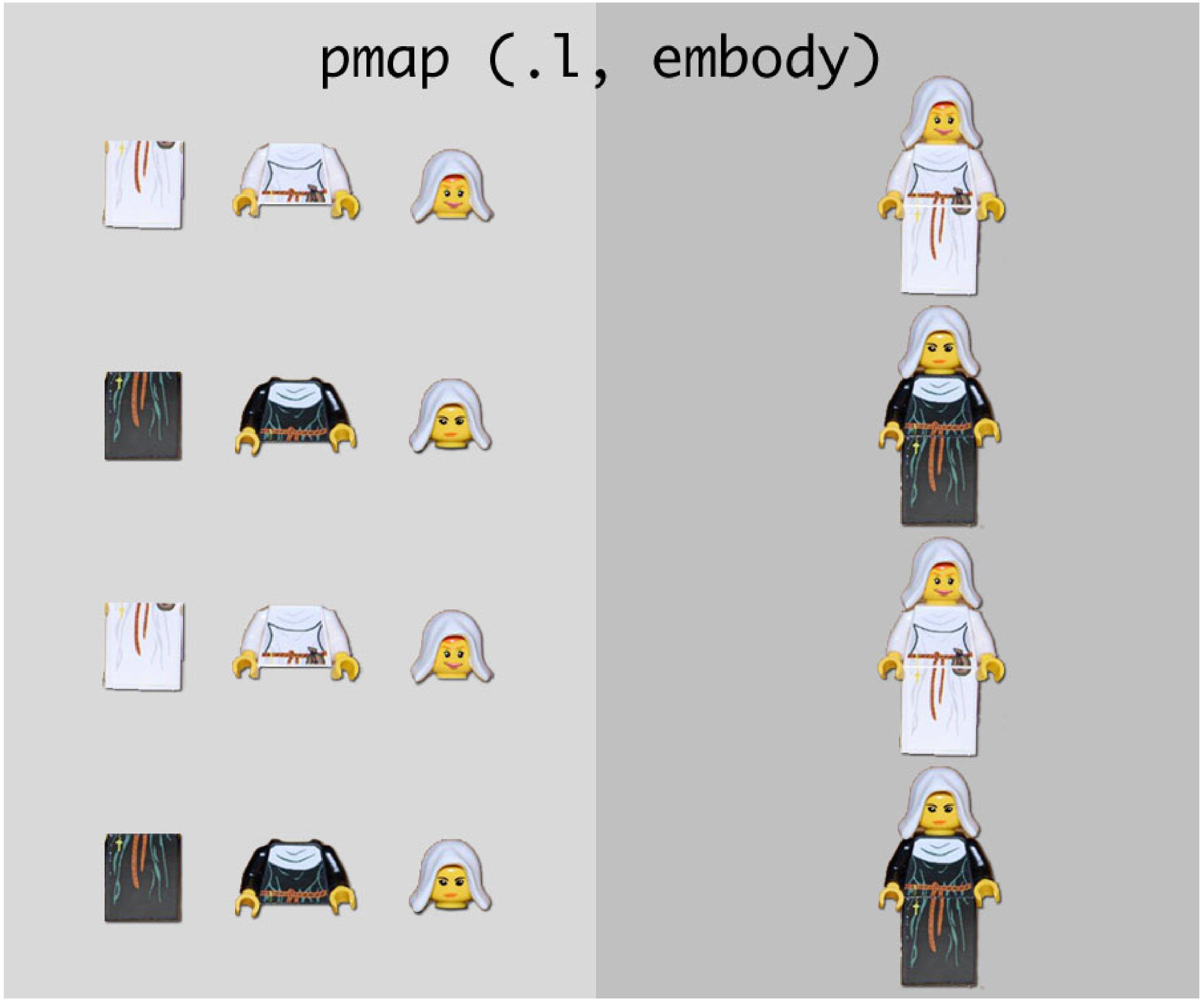
```
## [[1]]
## [1] 30
##
## [[2]]
## [1] 30
##
## [[3]]
## [1] 30
```

```r
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
```

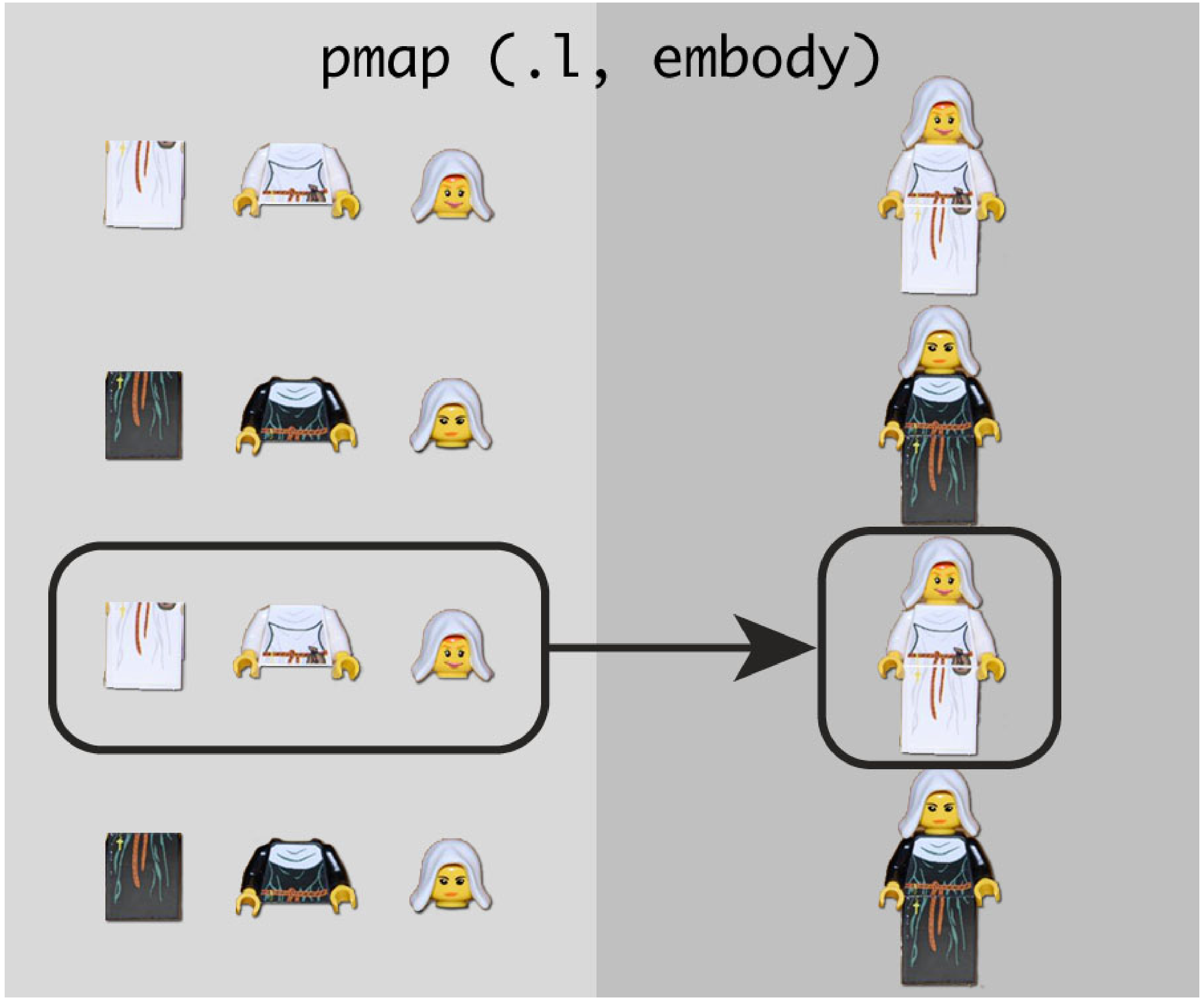
```r
pmap(list(a, b), ~sum(c(..1, ..2)))
```

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



```
pmap (.l, embody)
```

LEGO analogy by Jenny Bryan



LEGO analogy by Jenny Bryan

trial dataset

```r
remotes::install_url("https://github.mskcc.org/datadojo/biostatR/archive/master.zip")
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

```r
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

```
.[["cross_tab"]]
```

```
## [[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
map()	list
map_dbl()	double
map_int()	integer
map_lgl()	logical
map_dfr()	tibble (bind_rows)
map_dfc()	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
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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

```r
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
3. read all files in a folder
4. ***bootstrap analyses***
5. other purrr package functions

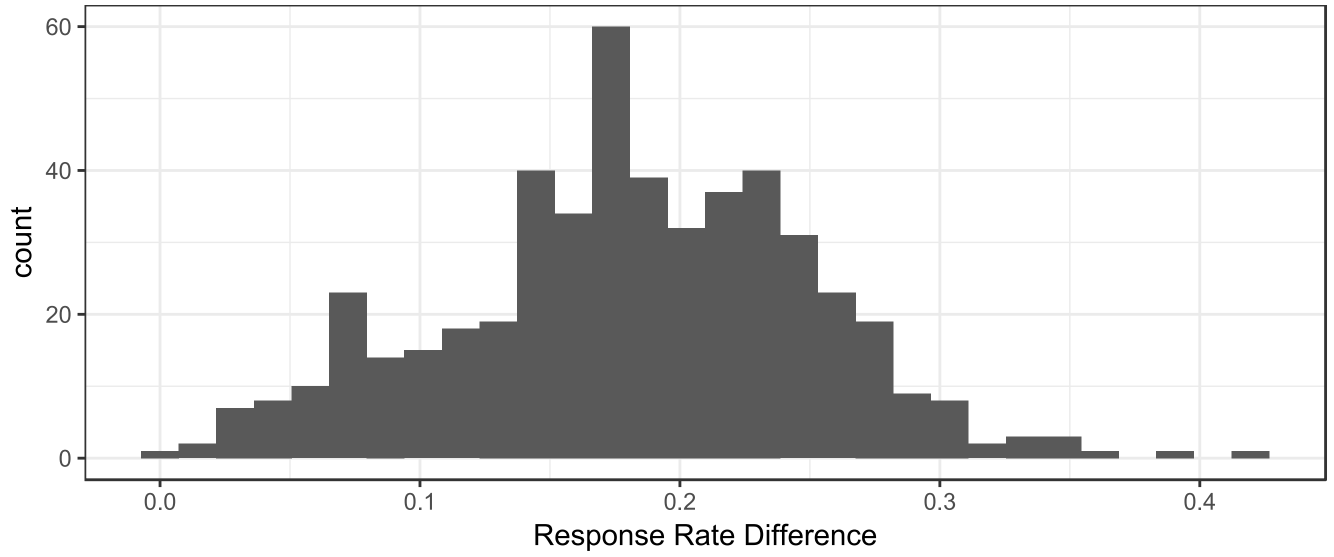
bootstrap analyses

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

```r
# 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

```r
# 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

difference in response rate: *18%*
bootstrap confidence interval: *4.6%, 32%*

bootstrap analyses

difference in response rate: *18%*
bootstrap confidence interval: *4.6%, 32%*
Wald confidence interval: *4.1%, 31%* — **Success!**

use cases

1. subgroup analyses
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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

```r
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 danieldsjoberg.com/purrr-for-biostatisticians
source code at github.com/ddsjoberg/purrr-for-biostatisticians