

purrr for biostatisticians



with examples

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purrr



www.rstudio.com

purrr's map functions

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

purrr::map vs base::apply

base apply is to _____ as purrr map is to _____ ?

purrr::map vs base::apply

base apply is to

as purrr map is to



www.impawards.com



base::apply

- first argument to `apply` is the data; the first argument to `MARGIN` is the function
- no consistent way to pass additional arguments; most use `args`, `data` uses `args`, and some require you to create a new anonymous function
- output from `apply` is not consistent

base::apply

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

- `lapply`, `sapply`, and `mapply` use `use.names` to suppress names in output; `apply` does not have this argument



purrr::map

- the `map` family has greater consistency among functions
- `map`, `map2`, and `map2_chr` 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 `map3` 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 modifiable



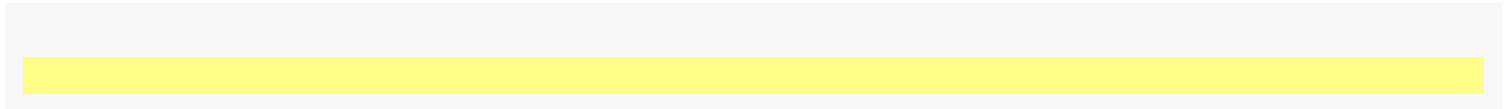
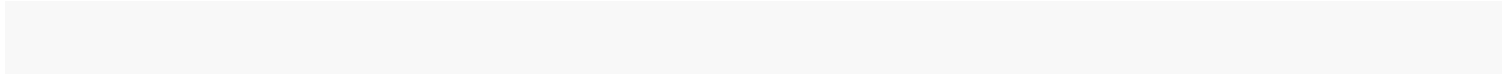
use cases

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

usage



usage



usage

pass a function name to

additional function arguments can be passed as well

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pass a function name to

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create a new function with

usage

pass a function name to

additional function arguments can be passed as well

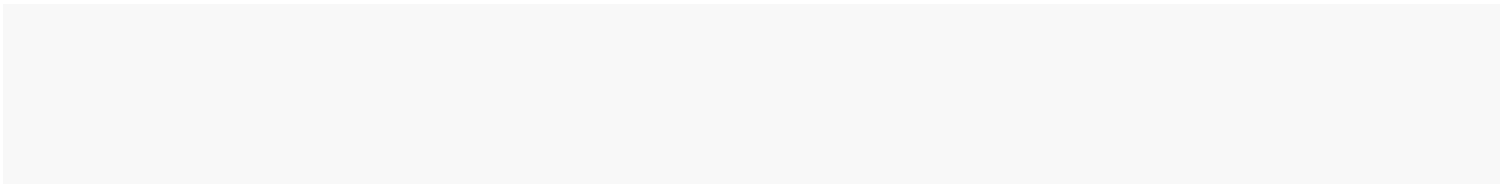
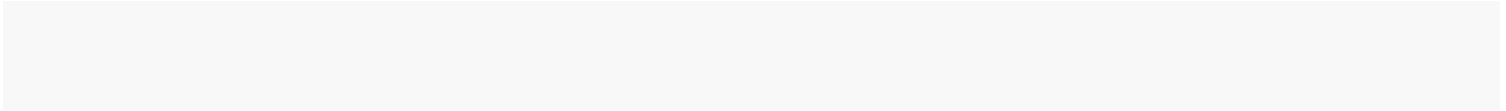
create a new function with

use the ' ' shortcut to create a function

usage



usage

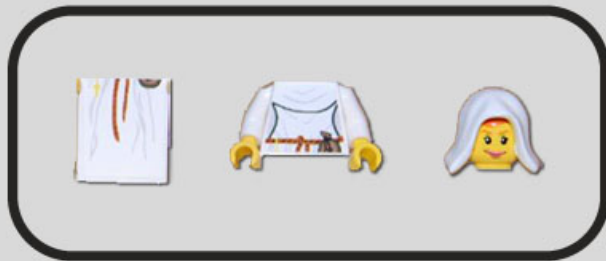


usage

pmap (.l, embody)



pmap (.l, embody)



trial dataset

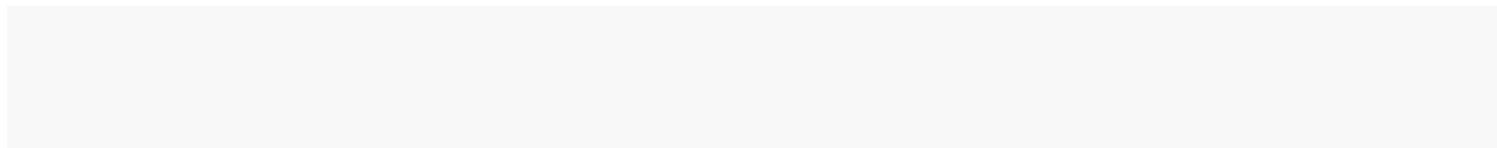
		N = 107	N = 93
Age, yrs	192	47 (39, 58)	46 (36, 54)
Marker Level, ng/mL	192	0.61 (0.22, 1.20)	0.72 (0.22, 1.63)
T Stage	200		
T1		25 (23%)	26 (28%)
T2		26 (24%)	23 (25%)
T3		29 (27%)	13 (14%)
T4		27 (25%)	31 (33%)
Grade	200		
I		38 (36%)	29 (31%)
II		34 (32%)	24 (26%)
III		35 (33%)	40 (43%)
Tumor Response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

use cases

- 1.
2. sensitivity analyses
3. read all files in a folder
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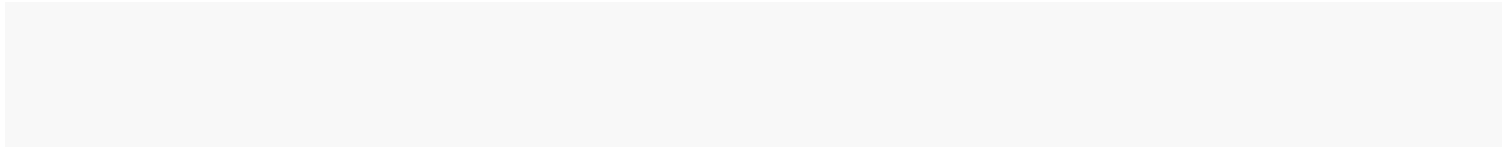
subgroup analysis

`tidyr::nest + purrr::map`



subgroup analysis

`tidyr::nest + purrr::map`



tibbles share the same structure as data frames

tibbles are a list of vectors, and it is possible to have a list column

very useful because a list can contain any other object: this means you can put any object in a tibble!

allows you to keep related objects together in a row, no matter how complex the individual objects are

subgroup analysis

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

subgroup analysis

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

subgroup analysis

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

output types

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

we can coerce the output type with

<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_dfr()` runs as it typically would with the added step of coercing the output at the end

tip: make sure your code works with `map_dfr()` before adding `map_dfc()`.

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sensitivity analyses

run your analysis among

- all patients ()
- excluding low grade patients ()

TRUE

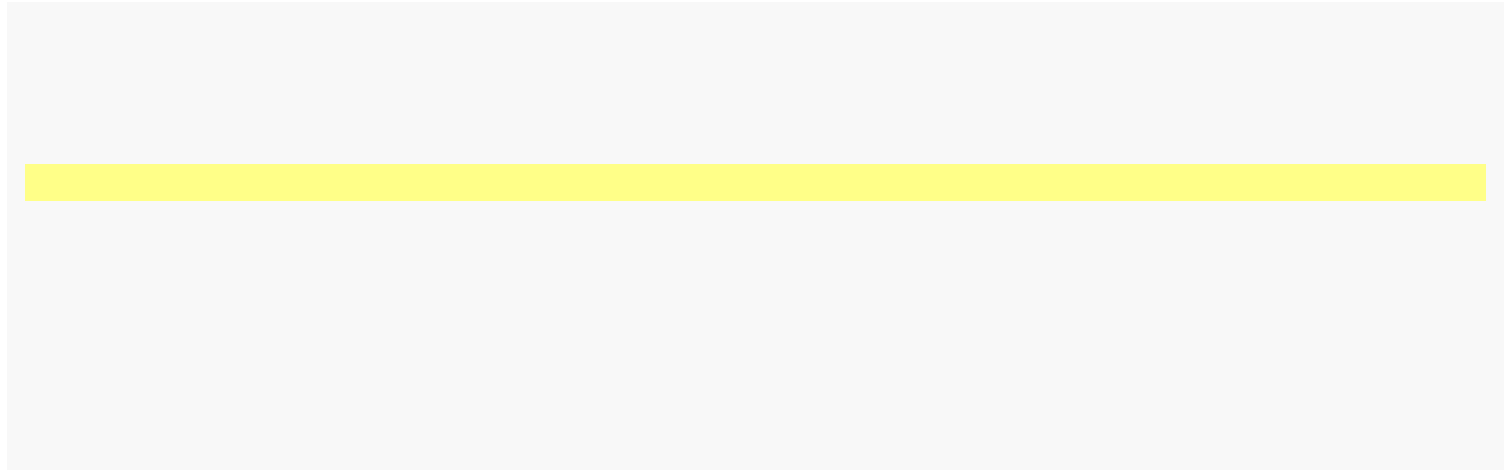
grade != 'I'

sensitivity analyses

run your analysis among

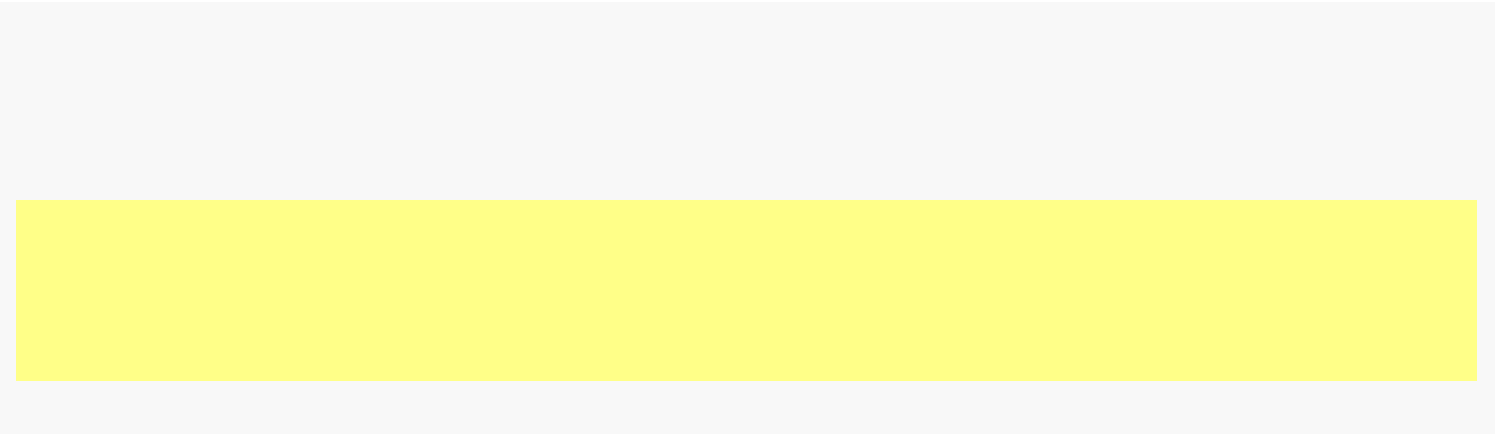
- all patients ()
- excluding low grade patients ()

sensitivity analyses



sensitivity analyses

you can also save figures in a tibble



use cases

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read files

store vector of the files you want to import



read files

store vector of the files you want to import

use `read_csv()` to read the files.

- returns a list where each element is a tibble

read files

append each of the data sets with the

- after files have been imported,

function

will create one final tibble

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include an identifier with a piped

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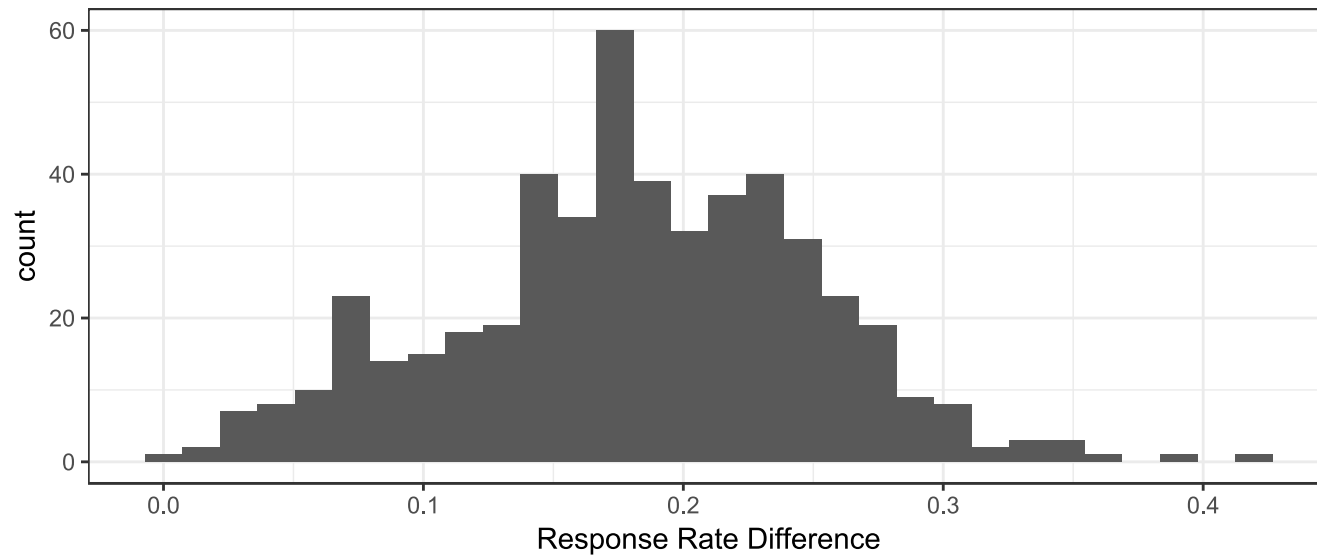
bootstrap analyses

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

bootstrap analyses



bootstrap analyses

the result

- 18% (95% CI 4.6%, 32%)

bootstrap analyses

the result

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how do the results compare to the the Wald CI?

bootstrap analyses

the result

- 18% (95% CI 4.6%, 32%)

how do the results compare to the the Wald CI?

- 18% (95% CI 4.1%, 31%)



use cases

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- 5.

other purrr functions

-
-
- and
- and
-
- , and



Yes, Lauren Hill was in !

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

names, or is short hand for if it does not if has

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and

keep or discard elements of a list or vector



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 (`%>%`)

like

without the factors...finally!

check out `as.list()`, `as.data.frame()`,

they are similar, but return lists rather than a tibble

, , and

these functions wrap functions so that instead of generating side effects through printed output, messages, warnings, and errors, they return enhanced output

wrapped function returns a list with components and

wrapped function instead returns a list with components
, , and

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

similar to and

done!



questions?

▣ slides available at danielsjoberg.com/purrr-for-biostatisticians

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

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