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 functions which allow you to replace many for loops* with code that is more succinct and easier to read

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

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as purrr map is to

base::apply

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

base::apply

- first argument to is the data; the first argument to is the function
- no consistent way to pass additional arguments; most use , uses , and some require you to create a new anonymous function
- output from is not consistent
- , , and uses to suppress names in output; does not have this argument

purrr::map

- the family has greater consistency among functions
- , , and inputs are the same and allow for flexible input
- consistent methods for passing additional arguments

purrr::map

- the family has greater consistency among functions
- , , and 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

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pass a functon name to

additional function arguments can be passed as well

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```

create a new function with

```

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```

create a new function with

```

```

use the shortcut to create a function

```

```

usage

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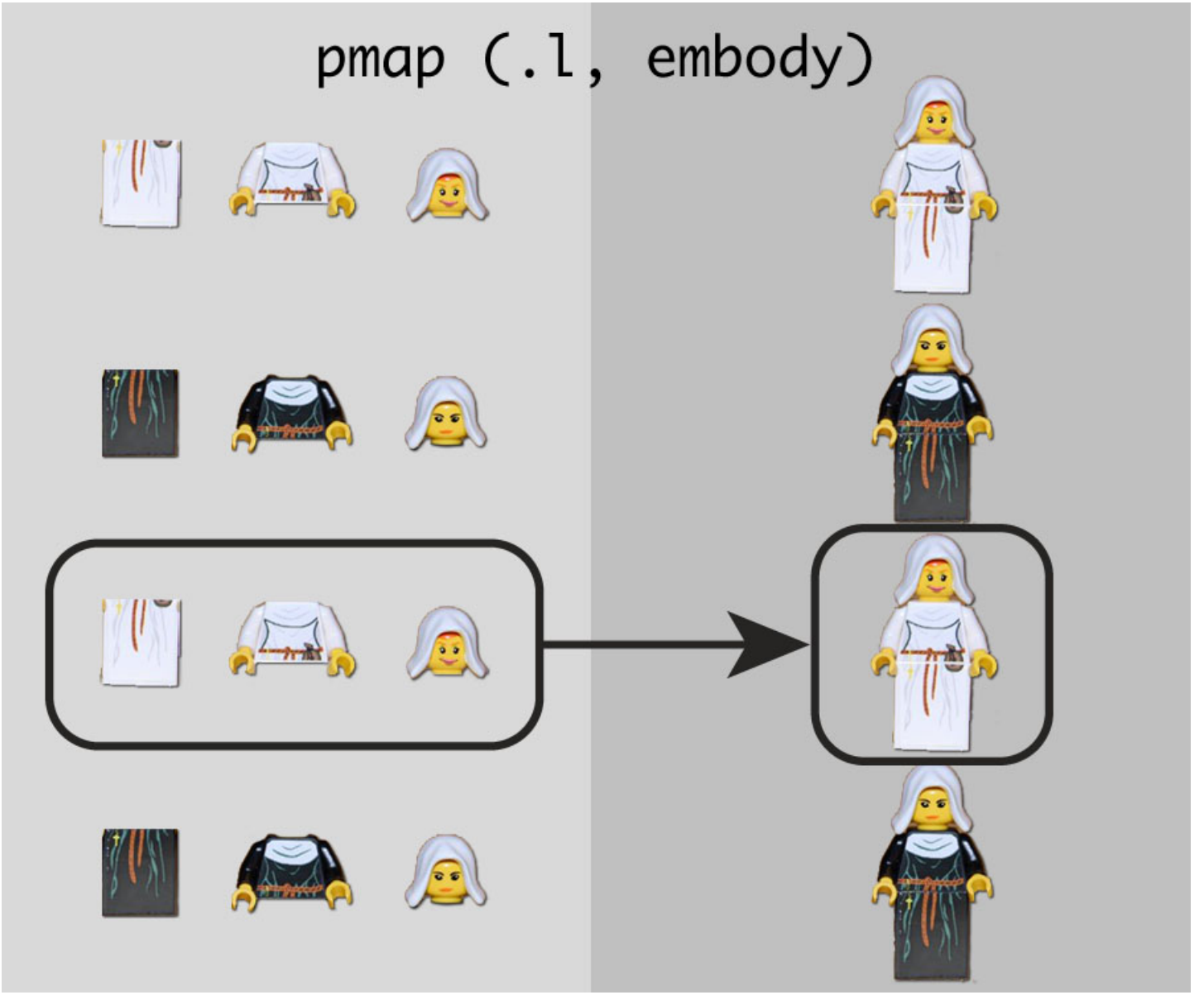
pmap (.l, embody)


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

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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 is a list

we can coerce the output type with

map()	list
map_dbl()	double
map_int()	integer
map_lgl()	logical
map_dfr()	tibble (bind_rows)
map_dfc()	tibble (bind_cols)

when using the functions, runs as it typically would with the added step of coercing the output at the end

tip: make sure your code works with before adding .

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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

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```
```

use to read the files.

- returns a list where each element is a tibble

```
```

read files

append each of the data sets with the function

- after files have been imported, will create one final tibble

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include an identifier with a piped

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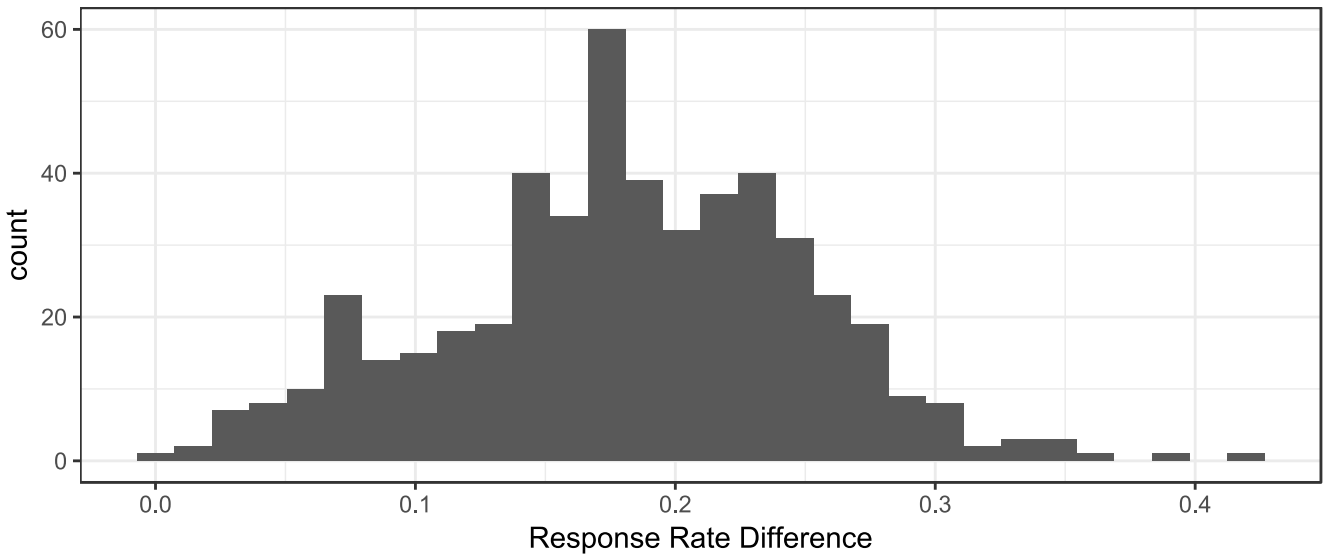
bootstrap analyses

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

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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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other purrr functions

-
-
- and
- and
-
- , , and

Yes, Lauren Hill was in !

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

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

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

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 , ,

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

similar to and

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

done!

questions?

slides available at danieldsjoberg.com/purrr-for-biostatisticians

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