

Working with multiple instances

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Motivation

- Most telemetry studies deal with more than one animal.
- Dealing with multiple animals can complicate analyses significantly.
- Some packages provide an infrastructure to deal with multiple animals (e.g. `adehabitat`, `move`).
- `amt` has very limited support for dealing with multiple animals, but relies on the infrastructure provided by the `purrr` package.

Examples

- Weekly home-range size of bears.
- Does home-range size differ between different sexes, treatments?
- Individual-level habitat selection?
- What is the mean step length for different animals during day and night?

Repeating tasks in R

Three possible ways to deal with multiple instances in R:

1. Copy and paste your code and make slight adaptations (**don't do this**).
2. Use a for-loop
3. Use functional programming

Let's consider the following problem: We want to calculate the mean step length of each fisher from the `amt_fisher` data set:

```
library(amt)
data(amt_fisher)
unique(amt_fisher$name)
```

```
[1] "Leroy"    "Ricky T" "Lupe"     "Lucile"
```

For the first animals Leroy¹

```
amt_fisher %>% filter(name == "Leroy") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 186.9954
```

¹Note, I am ignoring sampling rates here.

Now we could do the same for the other three individuals:

```
amt_fisher %>% filter(name == "Ricky T") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 41.9739
```

```
amt_fisher %>% filter(name == "Lupe") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 61.04558
```

```
amt_fisher %>% filter(name == "Lucile") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 85.95821
```

- We would also need an other vector, to save the results.
- While this approach might be OK for only a few individuals, it becomes very tedious for many animals or if you would like to add a an other grouping factor (say, we would also want to calculate the mean step for each day).
- for-loops can be useful here.

Note, that only part changes here:

```
amt_fisher %>% filter(name == "Ricky T") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 41.9739
```

```
amt_fisher %>% filter(name == "Lupe") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 61.04558
```

```
amt_fisher %>% filter(name == "Lucile") %>%  
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 85.95821
```

We could use a variable here:

```
i <- "Ricky T"
amt_fisher %>% filter(name == i) %>%
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 41.9739
```

```
i <- "Lupe"
amt_fisher %>% filter(name == i) %>%
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 61.04558
```

```
i <- "Lucile"
amt_fisher %>% filter(name == i) %>%
  step_lengths() %>% mean(na.rm = TRUE)
```

```
[1] 85.95821
```

- `i` takes the name of the animal and changes.
- Everything else is the **same**.

A for-loop has one variable, that changes for each go.

```
for (i in c("Leroy", "Ricky T", "Lupe", "Lucile")) {  
  # Do something  
}
```

The body of the function (embraced in curly brackets { }) is executed **four** times. Each time the value of `i` changes.

We can use this to calculate the mean step length:

```
for (i in c("Leroy", "Ricky T", "Lupe", "Lucile")) {  
  amt_fisher %>% filter(name == i) %>%  
    step_lengths() %>% mean(na.rm = TRUE)  
}
```

Finally we have to take care of the results and save this in a new variable, which I called `res` here.

```
res <- c()
j <- 1
for (i in c("Leroy", "Ricky T", "Lupe", "Lucile")) {
  res[j] <- amt_fisher %>% filter(name == i) %>%
    step_lengths() %>% mean(na.rm = TRUE)
  j <- j + 1
}
```

- for-loops are a significant improvement to the approach #1.
- However, for-loops *can* become a bit tedious if we have multiple grouping instances. We potentially need nested for-loops.

A slightly deeper look at R

- tibbles are *modern* data frames.
- A tibble can have list columns.
- A list is an other data structure in R, that can hold any other data structure.

With list columns it is easy to have more complex splits of your data (e.g., animals/seasons/weeks).

Lists

What is a list?

Lists are yet another data structures for R. Lists can contain any object (even other lists).

```
l <- list("a", b = 1:10, x = list(list(1:10)))  
str(l)
```

```
List of 3  
$ : chr "a"  
$ b: int [1:10] 1 2 3 4 5 6 7 8 9 10  
$ x:List of 1  
..$ :List of 1  
.. ..$ : int [1:10] 1 2 3 4 5 6 7 8 9 10
```


Examples for lists

```
x <- list(a = 1:3, b = list(1:3))  
x[[1]]
```

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

```
x$a
```

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

```
x[["b"]]
```

```
[[1]]
```

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

Functional programming in R

What is functional programming?

Simply put, FP is exactly what it sounds like. If you are doing something more than once, it belongs in a function. In FP, functions are the primary method with which you should carry out tasks. All actions are just (often creative) implementations of functions you've written. towardsdatascience.com

The apply-family

These functions apply a function on a `matrix`, `vector` or `list`.

For matrices:

- `apply` (we wont cover this here in more detail)

For vectors and lists

- `lapply`
- `sapply`

lapply

To apply a function to each element of a list (or a vector) and the result should be a list, then `lapply` can be used.

```
l <- list(1:3, 2)
lapply(l, length)
```

```
[[1]]
[1] 3
```

```
[[2]]
[1] 1
```

We could achieve the same with a a for-loop:

```
res <- list()
for (i in 1:2) {
  l[[i]] <- length(l[[i]])
}
```

Here it would make more sense to use `sapply` (R will try to simplify the data structure of the result).

```
sapply(1, length)
```

```
[1] 1 1
```

Note, we used the shortest possible way, it is also possible to explicitly work with the object the function is applied to.

```
sapply(1, function(x) length(x))
```

```
[1] 1 1
```

Since `length` only uses one argument (here `x`), we do not have to explicitly call the function

The purrr package provides a more type-stable way to `*apply()` functions. These are called `map_*()`.

- `lapply` -> `map`
- `sapply` -> `map_*`
 - `map_lgl` for logical values
 - `map_dbl` for doubles
 - `map_int` for integers
 - `map_chr` for text

In addition there variants of all `map*` functions take two inputs (`map2_*`) and many inputs (`pmap*`).


```
library(purrr)
map(1, length)
```

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

```
[[2]]
[1] 1
```

Better

```
map_int(1, length)
```

```
[1] 1 1
```

Again, it is possible to access the object directly. This can be done as before with `function(<var>)`, or by default with `.` or `.x` together with `~`.

```
map_int(1, function(x) length(x))
```

```
[1] 1 1
```

```
map_int(1, ~ length(.))
```

```
[1] 1 1
```

```
map_int(1, ~ length(.x))
```

```
[1] 1 1
```

An example for map2_*:

```
a <- 1:4
```

```
b <- 4:1
```

```
map2_dbl(a, b, ~ .x + .y)
```

```
[1] 5 5 5 5
```

Nest and unnest

An example data set

```
set.seed(12)
dat <- data.frame(
  id = rep(1:10, each = 10),
  x = runif(100),
  y = runif(100)
)
```

We can use `nest` and `unnest` to create so called `list-columns`.

```
dat %>% nest(data = c(x, y))
```

```
# A tibble: 10 x 2
```

```
  id data
```

```
  <int> <list>
```

```
1     1 <tibble [10 x 2]>
2     2 <tibble [10 x 2]>
3     3 <tibble [10 x 2]>
4     4 <tibble [10 x 2]>
5     5 <tibble [10 x 2]>
6     6 <tibble [10 x 2]>
7     7 <tibble [10 x 2]>
8     8 <tibble [10 x 2]>
9     9 <tibble [10 x 2]>
10    10 <tibble [10 x 2]>
```

```
dat %>% nest(data = -id)
```

```
# A tibble: 10 x 2
```

```
  id data
```

```
  <int> <list>
```

```
1     1 <tibble [10 x 2]>
2     2 <tibble [10 x 2]>
3     3 <tibble [10 x 2]>
4     4 <tibble [10 x 2]>
5     5 <tibble [10 x 2]>
6     6 <tibble [10 x 2]>
7     7 <tibble [10 x 2]>
8     8 <tibble [10 x 2]>
9     9 <tibble [10 x 2]>
10    10 <tibble [10 x 2]>
```

We can then work on the nested column(s), using mutate in combination with map_*:

```
dat %>% nest(data = -id) %>%  
  mutate(centroid.x = map_dbl(data, ~ mean(.x$x)))
```

```
# A tibble: 10 x 3  
      id data                centroid.x  
  <int> <list>                <dbl>  
1     1 <tibble [10 x 2]>      0.315  
2     2 <tibble [10 x 2]>      0.444  
3     3 <tibble [10 x 2]>      0.410  
4     4 <tibble [10 x 2]>      0.672  
5     5 <tibble [10 x 2]>      0.459  
6     6 <tibble [10 x 2]>      0.562  
7     7 <tibble [10 x 2]>      0.519  
8     8 <tibble [10 x 2]>      0.575  
9     9 <tibble [10 x 2]>      0.418  
10    10 <tibble [10 x 2]>      0.422
```

Lets come back to our example

First, lets use `nest()`:

```
amt_fisher %>% nest(data = -name)
```

```
# A tibble: 4 x 2  
  name      data  
  <chr>    <list>  
1 Leroy    <trck_xyt [919 x 5]>  
2 Ricky T <trck_xyt [8,958 x 5]>  
3 Lupe     <trck_xyt [3,004 x 5]>  
4 Lucile   <trck_xyt [1,349 x 5]>
```

Now we can iterate over all animals

```
amt_fisher %>% nest(data = -name) %>%  
  mutate(mean.sl = map_dbl(data, ~ step_lengths(.x) %>%  
    mean(na.rm = TRUE)))
```

```
# A tibble: 4 x 3
```

	name	data	mean.sl
	<chr>	<list>	<dbl>
1	Leroy	<trck_xyt [919 x 5]>	187.
2	Ricky T	<trck_xyt [8,958 x 5]>	42.0
3	Lupe	<trck_xyt [3,004 x 5]>	61.0
4	Lucile	<trck_xyt [1,349 x 5]>	86.0

The approach of list-columns makes it easy to have several grouping instances.

```
amt_fisher %>% mutate(wk = lubridate::week(t_)) %>%
  nest(data = -c(name, wk)) %>%
  mutate(mean.sl = map_dbl(data, ~ step_lengths(.x) %>%
    mean(na.rm = TRUE)))
```

```
# A tibble: 21 x 4
```

	name	wk	data	mean.sl
	<chr>	<dbl>	<list>	<dbl>
1	Leroy	6	<trck_xyt [47 x 5]>	12.6
2	Leroy	7	<trck_xyt [330 x 5]>	204.
3	Leroy	8	<trck_xyt [261 x 5]>	239.
4	Leroy	9	<trck_xyt [281 x 5]>	145.
5	Ricky T	6	<trck_xyt [232 x 5]>	40.6
6	Ricky T	7	<trck_xyt [737 x 5]>	40.3
7	Ricky T	8	<trck_xyt [1,345 x 5]>	46.1
8	Ricky T	9	<trck_xyt [1,488 x 5]>	47.1
9	Ricky T	10	<trck_xyt [1,290 x 5]>	42.3
10	Ricky T	11	<trck_xyt [1,280 x 5]>	36.2

11 2 2 1 1 4 4 2 2 2 2 2 2 2 2 2 2

Take-home messages

1. Available data structures can be used to deal with multiple animal.
2. Lists are just other “containers” to hold some data structures.
3. List columns are a great way to organize complex data structures.

Key resources/publications

Movement ecology

- Bunnefeld, N., Börger, L., van Moorter, B., Rolandsen, C. M., Dettki, H., Solberg, E. J., & Ericsson, G. (2011). A model-driven approach to quantify migration patterns: individual, regional and yearly differences. *Journal of Animal Ecology*, 80(2), 466-476.
- Bjørneraas et al. 2010: Screening Global Positioning System Location Data for Errors Using Animal Movement Characteristics.
<https://doi.org/10.1111/j.1937-2817.2010.tb01258.x>
- Joo, R., Boone, M. E., Clay, T. A., Patrick, S. C., Clusella-Trullas, S., & Basille, M. (2020). Navigating through the R packages for movement. *Journal of Animal Ecology*, 89(1), 248-267.

R resource

- Lovlace, R. et al. (2019). Geocomputation with R:
<https://geocompr.robinlovelace.net/>.
- Wickham, H. R for data science: <https://r4ds.had.co.nz/>