Doing things over and over again: Functions and Loops

For Loops

For each thing in some group of things, do something.

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```
for( <THING>  in  <GROUP OF THINGS ){

  <DO SOMETHING>

}
```

For Loops

For each thing in some group of things, do something.

```
for(i in 1:10){
  print(i)
}
```

For Loops

For each thing in some group of things, do something.

```
for(i in 1:10){
  print(i)
}
```

i is a counter

For Loops

For each thing in some group of things, do something.

```
for(i in 1:10){
  print(i)
}
```

```
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
[1] 10
```

For Loops

For each thing in some group of things, do something.

```
fruits <- c("apple", "banana", "canteloupe")


for(i in 1:length(fruits)){

  print(fruits[i])

}
```

square brackets to subset
We don't want to print **i** itself – we want to print the **i**th member of our vector.

For Loops

For each thing in some group of things, do something.

```
fruits <- c("apple", "banana", "canteloupe")


for(i in 1:length(fruits)){

  print(fruits[i])

}
```

For Loops

For each thing in some group of things, do something.

```
fruits <- c("apple", "banana", "canteloupe")


for(i in 1:length(fruits)){
  print(fruits[i])
}
```

```
[1] "apple"
[1] "banana"
[1] "canteloupe"
```

For Loops

For each thing in some group of things, do something.

- Counting (indexing) starts at 1
- To save results, you have to pre-allocate the output – i.e., make an empty vector before your loop

Safer indexing

For each thing in some group of things, do something.

```
for(i in 1:length(fruits)){
  print(fruits[i])
}
```

```
for(i in seq_along(fruits)){
  print(fruits[i])
}
```

```
[1] "apple"
[1] "banana"
[1] "canteloupe"
```

A few tips

1. Get code working outside a loop
2. Manually set “i” and make sure you get what you expect from the body of the loop

```
i <- 1
print(fruits[i])
```

```
"apple"
```

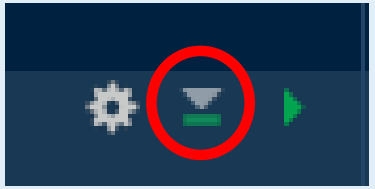
3. Make sure it works on a different one too

```
i <- 2
print(fruits[i])
```

```
“banana"
```

Your Turn 1: Make multiple graphs in a loop

1. Navigate to “Your Turn 1” in the .Rmd file
2. Use this symbol to run all the prior code in the file:



3. Modify the bare-bones `my_plot` function if desired, and run that code chunk.
4. Make vector of unique *station_code* s in the data frame.
5. Fill in the skeleton loop code: for each member of the `station_code` vector, make a graph using the `my_plot` function.

Your Turn 1: Answers

```
my_stns <- unique(wq_trimmed$station_code)


for(i in seq_along(my_stns)){

  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  print(my_plot(wq_sub, sal, do_pct, station_code))
}
```

Your Turn 1: Answers

Notice:

1. *wq_sub* and *i* both appear in your Global Environment.
2. The `my_plot` function was wrapped inside a `print` function.

We printed the plot, but you could do other things like save it with `ggsave()`. (You'll need to figure out how to generate a unique name for each file! It involves the `paste()` function.)

Pre-allocating memory for output

When you want to do more than just print things.

Of course, we'll start by just printing.

```
my_stns <- unique(wq_trimmed$station_code)

for(i in seq_along(my_stns)){
  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  print(my_stns[i])
  print(mean(wq_sub$sal, na.rm = TRUE))
}
```

Pre-allocating memory for output

When you want to do more than just print things.

Of course, we'll start by just printing.

```
my_stns <- unique(wq_trimmed$station_code)

for(i in seq_along(my_stns)){
  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  print(my_stns[i])
  print(mean(wq_sub$sal, na.rm = TRUE))
}
```

Pre-allocating memory for output

When you want to do more than just print things.

Of course, we'll start by just printing.

```
my_stns <- unique(wq_trimmed$station_code)

for(i in seq_along(my_stns)){
  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  print(my_stns[i])
  print(mean(wq_sub$sal, na.rm = TRUE))
}
```

```
[1] "gndblwq"
[1] 19.68066
[1] "gtmpcwq"
[1] 20.20109
[1] "kachdwq"
[1] 30.12615
[1] "niwolwq"
[1] 30.91247
[1] "rkblhwq"
[1] 30.40225
```

Pre-allocating memory for output

What we *want* is probably a data frame that looks like this:

Station	Mean salinity
gndblwq	19.68
gtmpcwq	20.20
kachdwq	30.12
niwolwq	30.91
rkblhwq	30.40

Pre-allocating memory for output

Data frames make loops very, veeeeeery slow.

So we're going to store output in vectors, then bind them together at the end.

```
stns_out <- rep("dummy_value", length(my_stns))
mean_sal_out <- rep(0, length(my_stns))

stns_out; mean_sal_out

[1] "dummy_value" "dummy_value" "dummy_value"
[4] "dummy_value" "dummy_value"

[1] 0 0 0 0 0
```

Pre-allocating memory for output

Now, to loop!

```
for(i in seq_along(my_stns)){
  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  stns_out[i] <- my_stns[i]
  mean_sal_out[i] <- mean(wq_sub$sal, na.rm = TRUE)
}

stns_out; mean_sal_out
```

Pre-allocating memory for output

Now, to loop!

```
for(i in seq_along(my_stns)){
  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  stns_out[i] <- my_stns[i]
  mean_sal_out[i] <- mean(wq_sub$sal, na.rm = TRUE)
}

stns_out; mean_sal_out
```

```
[1] "gndblwq" "gtmpcwq"
[3] "kachdwq" "niwolwq"
[5] "rkblhwq"

[1] 19.68066 20.20109 30.12615
[4] 30.91247 30.40225
```

Pre-allocating memory for output

```
for(i in seq_along(my_stns)){
  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  stns_out[i] <- my_stns[i]
  mean_sal_out[i] <- mean(wq_sub$sal, na.rm = TRUE)
}
```

```
cbind(stns_out, mean_sal_out)
```

```
     stns_out  mean_sal_out
[1,] "gndblwq" "19.6806614086868"
[2,] "gtmpcwq" "20.2010917213249"
[3,] "kachdwq" "30.1261500701366"
[4,] "niwolwq" "30.9124666667409"
[5,] "rkblhwq" "30.4022544404481"
```

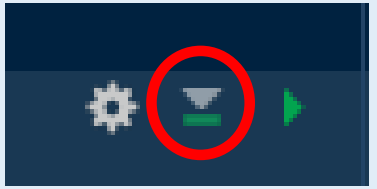
Pre-allocating memory for output

What did we do?

1. Created vectors to hold our output as it was generated
2. Replaced `print()` with a command to store our value in our desired output vector
3. Used “i” to specify *where* in the output vector our value needed to go for each iteration of the loop
4. Used `cbind()` to glue our output vectors together.

Your Turn 2: Make your own loop

1. Navigate to “Your Turn 2” in the .Rmd file
2. Use this symbol to run all the prior code in the file:



3. Write a loop, in which you:
   a. calculate mean temperature for each station
   b. calculate mean depth for each station
   c. bind these together, along with an identifying vector for “station_code”
4. Remember to set up output vectors *first*!

Your Turn 2: Answers

```
my_stns <- unique(wq_trimmed$station_code)
stns_out <- rep("stn", length(my_stns))
sal_out <- rep(0, length(my_stns))
depth_out <- rep(0, length(my_stns))


for(i in seq_along(my_stns)){
  stns_out[i] <- my_stns[i]

  wq_sub <- wq_trimmed %>%
    filter(station_code == my_stns[i])

  sal_out[i] <- mean(wq_sub$sal, na.rm = TRUE)
  depth_out[i] <- mean(wq_sub$depth, na.rm = TRUE)
}

cbind(stns_out, sal_out, depth_out)
```