

Pipe operator

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Necessary packages

```
library(magrittr)
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.0 --

## v ggplot2 3.3.0      v purrr  0.3.4
## v tibble  3.0.1      v dplyr  0.8.5
## v tidyr   1.0.3      v stringr 1.4.0
## v readr   1.3.1      v forcats 0.5.0

## -- Conflicts ----- tidyverse_conflicts() --
## x tidyr::extract()   masks magrittr::extract()
## x dplyr::filter()    masks stats::filter()
## x dplyr::lag()        masks stats::lag()
## x purrr::set_names() masks magrittr::set_names()
```

```
library(stringr)
```

1. Explore the outputs of the following functions.

```
x <- c(1,2)
sum(x, 3)
```

```
[1] 6
```

```
x %>% sum(3)
```

```
[1] 6
```

```
sum(x, 3) == x %>% sum(3)
```

```
[1] TRUE
```

```
seq(3, 10, 2)
```

```
[1] 3 5 7 9
```

```
3 %>% seq(10, 2)
```

```
[1] 3 5 7 9
```

```
10 %>% seq(3, ., 2)
```

```
[1] 3 5 7 9
```

```
# method 1  
filter(iris, Sepal.Length >= 7.0)
```

| | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species |
|----|--------------|-------------|--------------|-------------|------------|
| 1 | 7.0 | 3.2 | 4.7 | 1.4 | versicolor |
| 2 | 7.1 | 3.0 | 5.9 | 2.1 | virginica |
| 3 | 7.6 | 3.0 | 6.6 | 2.1 | virginica |
| 4 | 7.3 | 2.9 | 6.3 | 1.8 | virginica |
| 5 | 7.2 | 3.6 | 6.1 | 2.5 | virginica |
| 6 | 7.7 | 3.8 | 6.7 | 2.2 | virginica |
| 7 | 7.7 | 2.6 | 6.9 | 2.3 | virginica |
| 8 | 7.7 | 2.8 | 6.7 | 2.0 | virginica |
| 9 | 7.2 | 3.2 | 6.0 | 1.8 | virginica |
| 10 | 7.2 | 3.0 | 5.8 | 1.6 | virginica |
| 11 | 7.4 | 2.8 | 6.1 | 1.9 | virginica |
| 12 | 7.9 | 3.8 | 6.4 | 2.0 | virginica |
| 13 | 7.7 | 3.0 | 6.1 | 2.3 | virginica |

```
# method 2 - using pipe  
iris %>% filter(Sepal.Length >= 7.0)
```

| | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species |
|----|--------------|-------------|--------------|-------------|------------|
| 1 | 7.0 | 3.2 | 4.7 | 1.4 | versicolor |
| 2 | 7.1 | 3.0 | 5.9 | 2.1 | virginica |
| 3 | 7.6 | 3.0 | 6.6 | 2.1 | virginica |
| 4 | 7.3 | 2.9 | 6.3 | 1.8 | virginica |
| 5 | 7.2 | 3.6 | 6.1 | 2.5 | virginica |
| 6 | 7.7 | 3.8 | 6.7 | 2.2 | virginica |
| 7 | 7.7 | 2.6 | 6.9 | 2.3 | virginica |
| 8 | 7.7 | 2.8 | 6.7 | 2.0 | virginica |
| 9 | 7.2 | 3.2 | 6.0 | 1.8 | virginica |
| 10 | 7.2 | 3.0 | 5.8 | 1.6 | virginica |
| 11 | 7.4 | 2.8 | 6.1 | 1.9 | virginica |
| 12 | 7.9 | 3.8 | 6.4 | 2.0 | virginica |
| 13 | 7.7 | 3.0 | 6.1 | 2.3 | virginica |

```
# method 1  
ir <- as_tibble(iris)  
select(ir, Species)
```

```
# A tibble: 150 x 1  
  Species
```

```

      <fct>
1 setosa
2 setosa
3 setosa
4 setosa
5 setosa
6 setosa
7 setosa
8 setosa
9 setosa
10 setosa
# ... with 140 more rows

```

```

# method 2 - using pipe
iris %>% as_tibble() %>% select(Species)

```

```

# A tibble: 150 x 1
  Species
  <fct>
1 setosa
2 setosa
3 setosa
4 setosa
5 setosa
6 setosa
7 setosa
8 setosa
9 setosa
10 setosa
# ... with 140 more rows

```

2. Write the following code using the pipe operator.

```

str_c("good", sample(c("health", "food", "work", "day"), 1))

```

```

[1] "goodday"

```

What does the function `str_c` do?

Joins two or more vectors element-wise into a single character vector.

Answer:

```

c("health", "food", "work", "day") %>%
  sample(1) %>%
  str_c("good", .)

```

```

[1] "goodfood"

```

3. Write the following code using the pipe operator.

```
summarize(filter(iris, Species=="setosa"), median(Sepal.Length))
```

```
  median(Sepal.Length)  
1                5
```

Answer:

```
iris %>%  
  filter(Species=="setosa") %>%  
  summarize(median(Sepal.Length))
```

```
  median(Sepal.Length)  
1                5
```