

Introduction to R pipes and dplyr

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The magrittr pipe operator

An R package called `magrittr` popularized a new operator called a pipe (Note: pipes are an older computing concept dating back to the origins of the Unix operating)

- ▶ The pipe operator is `%>%`

Using pipes:

- ▶ `x %>% f()` is equivalent to `f(x)`
- ▶ `x %>% f(y)` is equivalent to `f(x,y)`.

Examples:

- ▶ Single argument function:

```
pi %>% cos()  
[1] -1
```

- ▶ For single argument functions, after the pipe you can drop the parentheses:

```
pi %>% cos  # same as above  
[1] -1
```

- ▶ Multi-argument functions

```
100 %>% log(base=10) # 100 is treated as the first argument  
[1] 2
```

Building pipelines with the pipe operator

The pipe operator allows us to build analysis “pipelines”.

A pipeline series of function calls that filter and/or transform our data

```
letters %>%           # start with letters vector
  str_to_upper %>%    # convert to upper case
  tail(10) %>%        # get last 10 elements
  str_flatten("-")     # join into single string, separated by '-'
[1] "Q-R-S-T-U-V-W-X-Y-Z"
```

The pipe operator helps to make our intent clearer, as compared to nested function calls:

```
str_flatten(tail(str_to_upper(letters), 10), "-")
[1] "Q-R-S-T-U-V-W-X-Y-Z"
```

The “built-in” pipe operator (R 4.1+)

The magrittr pipe operator became popular enough that the R developers added a native pipe operator to the R language starting in release 4.1.

- ▶ The native pipe operator is `|>`

The native pipe operator works similarly to the magrittr pipe:

- ▶ `x |> f()` is equivalent to `f(x)`
- ▶ `x |> f(y)` is equivalent to `f(x,y)`.

magrittr pipe allows you to drop parentheses for single argument functions, but this is not allowed with the native pipe:

```
pi %>% cos    # equivalent to pi %>% cos()  
pi |> cos     # this is an error with the native pipe  
pi |> cos()   # must add parentheses with native pipe
```

Placeholder, magrittr pipes

magrittr pipe allows you to use a “placeholder” symbol (.) for cases where the object your piping is not the first argument in the function being called:

the period (.) is the placeholder

```
c("A", "B", "C") %>%  
  data.frame(x = c(1,2,3), y = .)  
  x y  
1 1 A  
2 2 B  
3 3 C
```

magrittr placeholder can appear multiple times:

```
c("A", "B", "C") %>%  
  tibble(x = c(1,2,3), y = ., z = str_to_lower(.))  
# A tibble: 3 x 3  
      x y      z  
  <dbl> <chr> <chr>  
1     1 1 A      a  
2     2 2 B      b  
3     3 3 C      c
```

Placeholder, native pipes

A placeholder symbol (`_`) for use with the native pipe was introduced in R 4.2, but it has several limitations:

- ▶ Can only appear once
- ▶ Can only be used with named arguments

This works:

```
c("A", "B", "C") |>
  tibble(x = c(1,2,3), y = _)
# A tibble: 3 x 2
      x y
  <dbl> <chr>
1     1 A
2     2 B
3     3 C
```

But this doesn't:

```
c("A", "B", "C") |>
  tibble(x = c(1,2,3), y = _, z = str_to_lower(_))
```

What is dplyr?

dplyr is a package that provides a “grammar for data manipulation”

Core “verbs” in the dplyr package:

Column manipulation:

- ▶ `select()`
- ▶ `mutate()`

Row manipulation:

- ▶ `filter()`
- ▶ `arrange()`

Collapsing and Grouping:

- ▶ `summarize()`
- ▶ `group_by()`

All these functions return new data frames instead of modifying existing data frames

select() subsets columns

```
# select two columns
```

```
select(iris, Sepal.Length, Petal.Length) |> head(3)
```

	Sepal.Length	Petal.Length
1	5.1	1.4
2	4.9	1.4
3	4.7	1.3

```
# select everything BUT the species column
```

```
select(iris, -Species) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	5.1	3.5	1.4	0.2
2	4.9	3.0	1.4	0.2
3	4.7	3.2	1.3	0.2

`select()` has some helper functions for powerful filtering

See <https://tidyselect.r-lib.org/reference/language.html>

- ▶ `var1:var10`: variables lying between `var1` on the left and `var10` on the right. Also works with numeric indices.
- ▶ `everything()`: all variables.
- ▶ `all_of(vars)/any_of(vars)`: matches names stored in the character vector `vars`.
- ▶ `last_col()`: furthest column on the right.
- ▶ `where(predicate)`: all variables where predicate function returns TRUE.
e.g `where(is.numeric)`
- ▶ `starts_with()`: Starts with an exact prefix.
- ▶ `ends_with()`: Ends with an exact suffix.
- ▶ `contains()`: Contains a literal string.
- ▶ `matches()`: Matches a regular expression.
- ▶ `num_range()`: Matches a numerical range like `x01`, `x02`, `x03`.

select() helper examples

```
select(iris, starts_with("Petal")) |> head(3)
```

	Petal.Length	Petal.Width
1	1.4	0.2
2	1.4	0.2
3	1.3	0.2

```
select(iris, ends_with("Length")) |> head(3)
```

	Sepal.Length	Petal.Length
1	5.1	1.4
2	4.9	1.4
3	4.7	1.3

```
select(iris, where(is.numeric)) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	5.1	3.5	1.4	0.2
2	4.9	3.0	1.4	0.2
3	4.7	3.2	1.3	0.2

mutate() adds or transforms columns

```
mutate(iris, Species = str_to_upper(Species)) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	SETOSA
2	4.9	3.0	1.4	0.2	SETOSA
3	4.7	3.2	1.3	0.2	SETOSA

mutate can refer to multiple existing columns

```
iris |>
  select(starts_with("Sepal")) |>
  mutate(Sepal_Sum = Sepal.Width + Sepal.Length) |>
  head(3)
```

	Sepal.Length	Sepal.Width	Sepal_Sum
1	5.1	3.5	8.6
2	4.9	3.0	7.9
3	4.7	3.2	7.9

can refer to columns created "on the fly"

```
iris |>
  select(starts_with("Sepal")) |>
  mutate(Sepal_Sum = Sepal.Width + Sepal.Length,
         Sepal_Width_Ratio = Sepal.Width / Sepal_Sum) |>
  head(3)
```

	Sepal.Length	Sepal.Width	Sepal_Sum	Sepal_Width_Ratio
1	5.1	3.5	8.6	0.4069767
2	4.9	3.0	7.9	0.3797468
3	4.7	3.2	7.9	0.4050633

`filter()` selects rows that match criteria

```
# get only the I. setosa specimens
```

```
filter(iris, Species == "setosa") |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa

```
# filter on multiple criteria, treated as "AND"
```

```
filter(iris, Species == "setosa", Sepal.Length < 5) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa

`arrange()` sorts rows according to values of one or more columns

```
# sort by Sepal.Length
```

```
arrange(iris, Sepal.Length) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	4.3	3.0	1.1	0.1	setosa
2	4.4	2.9	1.4	0.2	setosa
3	4.4	3.0	1.3	0.2	setosa

```
# sort on multiple columns: by Sepal.Length then by Petal.Length
```

```
arrange(iris, Sepal.Length, Petal.Length) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	4.3	3.0	1.1	0.1	setosa
2	4.4	3.0	1.3	0.2	setosa
3	4.4	3.2	1.3	0.2	setosa

```
# sort in descending order using helper desc()
```

```
arrange(iris, desc(Sepal.Length)) |> head(3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	7.9	3.8	6.4	2.0	virginica
2	7.7	3.8	6.7	2.2	virginica
3	7.7	2.6	6.9	2.3	virginica

summarize() transforms and collapses

summarize() applies functions to one or more variables (columns) in the data frame, reducing a vector of values to a single value and returning the results in a data frame

```
summarize(iris,  
           avg.Sepal.Length = mean(Sepal.Length),  
           avg.Petal.Length = mean(Petal.Length))  
  avg.Sepal.Length avg.Petal.Length  
1      5.843333      3.758
```

group_by() is used for conditioning (faceting) and transforming

```
# apply grouping
grouped.df <- group_by(iris, Species)

# summarize grouped data frame
summarize(grouped.df,
           avg.Sepal.Length = mean(Sepal.Length),
           avg.Petal.Length = mean(Petal.Length))

# A tibble: 3 x 3
  Species      avg.Sepal.Length avg.Petal.Length
  <fct>          <dbl>          <dbl>
1 setosa         5.01            1.46
2 versicolor     5.94            4.26
3 virginica      6.59            5.55
```

The dplyr verbs functions are designed to work well with piping!

```
iris |>
  filter(Species != "virginica") |>
  group_by(Species) |>
  summarize(avg.Sepal.Length = mean(Sepal.Length),
            avg.Sepal.Width = mean(Sepal.Width))
# A tibble: 2 x 3
  Species      avg.Sepal.Length avg.Sepal.Width
  <fct>          <dbl>          <dbl>
1 setosa          5.01          3.43
2 versicolor      5.94          2.77
```


dplyr pipelines feed naturally into ggplot

But note that ggplot layers are “added” *not* piped:

```
iris |>
  filter(Species != "virginica") |>
  ggplot(aes(x = Sepal.Length, y = Sepal.Width, color = Species)) +
  geom_point(size=3) +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Morphology for non-virginica Iris species") +
  theme_classic() +
  theme(legend.justification = c(1, 1), legend.position = c(1, 1))
```

