Manipulating columns

Getting and Cleaning Data

```
msleep %>%
  filter(order == "Primates", sleep_total > 10) %>%
  select(name, sleep_rem, sleep_cycle, sleep_total) %>%
  arrange(name) %>%
  mutate(sleep_total_min = sleep_total * 60)
```

```
# A tibble: 5 x 5
                 sleep_rem sleep_cycle sleep_total /sleep_total_min
  name
                                     <db1>
                                                   \langle db1 \rangle
                                                                      <db1>
  <chr>
                      \langle dh1 \rangle
1 Macaque
                         1.2
                                      0.75
                                                    10.1
                                                                         606
2 Owl monkey
                        1.8
                                                    17
                                                                       1020
                                     NA
                                                    10.9
3 Patas monkey
                      1.1
                                     NA
                                                                         654
                                     NA
                                                    11
                                                                         660
4 Potto
                       NA
5 Slow loris
                                                    11
                                                                         660
                       NA
                                     NA
```

A whole new column!

```
msleep %>%
  filter(order == "Primates", sleep_total > 10) %>%
  select(name, sleep_rem, sleep_cycle, sleep_total) %>%
  arrange(name) %>%
  mutate(new_sleep = "msleep_data")
```

```
# A tibble: 5 x 5
               sleep_rem sleep_cycle sleep_total new_sleep
  name
  <chr>
                   <db1>
                               <db1>
                                            <dbl> <chr>
                                0.75
                                             10.1 msleep_data
1 Macague
                     1.2
2 Owl monkey
                     1.8
                               NA
                                             17
                                                  msleep_data
3 Patas monkey
                   1.1
                               NA
                                             10.9 msleep_data
4 Potto
                    NA
                               NA
                                             11
                                                  msleep_data
5 Slow loris
                    NA
                               NA
                                             11
                                                  msleep_data
```

A whole new column that is equal to the same value in all rows

```
# Save the results of filter, select and arrange to a dataframe
sleepy_primates <- msleep %>%
  filter(order == "Primates", sleep_total > 10) %>%
  select(name, sleep_rem, sleep_cycle, sleep_total) %>%
  arrange(name)
```

To create a new column with the sleep total converted to minutes
sleepy_primates\$sleep_total_min <- sleepy_primates\$sleep_total * 60</pre>

To add a column with the same value in each row
sleepy_primates\$new_sleep <- "msleep_data"</pre>

```
# Getting rid of the column bodywt
msleep %>%
  filter(order == "Primates", sleep_total > 10) %>%
  select(-bodywt)
```

# A tibble: 5 x 10 Now our dataset has only 10 columns instead of 11!										
	name	genus	vore	order	conservation	sleep_total	sleep_rem	sleep_cycle	awake	brainwt
	<chr></chr>	<chr></chr>	<chr></chr>	<chr></chr>	<chr></chr>	<db1></db1>	<db1></db1>	<db1></db1>	<db1></db1>	<db1></db1>
1	Owl monkey	Aotus	omni	Primates	NA	17	1.8	NA	7	0.0155
2	Patas monkey	Erythrocebus	omni	Primates	lc	10.9	1.1	NA	13.1	0.115
3	Macaque	Macaca	omni	Primates	NA	10.1	1.2	0.75	13.9	0.179
4	Slow loris	Nyctibeus	carni	Primates	NA	11	NA	NA	13	0.0125
5	Potto	Perodicticus	omni	Primates	lc	11	NA	NA	13	NA

> conservation # A tibble: 11 x 1 **Tidy data violation!** conservation abbreviation` Space in column name should be an underscore. <chr> 1 EX = ExtinctTidy data violation! 2 EW = Extinct in the wild There are two pieces of 3 CR = Critically Endangered information in a column: (1) 4 EN = Endangeredabbreviation and (2) description. 5 VU = Vulnerable6 NT = Near Threatened 7 LC = Least Concern 8 DD = Data deficient 9 NE = Not evaluated 10 PE = Probably extinct (informal) 11 PEW = Probably extinct in the wild (informal)

```
> conservation %>%
    separate(`conservation abbreviation`,
             into = c("abbreviation", "description"), sep = " = ")
# A tibble: 11 x 2
   abbreviation description
   <chr>
                <chr>
   EX
                Extinct
   EW
                Extinct in the wild
   CR
                Critically Endangered
   EN
                Endangered
  VU
                Vulnerable
  NT
                Near Threatened
   LC
                Least Concern
   DD
                Data deficient
   NE
                Not evaluated
10
  PE
                Probably extinct (informal)
                Probably extinct in the wild (informal)
11 PEW
```

```
> conservation %>%
    separate(`conservation abbreviation`,
             into = c("abbreviation", "description"), sep = " = ") %>%
   unite(united_col, abbreviation, description, sep=" = ")
 A tibble: 11 x 1
  united_col
   <chr>
 1 EX = Extinct
2 EW = Extinct in the wild
 3 CR = Critically Endangered
4 EN = Endangered
 5 VU = Vulnerable
6 NT = Near Threatened
 7 LC = Least Concern
8 DD = Data deficient
9 NE = Not evaluated
10 PE = Probably extinct (informal)
11 PEW = Probably extinct in the wild (informal)
```

```
> conservation %>%
   clean_names()
# A tibble: 11 x 1
   conservation abbreviation
   <chr>>
                       Adds underscore to column name
 1 EX = Extinct
 2 EW = Extinct in the wild
3 CR = Critically Endangered
4 EN = Endangered
 5 VU = Vulnerable
 6 NT = Near Threatened
 7 LC = Least Concern
 8 DD = Data deficient
 9 NE = Not evaluated
10 PE = Probably extinct (informal)
11 PEW = Probably extinct in the wild (informal)
```

Summarizing: Manipulating Data

Getting and Cleaning Data