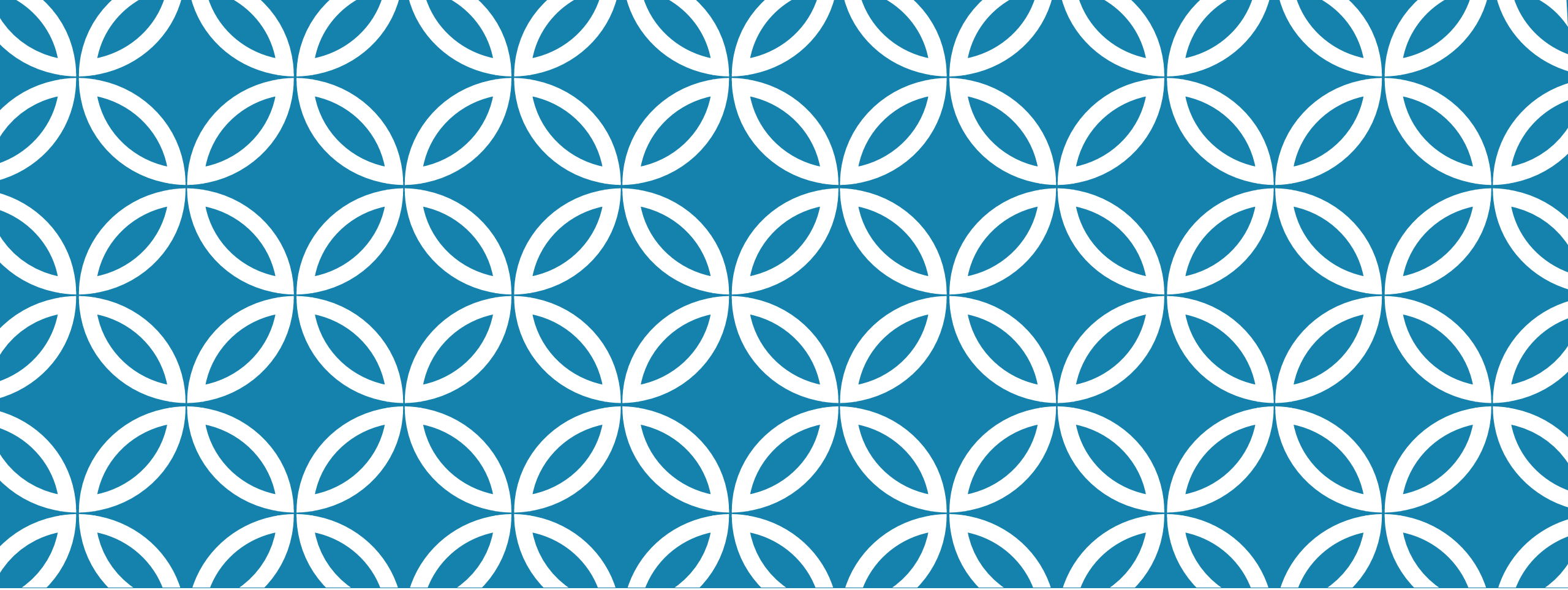


Introduction to R Workshop

Session 5

Data Understanding: Stats

May 6, 2019

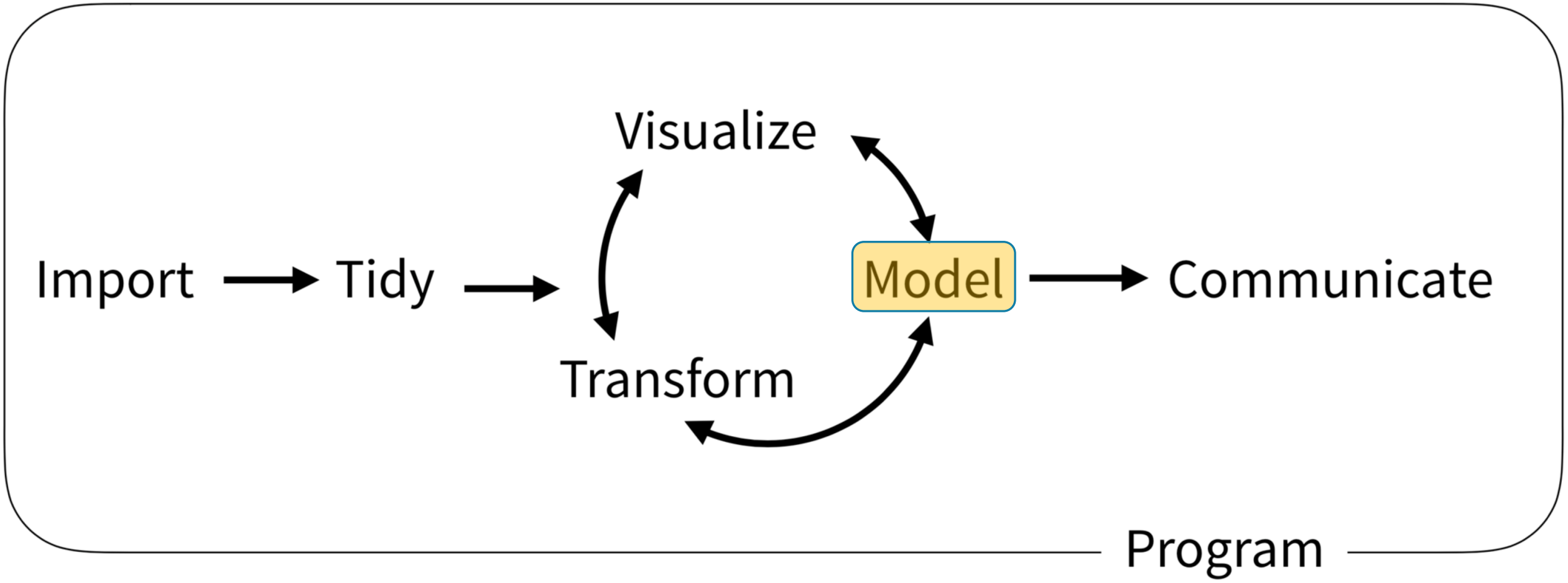
7:00 am - 8:00 am	BREAKFAST BALLROOM LOBBY 2ND FLOOR
8:00 am - 8:10 am	Instructor and Course Introduction
8:10 am - 9:50 am	Introduction to R and RStudio for Reproducible Reporting
9:50 am - 10:10 am	REFRESHMENT BREAK - BALLROOM LOBBY 2ND FLOOR
10:10 am - 11:50 am	Data Wrangling
12:00 pm - 1:00 pm	LUNCH BALLROOM LOBBY 2ND FLOOR
1:00 pm - 2:50 pm	Data Understanding
2:50 pm - 3:10 pm	REFRESHMENT BREAK - BALLROOM LOBBY - 2ND FLOOR
3:10 pm - 5:00 pm	Exploratory Data Analysis

Objectives

Be able to…

1. Summarize variables, including calculation of summary statistics
2. Break apart data frames observations into groups
3. Use standard statistical modeling functions
4. Compare variables' distributions

Typical Data Science Pipeline

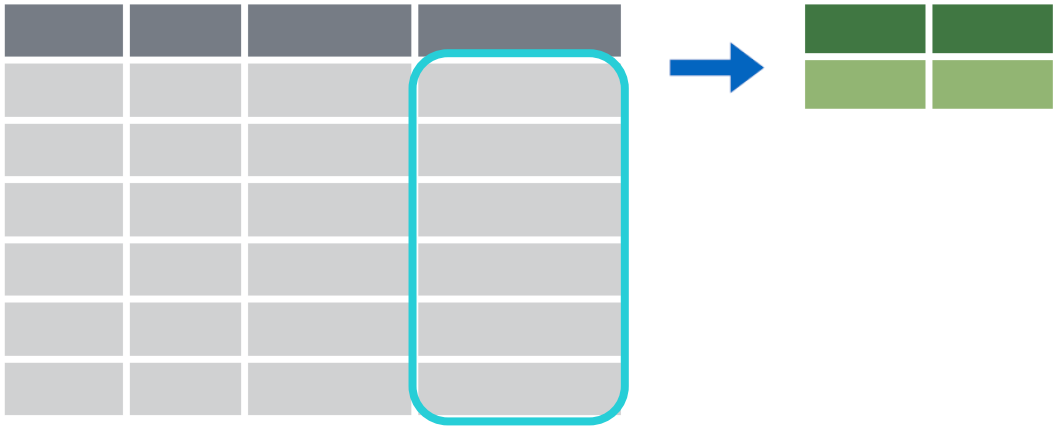


From *R for Data Science* (https://r4ds.had.co.nz/introduction.html)

Summarize()

summarize()

- Make summaries of your data



summarize()

- Make summaries of your data

```
orders %>%
    summarize(new_variable = calculation)
```

name for new variable

Value or function

summarize()

- Make summaries of your data

function that returns number of observations

```
orders %>%
    select(order_id, patient_id) %>%
    head(4) %>%
    summarize(order_count = n())
```

order_id	patient_id
19766	511388
88444	511388
40477	508061
97641	508061

→

order_count
4

summarize()

- Make summaries of your data

```
orders %>%
    select(order_id, patient_id) %>%
    head(4) %>%
    summarize(order_count = n(),
              pt_count = n_distinct(patient_id))
```

function that returns number of distinct values

order_id	patient_id
19766	511388
88444	511388
40477	508061
97641	508061

→

order_count	pt_count
4	2

Your Turn 1

Add onto the code in the above chunk to calculate:

1) Mean count of orders per patient

2) Mean count of orders per department

Calculate:

1) Mean count of orders per patient

```
orders_1 <- orders %>%
      summarize(order_count = n(),
                pt_count = n_distinct(patient_id)) %>%
      mutate(pt_order_count_mean = order_count / pt_count)
```

order_count <int>	pt_count <int>	pt_order_count_mean <dbl>
45002	9406	4.784393

1 row

Calculate:

2) Mean count of orders per department

```
orders_1 <- orders %>%
      summarize(order_count = n(),
                dept_count = n_distinct(department)) %>%
      mutate(dept_order_count_mean = order_count / dept_count)
```

order_count <int>	dept_count <int>	dept_order_count_mean <dbl>
45002	20	2250.1

1 row

Vector Functions

TO USE WITH MUTATE ()

COUNTS

dplyr::**n()** - number of values/rows
dplyr::**n_distinct()** - # of uniques
sum(!is.na()) - # of non-NA's

LOCATION

mean() - mean, also **mean(!is.na())**
median() - median

LOGICALS

mean() - Proportion of TRUE's
sum() - # of TRUE's

POSITION/ORDER

dplyr::**first()** - first value
dplyr::**last()** - last value
dplyr::**nth()** - value in nth location of vector

RANK

quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

IQR() - Inter-Quartile Range
mad() - median absolute deviation
sd() - standard deviation
var() - variance

Summary Functions

TO USE WITH SUMMARISE ()

summarise() applies summary functions to columns to create a new table. Summary functions take vectors as input and return single values as output.

summary function

COUNTS

dplyr::**n()** - number of values/rows
dplyr::**n_distinct()** - # of uniques
sum(!is.na()) - # of non-NA's

LOCATION

mean() - mean, also **mean(!is.na())**
median() - median

LOGICALS

mean() - Proportion of TRUE's
sum() - # of TRUE's

POSITION/ORDER

dplyr::**first()** - first value
dplyr::last() - last value
dplyr::nth() - value in nth location of vector

RANK

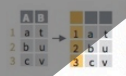
quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

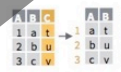
IQR() - Inter-Quartile Range
mad() - median absolute deviation
sd() - standard deviation
var() - variance

Row Names

Tidy data does not use rownames, which store a variable outside of the columns. To work with the rownames, first move them into a column.



rownames_to_column()
Move row names into col.
a <- rownames_to_column(iris, var = "C")

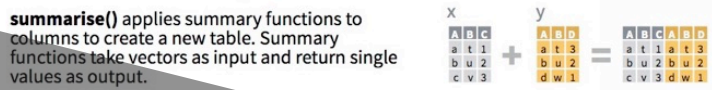


column_to_rownames()
Move col in row names.
column_to_rownames(a, var = "C")

Also **has_rownames()**, **remove_rownames()**

Combine Tables

COMBINE VARIABLES



Use **bind_cols()** to paste tables beside each other as they are.

bind_cols(…) Returns tables placed side by side as a single table.
BE SURE THAT ROWS ALIGN.

Use a "**Mutating Join**" to join one table to columns from another, matching values with the rows that they correspond to. Each join retains a different combination of values from the tables.

left_join(x, y, by = NULL, copy=FALSE, suffix=c(".x",".y"),…)
Join matching values from y to x.

right_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),…)
Join matching values from x to y.

inner_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),…)
Join data. Retain only rows with matches.

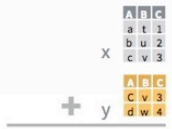
full_join(x, y, by = NULL, copy=FALSE, suffix=c(".x",".y"),…)
Join data. Retain all values, all rows.

Use **by = c("col1", "col2")** to specify the column(s) to match on.
left_join(x, y, by = "A")

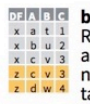
Use a named vector, **by = c("col1" = "col2")**, to match on columns with different names in each data set.
left_join(x, y, by = c("C" = "D"))

Use **suffix** to specify suffix to give to duplicate column names.
left_join(x, y, by = c("C" = "D"), suffix = c("1", "2"))

COMBINE CASES



Use **bind_rows()** to paste tables below each other as they are.



bind_rows(…, .id = NULL)
Returns tables one on top of the other as a single table. Set .id to a column name to add a column of the original table names (as pictured)

intersect(x, y, …)
Rows that appear in both x and y.

setdiff(x, y, …)
Rows that appear in x but not y.

union(x, y, …)
Rows that appear in x or y.
(Duplicates removed). union_all() retains duplicates.

Use **setequal()** to test whether two data sets contain the exact same rows (in any order).

EXTRACT ROWS

Use a "**Filtering Join**" to filter one table against the rows of another.

semi_join(x, y, by = NULL, …)
Return rows of x that have a match in y.
USEFUL TO SEE WHAT WILL BE JOINED.

anti_join(x, y, by = NULL, …)
Return rows of x that do not have a match in y. USEFUL TO SEE WHAT WILL NOT BE JOINED.

Your Turn 2

Use *summarize()* to calculate:

1) The date of the first (or minimum) order

2) The median time difference between *order_time* and *result_time*

Hint Refer to help for *NA* handling

Calculate:

1) The minimum or first order date

```
orders %>%
    summarize(order_time_min = min(order_time))
```

order_time_min
<S3: POSIXct>
2017-08-13 11:59:00

1 row

Calculate:

2) The median time difference between order_time and result_time

```
orders %>%
       mutate(result_interval = result_time - order_time) %>%
       summarize(result_interval_med = median(result_interval, na.rm = TRUE))
```

result_interval_med
<time>
18360 secs

1 row

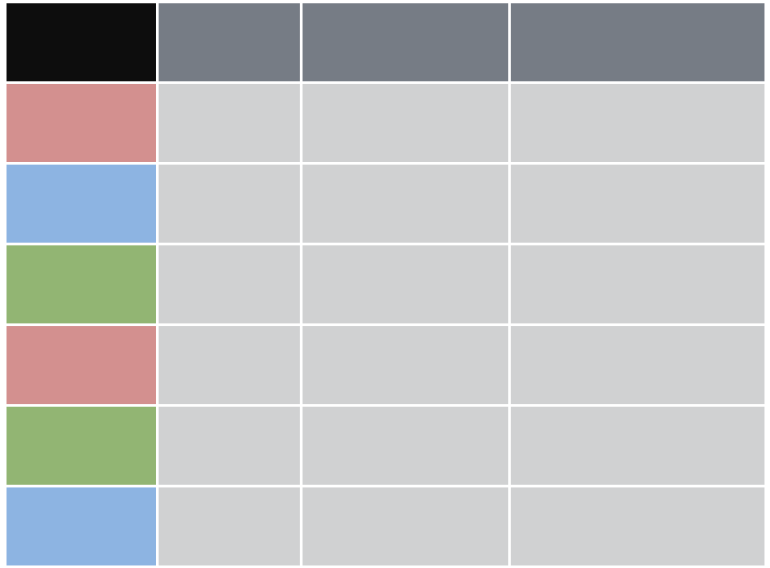
Your Turn 3

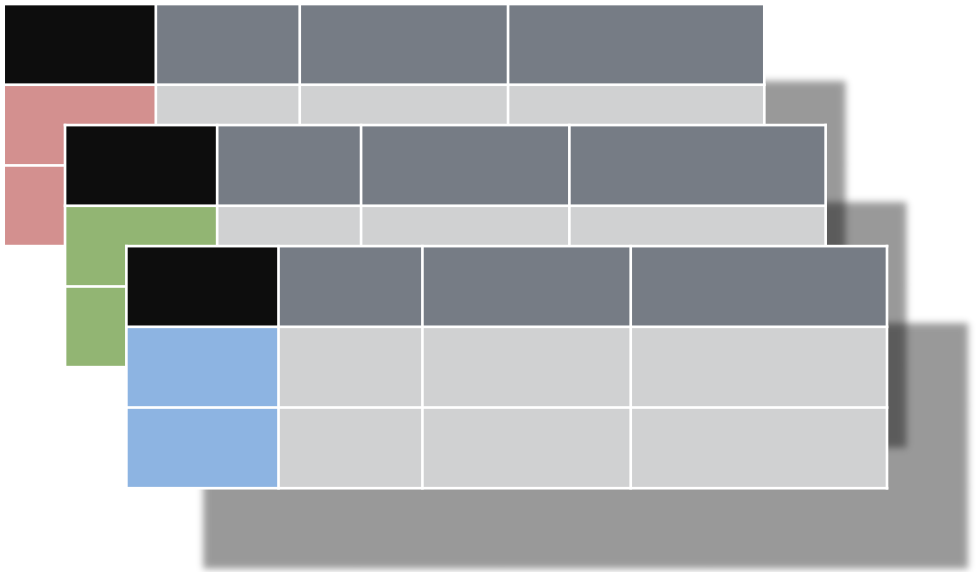
Consider:

How would you calculate the median number of orders for each patient?

group_by()

group_by()





group_by()

- *Grouping observations based on a specific variable's values*

```
orders %>%
    group_by(variable)
```

name of variable to group by

group_by()

- *Group observations by patient_id*

```
orders %>%
    group_by(patient_id)
```

```
# A tibble: 45,002 x 17
# Groups:   patient_id [9,406]
   order_id patient_id description proc_code
      <dbl>      <dbl> <chr>       <chr>
 1    19766     511388 PROTHROMBI… PRO
 2    88444     511388 BASIC META… BMP
 3    40477     508061 THYROID ST… TSH
 4    97641     508061 T4, FREE    T4FR
```

group_by()

- *Group observations by patient_id and department*

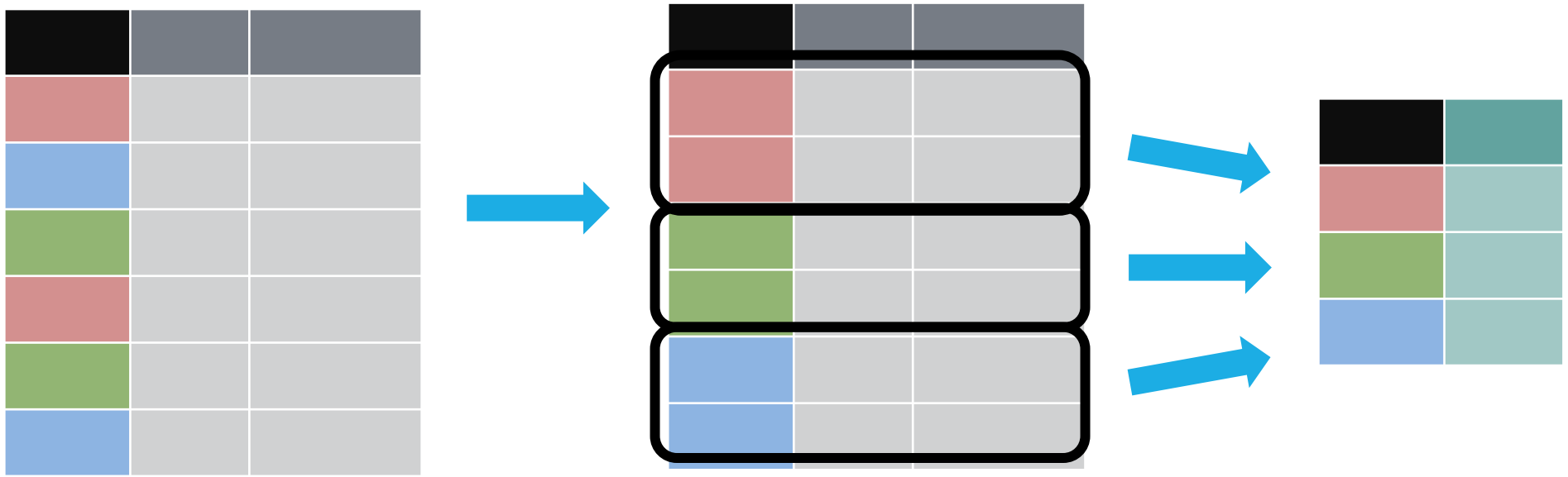
```
orders %>%
    group_by(patient_id, department)
```

```
# A tibble: 45,002 x 17
# Groups:   patient_id, department [10,102]
   order_id patient_id description proc_code
      <dbl>      <dbl> <chr>       <chr>
 1    19766     511388 PROTHROMBI… PRO
 2    88444     511388 BASIC META… BMP
 3    40477     508061 THYROID ST… TSH
 4    97641     508061 T4, FREE    T4FR
```

group_by() %>% summarize()

group_by() %>% summarize()

Make summaries of your data *by group*



Re-calculate the mean order count per patient

- ***Recall*** *that we previously used summarize() and mutate() like this:*

```
orders %>%
     summarize(order_count = n(),
               pt_count = n_distinct(patient_id)) %>%
     mutate(pt_order_count_mean = order_count / pt_count)
```

```
# A tibble: 1 x 3
  order_count pt_count pt_order_count_mean
        <int>    <int>                <dbl>
1       45002     9406             4.784393
```

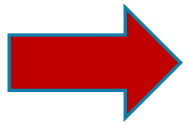
Calculate the mean order count per patient

- *Let's now use group_by() and summarize()…*

```
orders %>%
      group_by(patient_id) %>%
      summarize(order_count = n()) %>%
      summarize(pt_order_count_mean = mean(order_count))
```

1

```
# A tibble: 9,406 x 2
   patient_id order_count
        <dbl>       <int>
1      500001           1
2      500002           7
3      500003           5
4      500005           1
5      500006           5
```



2

```
# A tibble: 1 x 1
  pt_order_count_mean
                <dbl>
1            4.784393
```

Your Turn 4

Calculate:

1) The median number of orders per patient

2) The maximum number of TSH orders per patient

3) (**Bonus**) The 5th and 95th percentile of the number of orders per patient (*Hint: look up function `quantile()`*)

Calculate:

1) The median number of orders per patient

```
orders %>%
       group_by(patient_id) %>%
       summarize(order_count = n()) %>%
       summarize(pt_order_count_median = median(order_count))
```

pt_order_count_median
<dbl>
4

1 row

Calculate:

2) The maximum number of TSH orders per patient

```
orders %>%
       filter(proc_code == "TSH") %>%
       group_by(patient_id) %>%
       summarize(order_count = n()) %>%
       summarize(pt_order_count_max = max(order_count))
```

pt_order_count_max
<dbl>
6

1 row

Calculate:

3) (*Bonus*) The 5th and 95th percentile of the number of orders per patient

```
orders %>%
       group_by(patient_id) %>%
       summarize(order_count = n()) %>%
       summarize(pt_order_count_q05 = quantile(order_count, probs=0.05),
                 pt_order_count_q95 = quantile(order_count, probs=0.95))
```

pt_order_count_q05 <dbl>	pt_order_count_q95 <dbl>
1	13

1 row

Your Turn 5

Calculate the mean order count per patient for each department

Hint: summarize() rolls up a single grouping variable at a time

Calculate the mean order count per patient for each department

```
orders %>%
        group_by(department, patient_id) %>%
        summarize(order_count = n()) %>%
        summarize(pt_order_count_mean = mean(order_count))
```

1

```
# A tibble: 10,102 x 3
# Groups:   department [?]
                department patient_id order_count
                     <chr>      <dbl>       <int>
 1 BEHAVIORAL HEALTH CLINIC     500126           1
 2 BEHAVIORAL HEALTH CLINIC     500251           9
 3 BEHAVIORAL HEALTH CLINIC     500385          13
 4 BEHAVIORAL HEALTH CLINIC     500395           1
 5 BEHAVIORAL HEALTH CLINIC     500519           1
```

2

```
# A tibble: 20 x 2
                    department pt_order_count_mean
                         <chr>               <dbl>
 1      BEHAVIORAL HEALTH CLINIC            5.651685
 2            CARDIOLOGY CLINIC             3.916031
 3         ENDOCRINOLOGY CLINIC             3.416092
 4       FAMILY MEDICINE CLINIC             3.609278
 5   GASTROENTEROLOGY CLINIC                4.540698
```

Compare two sets of count data

Compare sample distributions

- *Create the order counts per patient for each department*

```
orders %>%
       filter(department %in% c("INTERNAL MEDICINE CLINIC",
                                "FAMILY MEDICINE CLINIC")) %>%
       group_by(department, patient_id) %>%
       summarize(order_count = n()) %>%
       ungroup() -> orders_per_pt_dept
```

```
# A tibble: 9,831 x 17
# Groups:   department, patient_id [2,632]
   order_id patient_id                  description
      <dbl>      <dbl>                        <chr>
 1    19766     511388                      PROTHRO
 2    88444     511388          BASIC METABOLIC PANEL
 3    50728     501184 COMPREHENSIVE METABOLIC PANEL
 4    91635     501184                  CBC (HEMOGRAM)
```

1

```
# A tibble: 2,632 x 3
# Groups:   department [?]
                department patient_id order_count
                     <chr>      <dbl>       <int>
 1 FAMILY MEDICINE CLINIC     500003           5
 2 FAMILY MEDICINE CLINIC     500022           4
 3 FAMILY MEDICINE CLINIC     500024          14
 4 FAMILY MEDICINE CLINIC     500034           2
 5 FAMILY MEDICINE CLINIC     500042           4
```

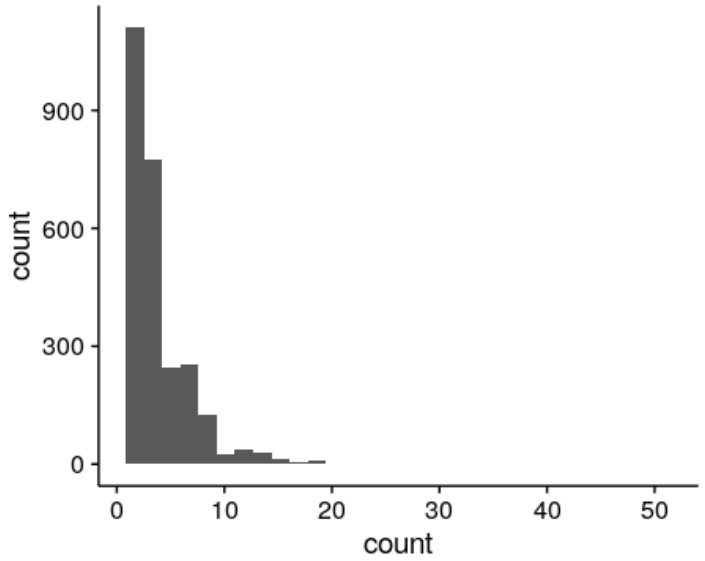
2

```
# A tibble: 2,632 x 3
                department patient_id order_count
                     <chr>      <dbl>       <int>
 1 FAMILY MEDICINE CLINIC     500003           5
 2 FAMILY MEDICINE CLINIC     500022           4
 3 FAMILY MEDICINE CLINIC     500024          14
 4 FAMILY MEDICINE CLINIC     500034           2
 5 FAMILY MEDICINE CLINIC     500042           4
```

3

Visualize the distribution of order counts

```
orders_per_pt_dept %>%
        ggplot() +
        geom_histogram(aes(x = order_count))
```



orders_per_pt_dept

department <chr>	patient_id <dbl>	order_count <int>
FAMILY MEDICINE CLINIC	500003	5
FAMILY MEDICINE CLINIC	500022	4
FAMILY MEDICINE CLINIC	500024	14
FAMILY MEDICINE CLINIC	500034	2
FAMILY MEDICINE CLINIC	500042	4
FAMILY MEDICINE CLINIC	500043	9

6 rows

Describe the central tendency of the order count

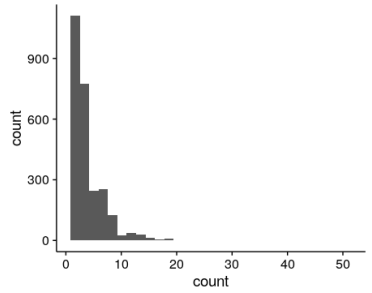
```
orders_per_pt_dept %>%
        group_by(department) %>%
        summarize(order_count_median = median(order_count),
                  order_count_mean = mean(order_count))
```

orders_per_pt_dept

department <chr>	patient_id <dbl>	order_count <int>
FAMILY MEDICINE CLINIC	500003	5
FAMILY MEDICINE CLINIC	500022	4
FAMILY MEDICINE CLINIC	500024	14
FAMILY MEDICINE CLINIC	500034	2
FAMILY MEDICINE CLINIC	500042	4
FAMILY MEDICINE CLINIC	500043	9

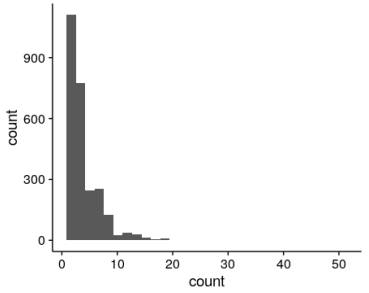
6 rows

```
# A tibble: 2 x 3
                  department order_count_median order_count_mean
                       <chr>              <dbl>            <dbl>
1   FAMILY MEDICINE CLINIC                  3         3.609278
2 INTERNAL MEDICINE CLINIC                  3         3.808664
```

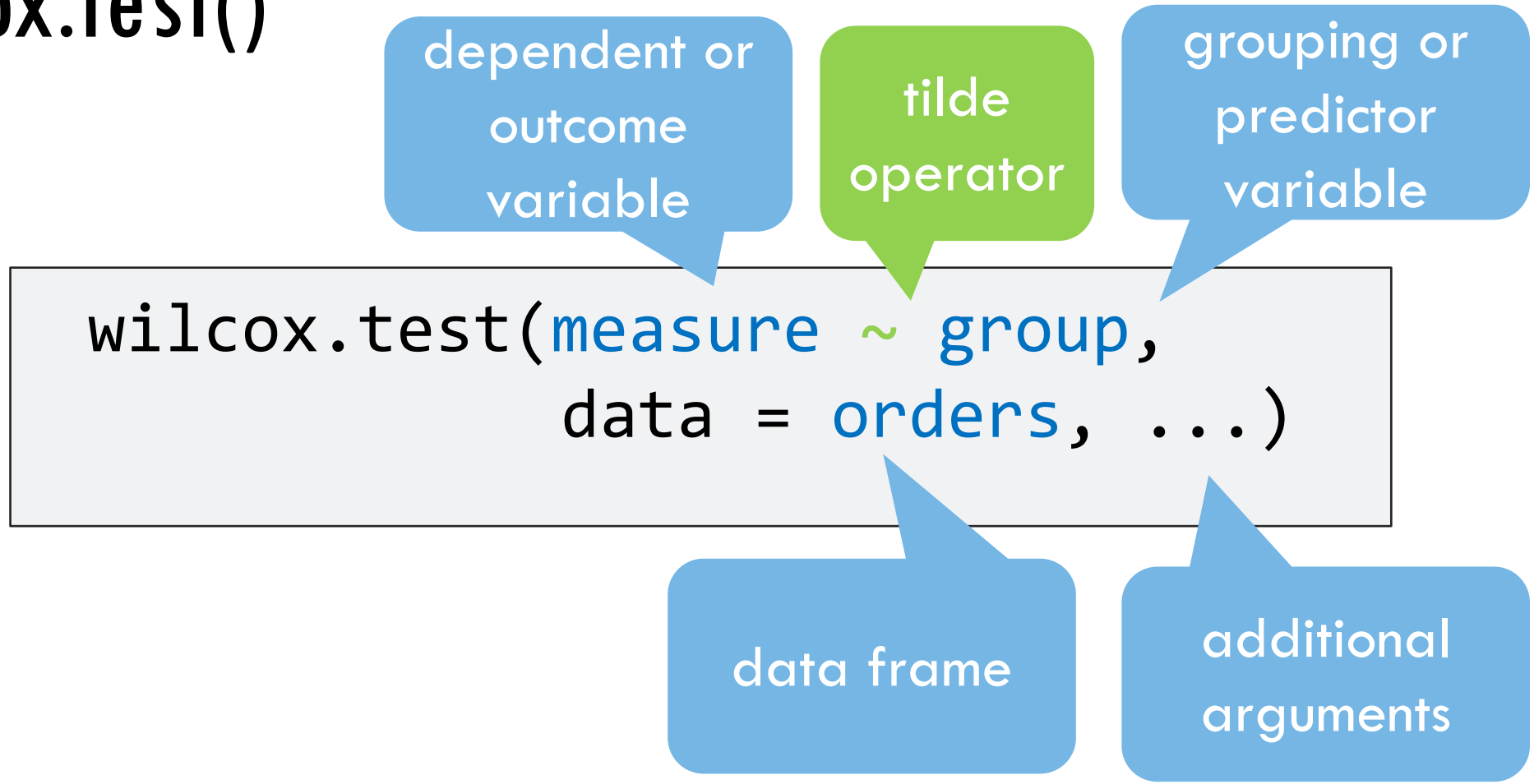


What test can compare count distributions?

Populations	Parametric	Non-parametric
Two populations	t-test	Mann-Whitney U
Many populations	ANOVA	Kruskal Wallis / one-way anova
Populations across several treatments/times	repeated measures ANOVA	Friedman test



wilcox.test()



Compare distributions by rank order

Compare order count distributions between 2 departments

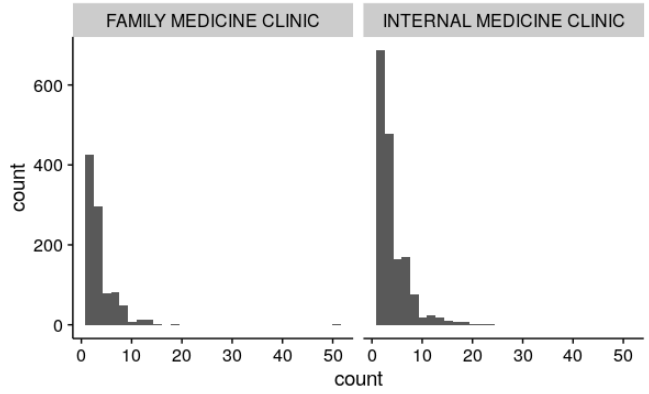
- *Wilcoxon rank-sum test*

```
wilcox.test(order_count ~ department,
            data = orders_per_pt_dept,
            alternative = "two.sided",
            paired = FALSE,
            conf.int = TRUE)
```

```
        Wilcoxon rank sum test with continuity correction

data:  count by department
W = 779510, p-value = 0.1521
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -3.210939e-06  1.571466e-05
sample estimates:
difference in location
         -4.511812e-05
```

```
# A tibble: 6 x 3
                department patient_id count
                     <chr>      <dbl> <int>
1 FAMILY MEDICINE CLINIC      500003     5
2 FAMILY MEDICINE CLINIC      500022     4
3 FAMILY MEDICINE CLINIC      500024    14
4 FAMILY MEDICINE CLINIC      500034     2
5 FAMILY MEDICINE CLINIC      500042     4
6 FAMILY MEDICINE CLINIC      500043     9
```



Your Turn 6

Compare order counts across the nephrology, cardiology, and gastroenterology departments.

**Hint: Convert department to a factor using function factor()*

Compare order counts across the nephrology, cardiology, and gastroenterology departments

```
orders %>%
       mutate(department = factor(department)) %>%
       filter(department %in% c("NEPHROLOGY CLINIC",
                                "CARDIOLOGY CLINIC",
                                "GASTROENTEROLOGY CLINIC")) %>%
       group_by(department, patient_id) %>%
       summarize(order_count = n()) %>%
       ungroup() %>%
       kruskal.test(order_count ~ department,
                    data = .)
```

```
        Kruskal-Wallis rank sum test

data:  order_count by department
Kruskal-Wallis chi-squared = 6.3171, df = 2, p-value = 0.04249
```