STAT 479: MIDTERM 1

- This exam lasts from 1:20 - 2:10pm on February 28, 2022. There are 7 questions.
- This exam is closed notes and closed computer.
- You may use a 1-page cheat sheet (8.5 x 11in or A4 size). You may use both sides, but the cheat sheet must be handwritten.
- If you need extra space, you may write on the back of the page. Please indicate somewhere that your answer continues.
- The instructors will only be able to answer clarifying questions during the exam. They will be sitting at the back of the room.

Question	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Total
Score Possible	2	2	4	4	6	6	6	30

Q1 [**2 points**]

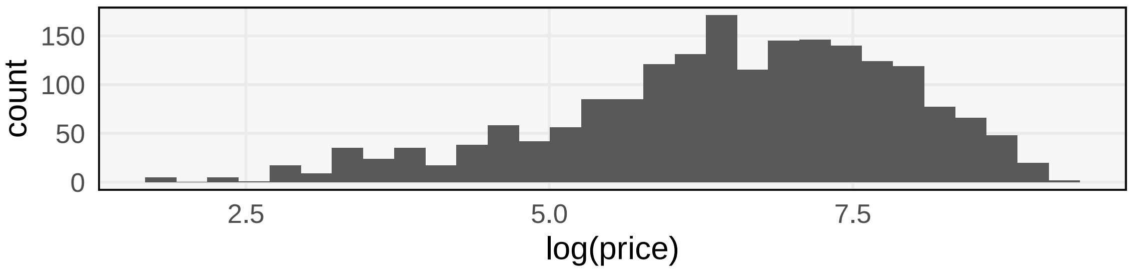
Circle all the true statements for compound and faceted figures.

a. Whenever possible, each panel in a faceted plot should be made to have its own y-axis scale.
b. When using the `patchwork` package, two plots `p1` and `p2` can be placed side-by-side using `p1 / p2`.
c. **When using the `patchwork` package, the `plot_layout` function can be used to collect legends.**
d. **Relative to interactively filtered displays, faceted plots are less taxing on the reader's memory.**

Q2 [**2 points**]

The code below generates a histogram of prices for a subset of items sold at Ikea, a furniture outlet.

```
ikea <- read_csv("https://uwmadison.box.com/shared/static/iat31h1wjg7abhd2889cput7k264bdzd.csv") %>%
  filter(category %in% c("Tables", "Bookcases", "Beds", "Cabinets", "Sofas", "Wardrobes"))
ggplot(ikea) +
  geom_histogram(aes(log(price)))
```



The four plots (i - iv) are generated by faceting this base plot by furniture category (the variable `category`). On the blank lines below, put the number of the plot that matches the corresponding faceting command, or leave the line empty if the corresponding plot does not appear.

ii a. `facet_grid(category ~ .)`

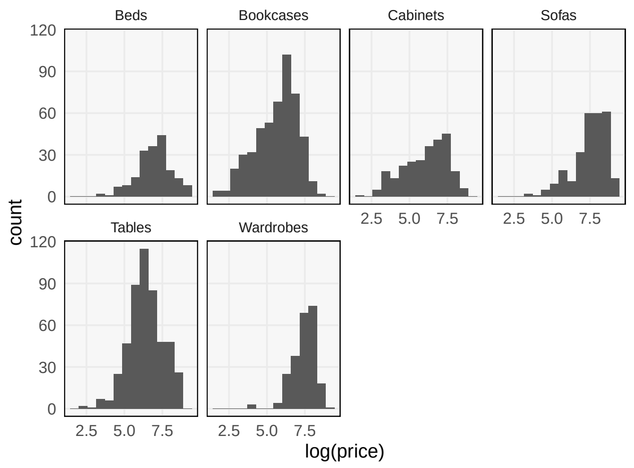
i b. `facet_wrap(~ category)`

iii c. `facet_wrap(~ category, scales = "free_y")`

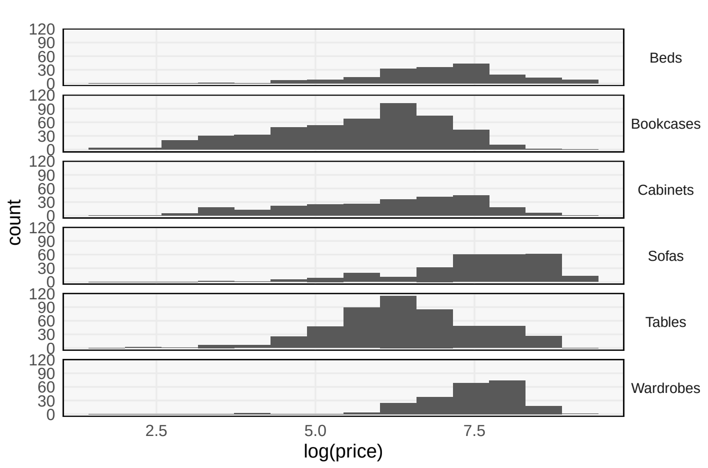
___ d. `facet_wrap(~ category, axes = "separate")`

iv e. `facet_wrap(~ reorder(category, price))`

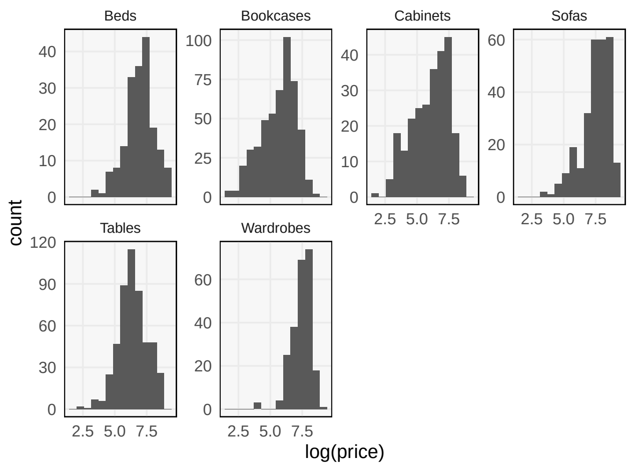
(i)



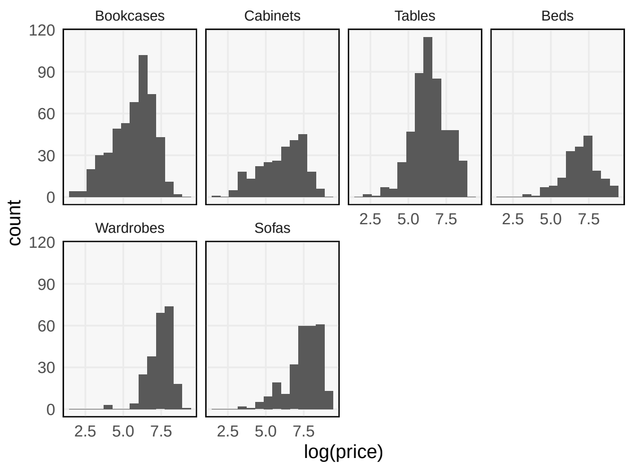
(ii)



(iii)



(iv)



Q3 [4 points]

Consider the sales data below.

```
##   region quarter sales
## 1      A      Q1     6
## 2      A      Q2     5
## 3      A      Q3     3
## 4      A      Q4     2
## 5      B      Q1     4
## 6      B      Q2     8
## 7      B      Q3     2
## 8      B      Q4     6
```

a. [2 points] Provide code to compute the total sales for each quarter, across both regions. The result should look like the table below.

```
sales %>%
  group_by(quarter) %>%
  summarise(total = sum(sales))
```

```
## # A tibble: 4 x 2
##   quarter total
##   <chr>   <dbl>
## 1 Q1         10
## 2 Q2         13
## 3 Q3          5
## 4 Q4          8
```

b. [2 points] Provide code to compute the proportion of each quarter's sales that came from each region. The result should look like the table below.

```
sales %>%
  group_by(quarter) %>%
  mutate(
    total = sum(sales),
    prop = sales / total
  ) %>%
  select(-total)
```

```
## # A tibble: 8 x 4
## # Groups:   quarter [4]
##   region quarter sales  prop
##   <chr>  <chr>   <dbl> <dbl>
## 1 A      Q1          6 0.6
## 2 A      Q2          5 0.385
## 3 A      Q3          3 0.6
## 4 A      Q4          2 0.25
## 5 B      Q1          4 0.4
## 6 B      Q2          8 0.615
## 7 B      Q3          2 0.4
## 8 B      Q4          6 0.75
```

We could also have ungrouped before computing the proportions,

```
sales %>%
  group_by(quarter) %>%
  mutate(total = sum(sales)) %>%
  ungroup() %>%
  mutate(prop = sales / total) %>%
  select(-total)
```

```
## # A tibble: 8 x 4
##   region quarter sales  prop
##   <chr>  <chr>   <dbl> <dbl>
## 1 A      Q1          6 0.6
## 2 A      Q2          5 0.385
## 3 A      Q3          3 0.6
## 4 A      Q4          2 0.25
## 5 B      Q1          4 0.4
## 6 B      Q2          8 0.615
## 7 B      Q3          2 0.4
## 8 B      Q4          6 0.75
```

Q4 [4 points]

Consider the `reactive()` and `observeEvent()` functions implemented by the `shiny` package. What are common use cases for the two functions? Be as specific as possible.

`reactive()`

- Often used to remove code duplication across `render*` contexts
- Often used to create filtered / updated datasets from one set of user inputs to another, before passing them to tables or plots.
- Often used to perform more intensive computations that are shared across several outputs

- Often used to trim redundancies in reactive graphs

`observeEvent()`

- Often used to modify reactive values.
- Often used for graphical queries, to modify distances with click inputs or selections with linked brushing inputs.
- Often used to execute code on `input` changes that are not necessary for specific rendered changes. For example, can be used to print messages or modify style elements without requiring new render calls.

Q5 [6 points]

Below, we provide three approaches to visualizing species abundance over time in an antibiotics dataset.

```
antibiotic <- read_csv("https://uwmadison.box.com/shared/static/5jmd9pku62291ek20lioevsw1c588ahx.csv")
antibiotic
```

```
## # A tibble: 972 x 7
##    species  sample value ind    time svalue antibiotic
##    <chr>    <chr>  <dbl> <chr> <dbl>  <dbl> <chr>
##  1 Unc05qi6 D1         0 D         1   NA   Antibiotic-free
##  2 Unc05qi6 D2         0 D         2   NA   Antibiotic-free
##  3 Unc05qi6 D3         0 D         3    0   Antibiotic-free
##  4 Unc05qi6 D4         0 D         4    0   Antibiotic-free
##  5 Unc05qi6 D5         0 D         5    0   Antibiotic-free
##  6 Unc05qi6 D6         0 D         6    0.2 Antibiotic-free
##  7 Unc05qi6 D7         0 D         7    0.2 Antibiotic-free
##  8 Unc05qi6 D8         1 D         8    0.2 Antibiotic-free
##  9 Unc05qi6 D9         0 D         9    0.2 Antibiotic-free
## 10 Unc05qi6 D10        0 D        10    0.2 Antibiotic-free
## # ... with 962 more rows
```

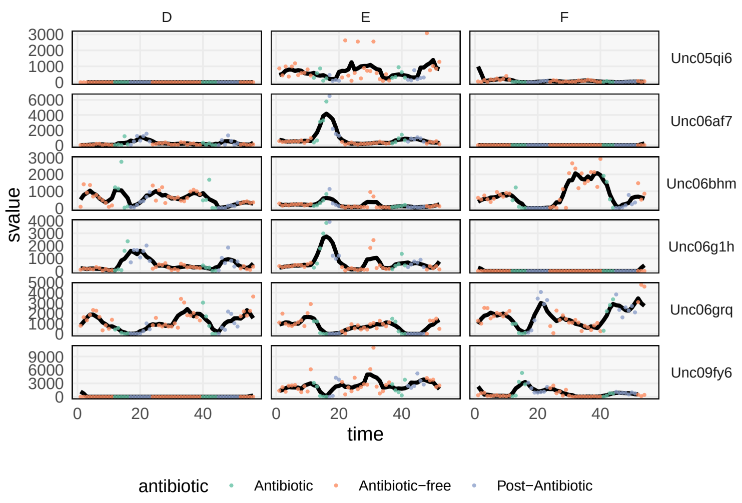
For each approach, describe,

- One type of visual comparison for which the visualization is well-suited.
- One type of visual comparison for which the visualization is poorly-suited.

Make sure to explain your reasoning.

a. [1.5 points] Approach 1

```
ggplot(antibiotic, aes(x = time)) +
  geom_line(aes(y = svalue), size = 1.2) +
  geom_point(aes(y = value, col = antibiotic), size = 0.5, alpha = 0.8) +
  facet_grid(species ~ ind, scale = "free_y") +
  scale_color_brewer(palette = "Set2") +
  theme(strip.text.y = element_text(angle = 0))
```



Effective:

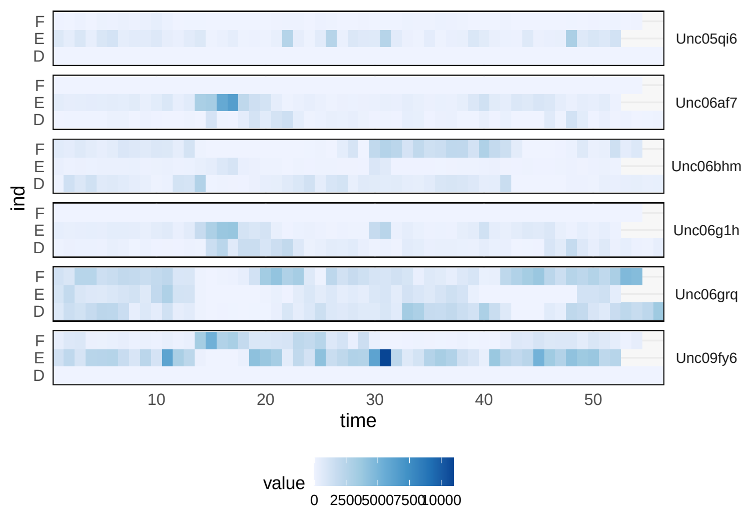
- Comparing abundances over time for each species and subject combination, even for rare species. It is easy to compare y-axis values within individual panels. Since the y-axis scales are not shared, trends in even the rare species are visible.
- Comparing species abundance across antibiotic treatment regimes. Since color is used to encode treatment regime, we can easily see how peaks or valleys coincide with the treatments.

Ineffective:

- Comparing abundances of different species for the same subject. Since the y-axes scales are not shared, it is hard to compare abundances across species.
- Ranking species by overall abundance within or across subjects. Again, this is a consequence of the unshared axis scales.
- Comparing trends in species abundances across subjects (especially D vs. F). Since our eyes have to travel left and right to compare species trends, it is harder to evaluate differences across subjects, compared to if they were all overlapping, for example.

b. [1.5 points] Approach 2

```r
ggplot(antibiotic) +
  geom_tile(aes(time, ind, fill = value)) +
  scale_x_continuous(expand = c(0, 0)) +
  scale_fill_distiller(direction = 1) +
  facet_grid(species ~ .) +
  theme(strip.text.y = element_text(angle = 0))
```



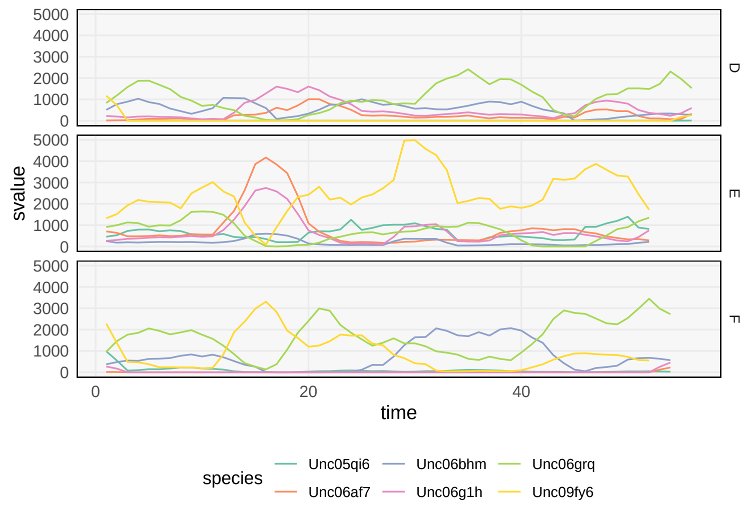
Effective

- For individual species, comparing trends over time across subjects. All the subjects are placed adjacent to one another within each panel, so our eyes don't have to travel such a large distance to make the comparison.
- Across species, recognizing shared increases or decreases at specific timepoints. Since the plot is so compact, all the values for a single timepoint are easily queryable.
- Recognizing the species and samples with the highest abundances. The cells with the darkest colors pop out from among the rest.

Ineffective

- Comparing the absolute abundances of a single species over time. It is difficult to compare shades of the same color.
- Evaluating the abundance of relatively rare species. These species all have light colors, and gradations smaller than the color scale bin size are not visible.
- Comparing species abundances for a single subject. We have to move our eyes across the three panels to make comparisons about a single species.

c. [1.5 points] Approach 3



Effective

- Within a single subject, ranking species by overall abundance. We can easily see which colors lie above the others within any given panel.

- Comparing abundance over time for a single subject and species. We can see increases and decreases clearly when plotting against a y-axis scale.
- Comparing overall species abundances across subjects. Since the same y-axis scale is used across panels, we can conclude that some subjects have more counts overall.

Ineffective

- Comparing trends for a single species across subjects. It is visually challenging to match colors across the three panels.
- Comparing trends for low abundance species. For low abundances, many of the lines overlap with one another.

d. [1.5 points] Sketch code that could be used to make one of the three visualizations above.

Code given in the blocks above.

Q6 [6 points]

The following questions refer to the NYC flights dataset. The first few lines are printed below.

```
library(nycflights13)
flights %>% select(carrier, air_time, distance)
```

```
## # A tibble: 336,776 x 3
##    carrier air_time distance
##    <chr>      <dbl>    <dbl>
##  1 UA           227     1400
##  2 UA           227     1416
##  3 AA           160     1089
##  4 B6           183     1576
##  5 DL           116      762
##  6 UA           150      719
##  7 B6           158     1065
##  8 EV            53      229
##  9 B6           140      944
## 10 AA           138      733
## # ... with 336,766 more rows
```

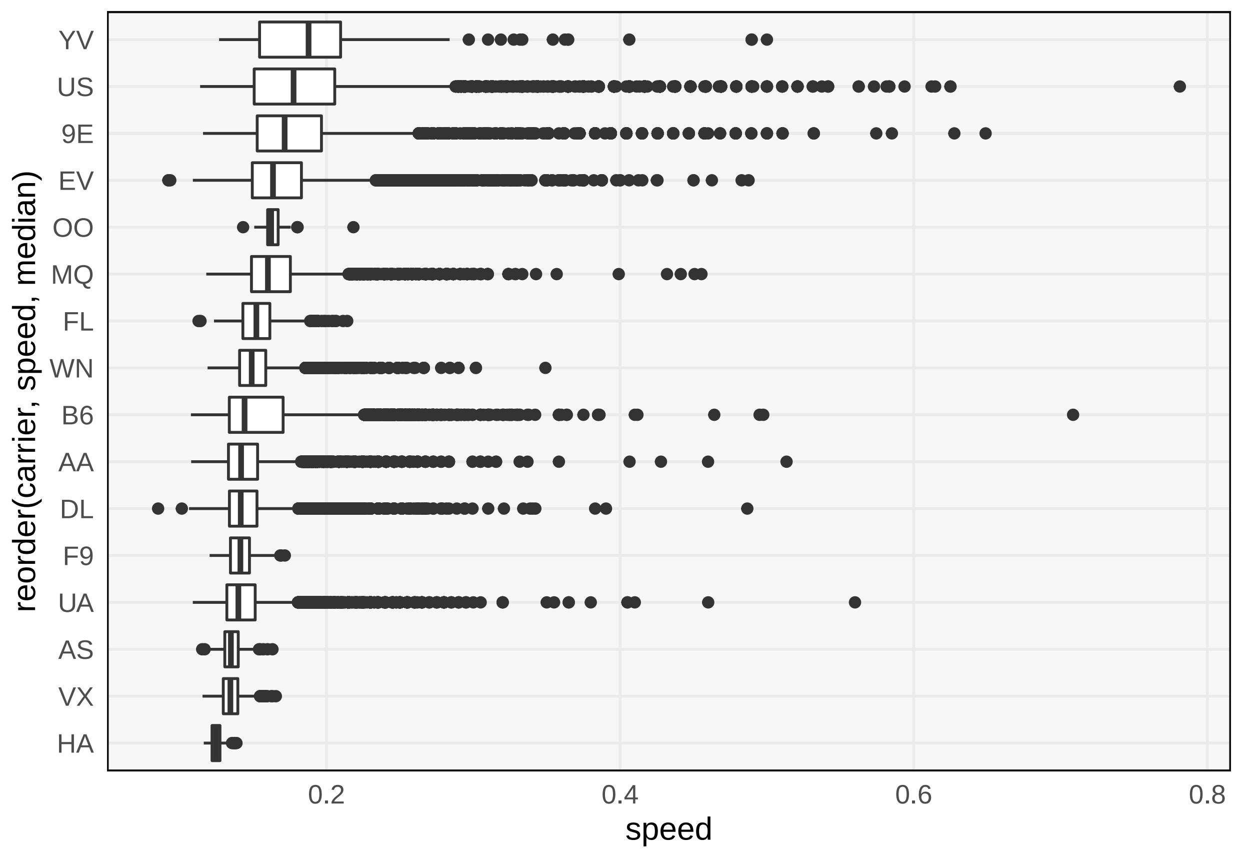
a. [3 points] Provide code to create a new column giving the average speed of the flight: `speed` $:= \frac{\texttt{distance}}{\texttt{air\_time}}$.

```
flights <- flights %>%
  mutate(speed = air_time / distance)
```

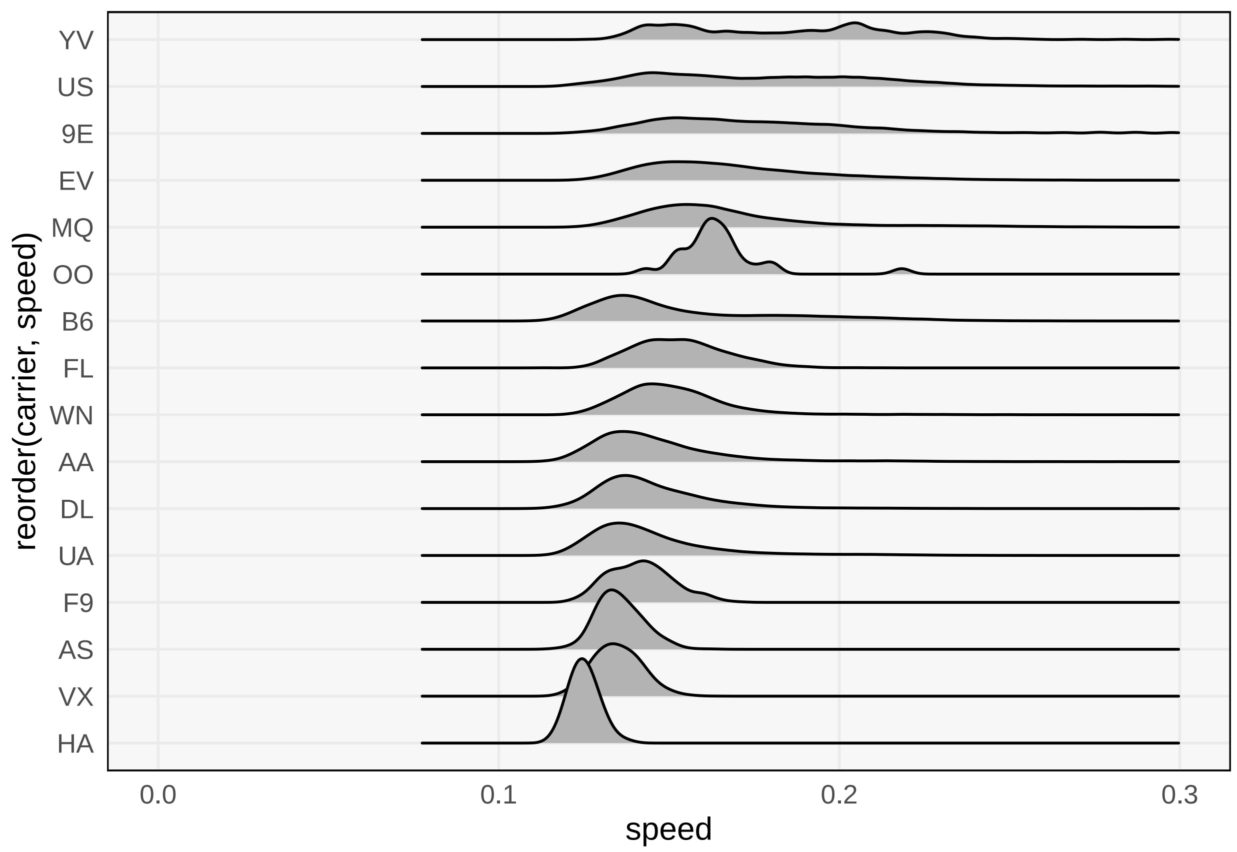
b. [3 points] Is there a large variation in flight speed across carriers? Design and sketch code for a visualization that could be used to answer this question (you may assume the output of (a)).

There are many possible answers to this. The best answers will avoid over-summarization and will provide customizations to support answering the query. Here are two approaches using a boxplot and a ridgelines plot.

```
flights <- filter(flights, !is.na(speed)) # this line is not needed in the soln
ggplot(flights) +
 geom_boxplot(aes(speed, reorder(carrier, speed, median)))
```



```r
library(ggridges)
ggplot(flights) +
  geom_density_ridges(aes(speed, reorder(carrier, speed))) +
  xlim(0, 0.3) # not expected in the soln
```



Q7 [**6 points**]

The code below sets up a Shiny app for interactively visualizing athlete weight and heights in the 2012 London Olympics. We would like to have an interactive scatterplot of `Weight` vs. `Height, cm` that updates which points (athletes) are highlighted depending on sports have been selected by a dropdown menu. Code for generating the scatterplot is provided in the function `scatterplot`.

```
library(shiny)
library(tidyverse)
olympics <- read_csv("https://uwmadison.box.com/shared/static/rzw8h2x6dp5693gdbpgxaf2koqijo12l.csv")

#' Scatterplot with highlighted points
#'
#' Assumes a column in df called "selected" saying whether points should be
#' larger / darker
scatterplot <- function(df) {
  ggplot(df) +
    geom_point(
      aes(Weight, `Height, cm`,
          alpha = as.numeric(selected),
          size = as.numeric(selected))
      ) +
    scale_alpha(range = c(0.05, .8)) +
    scale_size(range = c(0.1, 1))
}

ui <- fluidPage(
  selectInput("dropdown", "Select a Sport", choices = unique(olympics$Sport), multiple = TRUE),
  plotOutput("scatterplot")
)
```

```r
server <- function(input, output) {
  ### fill this in...
}
```

a. [3 points] Provide server code which would allow the scatterplot to update the highlighted athletes depending on the currently selected sports.

```r
server <- function(input, output) {
  output$scatterplot <- renderPlot({
    olympics %>%
      mutate(selected = Sport %in% input$dropdown) %>%
      scatterplot()
  })
}
```

b. [3 points] We have been asked to also print a table of the selected athletes. Assume the UI has the form,

```r
ui <- fluidPage(
  selectInput("dropdown", "Select a Sport", choices = unique(olympics$Sport), multiple = TRUE),
  plotOutput("scatterplot"),
  dataTableOutput("table")
)
```

Describe changes to your solution to (a) to meet the new requirements. How would you minimize code duplication? Be as specific as possible.

- We will need to add a `renderDataTable` call to print the data.table
- We can minimize code duplication by using a reactive expression to compute the version of the dataset highlighting which athletes are selected

```r
server <- function(input, output) {
  current_athletes <- reactive({
    olympics %>%
      mutate(selected = Sport %in% input$dropdown)
  })

  output$scatterplot <- renderPlot(scatterplot(current_athletes()))
  output$table <- renderDataTable({
    current_athletes() %>% filter(selected)
  })
}
```