Explore the data

Our modeling goal is to use k-means clustering to explore employment by race and gender. This is a good screencast for folks who are more new to k-means and want to understand how to apply it to a real-world data set.

```
library(tidyverse)

employed <- read_csv("https://raw.githubusercontent.com/rfordatascience/tidytuesday/master/data/2021/2021-02-23/employed.csv")
```

Let's start by focusing on the **industry** and **occupation** combinations available in this data, and average over the years available. We aren't looking at any time trends, but instead at the demographic relationships.

```
employed_tidy <- employed %>%
  filter(!is.na(employ_n)) %>%
  group_by(occupation = paste(industry, minor_occupation), race_gender)
%>%
  summarise(n = mean(employ_n)) %>%
  ungroup()
```

Let's create a `dataframe` read for k-means. We need to center and scale the variables we are going to use, since they are on such different scales: the proportions of each category who are Asian, Black, or women and the total number of people in each category.

```
employment_demo <- employed_tidy %>%
  filter(race_gender %in% c("Women", "Black or African American",
"Asian")) %>%
  pivot_wider(names_from = race_gender, values_from = n, values_fill =
0) %>%
  janitor::clean_names() %>%
  left_join(employed_tidy %>%
    filter(race_gender == "TOTAL") %>%
    select(-race_gender) %>%
    rename(total = n)) %>%
  filter(total > 1e3) %>%
  mutate(across(c(asian, black_or_african_american, women), ~ . /
(total)),
    total = log(total),
    across(where(is.numeric), ~ as.numeric(scale(.)))
  ) %>%
  mutate(occupation = snakecase::to_snake_case(occupation))

employment_demo
## # A tibble: 230 x 5
##    occupation                          asian black_or_african_a…
women  total
##
##  1 agriculture_and_related_construct… -0.553              -0.410
-1.31    -1.48
```

```
##  2 agriculture_and_related_farming_f… -0.943             -1.22
-0.509    0.706
##  3 agriculture_and_related_installat… -0.898             -1.28
-1.38    -0.992
##  4 agriculture_and_related_manage_me… -1.06              -1.66
-0.291    0.733
##  5 agriculture_and_related_managemen… -1.06              -1.65
-0.300    0.750
##  6 agriculture_and_related_office_an… -0.671             -1.54
2.23    -0.503
##  7 agriculture_and_related_productio… -0.385             -0.0372
-0.622   -0.950
##  8 agriculture_and_related_professio… -0.364             -1.17
0.00410 -0.782
##  9 agriculture_and_related_protectiv… -1.35              -0.647
-0.833   -1.39
## 10 agriculture_and_related_sales_and… -1.35              -1.44
0.425   -1.36
## # … with 220 more rows
```

Implement k-means clustering

Now we can implement k-means clustering, starting out with three centers. What does the output look like?

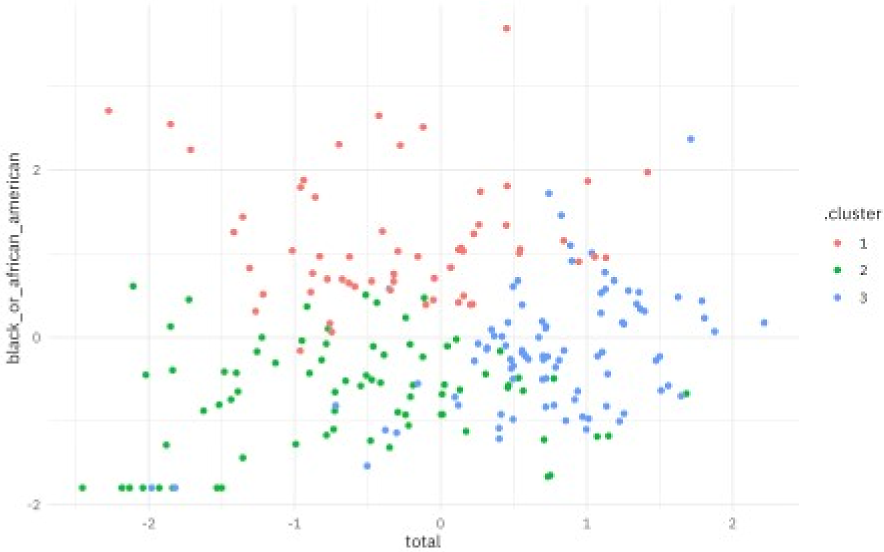
```
employment_clust <- kmeans(select(employment_demo, -occupation),
centers = 3)
summary(employment_clust)
##              Length Class  Mode
## cluster      230    -none- numeric
## centers       12    -none- numeric
## totss          1    -none- numeric
## withinss       3    -none- numeric
## tot.withinss   1    -none- numeric
## betweenss      1    -none- numeric
## size           3    -none- numeric
## iter           1    -none- numeric
## ifault         1    -none- numeric
```

The original format of the output isn't as practical to deal with in many circumstances, so we can load the broom package (part of tidymodels) and use verbs like `tidy()`. This will give us the centers of the clusters we found:

```
library(broom)
tidy(employment_clust)
## # A tibble: 3 x 7
##      asian black_or_african_american  women  total  size withinss
cluster
##
## 1  1.46                         -0.551  0.385  0.503    45     125. 1
## 2 -0.732                        -0.454 -0.820 -0.655    91     189. 2
## 3  0.00978                       0.704  0.610  0.393    94     211. 3
```

If we `augment()` the clustering results with our original data, we can plot any of the dimensions of our space, such as **total employed** vs. **proportion who are Black**. We can see here that there are really separable clusters but instead a smooth, continuous distribution from low to high along both dimensions. Switch out another dimension like `asian` to see that projection of the space.

```
augment(employment_clust, employment_demo) %>%
  ggplot(aes(total, black_or_african_american, color = .cluster)) +
  geom_point()
```

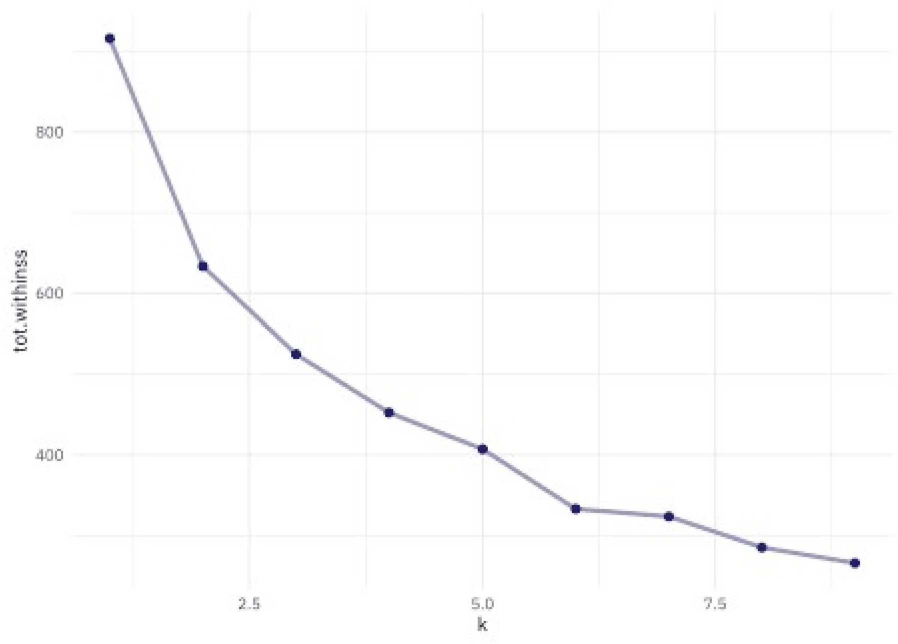


Choosing k

We used `k = 3` but how do we know that's right? There are lots of complicated or "more art than science" ways of choosing `k`. One way is to look at the total within-cluster sum of squares and see if it stops dropping off so quickly at some value for `k`. We can get that from another verb from broom, `glance()`; let's try lots of values for `k` and see what happens to the total sum of squares.

```
kclusts <-
  tibble(k = 1:9) %>%
  mutate(
    kclust = map(k, ~ kmeans(select(employment_demo, -occupation),
.x)),
    glanced = map(kclust, glance),
  )

kclusts %>%
  unnest(cols = c(glanced)) %>%
  ggplot(aes(k, tot.withinss)) +
  geom_line(alpha = 0.5, size = 1.2, color = "midnightblue") +
  geom_point(size = 2, color = "midnightblue")
```



I don't see a major "elbow" 💪 but I'd say that `k = 5` looks pretty reasonable. Let's fit k-means again.

```
final_clust <- kmeans(select(employment_demo, -occupation), centers =
5)
```

To visualize this final result, let's use plotly and add the `occupation` name to the hover so we can mouse around and see which occupations are more similar.

```
library(plotly)

p <- augment(final_clust, employment_demo) %>%
  ggplot(aes(total, women, color = .cluster, name = occupation)) +
  geom_point()

ggplotly(p, height = 500)
```

Remember that you can switch out the axes for `asian` or `black_or_african_american` to explore dimensions.