

727 HW5

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[Github Link](#)

```
cs_key <- read_file("API KEY.txt")

acs_il_c <- getCensus(name = "acs/acss5",
                       vintage = 2016,
                       vars = c("NAME",
                               "B01003_001E",
                               "B19013_001E",
                               "B19301_001E"),
                       region = "county:*",
                       regionin = "state:17",
                       key = cs_key) %>%
  rename(pop = B01003_001E,
        hh_income = B19013_001E,
        income = B19301_001E)

head(acs_il_c)
```

	state	county		NAME	pop	hh_income	income
1	17	067	Hancock County, Illinois	18633	50077	25647	
2	17	063	Grundy County, Illinois	50338	67162	30232	
3	17	091	Kankakee County, Illinois	111493	54697	25111	
4	17	043	DuPage County, Illinois	930514	81521	40547	
5	17	003	Alexander County, Illinois	7051	29071	16067	
6	17	129	Menard County, Illinois	12576	60420	31323	

```
il_map <- map_data("county", region = "illinois")
head(il_map)
```

long lat group order region subregion

```

1 -91.49563 40.21018      1      1 illinois     adams
2 -90.91121 40.19299      1      2 illinois     adams
3 -90.91121 40.19299      1      3 illinois     adams
4 -90.91121 40.10704      1      4 illinois     adams
5 -90.91121 39.83775      1      5 illinois     adams
6 -90.91694 39.75754      1      6 illinois     adams

```

```

acs_il_c <- acs_il_c %>%
  mutate(subregion = gsub(" County, Illinois", "", NAME) %>% tolower())

acs_map <- il_map %>%
  left_join(acs_il_c, by = "subregion")

head(acs_map)

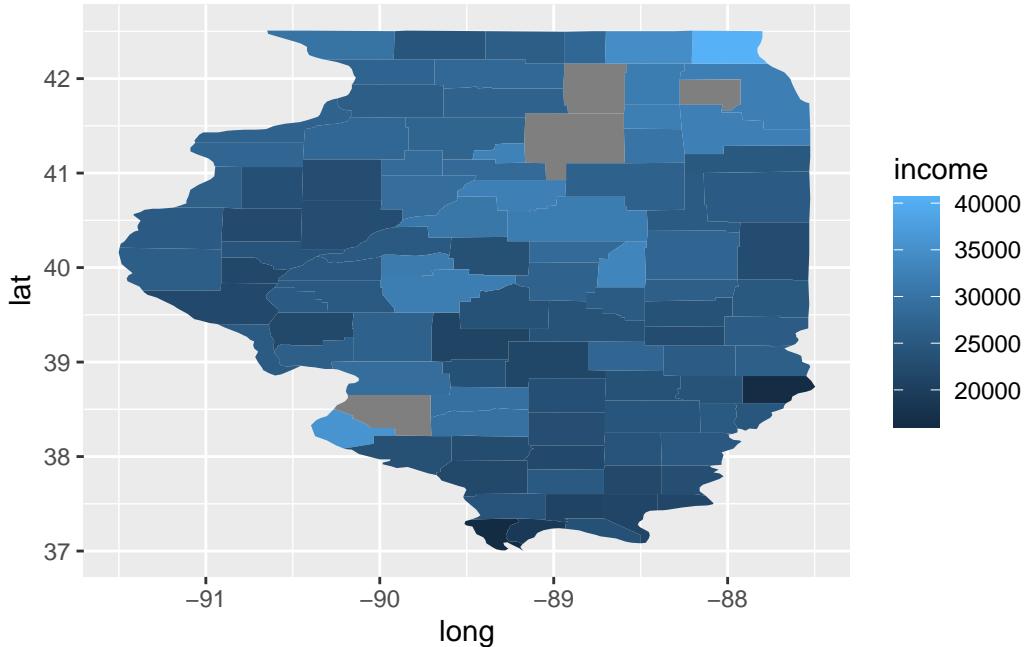
```

	long	lat	group	order	region	subregion	state	county
1	-91.49563	40.21018	1	1	illinois	adams	17	001
2	-90.91121	40.19299	1	2	illinois	adams	17	001
3	-90.91121	40.19299	1	3	illinois	adams	17	001
4	-90.91121	40.10704	1	4	illinois	adams	17	001
5	-90.91121	39.83775	1	5	illinois	adams	17	001
6	-90.91694	39.75754	1	6	illinois	adams	17	001
					NAME	pop	hh_income	income
1	Adams County, Illinois	66949				48065	26053	
2	Adams County, Illinois	66949				48065	26053	
3	Adams County, Illinois	66949				48065	26053	
4	Adams County, Illinois	66949				48065	26053	
5	Adams County, Illinois	66949				48065	26053	
6	Adams County, Illinois	66949				48065	26053	

```

ggplot(acs_map) +
  geom_polygon(aes(x = long,
                    y = lat,
                    group = group,
                    fill = income))

```



```

# Clean the data for clustering
# Extract unique county-level data (remove duplicate rows from map data)
acs_clean <- acs_il_c %>%
  select(subregion, pop, hh_income, income) %>%
  na.omit() # Remove any rows with missing values

# Create a matrix with county names as row names for clustering
acs_matrix <- acs_clean %>%
  select(pop, hh_income, income) %>%
  scale() # Standardize the variables

rownames(acs_matrix) <- acs_clean$subregion

# Create the distance matrix
dist_matrix <- dist(acs_matrix, method = "euclidean")

# Perform hierarchical clustering using Ward's method
hc_ward <- hclust(dist_matrix, method = "ward.D2")

# Plot the dendrogram
plot(hc_ward, main = "Dendrogram of Illinois Counties",
      xlab = "County", ylab = "Height", cex = 0.6)

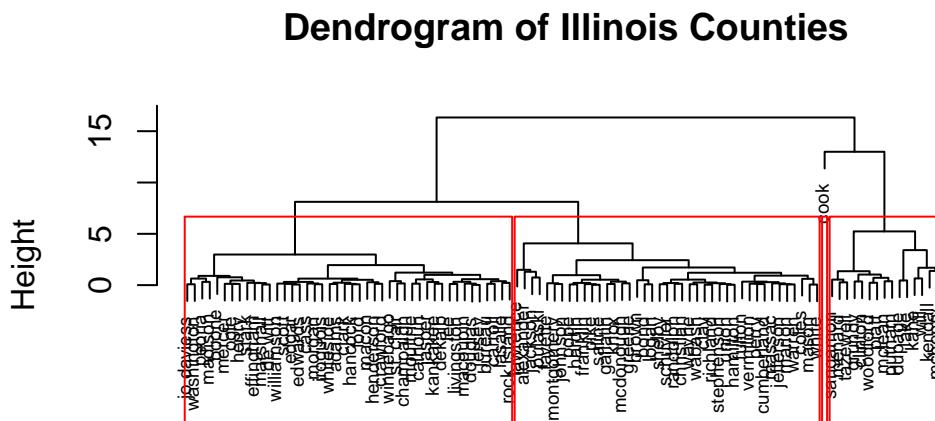
```

```

k <- 4

# Draw boxes around clusters
rect.hclust(hc_ward, k = k, border = "red")

```



County
hclust (*, "ward.D2")

```

# Cut the tree to create cluster assignments
clusters <- cutree(hc_ward, k = k)

# Create a data frame with cluster assignments
cluster_df <- data.frame(
  subregion = names(clusters),
  cluster = as.factor(clusters)
)

# Join cluster assignments with the original ACS data
acs_il_c <- acs_il_c %>%
  left_join(cluster_df, by = "subregion")

# Create new acs_map with cluster membership
acs_map <- il_map %>%
  left_join(acs_il_c, by = "subregion")

```

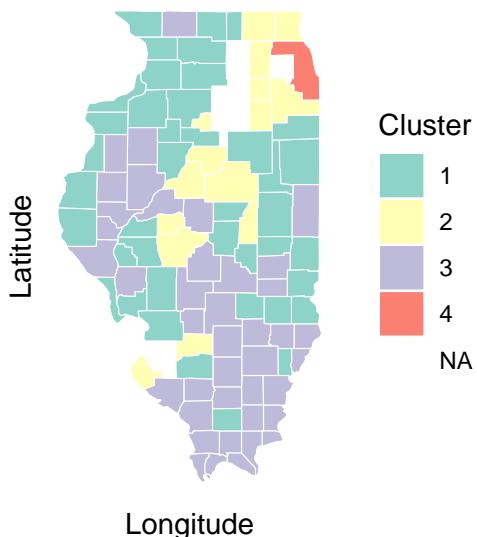
```

# Visualize the clusters on a map
ggplot(acs_map, aes(x = long, y = lat, group = group, fill = cluster)) +
  geom_polygon(color = "white", size = 0.2) +
  coord_fixed(1.3) +
  scale_fill_brewer(palette = "Set3", name = "Cluster") +
  theme_minimal() +
  labs(title = "Illinois County Clusters",
       subtitle = "Based on Population, Household Income, and Per Capita Income",
       x = "Longitude", y = "Latitude") +
  theme(panel.grid = element_blank(),
        axis.text = element_blank(),
        axis.ticks = element_blank())

```

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.

Illinois County Clusters
Based on Population, Household Income, and Per Capita Income



```

acs_il_t <- getCensus(name = "acs/acss5",
                       vintage = 2016,
                       vars = c("NAME",
                               "B01003_001E",
                               "B19013_001E",
                               "B19301_001E"),

```

```

            region = "tract:*",
            regionin = "state:17",
            key = cs_key) %>%
mutate(across(everything(), ~ifelse(. == -666666666, NA, .))) %>%
rename(pop = B01003_001E,
      hh_income = B19013_001E,
      income = B19301_001E)

head(acs_il_t)

```

	state	county	tract	NAME	pop
1	17	031	806002	Census Tract 8060.02, Cook County, Illinois	7304
2	17	031	806003	Census Tract 8060.03, Cook County, Illinois	7577
3	17	031	806400	Census Tract 8064, Cook County, Illinois	2684
4	17	031	806501	Census Tract 8065.01, Cook County, Illinois	2590
5	17	031	750600	Census Tract 7506, Cook County, Illinois	3594
6	17	031	310200	Census Tract 3102, Cook County, Illinois	1521
	hh_income	income			
1	56975	23750			
2	53769	25016			
3	62750	30154			
4	53583	20282			
5	40125	18347			
6	63250	31403			

```

# Clean the data for clustering
acs_il_t_clean <- acs_il_t %>%
  select(NAME, state, county, tract, pop, hh_income, income) %>%
  na.omit() # Remove rows with missing values

# Create a matrix for clustering (standardized)
acs_matrix_t <- acs_il_t_clean %>%
  select(pop, hh_income, income) %>%
  scale()

# Determine optimal K using within-cluster sum of squares
# Calculate WCSS for K = 1 to 20
set.seed(123)
wcss <- sapply(1:20, function(k) {
  kmeans(acs_matrix_t, centers = k, nstart = 25)$tot.withinss
})

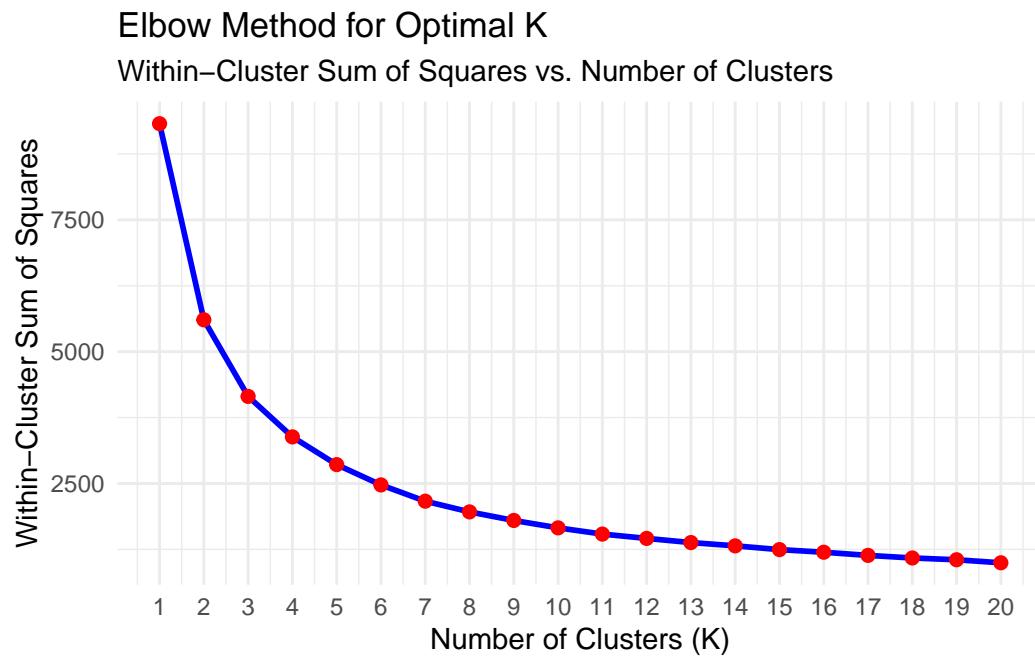
```

```

# Plot the elbow curve
wcss_df <- data.frame(K = 1:20, WCSS = wcss)

ggplot(wcss_df, aes(x = K, y = WCSS)) +
  geom_line(color = "blue", size = 1) +
  geom_point(color = "red", size = 2) +
  labs(title = "Elbow Method for Optimal K",
       subtitle = "Within-Cluster Sum of Squares vs. Number of Clusters",
       x = "Number of Clusters (K)",
       y = "Within-Cluster Sum of Squares") +
  theme_minimal() +
  scale_x_continuous(breaks = 1:20)

```



```

# Run K-means with optimal K
# Adjust based on elbow plot
# 6 seems to be optimal
optimal_k <- 6
set.seed(123)
kmeans_result <- kmeans(acs_matrix_t, centers = optimal_k, nstart = 25)

# Create a temporary data frame with cluster membership for analysis
temp_clustered <- acs_il_t_clean %>%

```

```

    mutate(cluster = as.factor(kmeans_result$cluster))

# Find mean statistics and most frequent county by cluster
cluster_summary <- temp_clustered %>%
  group_by(cluster) %>%
  summarise(
    mean_pop = mean(pop, na.rm = TRUE),
    mean_hh_income = mean(hh_income, na.rm = TRUE),
    mean_income = mean(income, na.rm = TRUE),
    n_tracts = n()
  )

print("Cluster Summary Statistics:")

```

[1] "Cluster Summary Statistics:"

```
print(cluster_summary)
```

	cluster	mean_pop	mean_hh_income	mean_income	n_tracts
	<fct>	<dbl>	<dbl>	<dbl>	<int>
1	1	4519.	92963.	45055.	527
2	2	3812.	135623.	77010.	154
3	3	5965.	53872.	24940.	690
4	4	2689.	32061.	17260.	764
5	5	3306.	58016.	29402.	914
6	6	11340.	93651.	39361.	60

```

# Find most frequent county in each cluster
most_frequent_county <- temp_clustered %>%
  group_by(cluster, county) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(cluster) %>%
  slice_max(count, n = 1) %>%
  select(cluster, most_frequent_county = county, count)

print(most_frequent_county)

```

```
# A tibble: 6 x 3
# Groups:   cluster [6]
```

```

cluster most_frequent_county count
<fct> <chr> <int>
1 1 031 220
2 2 031 97
3 3 031 326
4 4 031 379
5 5 031 282
6 6 197 12

# Combine summaries
full_summary <- cluster_summary %>%
  left_join(most_frequent_county, by = "cluster")

print(full_summary)

# A tibble: 6 x 7
  cluster mean_pop mean_hh_income mean_income n_tracts most_frequent_county
  <fct>     <dbl>        <dbl>       <dbl>      <int> <chr>
1 1         4519.      92963.     45055.      527 031
2 2         3812.      135623.    77010.      154 031
3 3         5965.      53872.     24940.      690 031
4 4         2689.      32061.     17260.      764 031
5 5         3306.      58016.     29402.      914 031
6 6        11340.     93651.     39361.      60  197
# i 1 more variable: count <int>

# Create a function for K-means clustering
kmeans_function <- function(k, data = acs_matrix_t, seed = 123) {
  set.seed(seed)
  result <- kmeans(data, centers = k, nstart = 25)
  return(result$cluster)
}

# Iterate over multiple K values (K = 2 to 10)
k_values <- 2:10

# Apply the function for each K and create new columns
# Names is cluster_i for each iteration
for (k in k_values) {
  col_name <- paste0("cluster_", k)
  acs_il_t_clean[[col_name]] <- as.factor(kmeans_function(k))
}

```

```
# Display the first rows of the updated dataset
head(acs_il_t_clean)
```

	NAME	state	county	tract	pop				
1	Census Tract 8060.02, Cook County, Illinois			17	031	806002	7304		
2	Census Tract 8060.03, Cook County, Illinois			17	031	806003	7577		
3	Census Tract 8064, Cook County, Illinois			17	031	806400	2684		
4	Census Tract 8065.01, Cook County, Illinois			17	031	806501	2590		
5	Census Tract 7506, Cook County, Illinois			17	031	750600	3594		
6	Census Tract 3102, Cook County, Illinois			17	031	310200	1521		
	hh_income	income	cluster_2	cluster_3	cluster_4	cluster_5	cluster_6	cluster_7	
1	56975	23750	2	3	1	4	3	6	
2	53769	25016	2	3	1	4	3	6	
3	62750	30154	2	2	3	5	5	3	
4	53583	20282	2	2	2	2	5	2	
5	40125	18347	2	2	2	2	4	2	
6	63250	31403	2	2	3	5	5	3	
	cluster_8	cluster_9	cluster_10						
1	8	7	8						
2	8	7	8						
3	3	6	7						
4	3	6	7						
5	1	4	10						
6	3	6	7						