

727 HW5

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[Github Link](#)

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

acs_il_c <- getCensus(name = "acs/acs5",
  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)

```

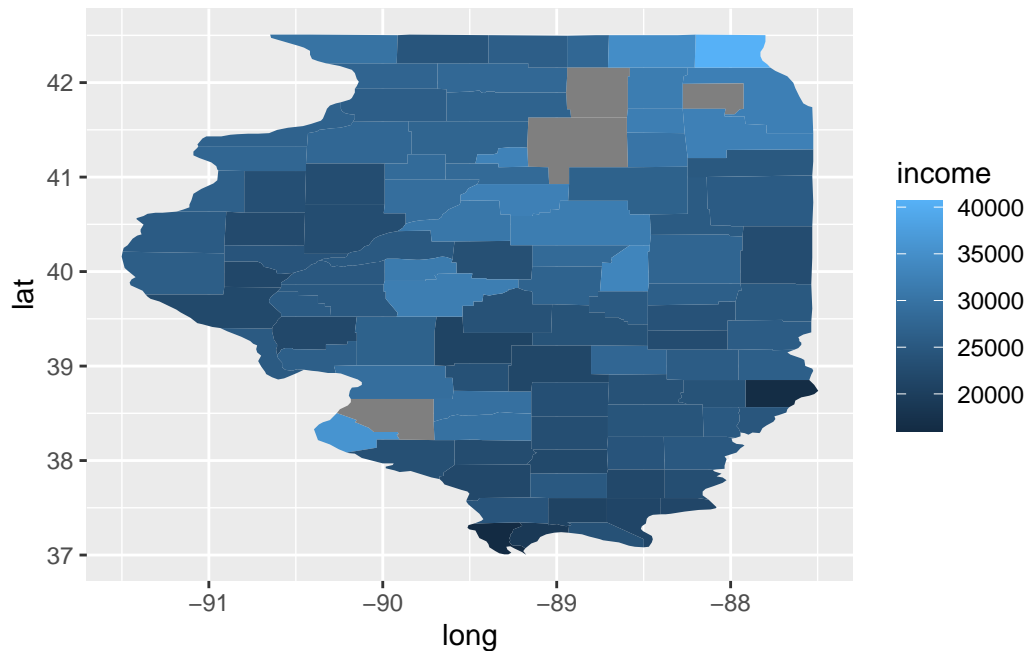
	long	lat	group	order	region	subregion	state	county
1	-91.49563	40.21018	1	1	illinois	adams	17	001
2	-90.91121	40.19299	1	2	illinois	adams	17	001
3	-90.91121	40.19299	1	3	illinois	adams	17	001
4	-90.91121	40.10704	1	4	illinois	adams	17	001
5	-90.91121	39.83775	1	5	illinois	adams	17	001
6	-90.91694	39.75754	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")

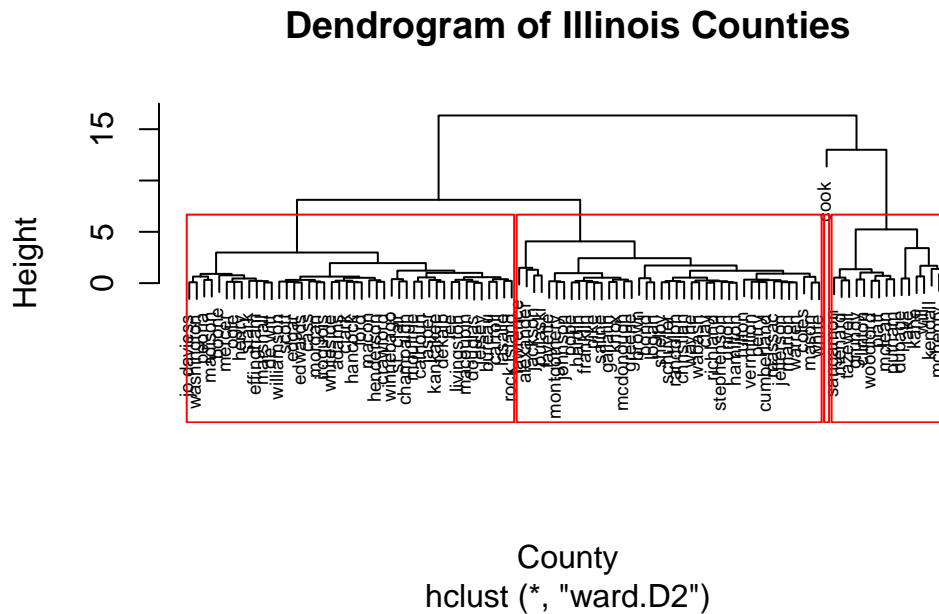
# Perform hierarchical clustering using Ward's method
hc_ward <- hclust(dist_matrix, method = "ward.D2")

# 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")
```



```
# 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)
)

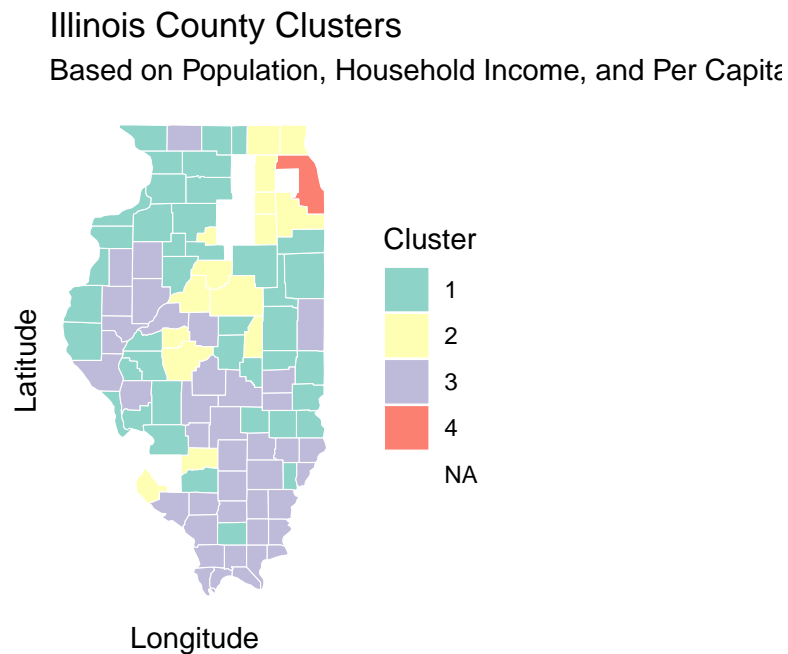
# Join cluster assignments with the original ACS data
acs_il_c <- acs_il_c %>%
  left_join(cluster_df, by = "subregion")

# 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.



```
acs_il_t <- getCensus(name = "acs/acs5",
                      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()

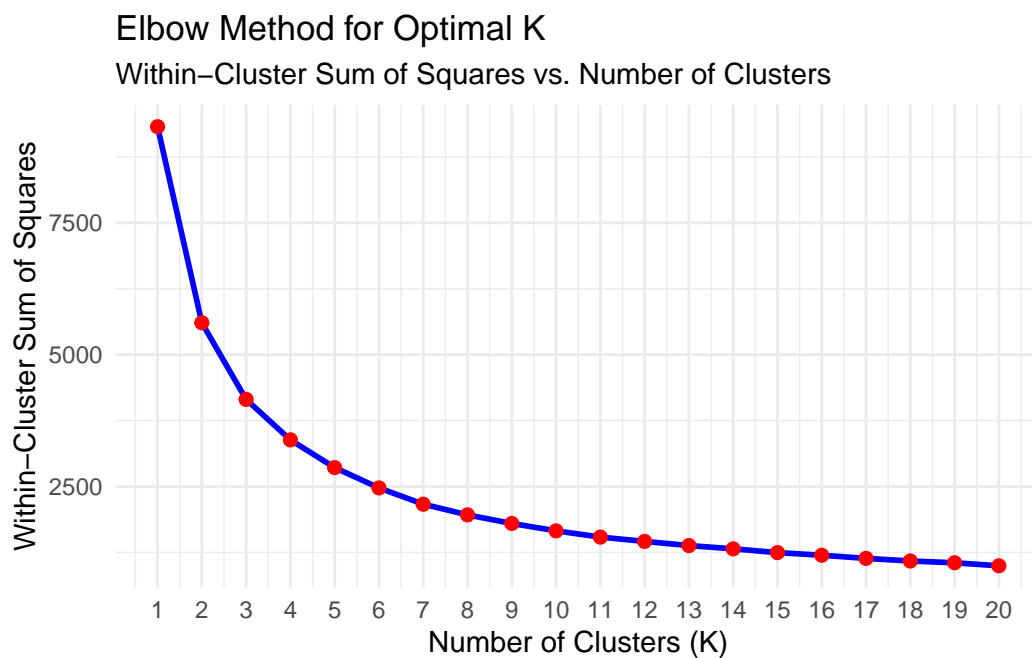
# Determine optimal K using within-cluster sum of squares
# Calculate WCSS for K = 1 to 20
set.seed(123)
wcss <- sapply(1:20, function(k) {
  kmeans(acs_matrix_t, centers = k, nstart = 25)$tot.withinss
})

```



```
# 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)
```

```

# A tibble: 6 x 5
  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						