Cranial Data

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Load Necessary Libraries

```r
library(readxl)
library(ggplot2)
library(dplyr)
```

```
## 
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
## 
##     filter, lag

## The following objects are masked from 'package:base':
## 
##     intersect, setdiff, setequal, union
```

Read the Excel File

```r
pbio_1001071_s004 <- read_excel("~/Desktop/CraniaAmericana/CranialCapacity/pbio.1001071.s004.xls")
```

```
## New names:
## * `` -> `...2`
## * `` -> `...3`
## * `` -> `...4`
## * `` -> `...5`
## * `` -> `...6`
## * `` -> `...7`
## * `` -> `...8`
## * `` -> `...9`
## * `` -> `...10`
## * `` -> `...11`
## * `` -> `...12`
```

```r
pbio_1001071_s004
```

```
## # A tibble: 338 x 12
##     Measurement Data: Com~1 ...2  ...3  ...4  ...5  ...6  ...7  ...8  ...9  ...10
##     <chr>                   <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
```

```
##  1 <NA>                    <NA>    <NA> <NA>  <NA>   <NA>  <NA>  <NA>  <NA>   <NA>
##  2 See key to columns bel~ <NA>    <NA> <NA>  <NA>   <NA>  <NA>  <NA>  <NA>   <NA>
##  3 <NA>                    <NA>    <NA> <NA>  <NA>   <NA>  <NA>  <NA>  <NA>   <NA>
##  4 <NA>                    Popu~   <NA> <NA>  Cran~  <NA>  <NA>  <NA>  <NA>   Quan~
##  5 Specimen #              Mort~   "Mor~ Cont~ Curr~ Curr~ Curr~ Mort~ Perc~  3 Di~
##  6 2                       Negr~   "Bla~ Afri~ 1297~ 79    82    83    0.01~  II
##  7 3                       Chin~   "\"M~ Asia~ 1381~ 84    87    89    0.02~  II
##  8 8                       Hind~   "Whi~ Asia~ 1165~ 71    74    73    -0.0~  II
##  9 14                      Angl~   "Whi~ Euro~ 1347~ 82    85    85    0      II
## 10 15                      Huron   "Nat~ Nati~ 1229~ 75    78    75    -0.0~  III
## # i 328 more rows
## # i abbreviated name:
## #   1: `Measurement Data: Comparison with Morton (1849) Shot-Based Capacities`
## # i 2 more variables: ...11 <chr>, ...12 <chr>
```

```r
# Renaming columns
colnames(pbio_1001071_s004) <- c("Measurement Data: Comparison with Morton
                                  (1849) Shot-Based Capacities", "...2", "...3",
                                  "...4", "...5", "...6", "...7", "...8", "...9",
                                  "...10", "...11", "...12")

# Keep only the relevant columns
cranial_data <- pbio_1001071_s004[, c("...2", "...4", "...8")]

# Print the cleaned column names to verify
print(colnames(cranial_data))
```

```
## [1] "...2" "...4" "...8"
```

```r
# Column header notes:
# "...2" = "Morton (1849) Affiliation"
# "...4" = "Continent-Based (6 Populations)"
# "...8" = "Morton Shot (in3)" = "The shot-based cranial capacity of the specimen, in cubic inches, fro~
# Convert columns to appropriate types
cranial_data$`...2` <- as.factor(cranial_data$`...2`)
cranial_data$`...8` <- as.numeric(cranial_data$`...8`)
```

```
## Warning: NAs introduced by coercion
```

```r
# Group by affiliation and calculate the mean cranial capacity
cranial_data_summary <- cranial_data %>%
  group_by(`...2`) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE))
```

Compare Whites

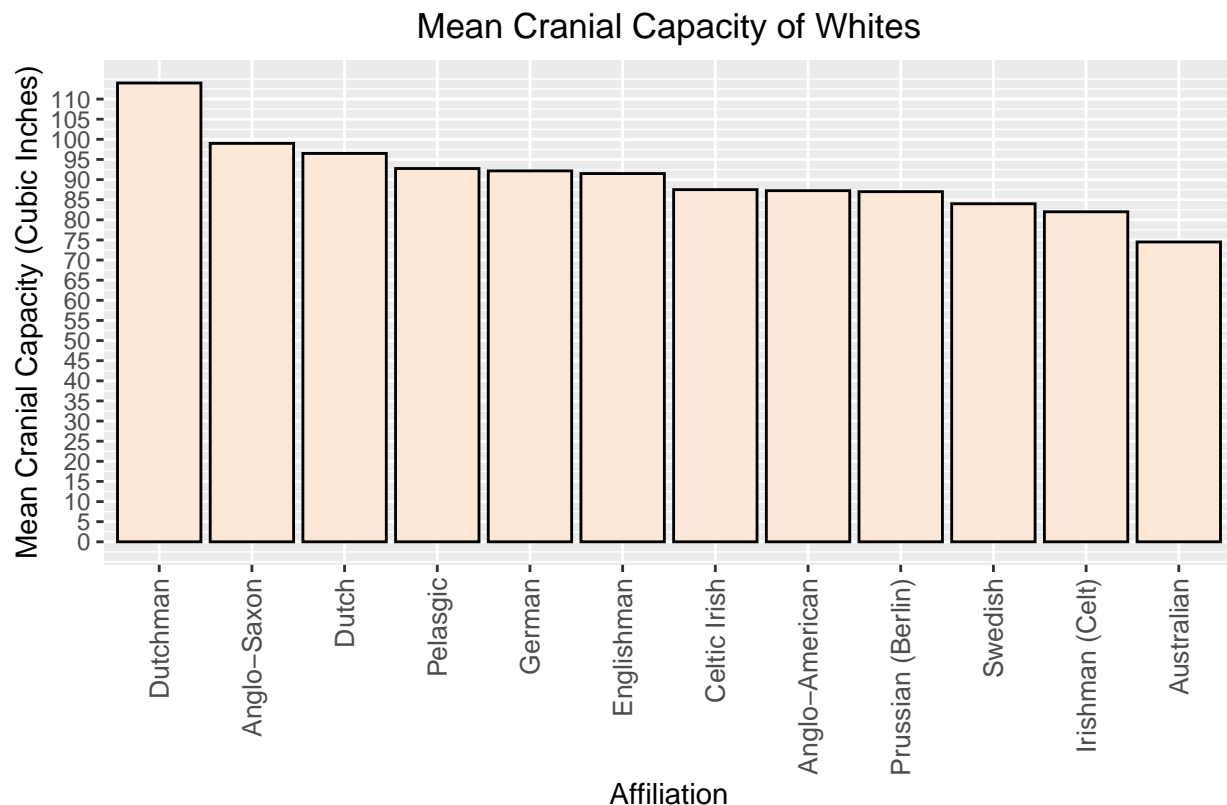```r
# Filter data to include only specified affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% c("Celtic Irish", "German", "Englishman", "Dutch", "Australian",
                       "Anglo-American", "Anglo-Saxon", "Prussian (Berlin)",
                       "Swedish", "Pelasgic", "Irishman (Celt)", "Dutchman"))
```

```r
# Group by affiliation and calculate the mean cranial capacity
cranial_data_summary <- filtered_cranial_data %>%
  group_by(`...2`) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE))

# Create the bar plot with sorting
ggplot(cranial_data_summary, aes(x = reorder(`...2`, -mean_cranial_capacity), y = mean_cranial_capacity
  geom_bar(stat = "identity", fill = "#fde7d6", color = "black") +
  labs(x = "Affiliation", y = "Mean Cranial Capacity (Cubic Inches)",
       title = "Mean Cranial Capacity of Whites",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  scale_y_continuous(breaks = seq(0, max(cranial_data_summary$mean_cranial_capacity, na.rm = TRUE), by =
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1, size = 10),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))
```


Mean Cranial Capacity of Whites

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.

Compare Whites to Negroes - Bar Graph

```r
# Filter data to include only specified affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% c("Celtic Irish", "German", "Englishman", "Dutch",
                       "Anglo-American", "Anglo-Saxon", "Prussian (Berlin)",
                       "Swedish", "Pelasgic", "Irishman (Celt)", "Dutchman",
                       "Negro", "Negress", "Native African", "Negro (US)",
                       "Native African Negro", "Hottentot", "Eboe", "Dey",
                       "Krooman", "Pessah (Negro)", "Golah",
```

```r
                            "Golah Negro (Liberia)", "Native African (Grabbo)",
                            "Native African (Bassa)", "Egyptian"))

# Group by affiliation and calculate the mean cranial capacity
cranial_data_summary <- filtered_cranial_data %>%
  group_by(`...2`) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE)) %>%
  arrange(desc(mean_cranial_capacity))  # Order by descending cranial capacity

# Define race group and colors
cranial_data_summary <- cranial_data_summary %>%
  mutate(race_group = ifelse(`...2` %in%
                            c("Negro", "Negress", "Native African", "Negro (US)",
                              "Native African Negro", "Hottentot", "Eboe", "Dey",
                              "Krooman", "Pessah (Negro)", "Golah",
                              "Golah Negro (Liberia)", "Native African (Grabbo)",
                              "Native African (Bassa)", "Egyptian"), "Negro", "White"))

# Create the bar plot
ggplot(cranial_data_summary, aes(x = reorder(`...2`, -mean_cranial_capacity), y = mean_cranial_capacity
  geom_bar(stat = "identity", color = "black") +
  scale_fill_manual(name = "Race Group", values = c("Negro" = "#260701", "White" = "#fde7d6")) +
  labs(x = "Affiliation", y = "Mean Cranial Capacity (Cubic Inches)",
       title = "Mean Cranial Capacity by Race",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  scale_y_continuous(breaks = seq(0, max(cranial_data_summary$mean_cranial_capacity, na.rm = TRUE), by =
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1, size = 8),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))
```
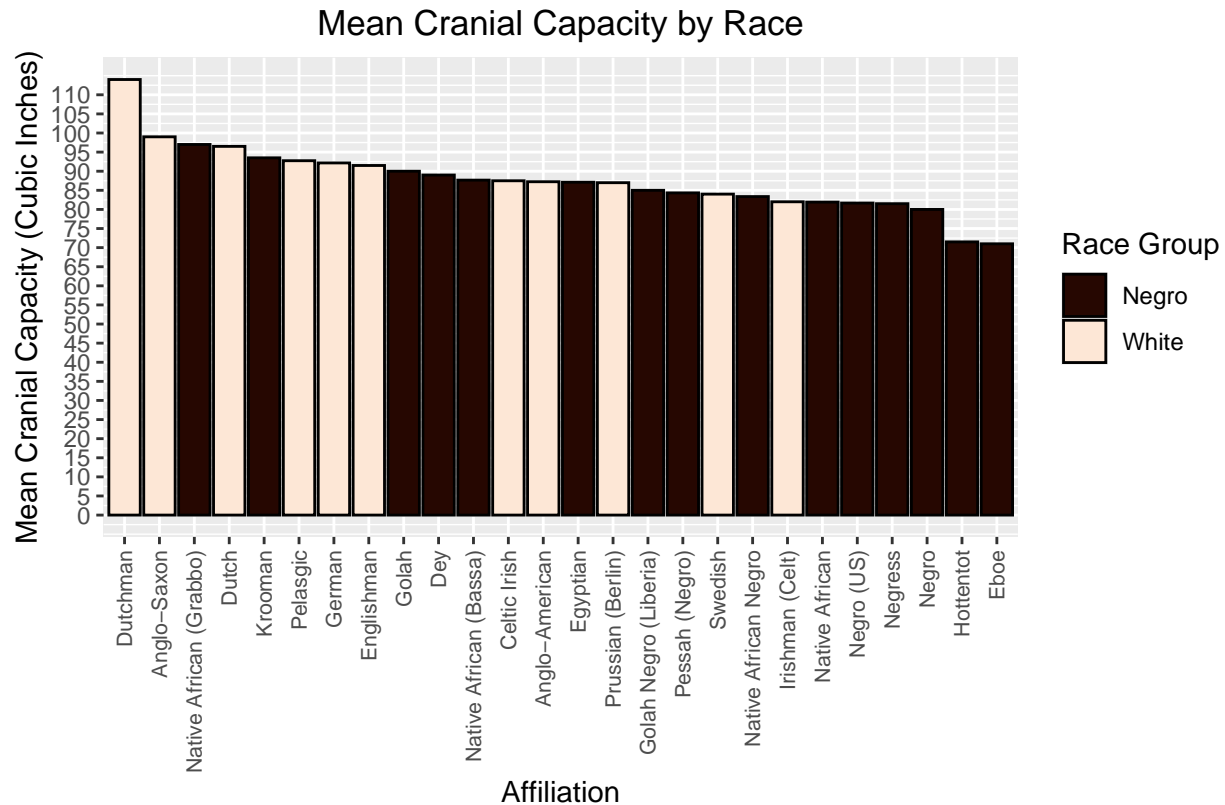
Mean Cranial Capacity by Race

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.
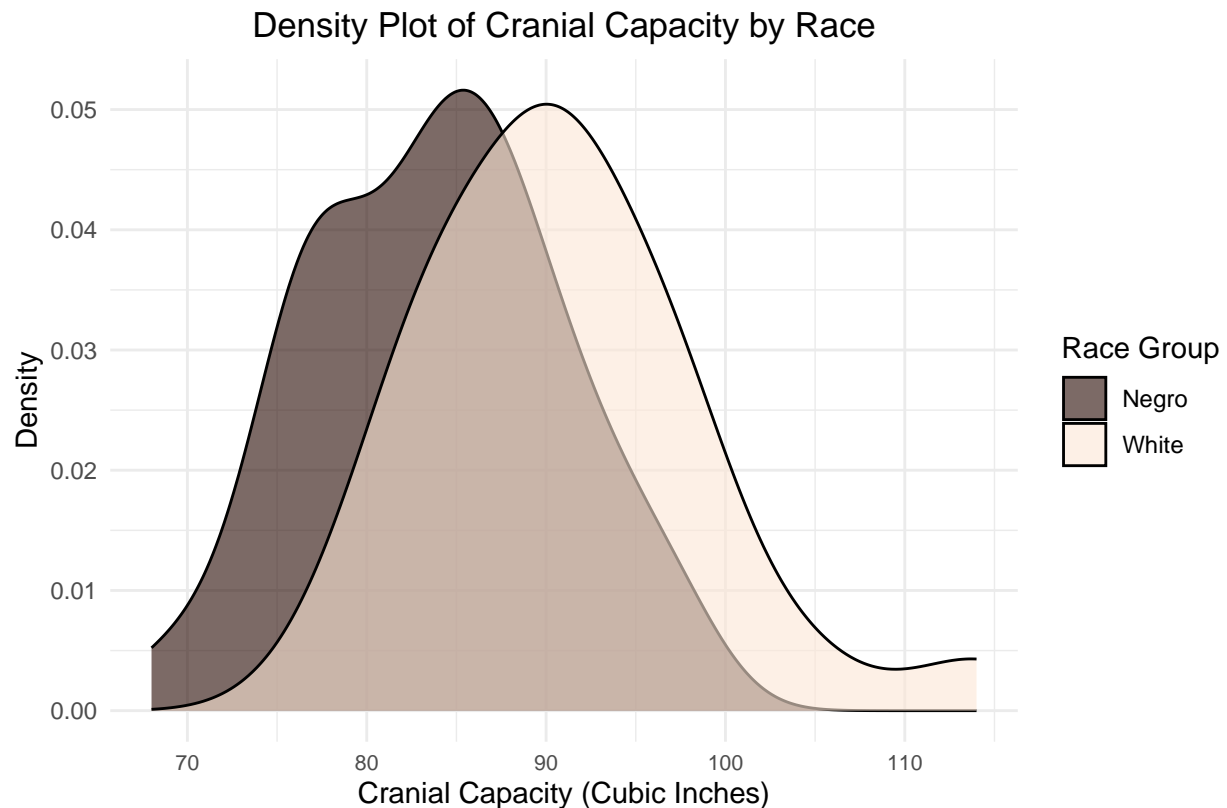
Compare Whites to Negroes - Density Plot

```
# Filter data to include only specified affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% c("Celtic Irish", "German", "Englishman", "Dutch",
                       "Anglo-American", "Anglo-Saxon", "Prussian (Berlin)",
                       "Swedish", "Pelasgic", "Irishman (Celt)", "Dutchman",
                       "Negro", "Negress", "Native African", "Negro (US)",
                       "Native African Negro", "Hottentot", "Eboe", "Dey",
                       "Krooman", "Pessah (Negro)", "Golah",
                       "Golah Negro (Liberia)", "Native African (Grabbo)",
                       "Native African (Bassa)", "Egyptian"))

# Define race group
filtered_cranial_data <- filtered_cranial_data %>%
  mutate(race_group = ifelse(`...2` %in%
                       c("Negro", "Negress", "Native African", "Negro (US)",
                         "Native African Negro", "Hottentot", "Eboe", "Dey",
                         "Krooman", "Pessah (Negro)", "Golah",
                         "Golah Negro (Liberia)", "Native African (Grabbo)",
                         "Native African (Bassa)", "Egyptian"), "Negro", "White"))

# Create the density plot
ggplot(filtered_cranial_data, aes(x = `...8`, fill = race_group)) +
  geom_density(alpha = 0.6, color = "black") +
  scale_fill_manual(values = c("Negro" = "#260701", "White" = "#fde7d6"), name = "Race Group") +
```

```
    labs(x = "Cranial Capacity (Cubic Inches)",
         y = "Density",
         title = "Density Plot of Cranial Capacity by Race",
         caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
    theme_minimal() +
    theme(axis.text.x = element_text(size = 8),
          plot.title = element_text(hjust = 0.5),
          plot.caption = element_text(hjust = 0))
```


Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.

Compare Whites Asians and Negroes - Bar Graph

```
# Filter data to include specified affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% c("Celtic Irish", "German", "Englishman", "Dutch",
                        "Anglo-American", "Anglo-Saxon", "Prussian (Berlin)",
                        "Swedish", "Pelasgic", "Irishman (Celt)", "Dutchman",
                        "Negro", "Negress", "Native African", "Negro (US)",
                        "Native African Negro", "Hottentot", "Eboe", "Dey",
                        "Krooman", "Pessah (Negro)", "Golah",
                        "Golah Negro (Liberia)", "Native African (Grabbo)",
                        "Native African (Bassa)", "Egyptian",
                        "Chinese", "Javanese", "Hindu of Bengal", "Malay (Ceylon)"))

# Define the race groups
filtered_cranial_data <- filtered_cranial_data %>%
  mutate(race_group = case_when(
```

```r
    `...2` %in% c("Negro", "Negress", "Native African", "Negro (US)",
                  "Native African Negro", "Hottentot", "Eboe", "Dey",
                  "Krooman", "Pessah (Negro)", "Golah",
                  "Golah Negro (Liberia)", "Native African (Grabbo)",
                  "Native African (Bassa)", "Egyptian") ~ "Negro",
    `...2` %in% c("Chinese", "Javanese", "Hindu of Bengal", "Malay (Ceylon)",
                  "Tagelos Malay", "Tagelos Malay", "Hindu", "Malay (Madura)",
                  "Malay (Borneo)", "Malay (Makassar)", "Malay (Amboyna)",
                  "Malay (Sambawa)", "Bengalee", "Malay (Malacca)", "Malay",
                  "Chinese (Canton)", "Malay (Macassar)", "Malay (Javanese)",
                  "Thugg of India") ~ "Asian",
    TRUE ~ "White"
  ))

# Group by affiliation and calculate the mean cranial capacity
cranial_data_summary <- filtered_cranial_data %>%
  group_by(`...2`, race_group) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE)) %>%
  arrange(desc(mean_cranial_capacity))  # Order by descending cranial capacity
```
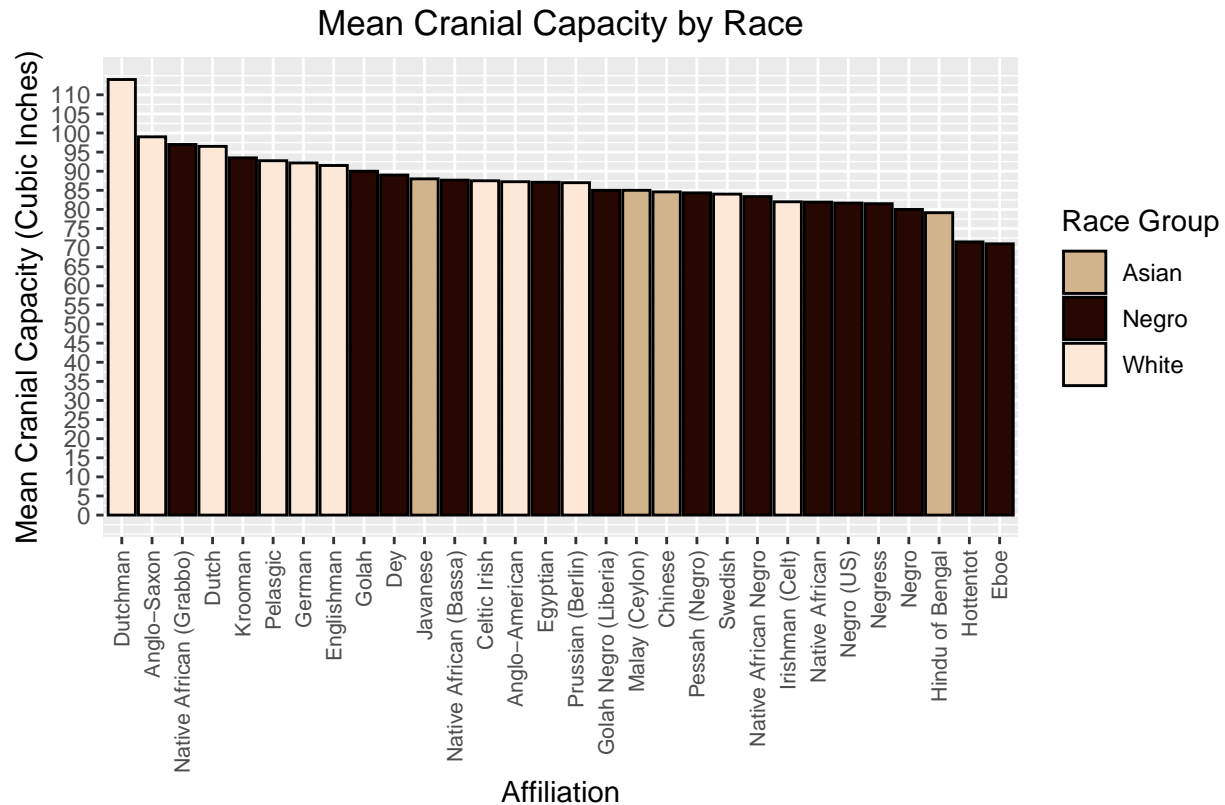
```
## `summarise()` has grouped output by '...2'. You can override using the
## `.groups` argument.
```

```r
# Create the bar plot
ggplot(cranial_data_summary, aes(x = reorder(`...2`, -mean_cranial_capacity), y = mean_cranial_capacity
  geom_bar(stat = "identity", color = "black") +
  scale_fill_manual(values = c("White" = "#fde7d6", "Negro" = "#260701", "Asian" = "Tan"),
                    name = "Race Group") +
  labs(x = "Affiliation", y = "Mean Cranial Capacity (Cubic Inches)",
       title = "Mean Cranial Capacity by Race",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  scale_y_continuous(breaks = seq(0, max(cranial_data_summary$mean_cranial_capacity, na.rm = TRUE), by =
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1, size = 8),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))
```

Mean Cranial Capacity by Race

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.

Compare Whites Asians and Negroes - Density Plot

```r
# Filter data to include specified affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% c("Celtic Irish", "German", "Englishman", "Dutch",
                       "Anglo-American", "Anglo-Saxon", "Prussian (Berlin)",
                       "Swedish", "Pelasgic", "Irishman (Celt)", "Dutchman",
                       "Negro", "Negress", "Native African", "Negro (US)",
                       "Native African Negro", "Hottentot", "Eboe", "Dey",
                       "Krooman", "Pessah (Negro)", "Golah",
                       "Golah Negro (Liberia)", "Native African (Grabbo)",
                       "Native African (Bassa)", "Egyptian",
                       "Chinese", "Javanese", "Hindu of Bengal", "Malay (Ceylon)"))

# Define the race groups
filtered_cranial_data <- filtered_cranial_data %>%
  mutate(race_group = case_when(
    `...2` %in% c("Negro", "Negress", "Native African", "Negro (US)",
                  "Native African Negro", "Hottentot", "Eboe", "Dey",
                  "Krooman", "Pessah (Negro)", "Golah",
                  "Golah Negro (Liberia)", "Native African (Grabbo)",
                  "Native African (Bassa)", "Egyptian") ~ "Negro",
    `...2` %in% c("Chinese", "Javanese", "Hindu of Bengal", "Malay (Ceylon)",
                  "Tagelos Malay", "Tagelos Malay", "Hindu", "Malay (Madura)",
                  "Malay (Borneo)", "Malay (Makassar)", "Malay (Amboyna)",
                  "Malay (Sambawa)", "Bengalee", "Malay (Malacca)", "Malay",
```

```
                  "Chinese (Canton)", "Malay (Macassar)", "Malay (Javanese)",
                  "Thugg of India") ~ "Asian",
    TRUE ~ "White"
  ))

# Group by affiliation and calculate the mean cranial capacity
cranial_data_summary <- filtered_cranial_data %>%
  group_by(`...2`, race_group) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE)) %>%
  arrange(desc(mean_cranial_capacity))  # Order by descending cranial capacity
```
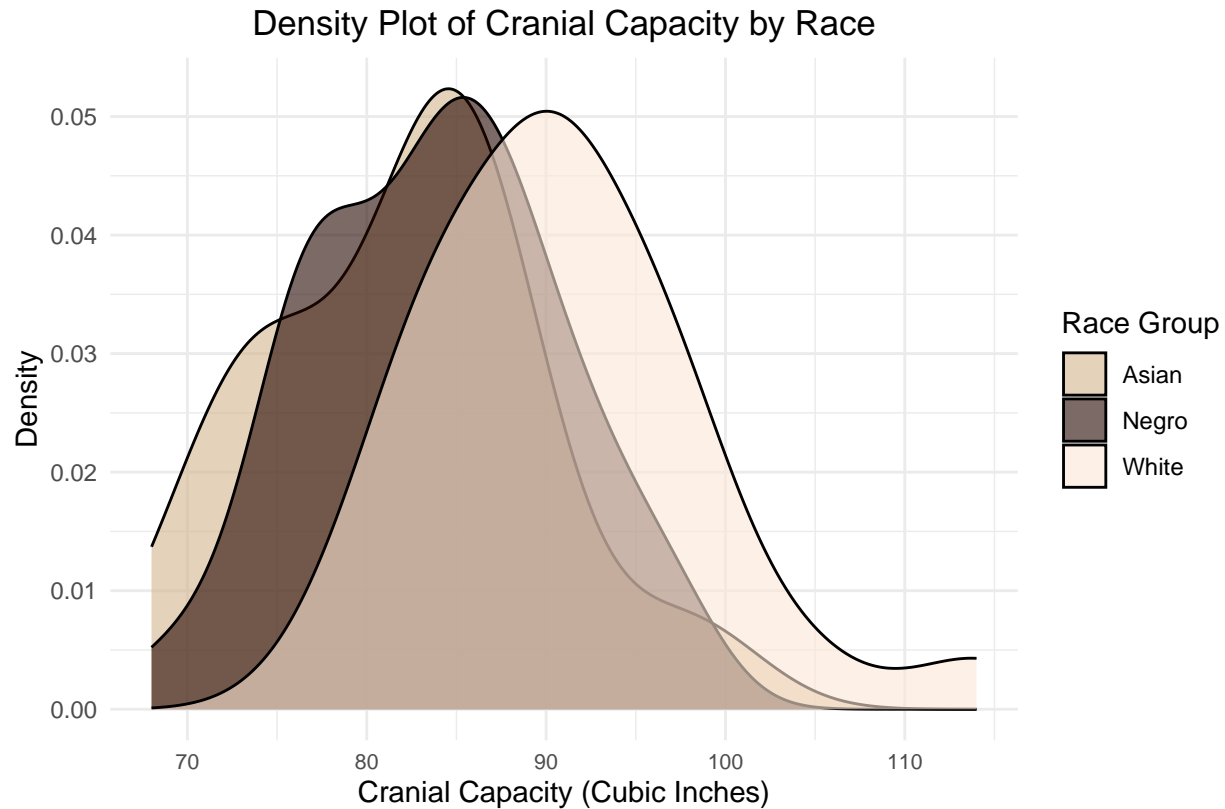
`summarise()` has grouped output by '...2'. You can override using the
`.groups` argument.

```
ggplot(filtered_cranial_data, aes(x = `...8`, fill = race_group)) +
  geom_density(alpha = 0.6, color = "black") +
  scale_fill_manual(values = c("White" = "#fde7d6", "Negro" = "#260701", "Asian" = "Tan"),
                    name = "Race Group") +
  labs(x = "Cranial Capacity (Cubic Inches)",
       y = "Density",
       title = "Density Plot of Cranial Capacity by Race",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  theme_minimal() +
  theme(axis.text.x = element_text(size = 8),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))
```

Density Plot of Cranial Capacity by Race

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.
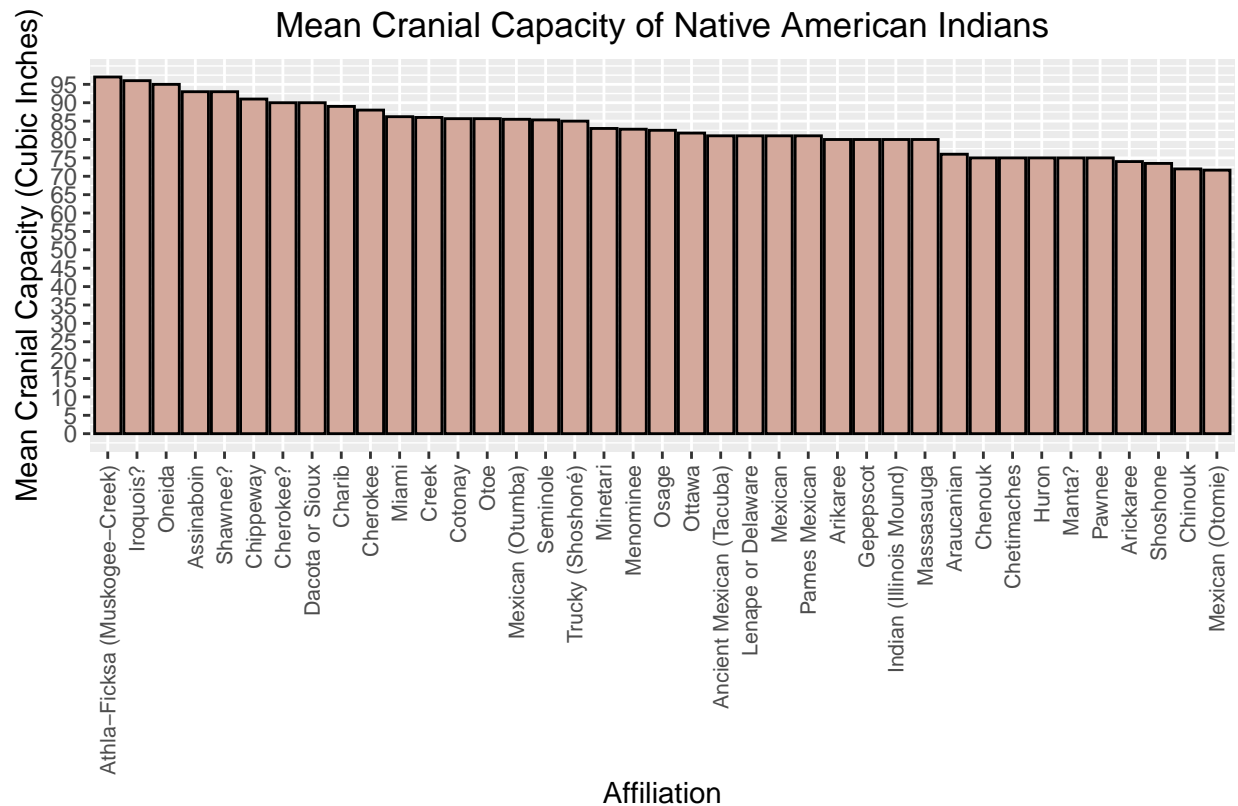
Compare Native American Indians

```r
# Filter data to include only specified Native American Indian affiliations
native_american_affiliations <- c("Huron", "Iroquois?", "Massasauga", "Oneida", "Mexican",
                                   "Menominee", "Osage", "Chetimaches", "Gepepscot", "Miami",
                                   "Manta?", "Shawnee?", "Creek", "Chinouk", "Pawnee", "Chenouk",
                                   "Athla-Ficksa (Muskogee-Creek)", "Seminole", "Dacota or Sioux",
                                   "Cherokee?", "Cherokee", "Arickaree", "Araucanian", "Assinaboin",
                                   "Osage", "Chippeway", "Shawnee?", "Charib", "Seminole",
                                   "Mexican (Otumba)", "Ancient Mexican (Tacuba)", "Cotonay",
                                   "Minetari", "Arikaree", "Creek", "Otoe", "Ottawa",
                                   "Lenape or Delaware", "Indian (Illinois Mound)", "Shoshone",
                                   "Trucky (Shoshoné)", "Mexican (Otomie)", "Pames Mexican")

filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% native_american_affiliations)

# Group by affiliation and calculate the mean cranial capacity
cranial_data_summary <- filtered_cranial_data %>%
  group_by(`...2`) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE)) %>%
  arrange(desc(mean_cranial_capacity))  # Order by descending cranial capacity

# Create the bar plot to compare the means
ggplot(cranial_data_summary, aes(x = reorder(`...2`, -mean_cranial_capacity), y = mean_cranial_capacity
  geom_bar(stat = "identity", fill = "#D4A99C", color = "black") +
```

```
    labs(x = "Affiliation", y = "Mean Cranial Capacity (Cubic Inches)",
         title = "Mean Cranial Capacity of Native American Indians",
         caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
    scale_y_continuous(breaks = seq(0, max(cranial_data_summary$mean_cranial_capacity, na.rm = TRUE), by =
    theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1, size = 8),
          plot.title = element_text(hjust = 0.5),
          plot.caption = element_text(hjust = 0),
          legend.position = "none")  # Remove the legend
```

Mean Cranial Capacity of Native American Indians

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.

Compare Bottom Six Negroes to Bottom Six Native American Indians - Bar Graph

```
# Filter data to include only specified Negro and Native American Indian affiliations
negro_affiliations <- c("Negro", "Negress", "Native African",
                        "Negro (US)", "Hottentot", "Eboe")

native_american_affiliations <- c("Manta?", "Pawnee", "Arickaree",
                                  "Shoshone", "Chinouk", "Mexican (Otomie)")

# Combine both sets of affiliations
combined_affiliations <- c(negro_affiliations, native_american_affiliations)

# Filter data to include only combined affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% combined_affiliations)

# Group by affiliation and calculate the mean cranial capacity
```
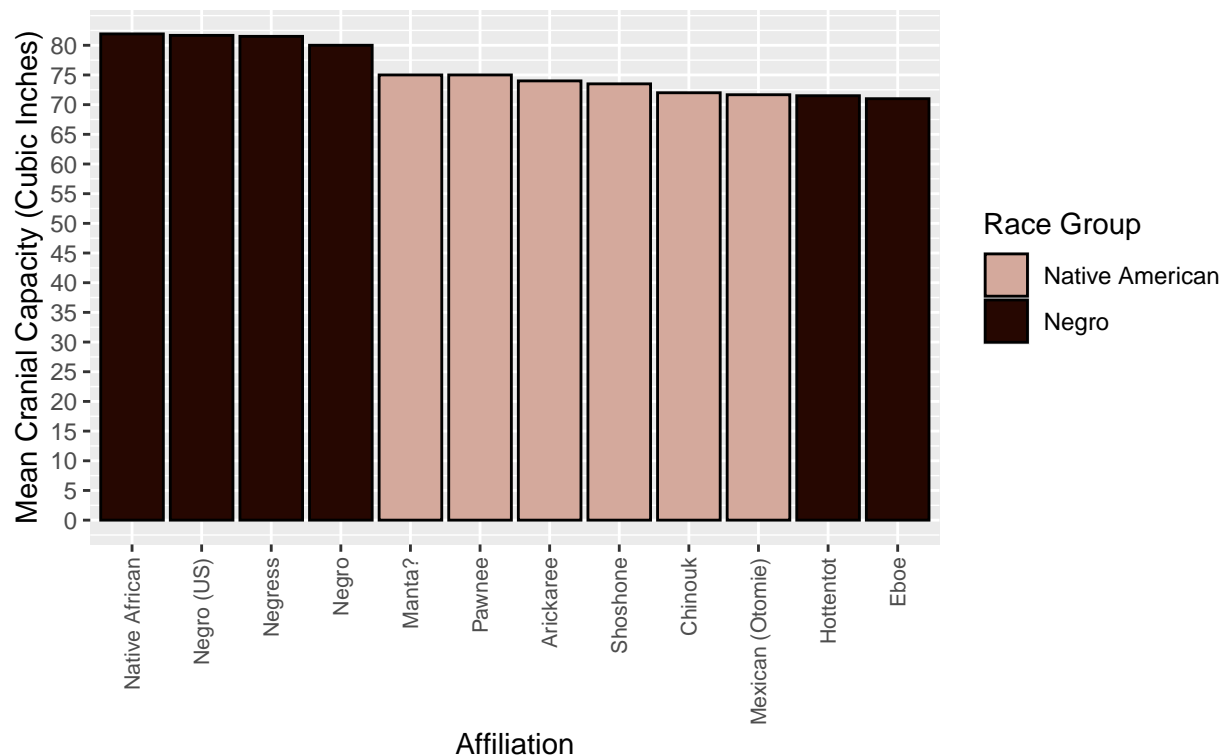
```r
cranial_data_summary <- filtered_cranial_data %>%
  group_by(`...2`) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE)) %>%
  arrange(desc(mean_cranial_capacity))  # Order by descending cranial capacity

# Define race group
cranial_data_summary <- cranial_data_summary %>%
  mutate(race_group = ifelse(`...2` %in% negro_affiliations, "Negro", "Native American"))

# Create the bar plot
ggplot(cranial_data_summary, aes(x = reorder(`...2`, -mean_cranial_capacity), y = mean_cranial_capacity
  geom_bar(stat = "identity", color = "black") +
  scale_fill_manual(values = c("Negro" = "#260701", "Native American" = "#D4A99C"), name = "Race Group")
  labs(x = "Affiliation", y = "Mean Cranial Capacity (Cubic Inches)",
       title = "Cranial Capacity: Lowest Negroes vs. Lowest Native Americans",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  scale_y_continuous(breaks = seq(0, max(cranial_data_summary$mean_cranial_capacity, na.rm = TRUE), by =
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1, size = 8),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))
```

Cranial Capacity: Lowest Negroes vs. Lowest Native Americans

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.

Compare Bottom Six Negroes to Bottom Six Native American Indians - Density Plot

```r
# Filter data to include only specified Negro and Native American Indian affiliations
negro_affiliations <- c("Negro", "Negress", "Native African",
                        "Negro (US)", "Hottentot", "Eboe")
```

```r
native_american_affiliations <- c("Manta?", "Pawnee", "Arickaree",
                                  "Shoshone", "Chinouk", "Mexican (Otomie)")

# Combine both sets of affiliations
combined_affiliations <- c(negro_affiliations, native_american_affiliations)

# Filter data to include only combined affiliations
filtered_cranial_data <- cranial_data %>%
  filter(`...2` %in% combined_affiliations)

# Define race group
filtered_cranial_data <- filtered_cranial_data %>%
  mutate(race_group = ifelse(`...2` %in% negro_affiliations, "Negro", "Native American"))

# Create the density plot
ggplot(filtered_cranial_data, aes(x = `...8`, fill = race_group)) +
  geom_density(alpha = 0.6, color = "black") +
  scale_fill_manual(values = c("Negro" = "#260701", "Native American" = "#D4A99C"), name = "Race Group")
  labs(x = "Cranial Capacity (Cubic Inches)",
       y = "Density",
       title = "Cranial Capacity: Lowest Negroes vs. Lowest Native Americans",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  theme_minimal() +
  theme(axis.text.x = element_text(size = 8),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))
```
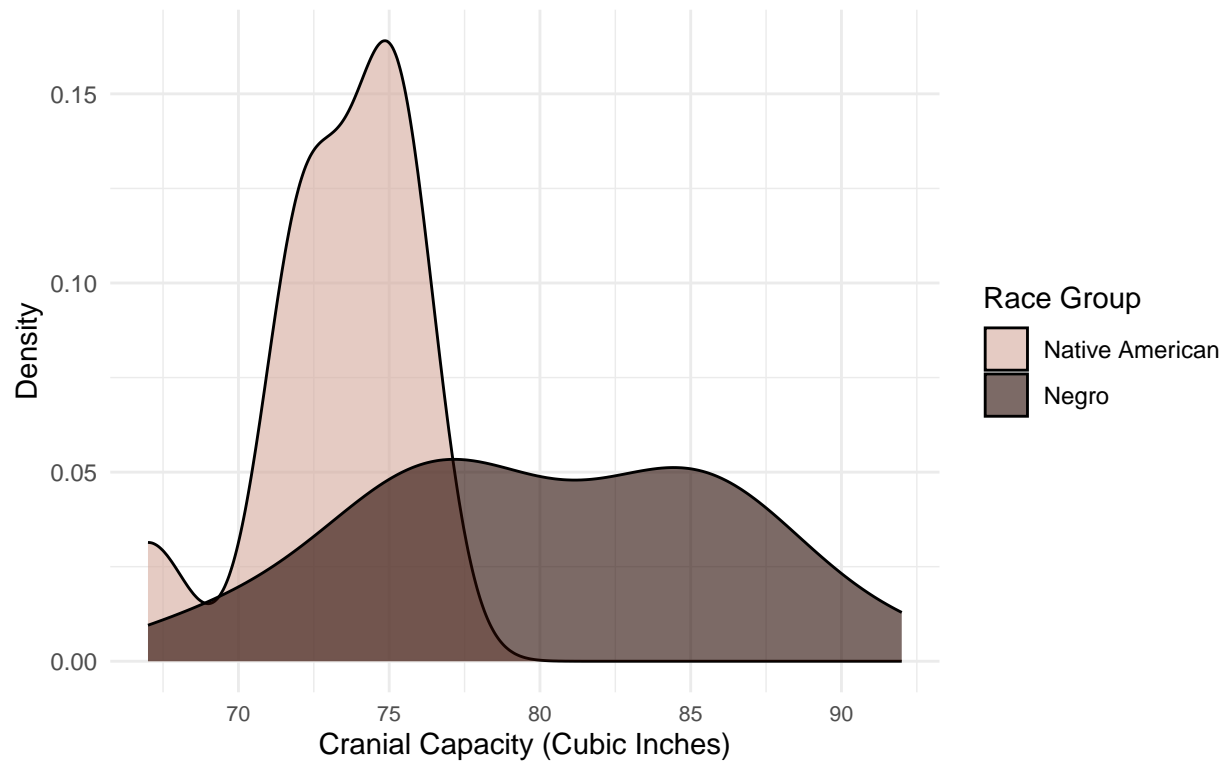
Cranial Capacity: Lowest Negroes vs. Lowest Native Americans

Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.

Compute the Mean for Each Continent

```r
# Filter out the "Australian" group and exclude rows with NA in the cranial capacity column
filtered_cranial_data_continent <- cranial_data %>%
  filter(`...4` != "Australian", !is.na(`...8`))

# Group by continent and calculate the mean cranial capacity
cranial_data_continent_summary <- filtered_cranial_data_continent %>%
  group_by(`...4`) %>%
  summarise(mean_cranial_capacity = mean(`...8`, na.rm = TRUE)) %>%
  arrange(desc(mean_cranial_capacity))  # Order by descending cranial capacity

# Print the summary to verify
print(cranial_data_continent_summary)
```

```
## # A tibble: 5 x 2
##   ...4                      mean_cranial_capacity
##   <chr>                               <dbl>
## 1 European/Caucasian-American          88.9
## 2 Native North American                84.1
## 3 African/African Diaspora             83.7
## 4 Asian/Pacific Islander               83.1
## 5 Native South American                75.5
```
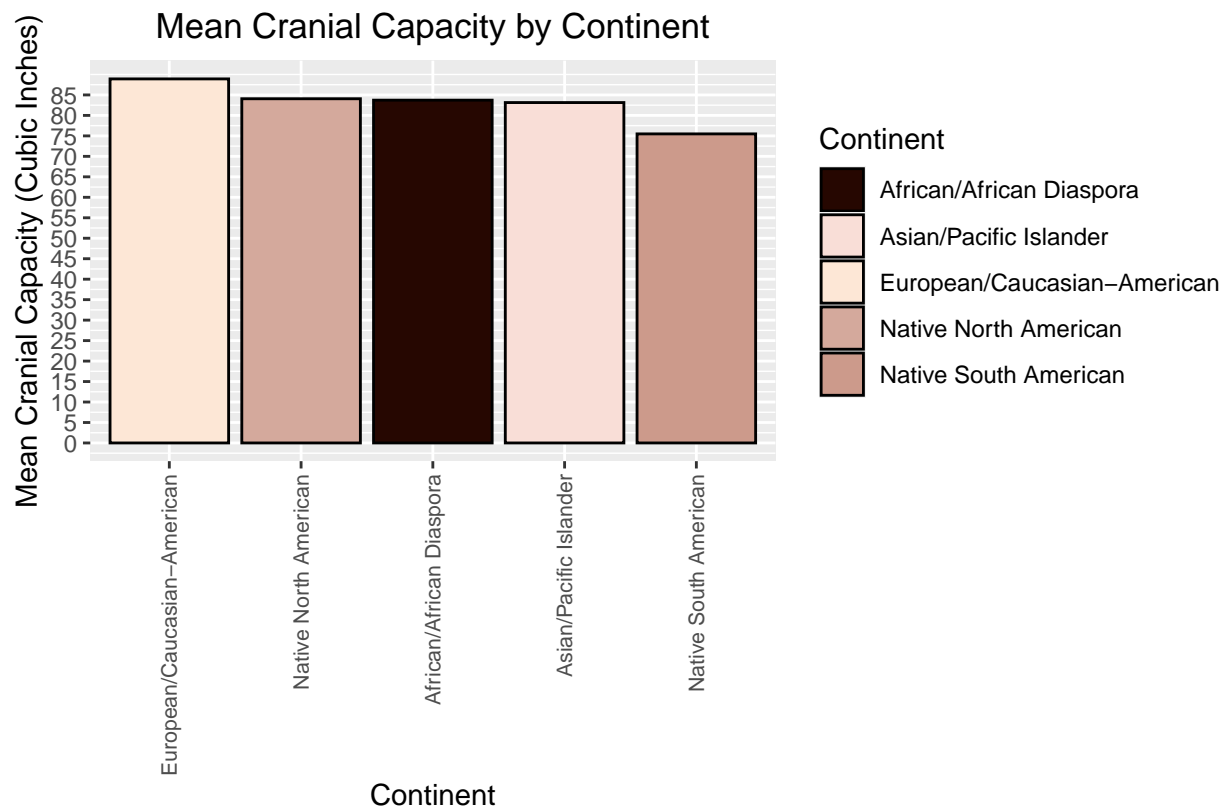
```r
# Define the colors for each continent
continent_colors <- c(
  "European/Caucasian-American" = "#FDE7D6",
  "Native North American" = "#D4A99C",
  "Native South American" = "#cc9a8b",
  "African/African Diaspora" = "#260701",
  "Asian/Pacific Islander" = "#F9DED7"
)

# Create the bar plot to compare the means
ggplot(cranial_data_continent_summary, aes(x = reorder(`...4`, -mean_cranial_capacity), y = mean_cranial
  geom_bar(stat = "identity", color = "black") +
  scale_fill_manual(values = continent_colors, name = "Continent") +
  labs(x = "Continent", y = "Mean Cranial Capacity (Cubic Inches)",
       title = "Mean Cranial Capacity by Continent",
       caption = "Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animal
  scale_y_continuous(breaks = seq(0, max(cranial_data_continent_summary$mean_cranial_capacity, na.rm = `
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1, size = 8),
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0))  # Adjust caption alignment
```


Source: Samuel George Morton (1849) Catalogue of Skulls of Man and the Inferior Animals, Third Edition.