CraniumData

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07/26/2024

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

```r
pbio_1001071_s003 <- read_excel("~/Desktop/CraniaAmericana/pbio.1001071.s003.xls")
```

```
## New names:
## * `` -> `...2`
## * `` -> `...3`
## * `` -> `...4`
## * `` -> `...5`
## * `` -> `...6`
## * `` -> `...7`
```

```r
pbio_1001071_s003
```

```
## # A tibble: 175 x 7
##    `Morton (1839) Crania Americana`        ...2  ...3  ...4  ...5  ...6  ...7
##    <chr>                                   <chr> <chr> <chr> <chr> <chr> <chr>
##  1 <NA>                                    <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
##  2 See bottom for key. Specimens listed in ~ <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
##  3 <NA>                                    <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
##  4 Specimen #                              Affi~ Plate FA    IC    Defo~ Mort~
##  5 75                                      Peru~ <NA>  72    83.5  <NA>  Peru~
##  6 76                                      Peru~ <NA>  73    64    <NA>  Peru~
##  7 77                                      Peru~ <NA>  75    75    <NA>  Peru~
##  8 79                                      Peru~ <NA>  74    74.5  <NA>  Peru~
##  9 81                                      Peru~ <NA>  76    79    <NA>  Peru~
## 10 82                                      Peru~ <NA>  79    75    <NA>  Peru~
## # i 165 more rows
```

```r
# Rename columns if necessary (example shown with column names from the image)
colnames(pbio_1001071_s003) <- c("Specimen#", "Affiliation", "Plate", "FA",
                                 "IC", "Deformed", "MortonGroup")
# Keep only the relevant columns
cranial_data <- pbio_1001071_s003[, c("Affiliation", "IC", "MortonGroup")]
# Print the cleaned column names to verify
print(colnames(cranial_data))
```

```
## [1] "Affiliation" "IC"          "MortonGroup"
```

```
# Ensure the IC column is numeric
cranial_data$IC <- as.numeric(cranial_data$IC)
```

Warning: NAs introduced by coercion

```
# Filter out "Affiliation" and "NA" from the Affiliation column
cranial_data_filtered <- cranial_data[!cranial_data$Affiliation %in%
                                      c("Affiliation", NA), ]
ggplot(cranial_data_filtered, aes(x = Affiliation, y = IC)) +
  geom_bar(stat = "identity", position = "dodge",
           fill = "gray", color = "black") +
  labs(title = "Cranial Capacity by Race",
       x = "Affiliation",
       y = "Cranial Capacity (Cubic Inches)",
       caption = "Source: Samuel George Morton (1839) Crania Americana; or,
       A Comparative View of the Skulls of Various Aboriginal Nations of North and South America") +
  scale_y_continuous(breaks = seq(0, 100, by = 5)) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1, size = 8),
        axis.text.y = element_text(size = 8),
        legend.position = "none",
        plot.title = element_text(hjust = 0.5),
        plot.caption = element_text(hjust = 0.5, size = 8))
```
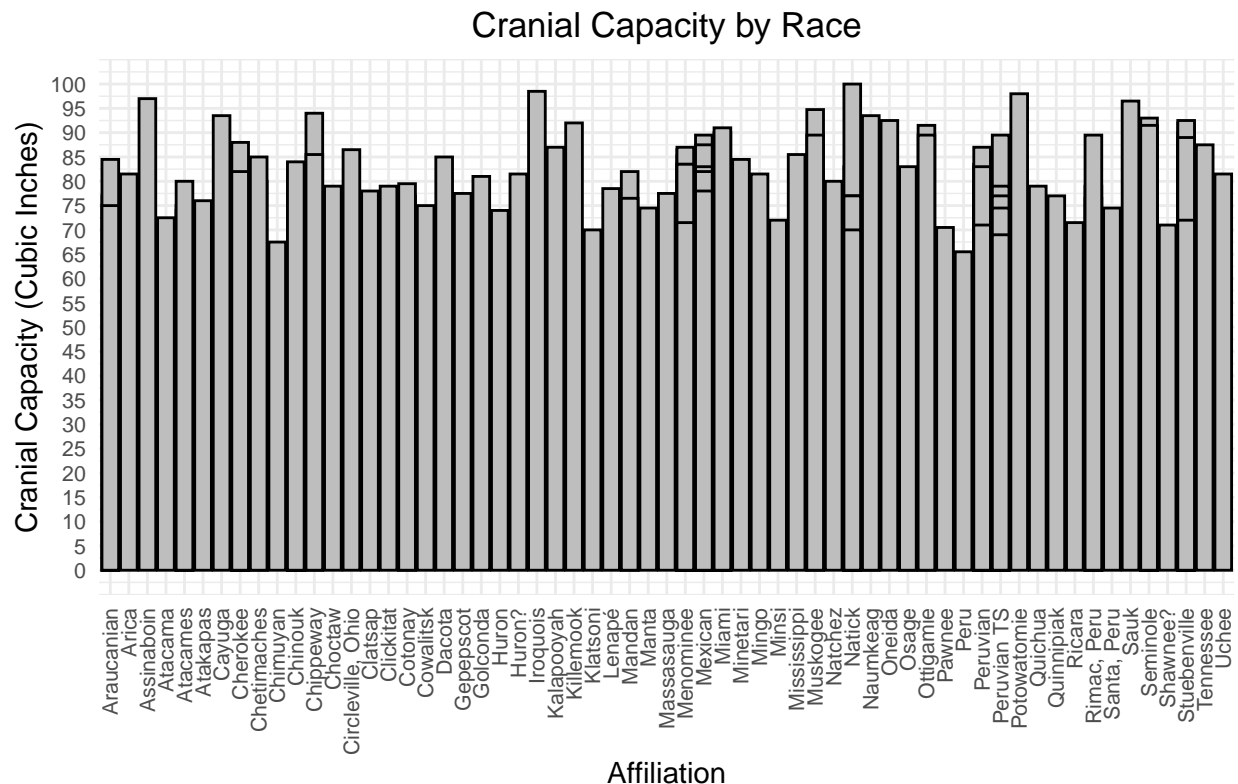
Warning: Removed 3 rows containing missing values (`geom_bar()`).

Source: Samuel George Morton (1839) Crania Americana; or,
A Comparative View of the Skulls of Various Aboriginal Nations of North and South America