

CDC 2023: Data visualizations for 1999-2008 Diabetes Data

Code ▼

9/30/23

This is an R Markdown (<http://rmarkdown.rstudio.com>) Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

Hide

```
library(tidyverse)
library(knitr)
```

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

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```
pop_change <- read_csv('HealthSciences_Dataset (2).csv', show_col_types = FALSE) |>
  select(patient_nbr, race, gender, age, number_diagnoses, diabetesMed, readmitted) |>
  filter(gender != 'Unknown/Invalid', race != '?')
```

pop_change

patient_nbr	race	gender	age	number_diagnoses	diabetesMed	
<dbl>	<chr>	<chr>	<chr>	<dbl>	<chr>	
8222157	Caucasian	Female	[0-10)	1	No	
55629189	Caucasian	Female	[10-20)	9	Yes	
86047875	AfricanAmerican	Female	[20-30)	6	Yes	
82442376	Caucasian	Male	[30-40)	7	Yes	
42519267	Caucasian	Male	[40-50)	5	Yes	
82637451	Caucasian	Male	[50-60)	9	Yes	
84259809	Caucasian	Male	[60-70)	7	Yes	
114882984	Caucasian	Male	[70-80)	8	Yes	
48330783	Caucasian	Female	[80-90)	8	Yes	
63555939	Caucasian	Female	[90-100)	8	Yes	

1-10 of 99,492 rows | 1-6 of 7 columns

Previous 1 2 3 4 5 6 ... 100 Next

#Some control data I am trying to add later

Hide

```
#control_data <- pop_change (
  #Ethnicity = c("Caucasian", "African American", "Other", "Asian", "Hispanic"),
  #Population = c(226962, 35470, 2448, 11279, 32832))
```

Hide

```
gender_percent <- pop_change |>
  group_by(gender) |>
  summarize(percent = n() /nrow(pop_change) * 100)

gender_percent
```

gender <chr>	percent <dbl>
Female	53.84855
Male	46.15145
2 rows	

Hide

```
race_percent <- pop_change |>
  group_by(race) |>
  summarize(percent = n() /nrow(pop_change) * 100)

race_percent
```

race <chr>	percent <dbl>
AfricanAmerican	19.3080851
Asian	0.6442729
Caucasian	76.4875568
Hispanic	2.0474008
Other	1.5126844
5 rows	

Hide

```
age_percent <- pop_change |>
  group_by(age) |>
  summarize(percent = n() /nrow(pop_change) * 100)
```

age_percent

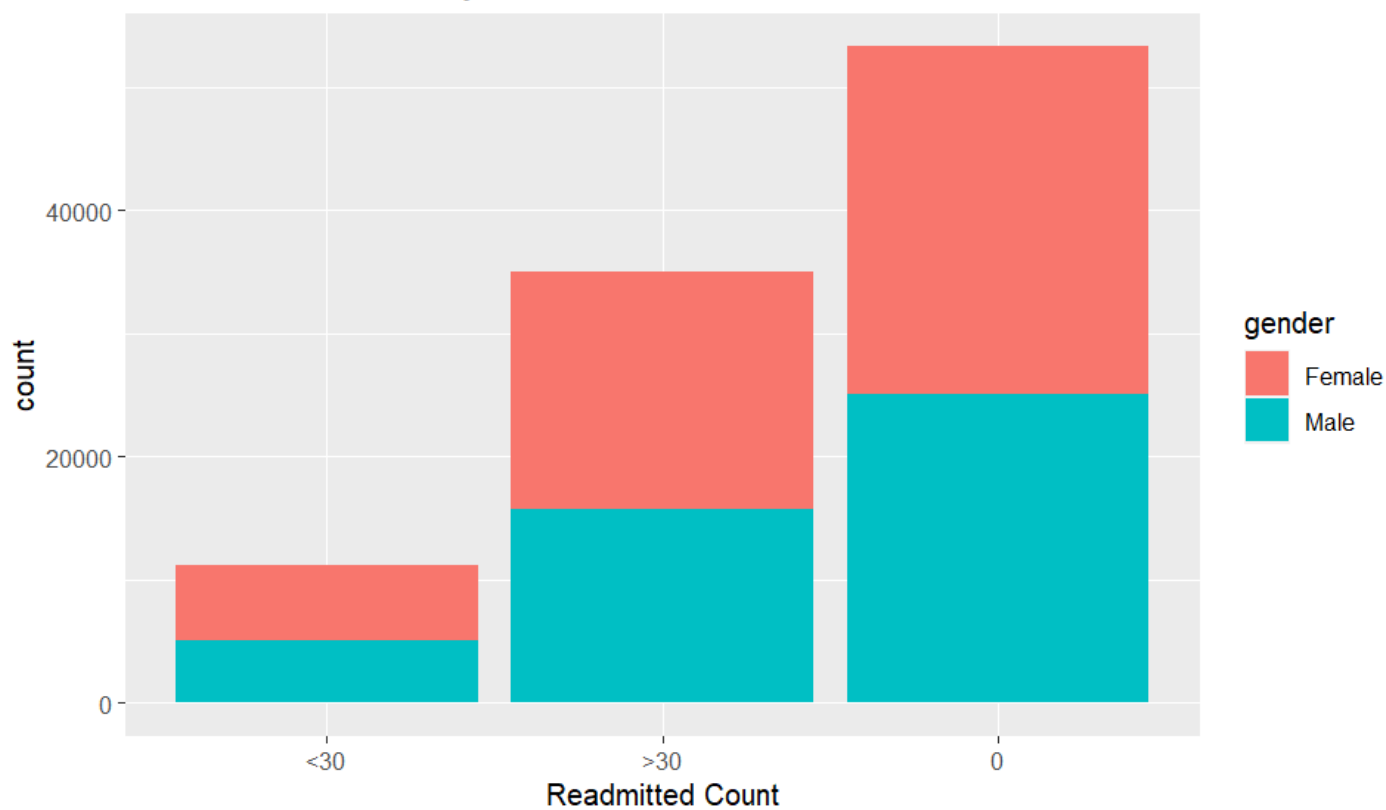
age <chr>	percent <dbl>
[0-10)	0.1608170
[10-20)	0.6854822
[20-30)	1.6192257
[30-40)	3.7178869
[40-50)	9.5133277
[50-60)	16.9812648
[60-70)	22.1002694
[70-80)	25.5980380
[80-90)	16.8857798
[90-100)	2.7379086

1-10 of 10 rows

Hide

```
pop_change |>
  mutate(readmitted = ifelse(readmitted == "NO", "0", readmitted)) |>
  ggplot(mapping = aes(x = readmitted, fill = gender)) +
  geom_bar() +
  labs(title = "Number readmitted by Gender",
       x = "Readmitted Count")
```

Number readmitted by Gender

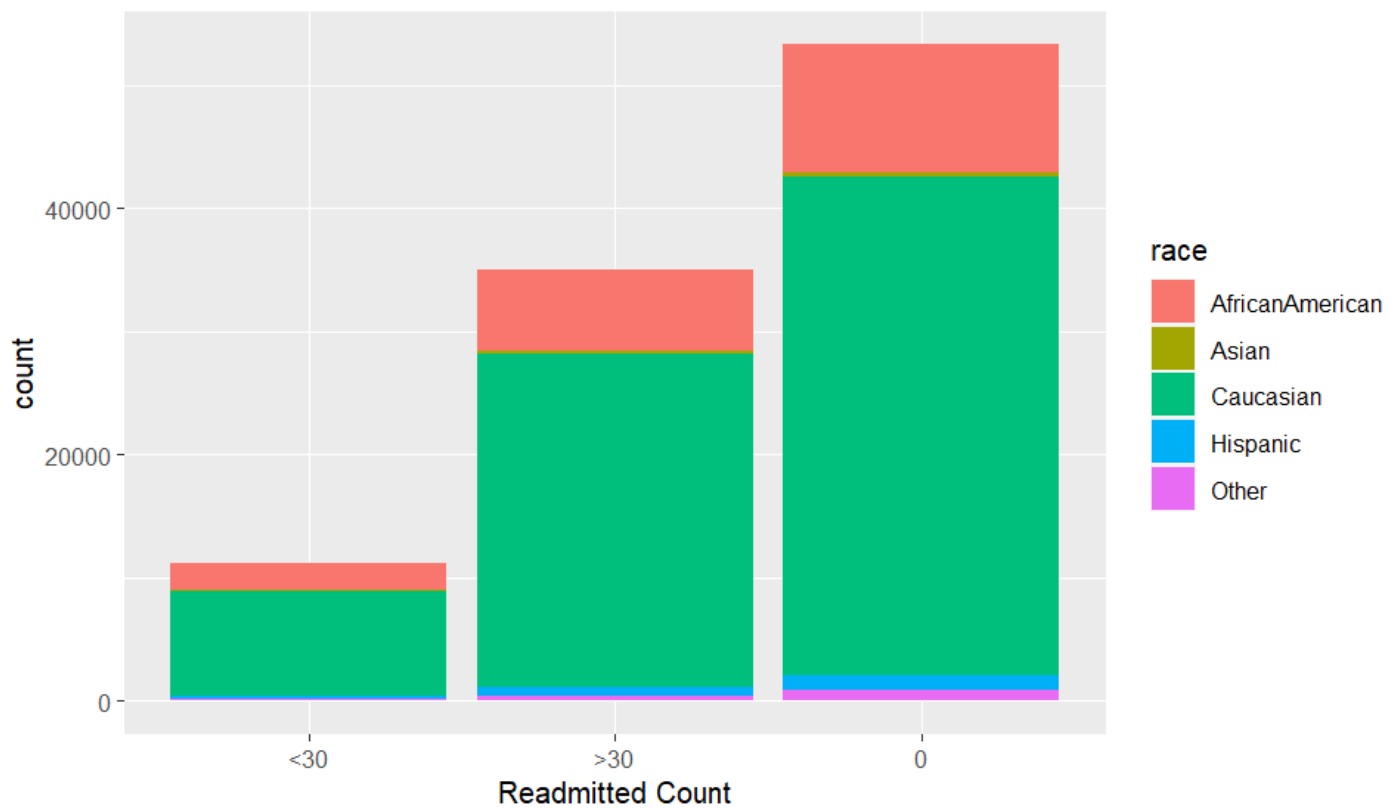
[Hide](#)

NA

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```
pop_change |>
  mutate(readmitted = ifelse(readmitted == "NO", "0", readmitted)) |>
  ggplot(mapping = aes(x = readmitted, fill = race)) +
  labs(title = "Number Readmitted by Race",
        x = "Readmitted Count") +
  geom_bar()
```

Number Readmitted by Race


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NA

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```
pop_change |>
  mutate(readmitted = ifelse(readmitted == "NO", "0", readmitted)) |>
  ggplot(mapping = aes(x = readmitted, fill = age)) +
  labs(title = "Number Readmitted by Age",
        x = "Readmitted Count") +
  geom_bar()
```

Number Readmitted by Age

