# Untitled

Samantha Rodriguez

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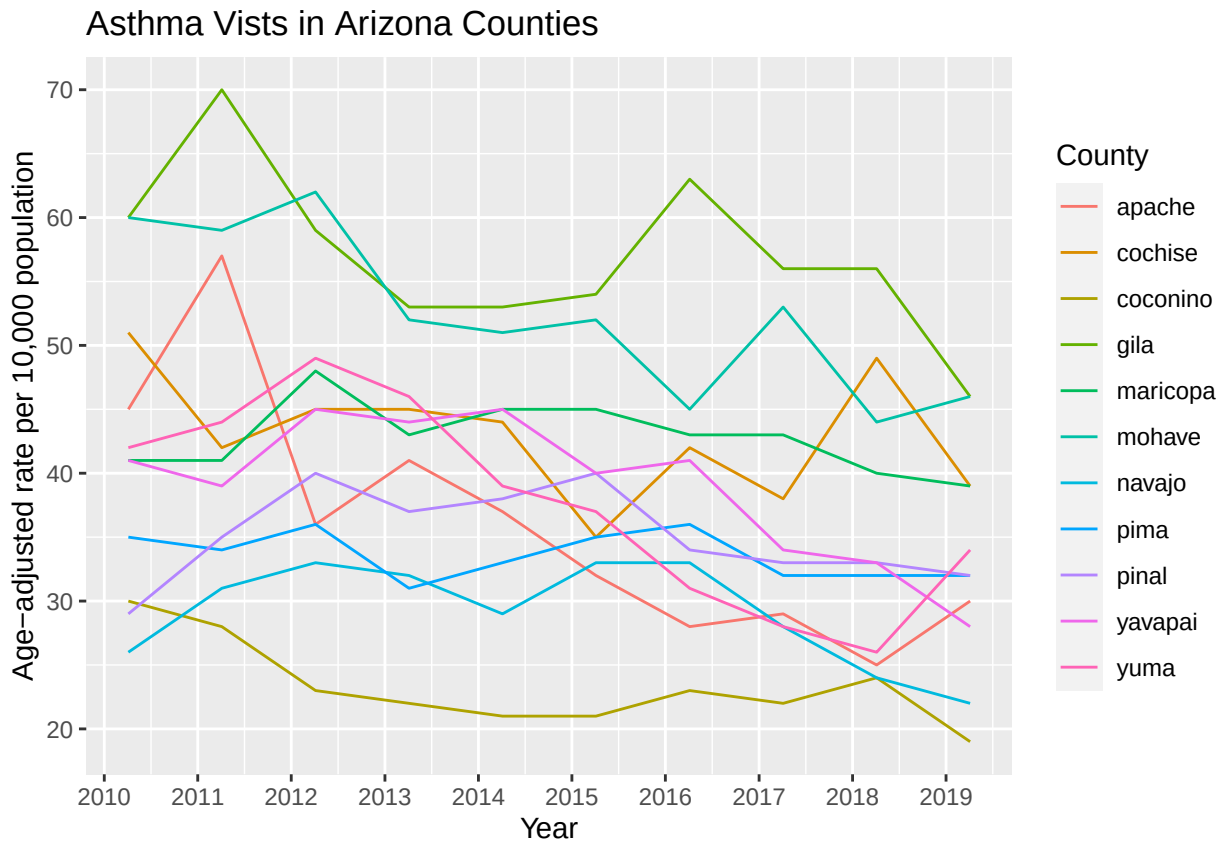
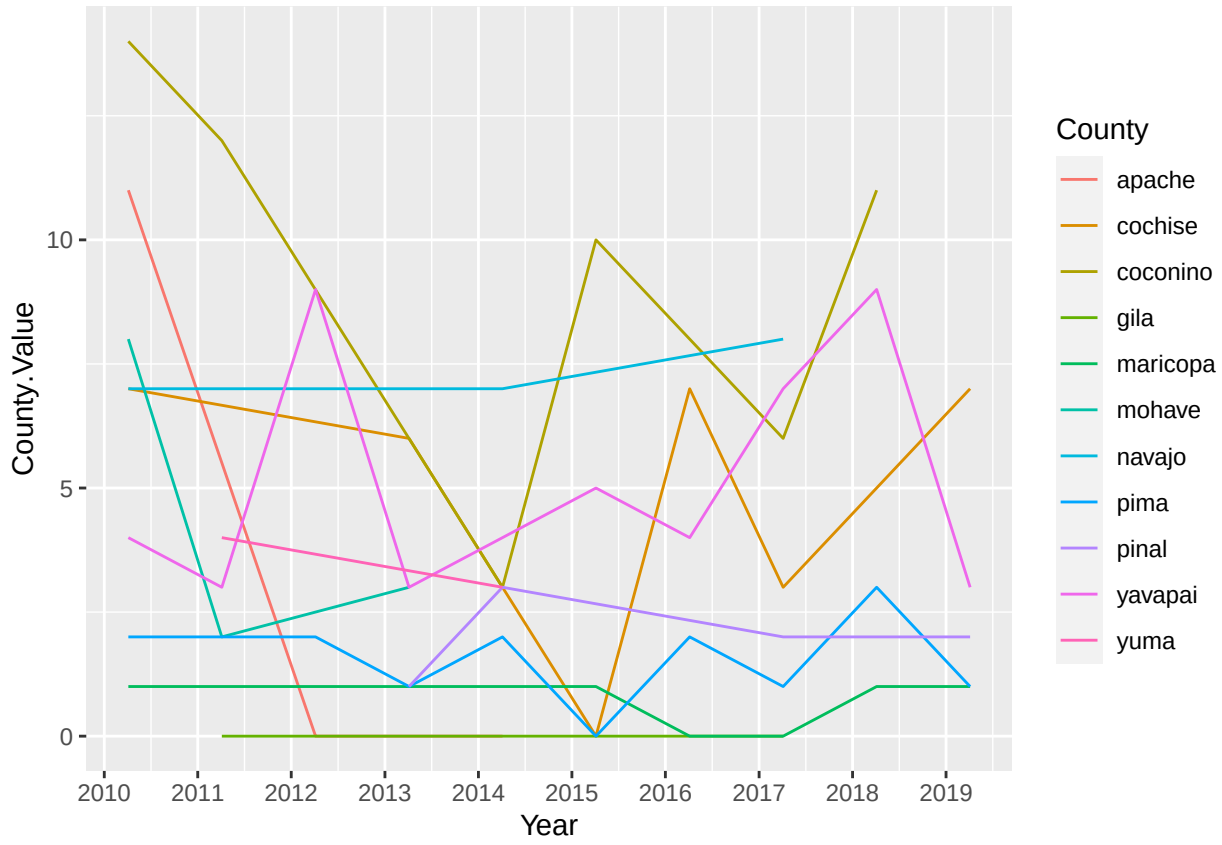
```
asthma <- hospitalData[hospitalData$Content.Area == "Asthma",]
ggplot(asthma, aes(x=Year, y=County.Value, color=County)) + geom_line() +
  scale_x_date(date_labels = "%Y", date_breaks = "1 year") +
  ggtitle("Asthma Vists in Arizona Counties") +
  ylab("Age-adjusted rate per 10,000 population")
```




```
cmp <- hospitalData[hospitalData$Content.Area == "Carbon Monoxide Poisoning",]
ggplot(cmp, aes(x=Year, y=County.Value, color=County)) + geom_line() +
  scale_x_date(date_labels = "%Y", date_breaks = "1 year")
```




```
asthma <- hospitalData[hospitalData$Content.Area == "Asthma" &
                         hospitalData$County == "COCONINO",]
asthma <- asthma %>% arrange(Year) %>% pull(County.Value)
plot(asthma)
acf(asthma)
pacf(asthma)
obj <- arima(asthma, order=c(1,0,0))
acf(obj$residuals)
predict(obj, n.ahead = 1)
```

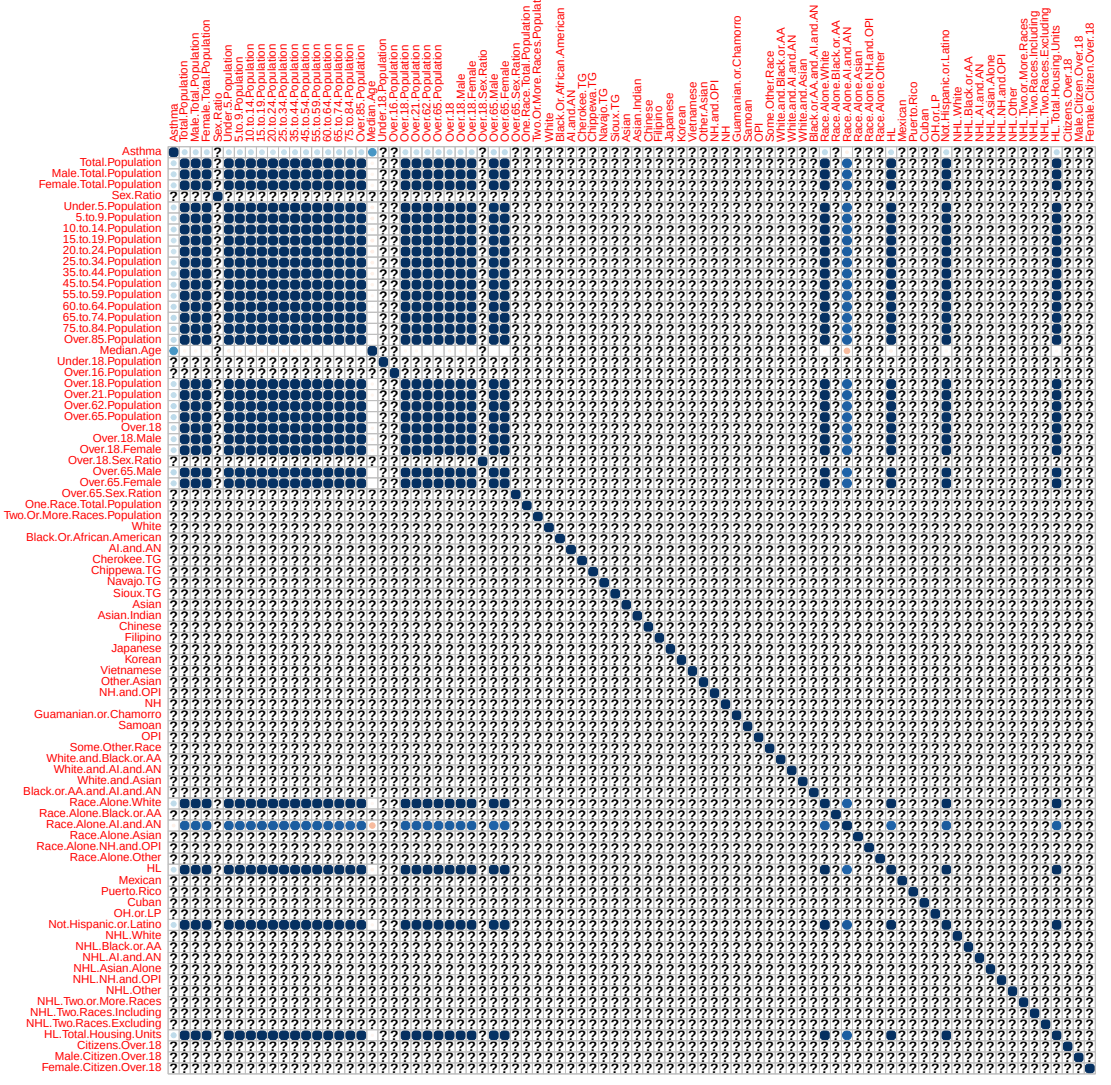
```
hospital.wider <- hospitalData %>% select(-State.Rate)
hospital.wider <- pivot_wider(hospital.wider, names_from = Content.Area,
                              values_from = County.Value)
```

```
asthma.wider <- hospital.wider %>% select(c(County.Year, Asthma))
asthma.data <- merge(asthma.wider, censusData)
```

```
# colnames(cor.data) <- c('x1', 'x2', 'x3', 'x4', 'x5', 'x6', 'x7', 'x8', 'x9',
#                         'x10', 'x11', 'x12', 'x13', 'x14', 'x15', 'x16', 'x17',
#                         'x18', 'x19', 'x20', 'x21', 'x22', 'x23', 'x24',
#                         'x25', 'x26', 'x27', 'x28', 'x29', 'x30', 'x31', 'x32',
#                         'x33', 'x34', 'x35',
#                         'x36', 'x37', 'x38', 'x39', 'x40', 'x41', 'x42', 'x43',
#                         'x44', 'x45', 'x46',
#                         'x47', 'x48', 'x49', 'x50', 'x51', 'x52', 'x53', 'x54',
```

```
#                           'x55', 'x56', 'x57',
#                           'x58', 'x59', 'x60', 'x61', 'x62', 'x63', 'x64', 'x65',
#                           'x66', 'x67', 'x68',
#                           'x69', 'x70', 'x71', 'x72', 'x73', 'x74', 'x75', 'x76',
#                           'x77', 'x78', 'x79',
#                           'x80', 'x81', 'x82', 'x83', 'x84', 'x85', 'x86', 'x87',
#                           'x88', 'x89', 'x90',
#                           'x91', 'x92')
```

```
cor.data <- asthma.data %>% select(-c(County.Year, Year, County))
corrplot::corrplot(cor(cor.data), tl.cex = 0.8)
```


Asthma
Total.Population
Male.Total.Population
Female.Total.Population
Sex.Ratio
Under.5.Population
5.to.9.Population
10.to.14.Population
15.to.19.Population
20.to.24.Population
25.to.34.Population
35.to.44.Population
45.to.54.Population
55.to.59.Population
60.to.64.Population
65.to.74.Population
75.to.84.Population
Over.85.Population
Median.Age
Under.18.Population
Over.16.Population
Over.18.Population
Over.21.Population
Over.62.Population
Over.65.Population
Over.18
Over.18.Male
Over.18.Female
Over.18.Sex.Ratio
Over.65.Male
Over.65.Female
Over.65.Sex.Ration
One.Race.Total.Population
Two.Or.More.Races.Population
White
Black.Or.African.American
AI.and.AN
Cherokee.TG
Chippewa.TG
Navajo.TG
Sioux.TG
Asian
Asian.Indian
Chinese
Filipino
Japanese
Korean
Vietnamese
Other.Asian
NH.and.OPI
NH
Guamanian.or.Chamorro
Samoan
OPI
Some.Other.Race
White.and.Black.or.AA
White.and.AI.and.AN
White.and.Asian
Black.or.AA.and.AI.and.AN
Race.Alone.White
Race.Alone.Black.or.AA
Race.Alone.AI.and.AN
Race.Alone.Asian
Race.Alone.NH.and.OPI
Race.Alone.Other
HL
Mexican
Puerto.Rico
Cuban
OH.or.LP
Not.Hispanic.or.Latino
NHL.White
NHL.Black.or.AA
NHL.AI.and.AN
NHL.Asian.Alone
NHL.NH.and.OPI
NHL.Other
NHL.Two.or.More.Races
NHL.Two.Races.Including
NHL.Two.Races.Excluding
HL.Total.Housing.Units
Citizens.Over.18
Male.Citizen.Over.18
Female.Citizen.Over.18
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1

```r
cor.v <- cor(cor.data)
pos.cor <- cor.v[cor.v > 0.5]
```