Why Do Patients Skip Doctor's Appointments?

In this project I apply ANOVA and Dominance Analysis to investigate the causes of why patients skip their scheduled doctor's appointments.

The data set comes from Kaggle (https://www.kaggle.com/joniarroba/noshowappointments) and includes demographic and contextual data for over 62,000 patients from Vitoria, Brazil.

```
library(dplyr)
library(tidyr)
library(ggplot2)
library(yhat)
library(ggthemes)
library(Cairo)
library(scales)
```

```
options(repr.plot.width=5, repr.plot.height=4)
options(scipen = 99)

# Import the data
appt <- read.csv("KaggleV2-May-2016.csv", header=T, stringsAsFactors = F)
# Convert gender and outcome variable to numeric
appt$Gender <- as.numeric(as.factor(appt$Gender)) - 1
appt[appt$No.show=="No", "No.show"] <- 0
appt[appt$No.show=="Yes", "No.show"] <- 1
appt$No.show <- as.numeric(appt$No.show)
# Extract the length of time in days between the patient scheduling the appointment and the appointment
appt$schedule_time_days <- as.numeric(as.Date(appt$AppointmentDay) - as.Date(appt$ScheduledDay))
# Extract the day of the week from the appointment date timestamp
appt$appt_day <- factor(weekdays(as.Date(appt$AppointmentDay)))
# Extract month from the appointment date timestamp
appt$appt_month <- factor(months(as.Date(appt$AppointmentDay)))
# Convert neighborhood to factor
appt$Neighbourhood <- factor(appt$Neighbourhood)
# Select relevant columns for ANOVA and dominance analysis
appt <- appt %>%
  select(14, 3, 6, 8:13, 15:17, 7)

head(appt)
```

```
##   No.show Gender Age Scholarship Hipertension Diabetes Alcoholism Handcap
## 1       0      0  62           0            1        0          0       0
## 2       0      1  56           0            0        0          0       0
## 3       0      0  62           0            0        0          0       0
## 4       0      0   8           0            0        0          0       0
## 5       0      0  56           0            1        1          0       0
## 6       0      0  76           0            1        0          0       0
##   SMS_received schedule_time_days appt_day appt_month     Neighbourhood
## 1            0                  0   Friday      April   JARDIM DA PENHA
## 2            0                  0   Friday      April   JARDIM DA PENHA
## 3            0                  0   Friday      April     MATA DA PRAIA
## 4            0                  0   Friday      April PONTAL DE CAMBURI
## 5            0                  0   Friday      April   JARDIM DA PENHA
## 6            0                  2   Friday      April        REPÃ<U+009A>BLICA
```

The outcome variable ('No.show') we're trying to investigate is whether or not a patient skipped their scheduled doctor's appointment. The data contains a variety of variables for each patient including age, medical conditions, appointment and scheduling dates, and neighborhood.

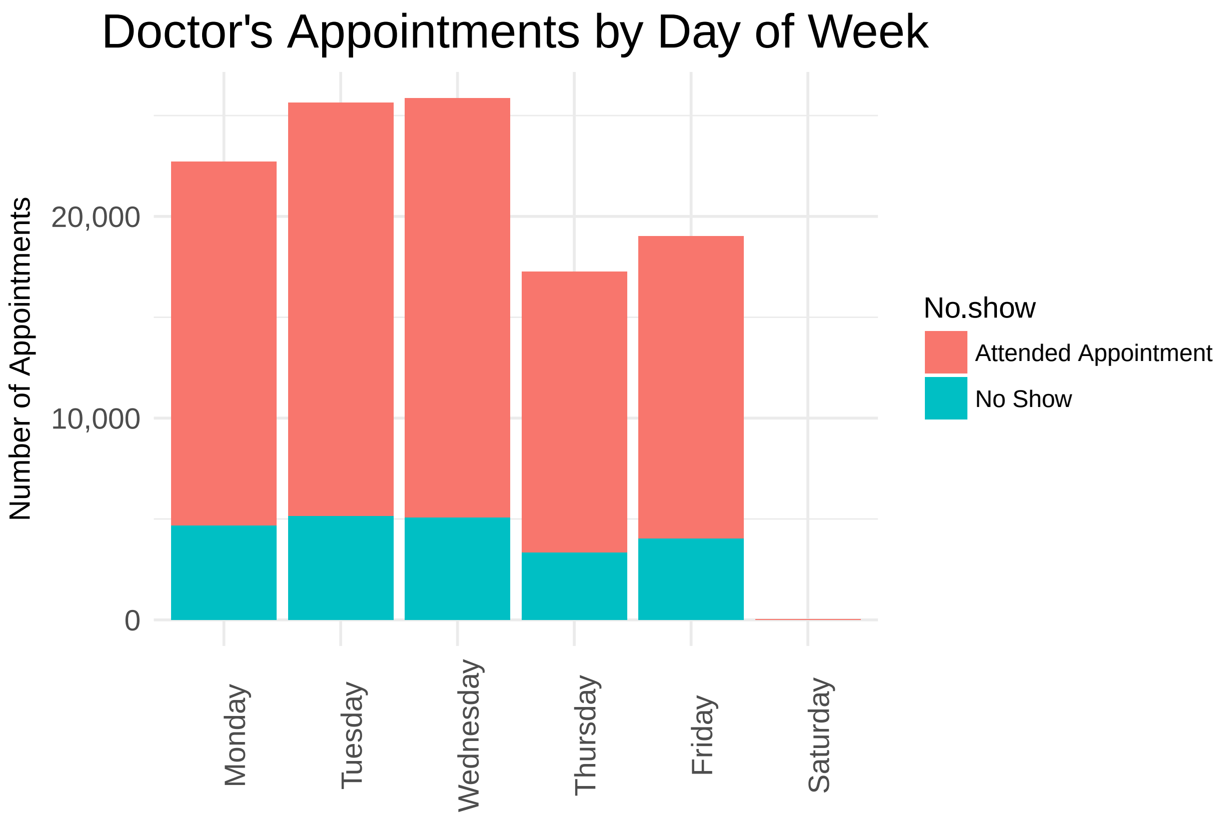
In order to determine if there are meaningful differences in the no-show percentages across the categorical variables in our data set we'll apply the Analysis of Variance (ANOVA) method. ANOVA is a method for comparing sample means across two or more groups, and determine if there is a statistically signficant difference in these means. By leveraging ANOVA with our data set we'll be able to determine if the day of the week, the month, or a patient's neighborhood has a meaningful impact on our outcome variable.

```r
# ANOVA for day of week
appt_day <- appt %>%
  select(appt_day, No.show)
av_day <- aov(No.show ~ appt_day, data=appt_day)
summary(av_day)
```

```
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## appt_day         5      4  0.8853   5.495 0.0000462 ***
## Residuals   110521  17808  0.1611
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The ANOVA analysis by day of week yielded an F value of 5.5 with a p-value less than .001, this means we can be 99.9% sure that the day of the week has an impact on the no-show percentages of the patients.

```r
# Visualize difference in no show averages across days of the week
appt_day$appt_day <- factor(appt_day$appt_day, levels = c("Monday", "Tuesday", "Wednesday", "Thursday",
appt_day$No.show <- as.character(appt_day$No.show)
appt_day[appt_day$No.show==1, "No.show"] <- "No Show"
appt_day[appt_day$No.show==0, "No.show"] <- "Attended Appointment"
ggplot(appt_day, aes(x=appt_day)) +
  geom_bar(aes(fill=No.show)) +
  ggtitle("Doctor's Appointments by Day of Week") +
  labs(x="", y="Number of Appointments") +
  theme_minimal() +
  scale_colour_tableau() +
  scale_y_continuous(labels = comma) +
  theme(plot.title = element_text(size=18, hjust=.5),
        axis.title = element_text(size=11),
        axis.text = element_text(size=11),
        axis.text.x = element_text(angle = 90))
```

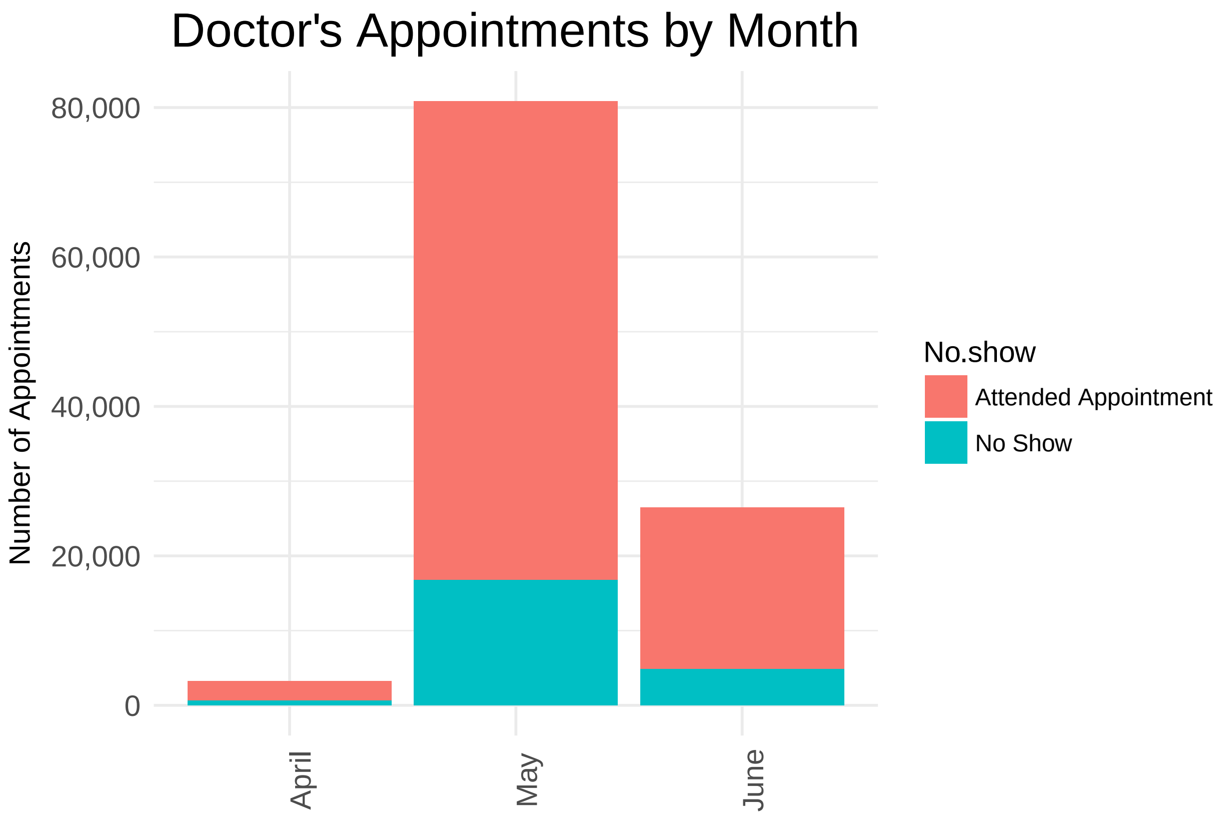


```
# ANOVA for month of appointment
appt_month <- appt %>%
  select(appt_month, No.show)
av_month <- aov(No.show ~ appt_month, data=appt_month)
summary(av_month)
```

```
##                  Df Sum Sq Mean Sq F value              Pr(>F)
## appt_month        2     11   5.474   33.99 0.00000000000000176 ***
## Residuals    110524  17801   0.161
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The ANOVA analysis by month of the appointment also yielded a very low p-value less than .001. When conducting ANOVA, the null hypothesis is that the group means across our categorical variable are equal. The low p-value indicates that we can reject the null hypothesis with 99.9% confidence.

```
# Visualize difference in no show averages across months of the year
appt_month$No.show <- as.character(appt_month$No.show)
appt_month$appt_month <- factor(appt_month$appt_month, levels=c("April", "May", "June"))
appt_month[appt_month$No.show==1, "No.show"] <- "No Show"
appt_month[appt_month$No.show==0, "No.show"] <- "Attended Appointment"
ggplot(appt_month, aes(x=appt_month)) +
  geom_bar(aes(fill=No.show)) +
  ggtitle("Doctor's Appointments by Month") +
  labs(x="", y="Number of Appointments") +
  theme_minimal() +
  scale_colour_tableau() +
  scale_y_continuous(labels = comma) +
  theme(plot.title = element_text(size=18, hjust=.5),
        axis.title = element_text(size=11),
        axis.text = element_text(size=11),
        axis.text.x = element_text(angle = 90))
```

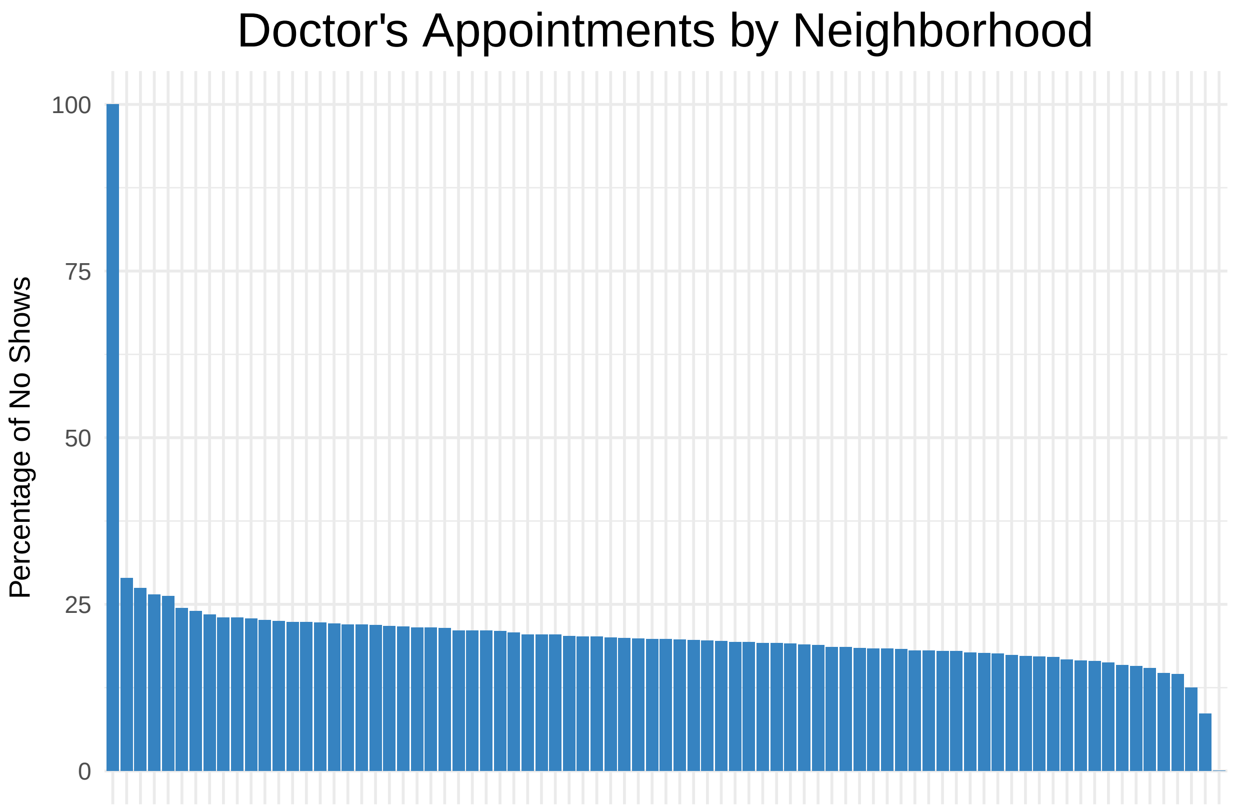


```
# ANOVA for neighborhood
appt_nbhd <- appt %>%
  select(Neighbourhood, No.show)
av_nbhd <- aov(No.show ~ Neighbourhood, data=appt_nbhd)
summary(av_nbhd)
```

```
##                    Df Sum Sq Mean Sq F value              Pr(>F)
## Neighbourhood     80     79  0.9910   6.172 <0.0000000000000002 ***
## Residuals     110446  17733  0.1606
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

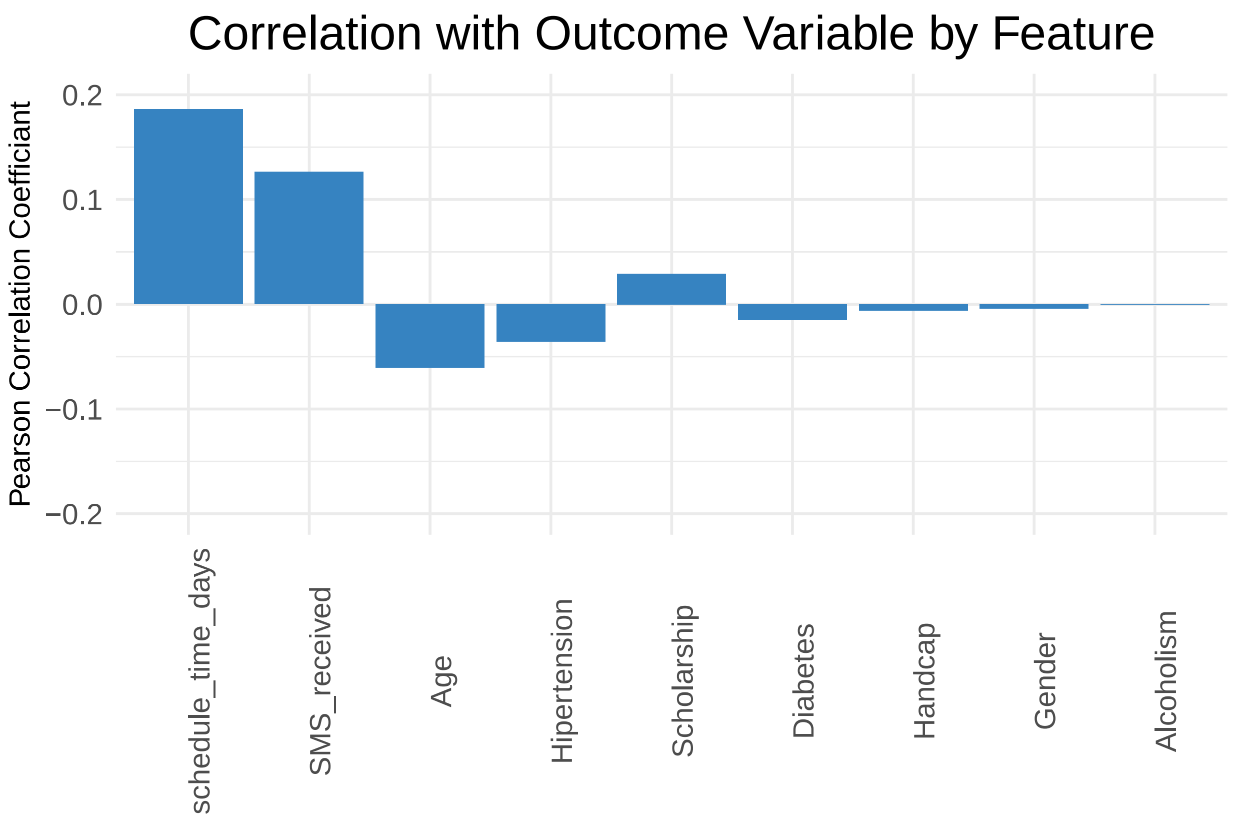
The p-value derived from the ANOVA analysis by neighborhood was also less than .001, meaning that we can be 99.9% confident that a patient's neighborhood has an effect on their rate of skipping doctor's appointments.

```
# Visualize difference in no show averages across neighborhoods
appt_nbhd_sum <- appt_nbhd %>%
  group_by(Neighbourhood) %>%
  summarize(pct_no_shows = mean(No.show, na.rm=T)*100) %>%
  arrange(desc(pct_no_shows))
appt_nbhd_sum$Neighbourhood <- factor(as.character(appt_nbhd_sum$Neighbourhood), levels = c(as.characte
ggplot(appt_nbhd_sum, aes(x=Neighbourhood, y=pct_no_shows)) +
  geom_bar(stat="identity",  fill="#3683c1") +
  ggtitle("Doctor's Appointments by Neighborhood") +
  labs(x="", y="Percentage of No Shows") +
  theme_minimal() +
  scale_y_continuous(labels = comma) +
  theme(plot.title = element_text(size=18, hjust=.5),
        axis.title = element_text(size=11),
        axis.text.x=element_blank())
```



In order to measure the extent to which the other features in our data set relate to the outcome variable we can apply the Pearson correlation. Pearson's Product Moment correlation coefficiant examines the extent to which two continuous variables relate to each other on a -1 to 1 scale (-1 representing a perfect negative linear relationship and 1 corresponding to a perfect postive linear relationship).

```
# Get pearson correlation between continous predictor variables and no show status
temp <- appt %>%
  select(Gender, Age, Scholarship, Hipertension, Diabetes, Alcoholism, Handcap, SMS_received, schedule_
temp_cor <- data.frame(apply(temp, 2, function(x) cor.test(x, appt$No.show, method='p')$estimate))
colnames(temp_cor) <- "pearson_correlation_coeff"
temp_cor <- temp_cor %>%
  mutate(feature = rownames(temp_cor)) %>%
  select(2,1) %>%
  arrange(desc(abs(pearson_correlation_coeff)))
temp_cor$feature <- factor(temp_cor$feature, levels = temp_cor$feature)
ggplot(temp_cor, aes(x=feature, y=pearson_correlation_coeff)) +
  geom_bar(stat="identity", fill="#3683c1") +
  ggtitle("Correlation with Outcome Variable by Feature") +
  labs(x="", y="Pearson Correlation Coefficiant") +
  theme_minimal() +
  scale_y_continuous(labels = comma) +
  expand_limits(y = c(-.2, .2)) +
  guides(fill=FALSE) +
  theme(plot.title = element_text(size=18, hjust=.5),
        axis.title = element_text(size=11),
        axis.text = element_text(size=11),
        axis.text.x = element_text(angle = 90))
```



Dominance Analysis is a lesser known statistical method that examines the extent to which the variance in the outcome variable can be attributed to each of the predictor variables (features). Dominance Analysis goes beyond examining correlations between each of the features by statistically controlling for confounding influences between features. In this method, a multivariate regression model is generated across all possible subsets of the features. The residuals of these models are compared to generate dominance weights, which represent the percentage of variance in the outcome variable that can be directly attributed to each of the features in the feature space.

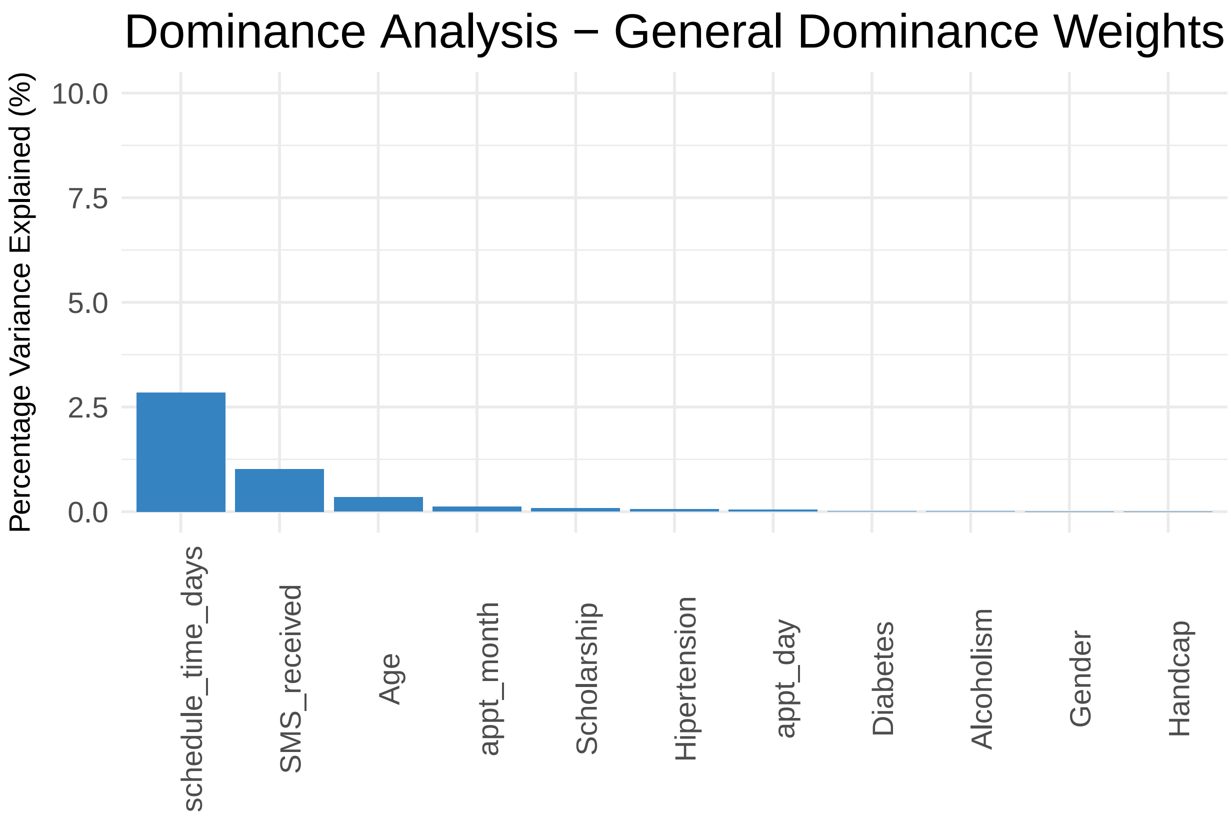
```
# Perform dominance analysis
# Conduct all possible subsets regression on the NPS data
aps <- aps(appt, dv = "No.show", ivlist = c("Gender", "Age", "Scholarship", "Hipertension", "Diabetes",
# With the output from all possible subsets regression, conduct dominance analysis
da <- dominance(aps)
total_variance_pred <- sum(da$GD)
```

```
da_results <- data.frame(da$GD)
da_results$feature <- row.names(da_results)
colnames(da_results) <- c("general_dominance_weights", "feature")
da_results <- da_results %>%
   select(2,1) %>%
   mutate(da_results_relative = general_dominance_weights / sum(general_dominance_weights, na.rm=T)) %>%
   arrange(desc(da_results_relative))

print(da_results)
```

```
##               feature general_dominance_weights da_results_relative
## 1  schedule_time_days             0.02848898600        0.6287648986
## 2        SMS_received             0.01020826475        0.2253010532
## 3                 Age             0.00341238260        0.0753128384
## 4          appt_month             0.00114864800        0.0253511846
## 5         Scholarship             0.00080614482        0.0177919833
## 6        Hipertension             0.00058074618        0.0128173327
## 7            appt_day             0.00043912570        0.0096917042
## 8            Diabetes             0.00010559092        0.0023304398
## 9          Alcoholism             0.00008570779        0.0018916099
## 10             Gender             0.00002075596        0.0004580936
## 11            Handcap             0.00001308816        0.0002888618
```

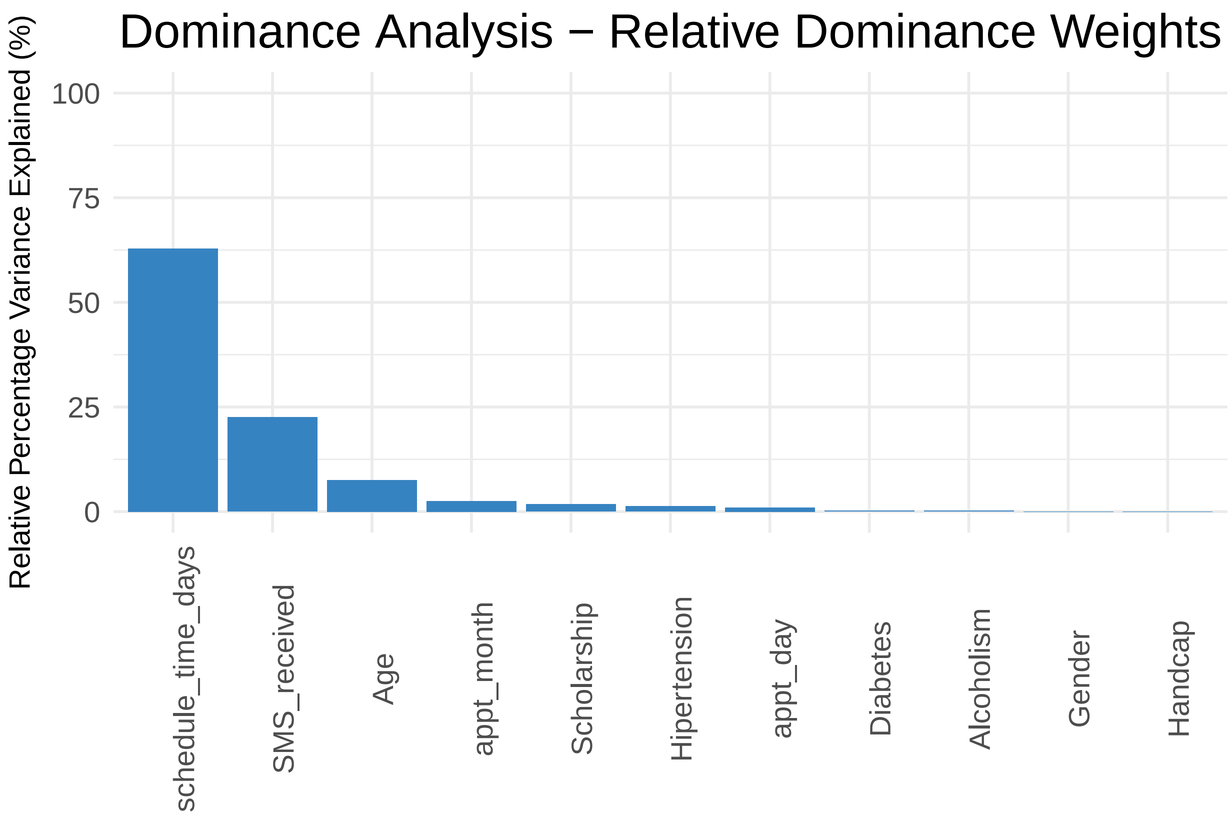
As we can see only a small percentage of the variance in the patient no show rate can be attributed to the variables in our data set.

```
da_results[,c(2,3)] <- da_results[,c(2,3)]*100
da_results$feature <- factor(da_results$feature, levels = c(da_results$feature))

ggplot(da_results, aes(x=feature, y=general_dominance_weights)) +
  geom_bar(stat="identity", fill="#3683c1") +
  expand_limits(y = 10) +
  ggtitle("Dominance Analysis - General Dominance Weights") +
  labs(x="", y="Percentage Variance Explained (%)") +
  theme_minimal() +
  scale_y_continuous(labels = comma) +
  theme(plot.title = element_text(size=18, hjust=.5),
        axis.title = element_text(size=11),
        axis.text = element_text(size=11),
        axis.text.x = element_text(angle = 90))
```



By converting the general dominance weights to relative percentages, we can examine the relative contribution of each feature's predictive ability.

```r
ggplot(da_results, aes(x=feature, y=da_results_relative)) +
  geom_bar(stat="identity", fill="#3683c1") +
  expand_limits(y=100) +
  ggtitle("Dominance Analysis - Relative Dominance Weights") +
  labs(x="", y="Relative Percentage Variance Explained (%)") +
  theme_minimal() +
  scale_y_continuous(labels = comma) +
  theme(plot.title = element_text(size=18, hjust=.5),
        axis.title = element_text(size=11),
        axis.text = element_text(size=11),
        axis.text.x = element_text(angle = 90))
```


Dominance Analysis − Relative Dominance Weights
Relative Percentage Variance Explained (%)
100
75
50
25
0
schedule_time_days
SMS_received
Age
appt_month
Scholarship
Hipertension
appt_day
Diabetes
Alcoholism
Gender
Handcap