PHD research notebook: Analying climate vs commodity loss - outputs from design matrix correlations

This is the subtitle

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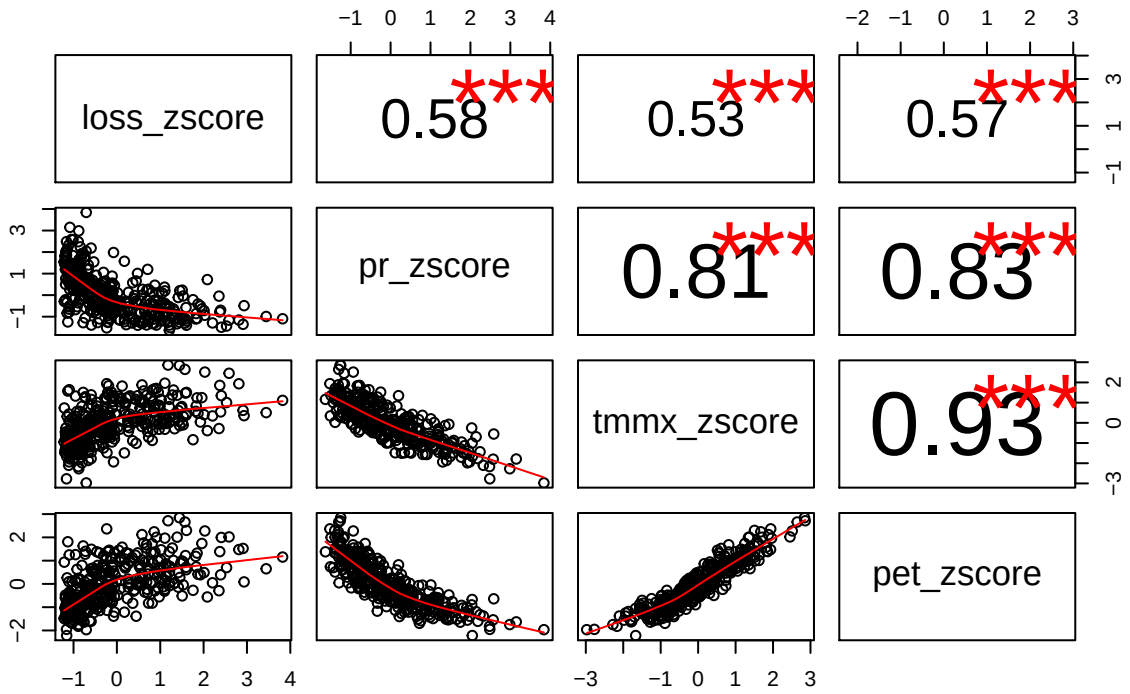
R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

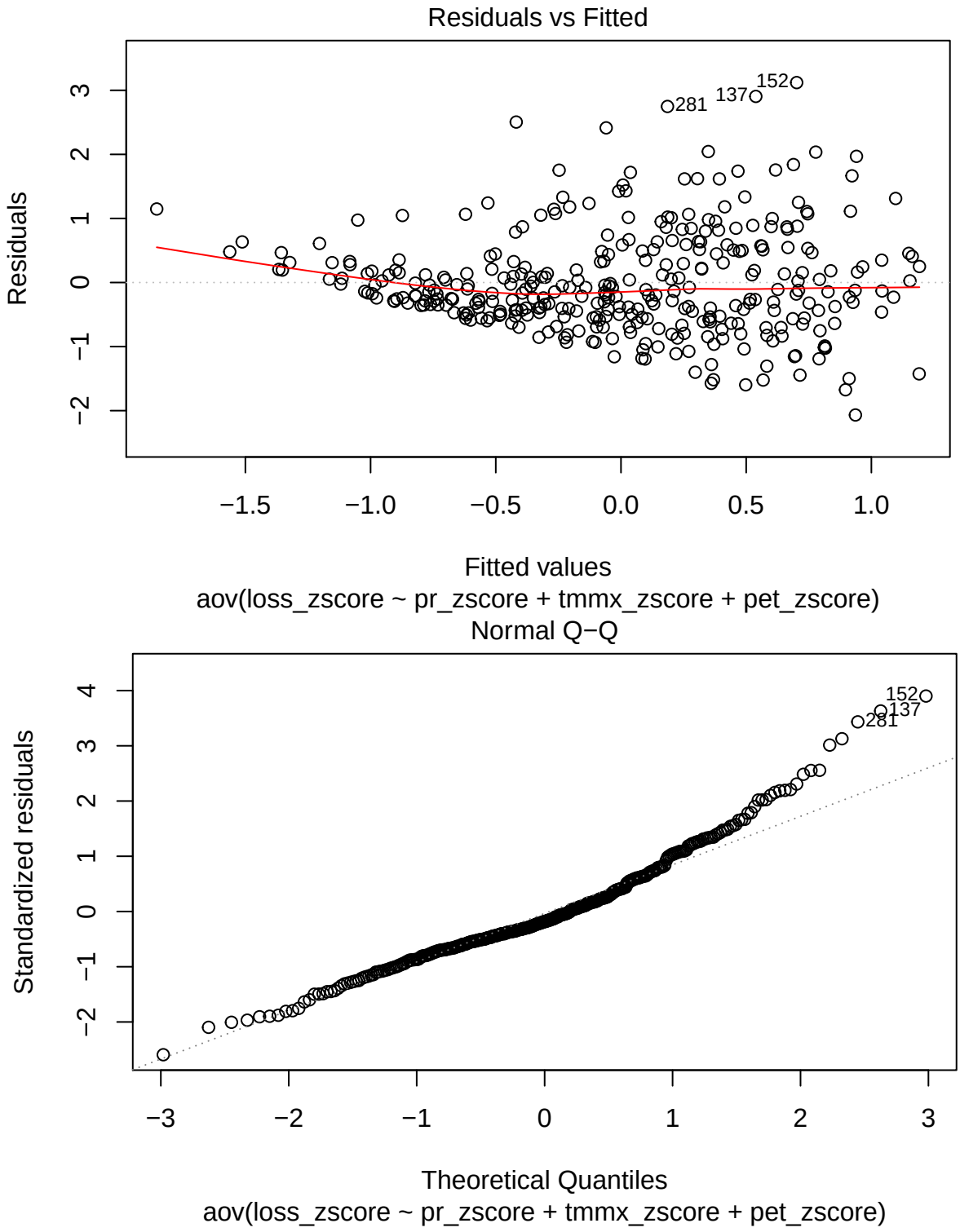
```
#---cor panel example 1

panel.cor <- function(x, y, digits=2, prefix="", cex.cor)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- abs(cor(x, y))
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  txt <- paste(prefix, txt, sep="")
  if(missing(cex.cor)) cex <- 0.8/strwidth(txt)

  test <- cor.test(x,y)
  # borrowed from printCoefmat
  Signif <- symnum(test$p.value, corr = FALSE, na = FALSE,
                   cutpoints = c(0, 0.001, 0.01, 0.05, 0.1, 1),
                   symbols = c("***", "**", "*", ".", " "))

  text(0.5, 0.5, txt, cex = cex * r)
  text(.8, .8, Signif, cex=cex, col=2)
}

var1 <- read.csv("/waf/tmp/pr_jun2_cube_root_acres_climatecorrelation.csv")
colnames(var1)[9] <- paste(colnames(var1)[2], "_zscore", sep="")
var2 <- read.csv("/waf/tmp/pet_jun2_cube_root_acres_climatecorrelation.csv")
colnames(var2)[9] <- paste(colnames(var2)[2], "_zscore", sep="")
var3 <- read.csv("/waf/tmp/tmmx_jun1_cube_root_acres_climatecorrelation.csv")
colnames(var3)[9] <- paste(colnames(var3)[2], "_zscore", sep="")

data1 <- cbind(var1, var2[9], var3[9])

pairs(loss_zscore ~ pr_zscore + tmmx_zscore + pet_zscore, data = data1,
      lower.panel=panel.smooth, upper.panel=panel.cor, main = "initial pairs plot")
```

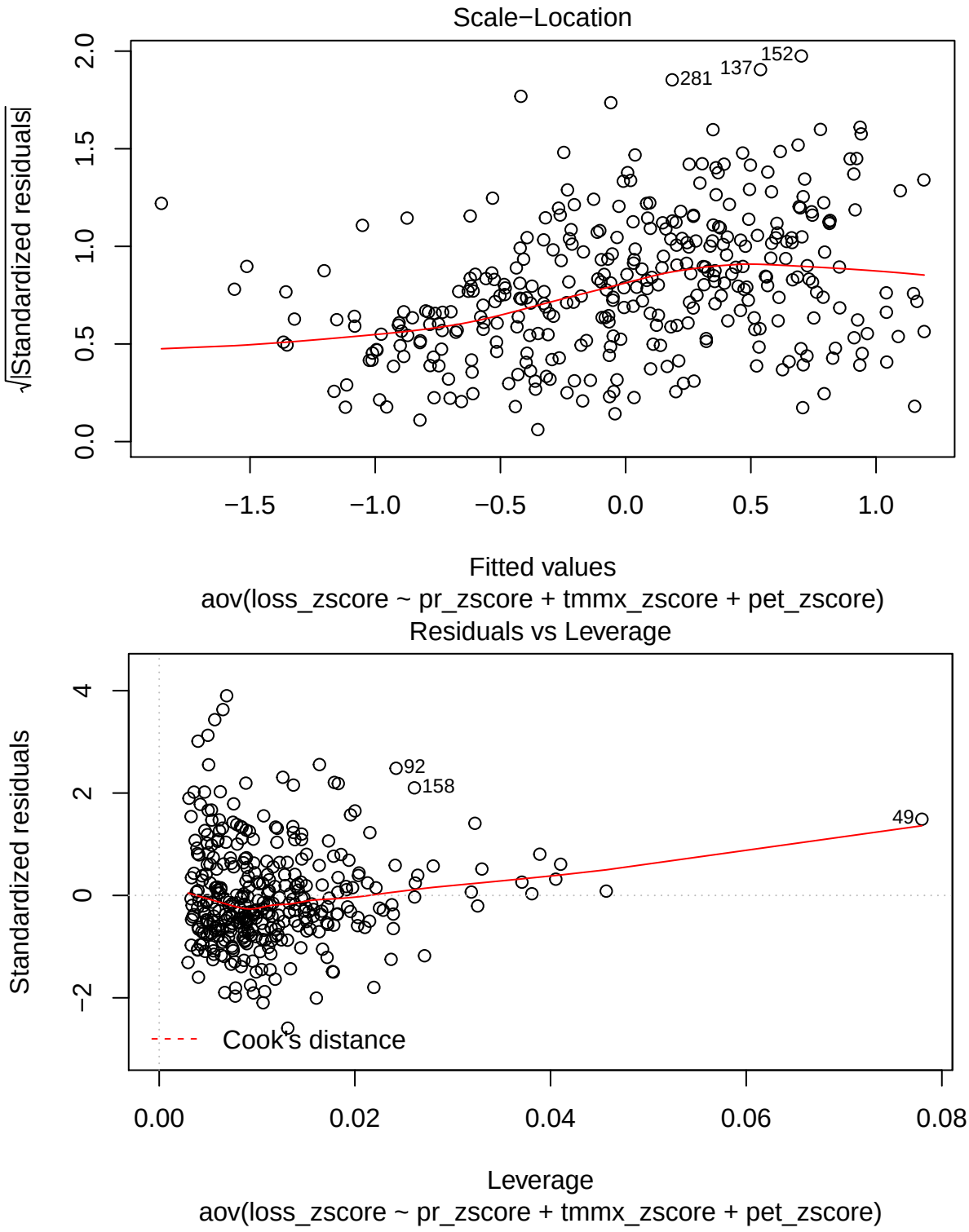


Including Plots

You can also embed plots, for example:

```
fit <- aov(loss_zscore ~ pr_zscore + tmmx_zscore + pet_zscore, data = data1)

#layout(matrix(c(1,2,3,4),2,2)) # optional layout
plot(fit) # diagnostic plots
```


Residuals vs Fitted
Residuals
Fitted values
aov(loss_zscore ~ pr_zscore + tmmx_zscore + pet_zscore)
Normal Q−Q
Standardized residuals
Theoretical Quantiles
aov(loss_zscore ~ pr_zscore + tmmx_zscore + pet_zscore)
152
137
281




```
summary(fit) # display Type I ANOVA table
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## pr_zscore     1 117.69  117.69 182.663 <2e-16 ***
## tmmx_zscore   1   3.72    3.72   5.771 0.0168 *
```

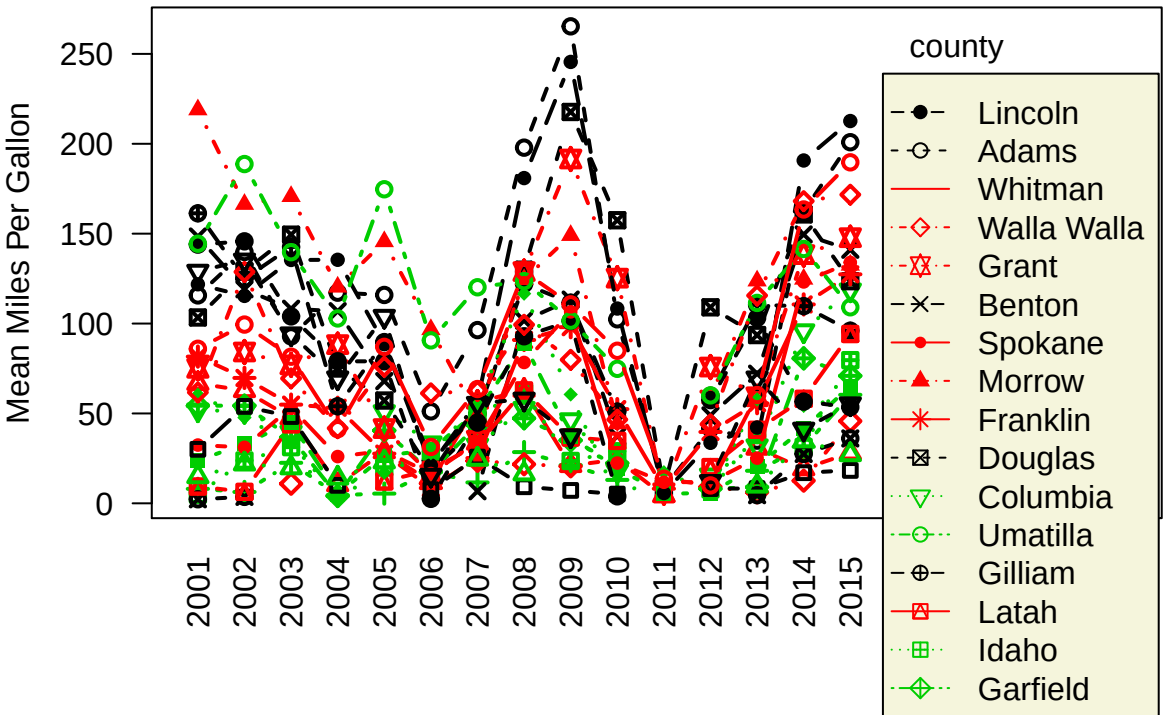
```
## pet_zscore    1   3.96    3.96   6.154 0.0136 *
## Residuals   344 221.63    0.64
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
drop1(fit,~.,test="F") # type III SS and F Tests
```

```
## Single term deletions
##
## Model:
## loss_zscore ~ pr_zscore + tmmx_zscore + pet_zscore
##             Df Sum of Sq    RSS     AIC F value    Pr(>F)
## <none>                  221.63 -149.01
## pr_zscore    1   13.6026 235.23 -130.28 21.1129 6.087e-06 ***
## tmmx_zscore  1    0.1423 221.77 -150.79  0.2208   0.63871
## pet_zscore   1    3.9648 225.60 -144.84  6.1539   0.01359 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

```
#attach(mtcars)
county <- factor(data1$county)
year <- factor(data1$year)
interaction.plot(year, county, data1$loss, type="b", col=c(1:3),
                 leg.bty="o", leg.bg="beige", lwd=2, pch=c(1:25),
                 xlab=" ",
                 ylab="Mean Miles Per Gallon",
                 main="Interaction Plot", las = 2)
```




```
regre <- mgcv::gam(pet_zscore ~ pr_zscore + tmmx_zscore, data=data1)
VIF1 <- (1/(1-.89))
```