```
<<loadData, results = hide, echo = FALSE>>=
# Polymerase chain reaction (PCR) data for 3 dose groups
pcrData <- read.csv("pcrData.csv")
@
```

There were **\Sexpr{dim(pcrData)[1]}** subjects measured across \Sexpr{length(unique(pcrData$Compound))} drug groups. A density plot of the data is produced with the lattice package:

```
<<densityPlot, echo = FALSE, fig = TRUE>>=
library(lattice)
trellis.par.set(col.whitebg())
print(
    densityplot(
        ~log(Cycles, base = 2),
        pcrData,
        groups = Compound,
        adjust = 1.5,
        pch = "|",
        auto.key = list(columns = 3)))
@
```

Here is a table of the mean cycles to threshold for each drug group:

```
<<meanTable, echo = FALSE, results = xml>>=
meanCycles <- tapply(
    log(pcrData$Cycles, base = 2),
    pcrData$Compound,
    mean)

odfTable(
    meanCycles,
    horizontal = TRUE)
@
```

Of course, we would normally look at diagnostics before going straight to the p-value

```
<<lmFit, results = verbatim>>=
linearModel <- lm(
    log(Cycles, base = 2) ~ Compound,
    data = pcrData)
anova(linearModel)
@
```