

# The puromycin study

## By Somebody

### Introduction

The first lines of data are:

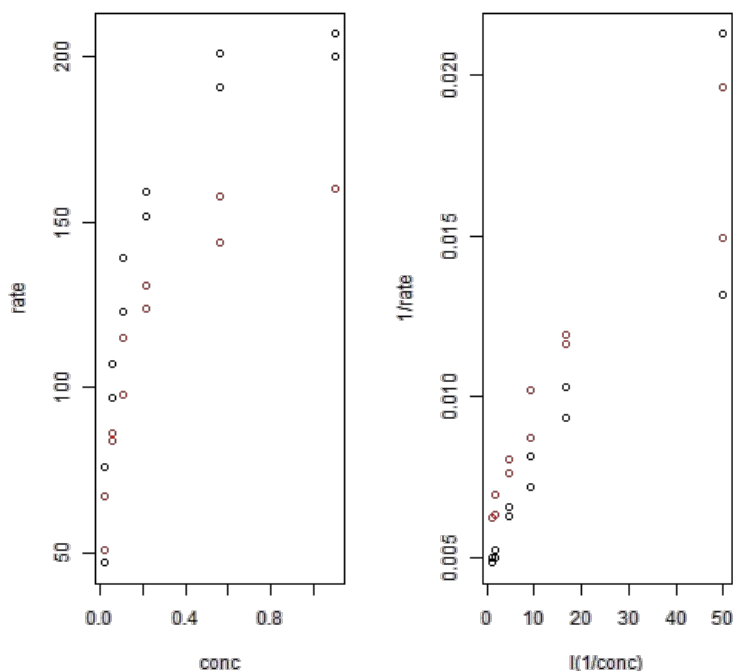
```
head(Puromycin, 3)
```

```
##   conc rate  state
## 1 0.02   76 treated
## 2 0.02   47 treated
## 3 0.06   97 treated
```

There are 23 observations.

### Transformation almost gives linearity

```
par(mfrow = c(1, 2))
plot(rate ~ conc, data = Puromycin, col = as.numeric(state))
plot(1/rate ~ I(1/conc), data = Puromycin, col = as.numeric(state))
```



### Fit a model to transformed data

```
m1 <- lm(1/rate ~ state + I(1/conc) + state * I(1/conc), data = Puromycin)
summary(m1)
```

```
##
## Call:
## lm(formula = 1/rate ~ state + I(1/conc) + state * I(1/conc),
##     data = Puromycin)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.004310 -0.000456 -0.000160  0.000924  0.003808
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.11e-03   6.27e-04   8.14 1.3e-07 ***
## stateuntreated  1.86e-03   9.20e-04   2.03  0.057 .
## I(1/conc)      2.47e-04   2.86e-05   8.64 5.2e-08 ***
## stateuntreated:I(1/conc) -3.22e-05  4.10e-05  -0.79  0.442
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00169 on 19 degrees of freedom
## Multiple R-squared:  0.876,    Adjusted R-squared:  0.856
```

## F-statistic: 44.6 on 3 and 19 DF, p-value: 8.51e-09