The Puromycin data

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The first lines of data are:

> head(Puromycin, 3)

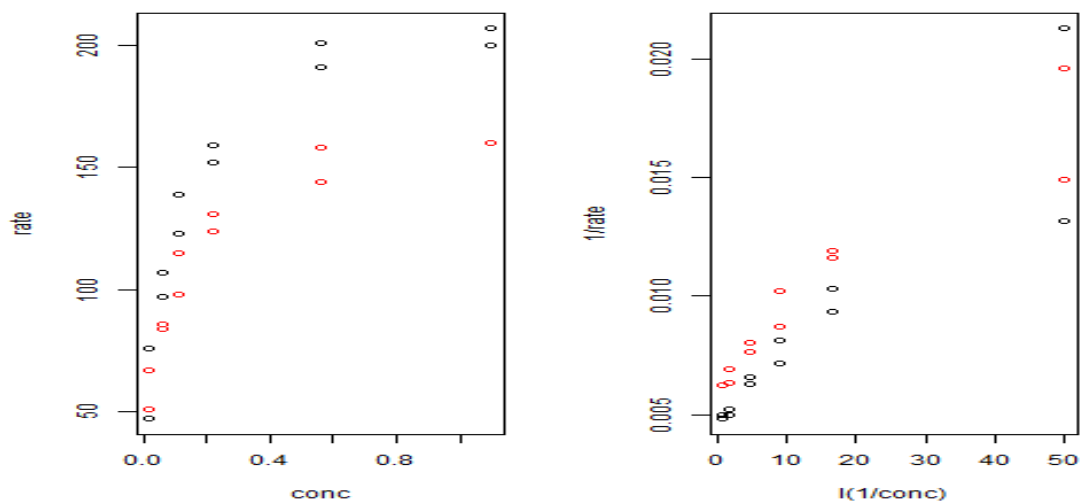|	conc	rate	state
1	0.02	76	treated
2	0.02	47	treated
3	0.06	97	treated

> nr = nrow(Puromycin)

There are 23 rows in the dataframe. (Notice that we may refer to R expression in the text). 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

> summary(m1)

- Call: lm(formula = 1/rate ~ state + I(1/conc) + state * I(1/conc), Call: data = Puromycin)
- Residuals

Min	1Q	Median	3Q	Max
-0.0043	-0.0005	-0.0002	0.0009	0.0038

- 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

- Residuals standard error: 0.002 on 19 degrees of freedom
- Multiple R-Squared:**0.876**
- Adjusted R-Squared:**0.856**
- F-statistics: **44.614** on 3 and 19 DF. P-value:**0**.
  Model diagnostics

  > par(mfrow = c(2, 2))

  > plot(m1)