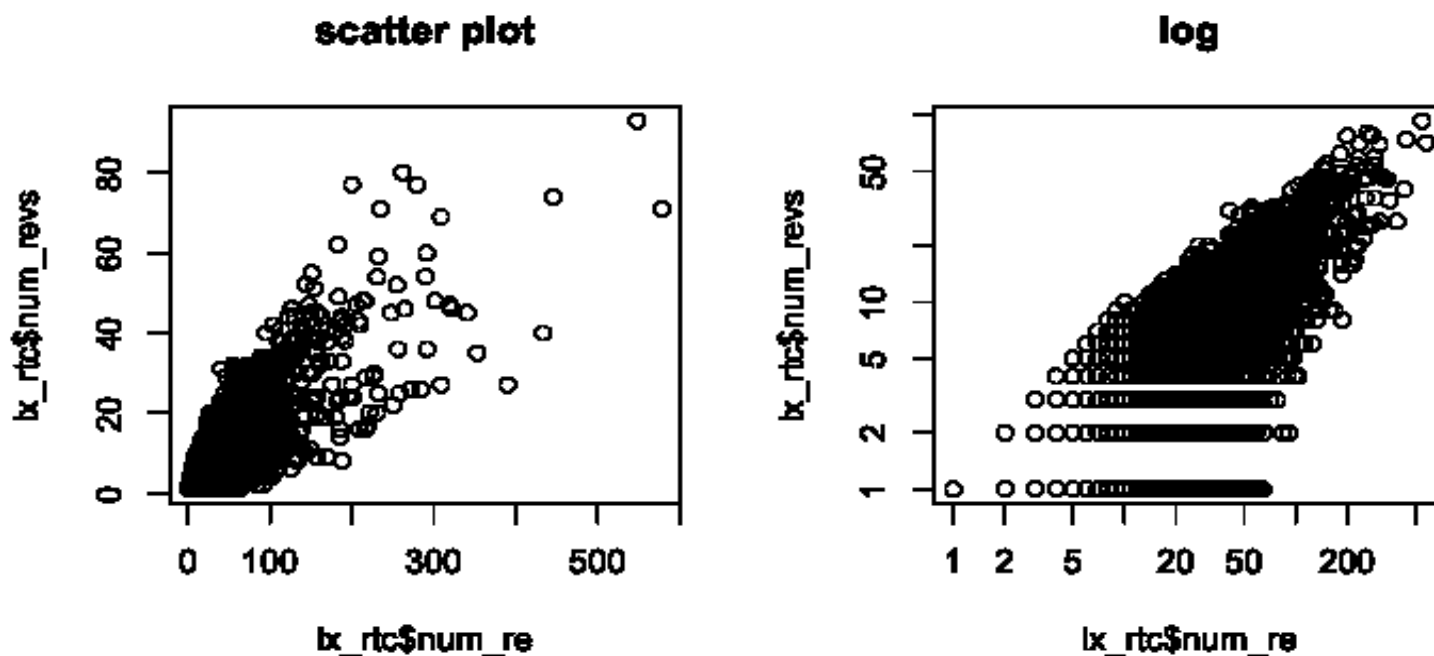


Practical Statistics

Peter C Rigby

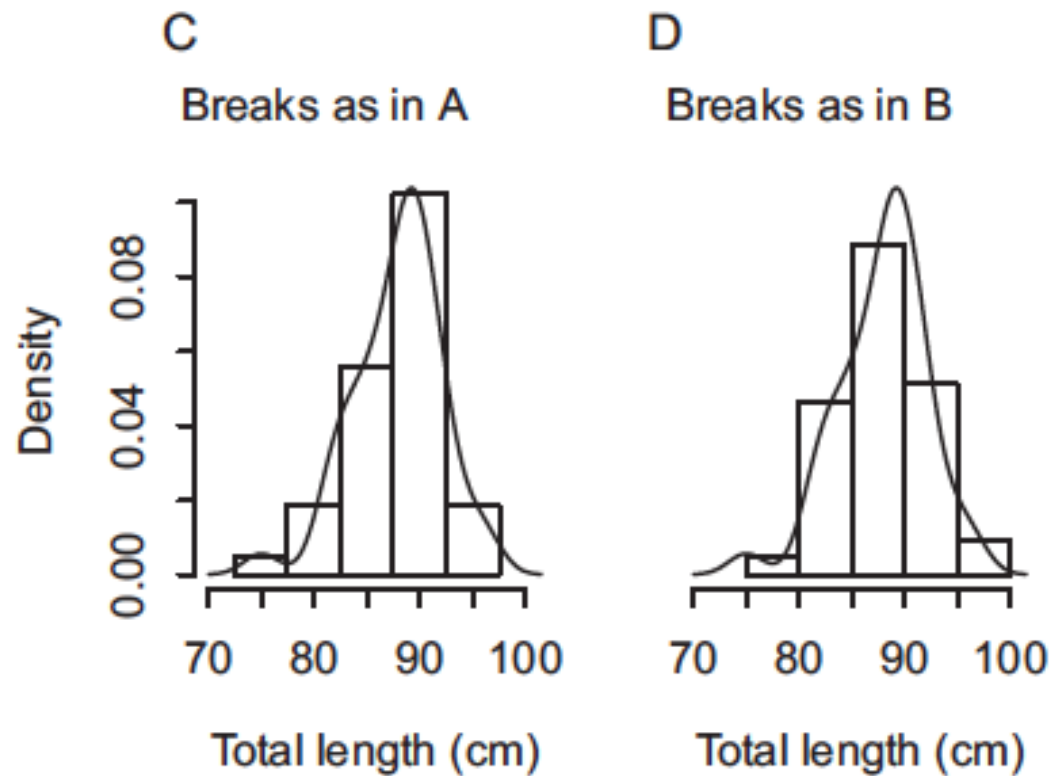
Step 1: Take a look at the data

Scatter Plots



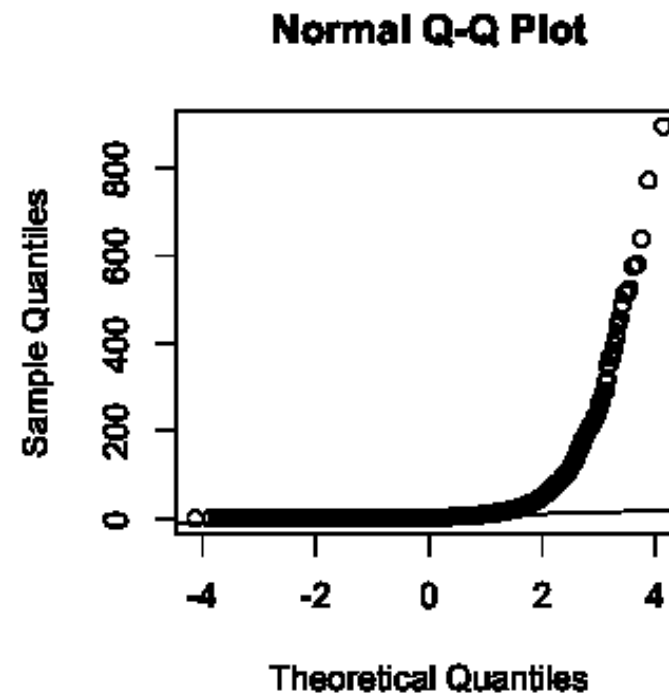
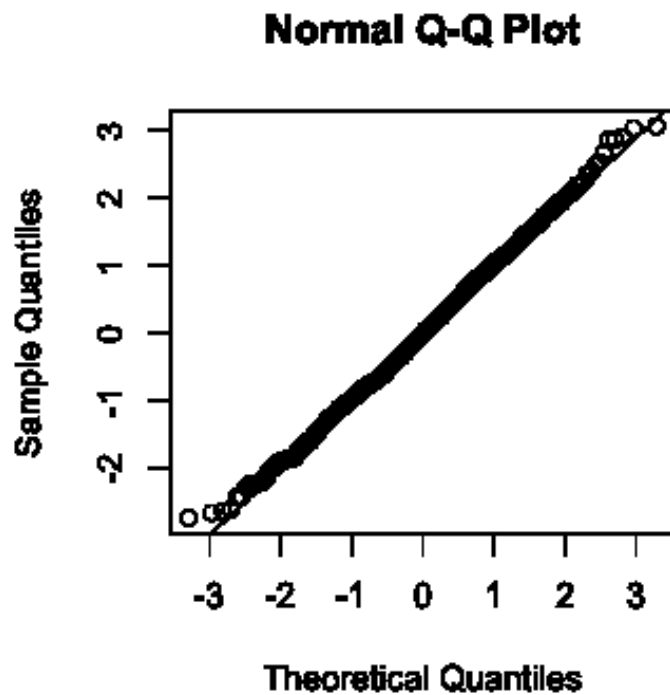
Scatter Plot is visual correlation “test”
- `plot(num_revs, num_re)`

Histograms



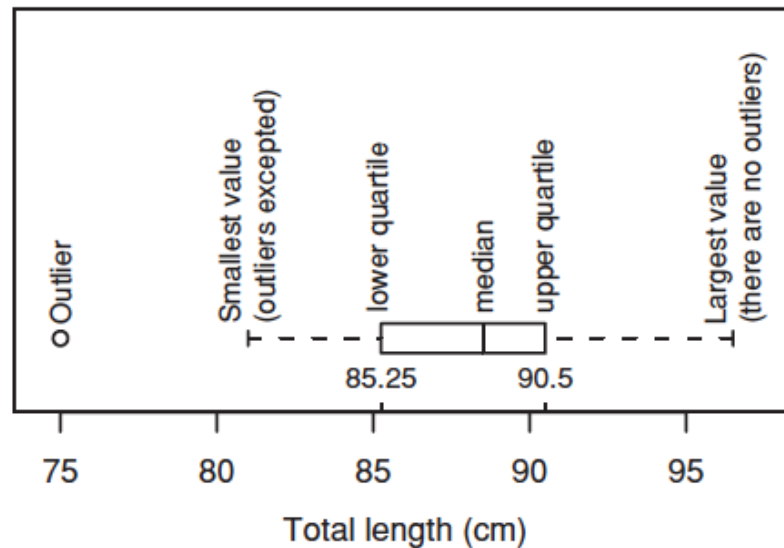
Histograms can distort the data

QQ Plot



Is the data normally distributed?
`qqnorm(bugs)`

Boxplot



Inter-quartile range
= $90.5 - 85.25$
= 5.25

Compare
 $0.75 \times \text{Inter-quartile range}$
= 3.9
with standard deviation
= 4.2

Visual version of the `r` summary function
`-boxplot(bugs, log = 'y')`

Step 2: Model the data

- Things to consider
 - Are your variables count, categorical, continuous?
- Do you want to compare two or more conditions?

Linear Model

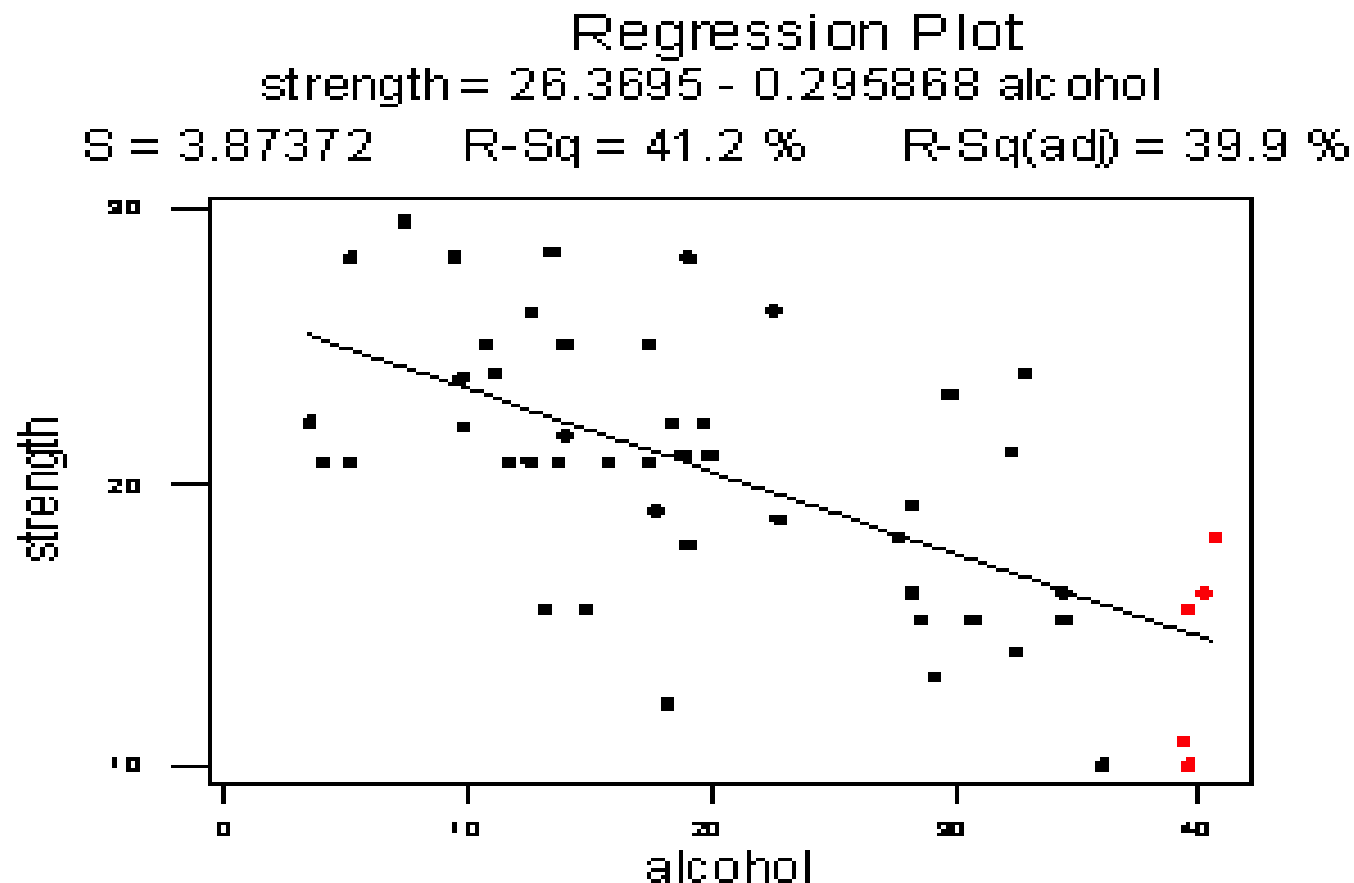
- y value, response, or dependent
- x value, predictor, or independent
- ϵ , error, or residuals
- b0 intercept
- b1 slope

$$y = b_0 + b_1x + \epsilon$$

```
m <- lm(rev_interval ~ num_re + num_revs)
```


Linear Model

$$\hat{y}_i = b_0 + b_1 x_i$$



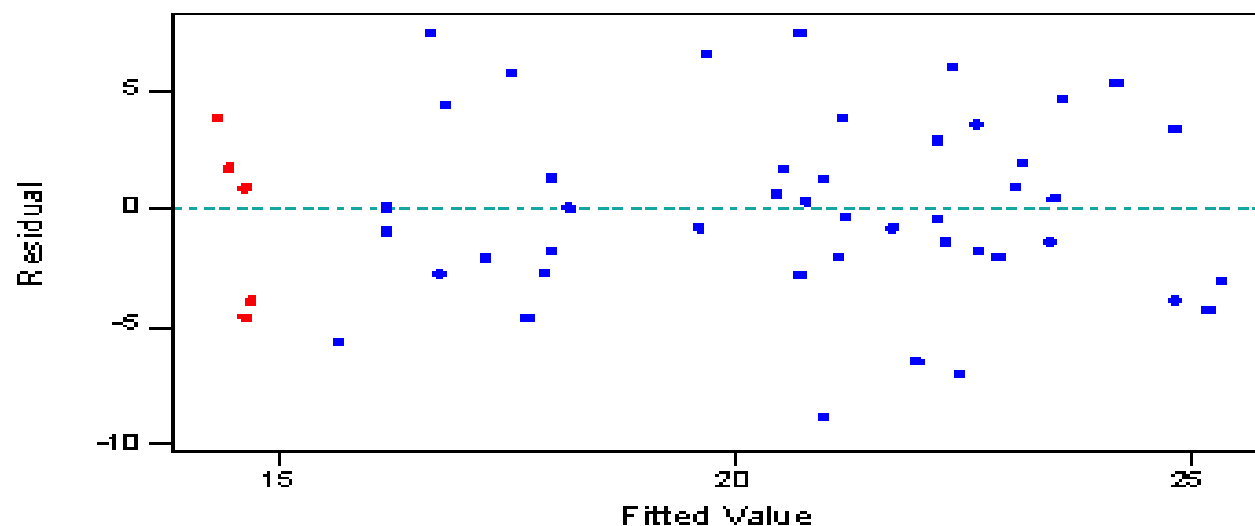
Model Assumptions

- Independence of observations
- Normality – the distributions of the residuals are normal.
- Equality (or "homogeneity") of variances, called homoscedasticity — the variance of data in groups should be the same.

Constant Variance the Error

$$\text{SSE} = \sum_{i=1}^n (y_i - \hat{y}_i)^2$$

Residuals Versus the Fitted Values
(response is strength)



Coefficient of determination R^2

Mean squared error $\text{MSE} = \frac{\text{SSE}}{n - 2}$

Total sum of squares $\text{SSTO} = \sum_{i=1}^n (y_i - \bar{y})^2$

Proportion of the variation in y explained by x

$$R^2 = \frac{\text{SSR}}{\text{SSTO}} = \frac{\text{SSTO} - \text{SSE}}{\text{SSTO}}$$

Generalized Linear Models

- Continuous
 - `gaussian(link = "identity")`
- Categorical
 - `binomial(link = "logit")`
- Count data
 - `poisson(link = "log")`
 - `glm(bugs ~ num_re, family = 'quasipoisson')`

Dispersion

- Overdispersion makes variables look more statistically significant.
 - Underdispersion has opposite effect
- Quasi function correct for dispersion
 - `quasibinomial(link = "logit")`
 - `quasipoisson(link = "log")`

Interpreting predictors

- You must apply inverse of link function to estimates interpret estimates
 - Poisson link function is log
 - Take the exp of each estimate

ANOVA

- Comparing two groups of data
 - `bugs ~ as.factor(module)`
 - `bugs ~ as.factor(devs)`
 - `Bugs ~ as.factor(organization)`
- The null hypothesis is that all groups are simply random samples of the same population.
- Example
 - <http://www.youtube.com/watch?v=Dwd3ha0P8uw>