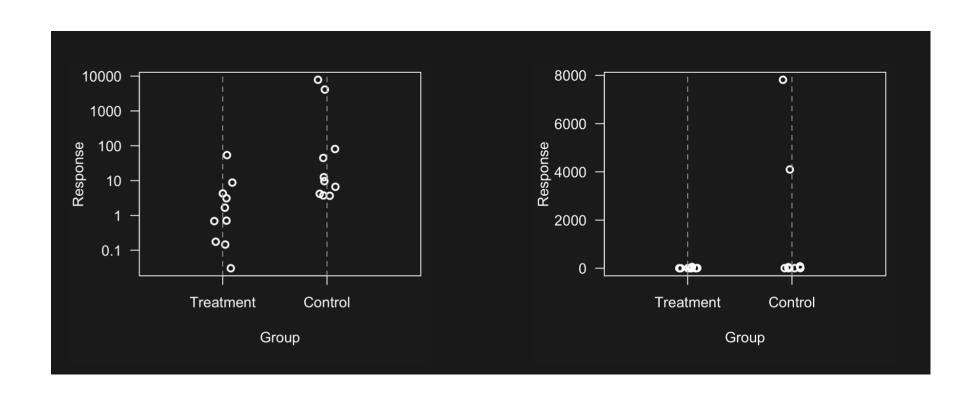
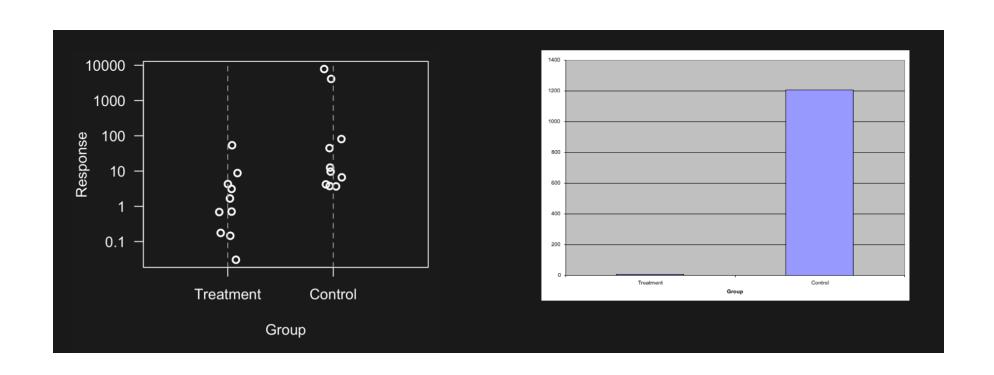
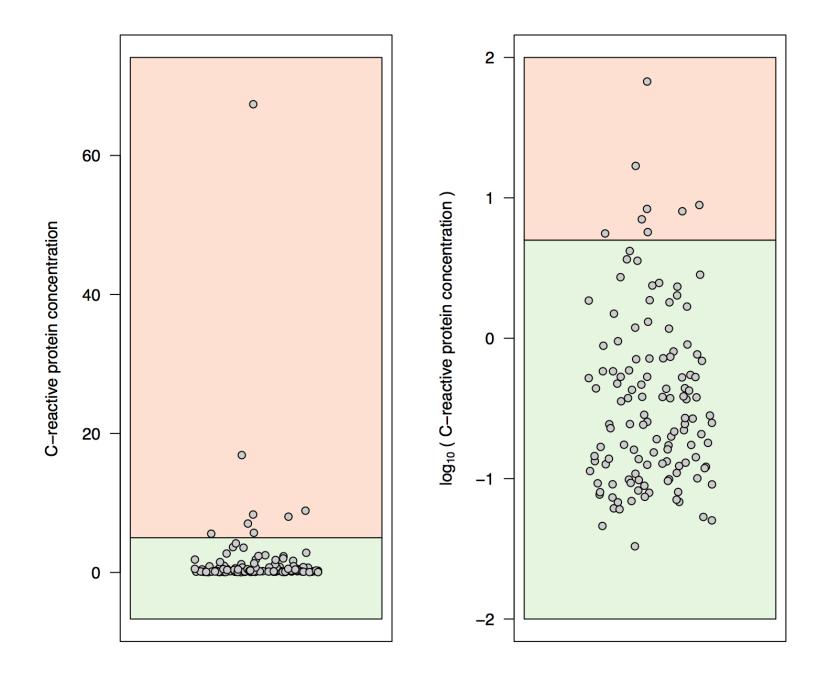
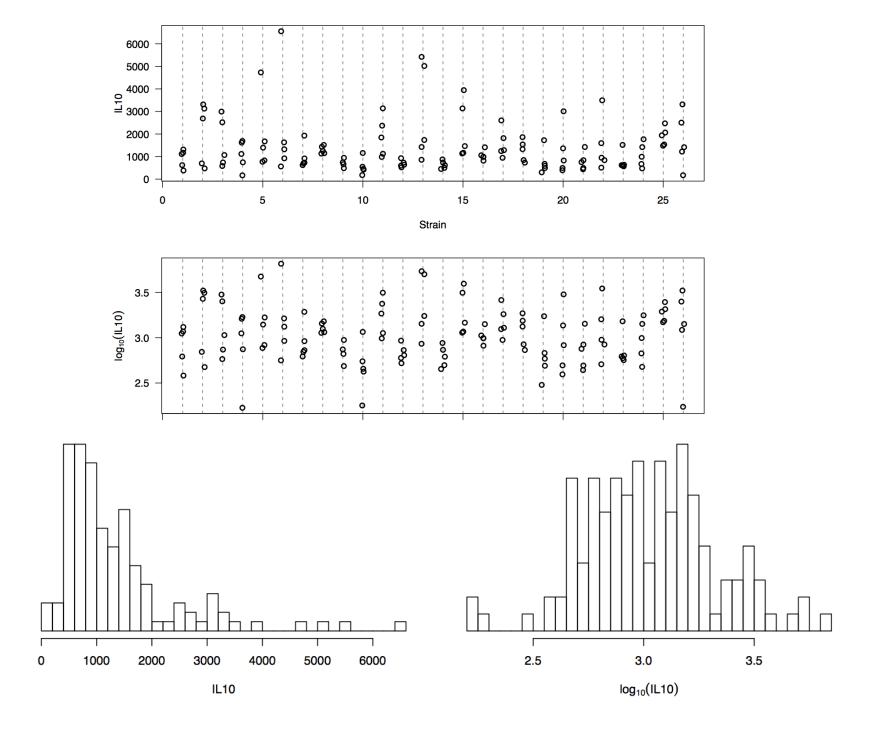
#### **Consider data transformations**

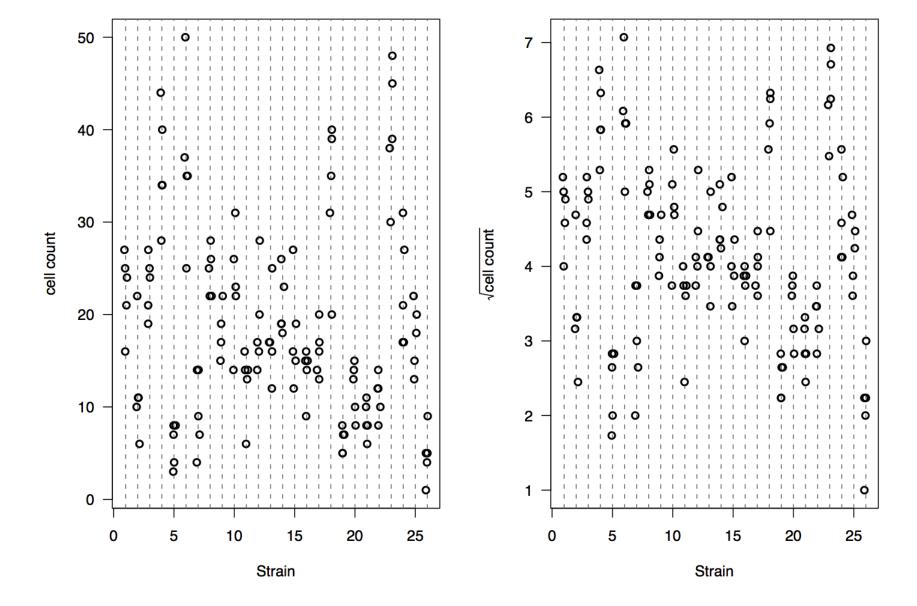


#### **Consider data transformations**



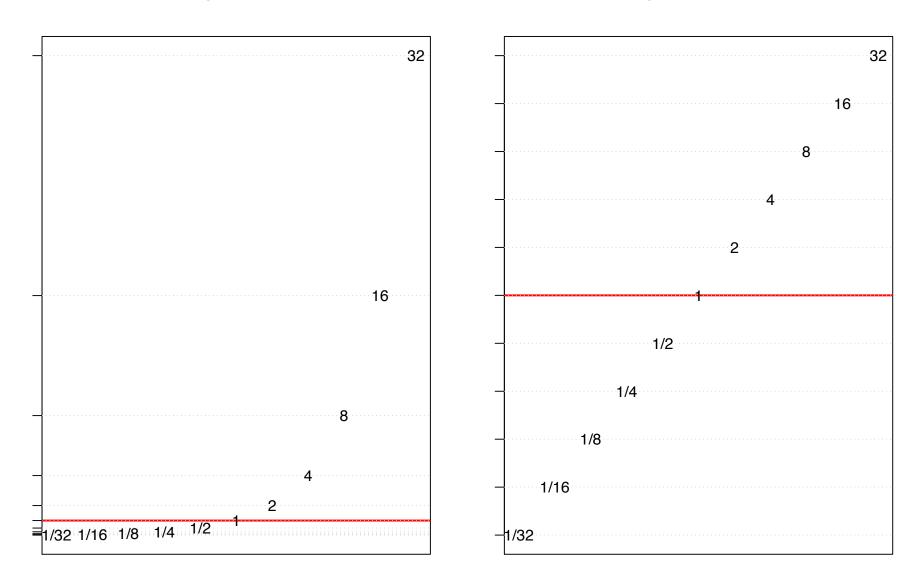




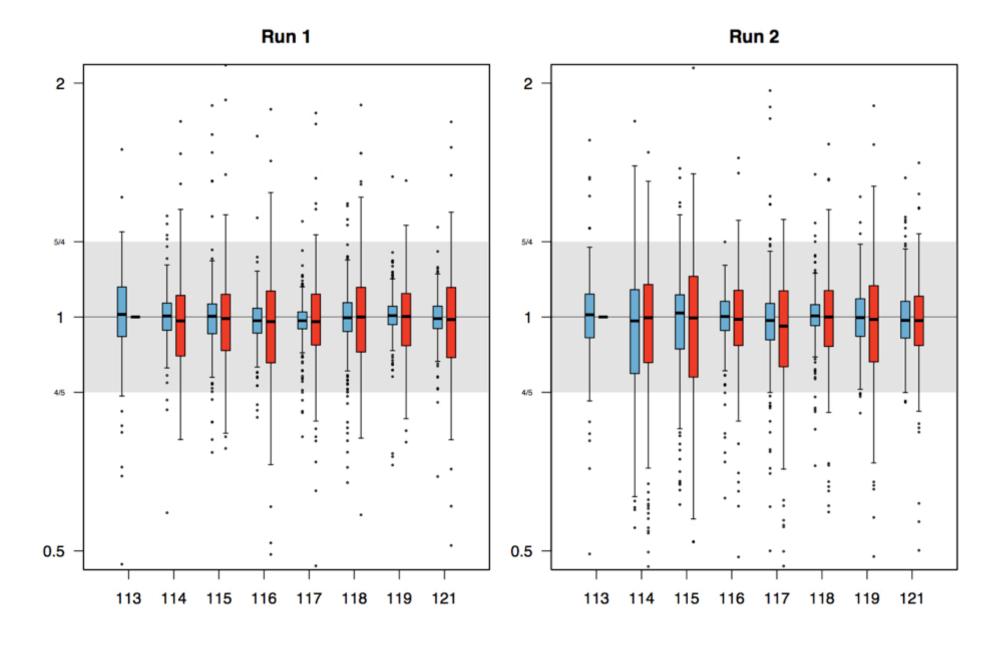


#### **Original scale**

#### Logarithmic scale



$$\log(X/Y) = \log(X) - \log(Y) = -(\log(Y) - \log(X)) = -\log(Y/X)$$



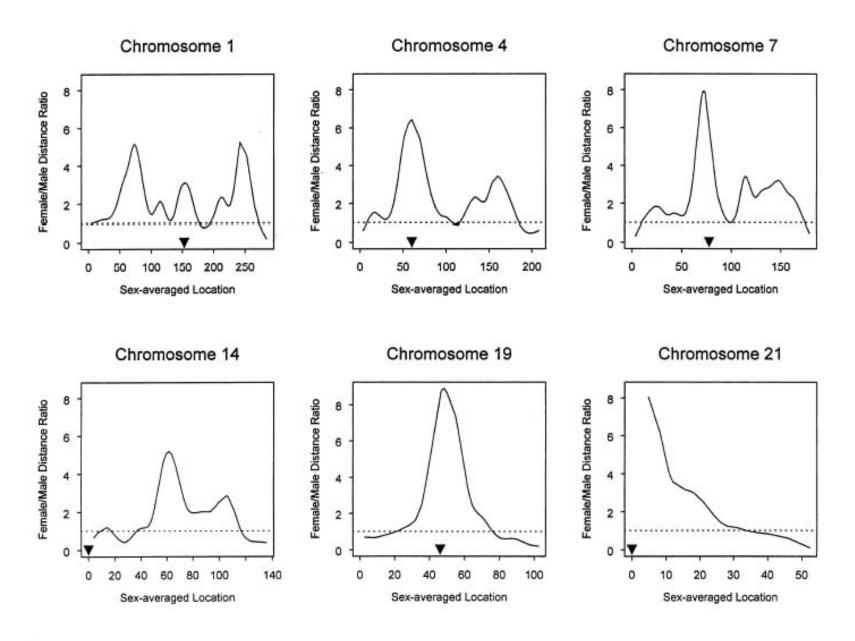


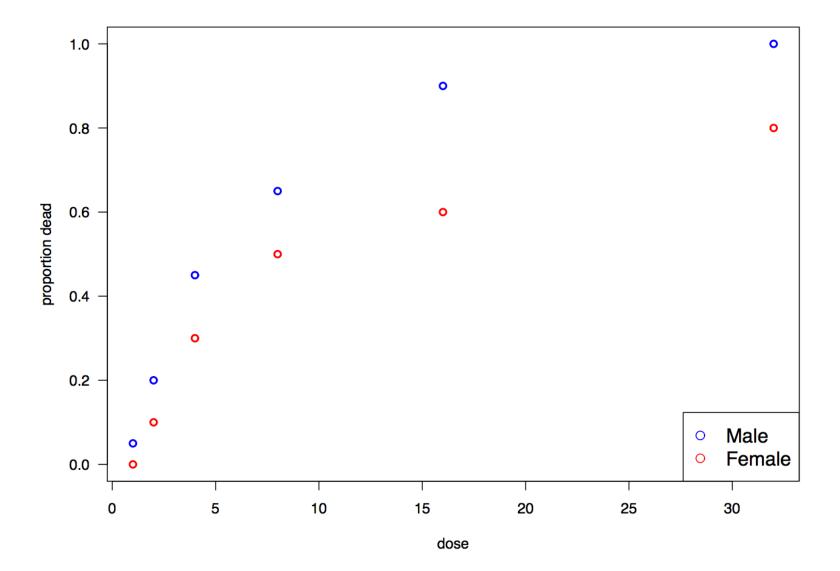
Figure 1 Plots of the female:male genetic-distance ratio against sex-averaged genetic location (in cM) along six selected chromosomes. Approximate locations of the centromeres are indicated by the triangles. The dashed lines correspond to equal female and male distances.

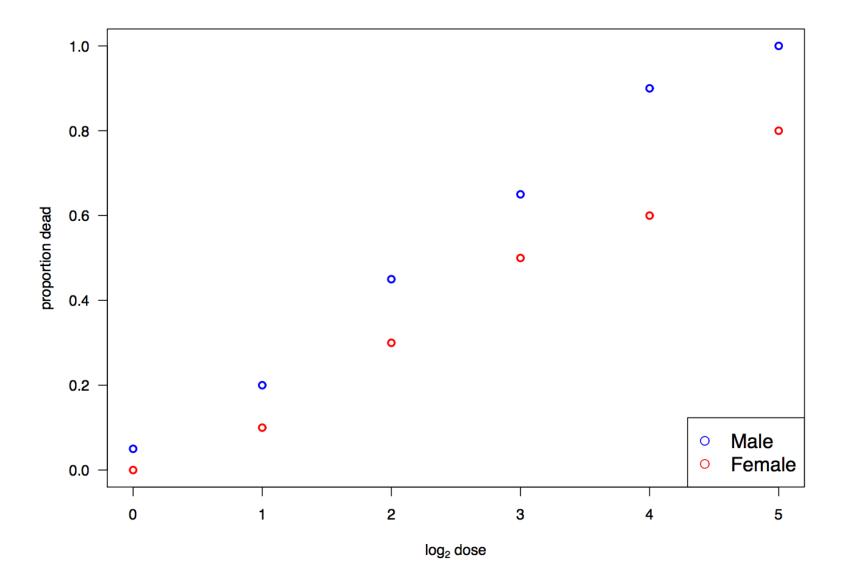
#### Tobacco budworm, Heliothis virescens

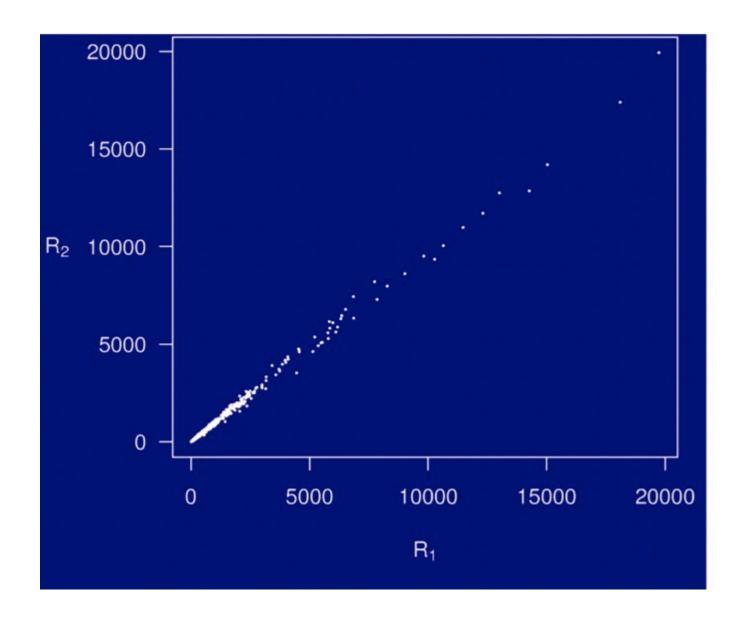
Batches of 20 male and 20 female worms were given a 3-day dose of pyrethroid *trans*-cypermethrin

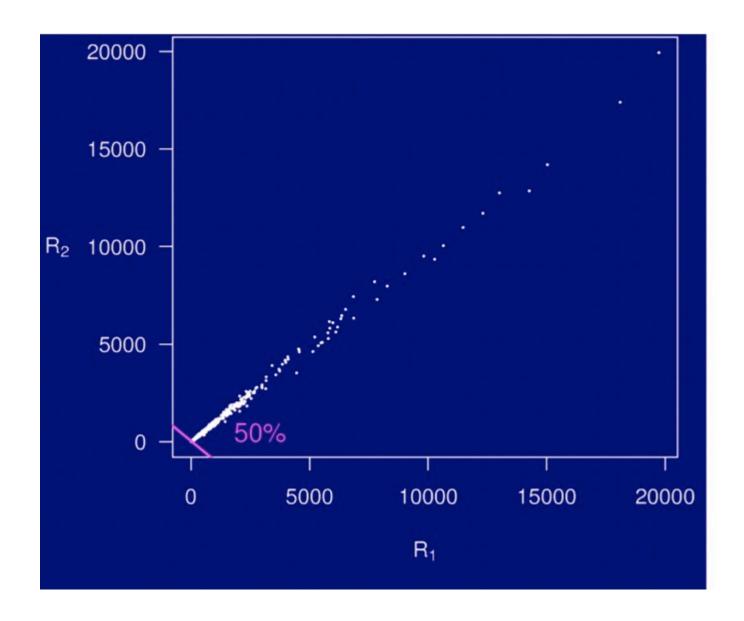
The no. dead or "knocked down" in each batch was noted.

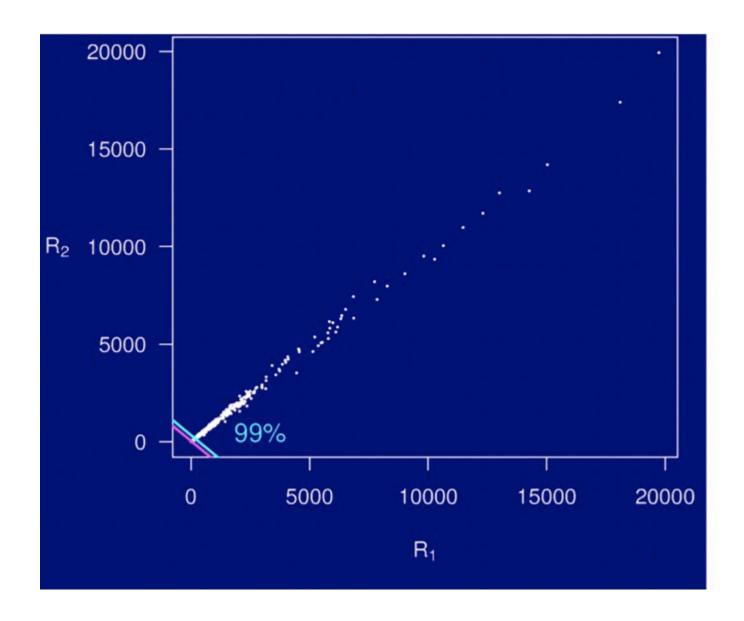
	Dose					
Sex	1	2	4	8	16	32
Male	1	4	9	13	18	20
Female	0	2	6	10	12	16

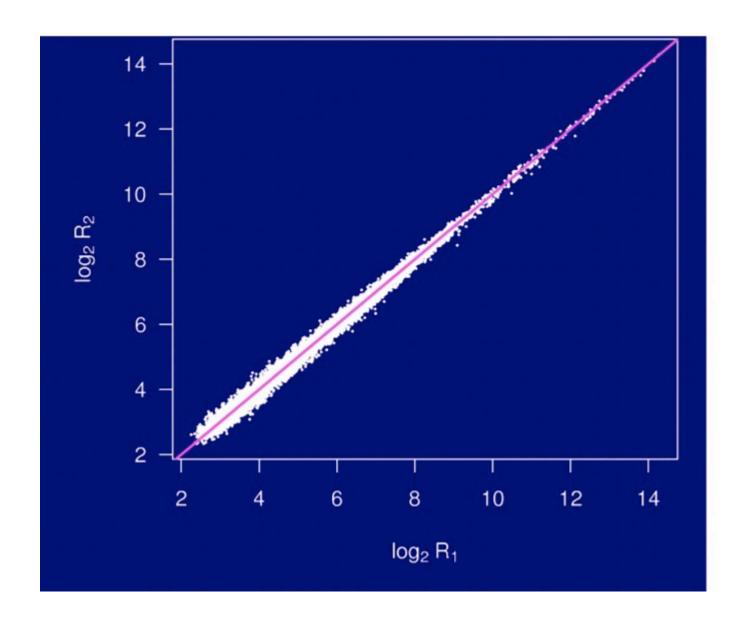


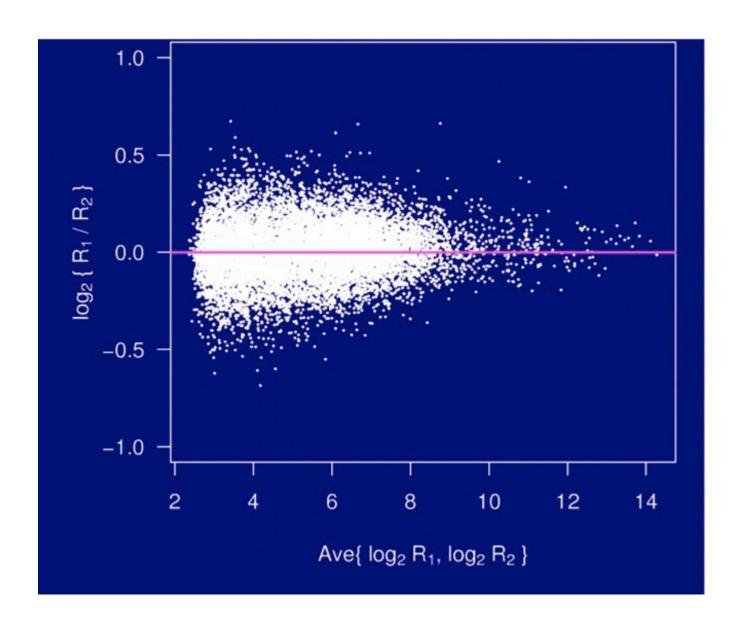












## **Summary statistics**

Location / Center

- mean (average)
- median
- mode
- geometric mean
- harmonic mean

Scale

- standard deviation (SD)
- inter-quartile range (IQR)
- range

Other

- quantile
- quartile
- quintile

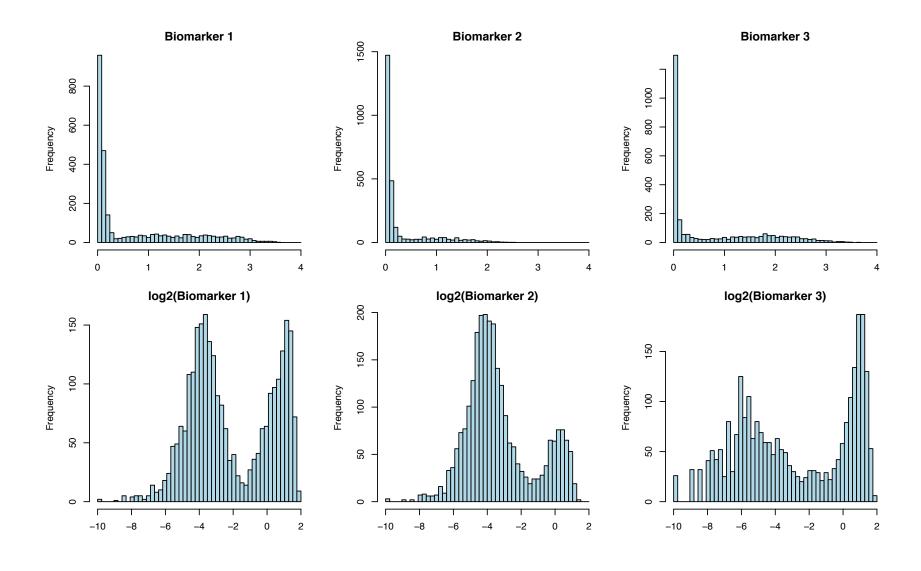
## **Summary statistics**

mean = 
$$\frac{1}{n} \sum_{i=1}^{n} x_i = (x_1 + x_2 + \ldots + x_n)/n$$

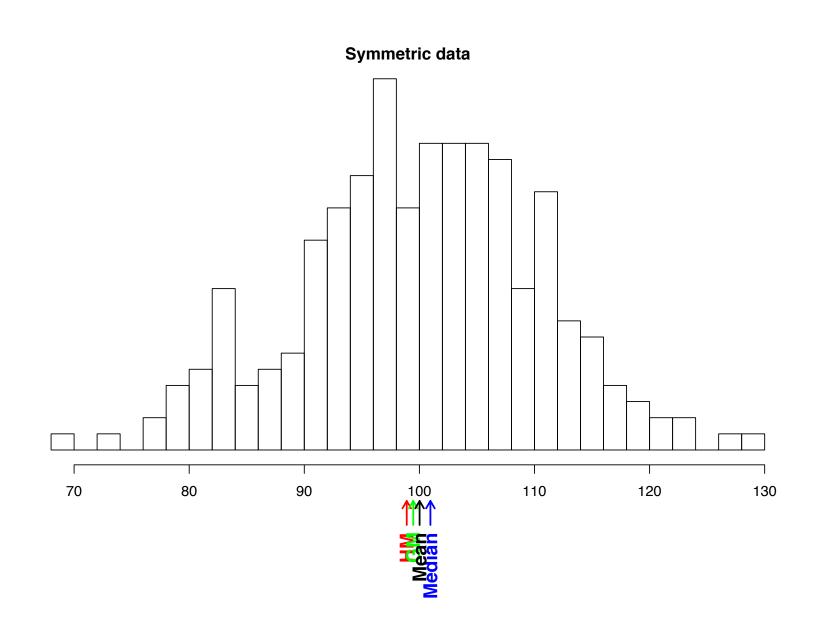
geometric mean 
$$= \sqrt[n]{\prod_{i=1}^n x_i} = \exp\left\{\frac{1}{n} \sum_{i=1}^n \log x_i\right\}$$

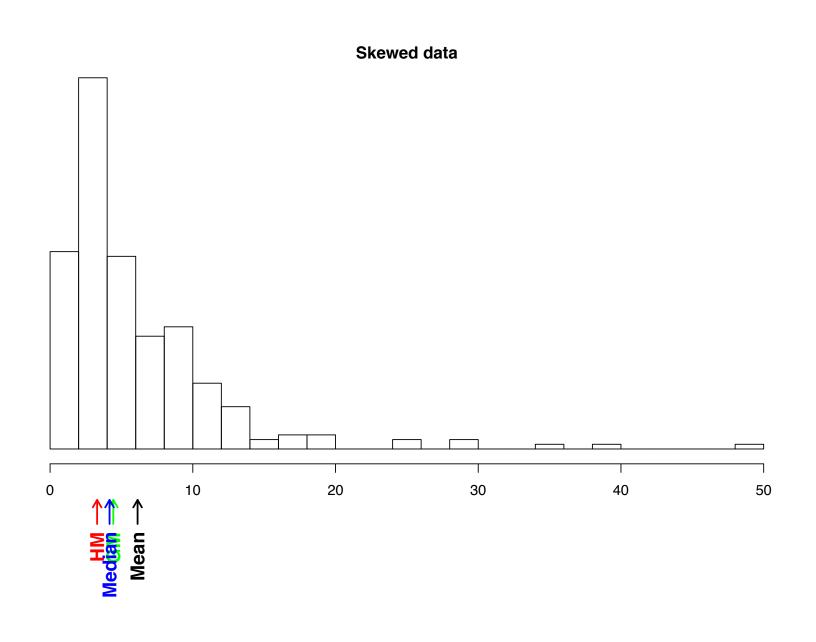
harmonic mean 
$$= 1/\left\{\frac{1}{n}\sum_{i=1}^{n}(1/x_i)\right\}$$

→ Note: these are all sample means.



- Forget about the mode.
- The mean is sensitive to outliers.
- The median is resistant to outliers.
- The geometric mean is used when a logarithmic transformation is appropriate (for example, when the distribution has a long right tail).
- The harmonic mean may be used when a reciprocal transformation is appropriate (very seldom).





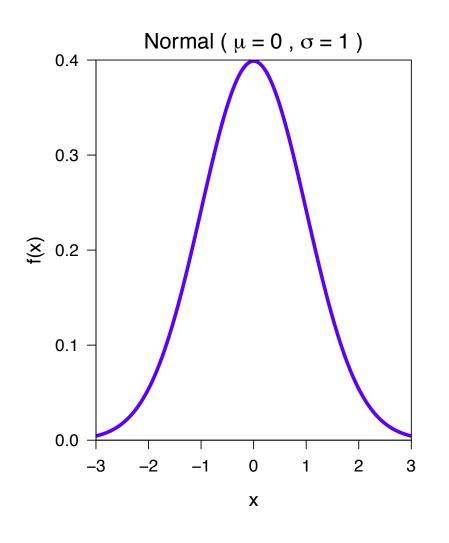
## A key point

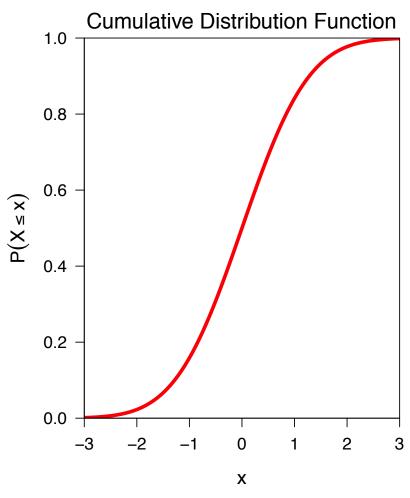
The different possible measures of the "center" of the distribution are all allowable.

You should consider the following though:

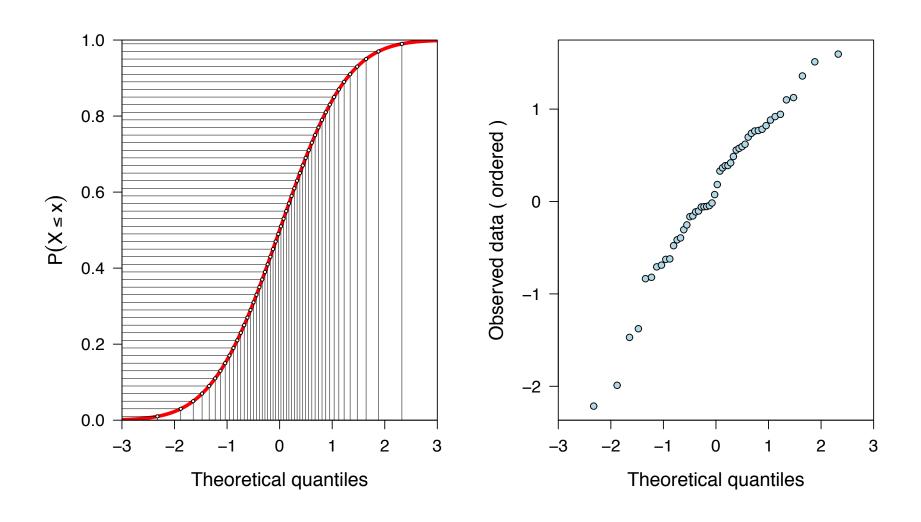
- Which is the best measure of the "typical" value in your particular setting?
- → Be sure to make clear which "average" you use.

# **QQ-plots**

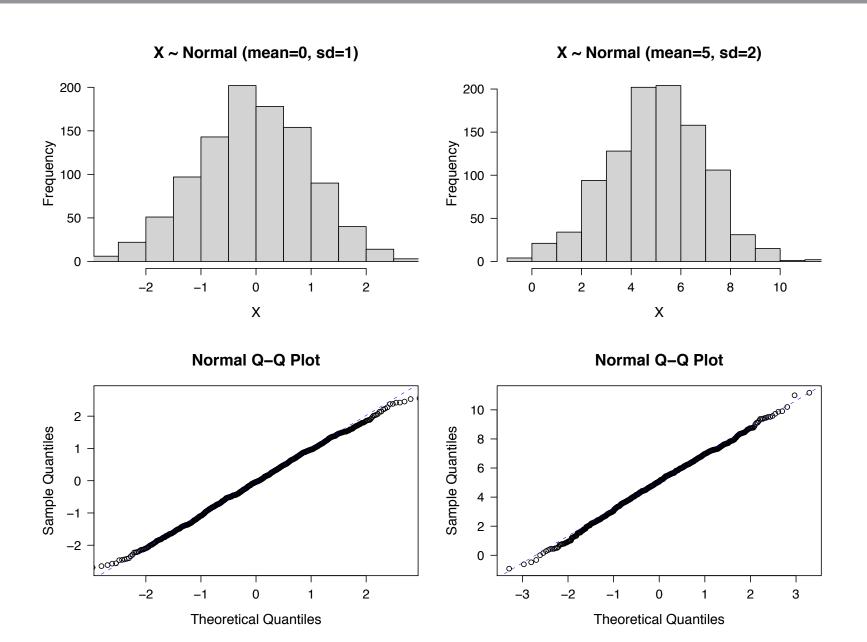




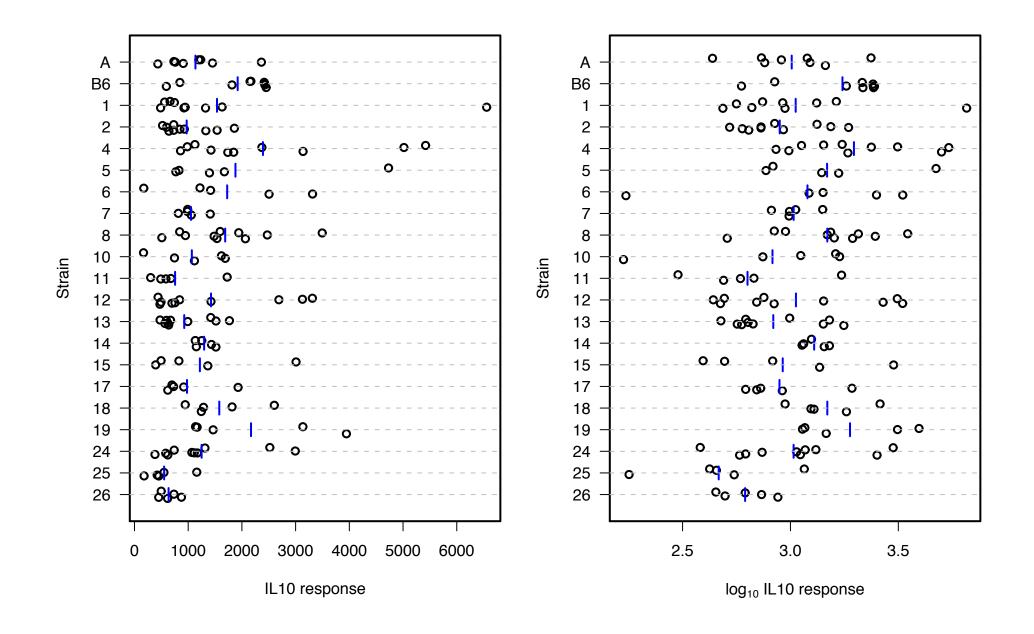
# **QQ-plots**



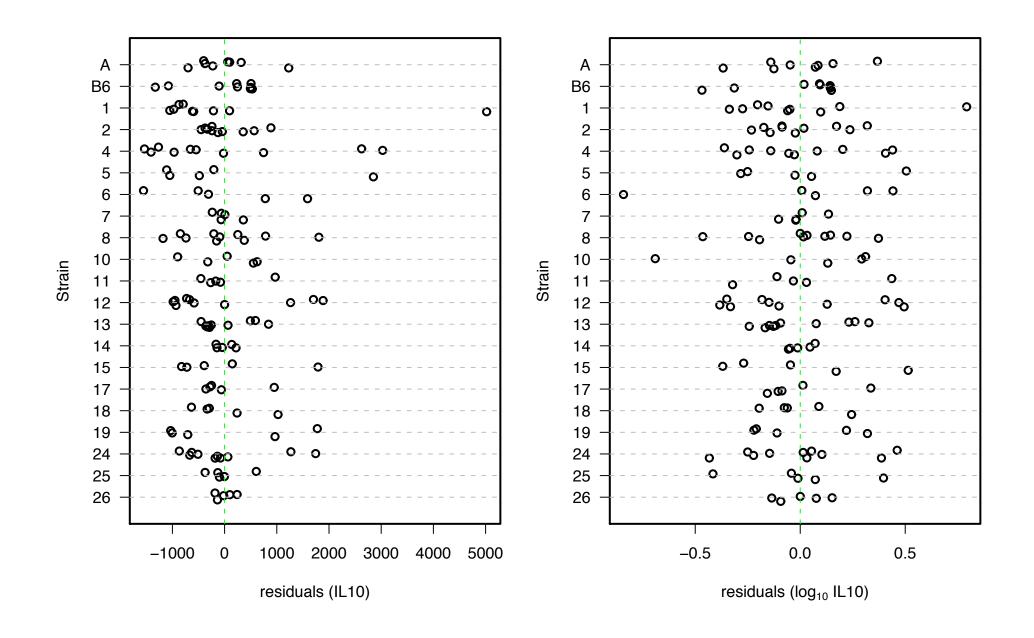
# **QQ-plots**



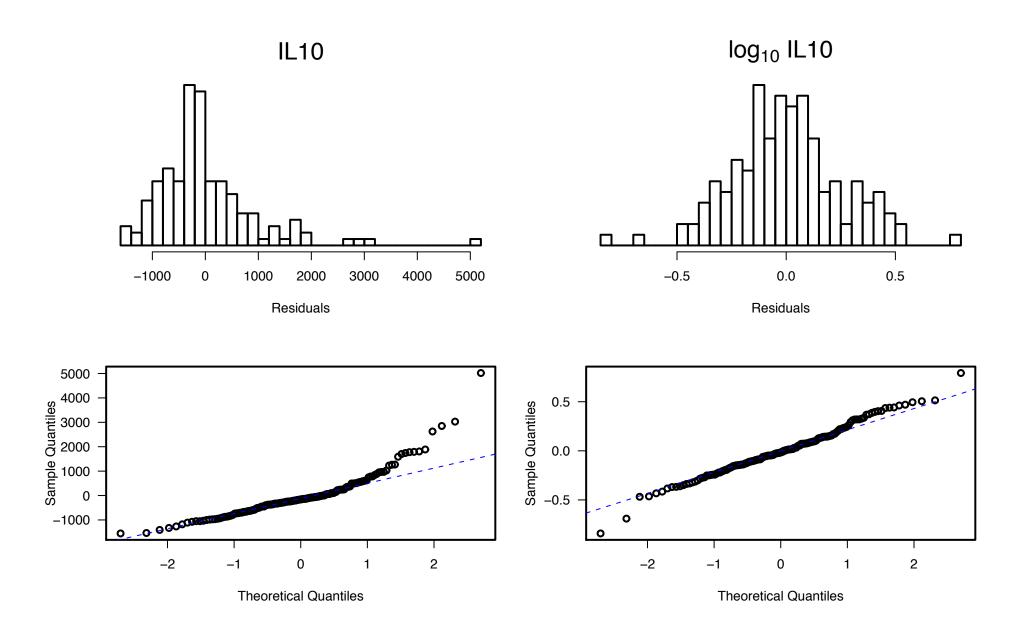
## **Example**



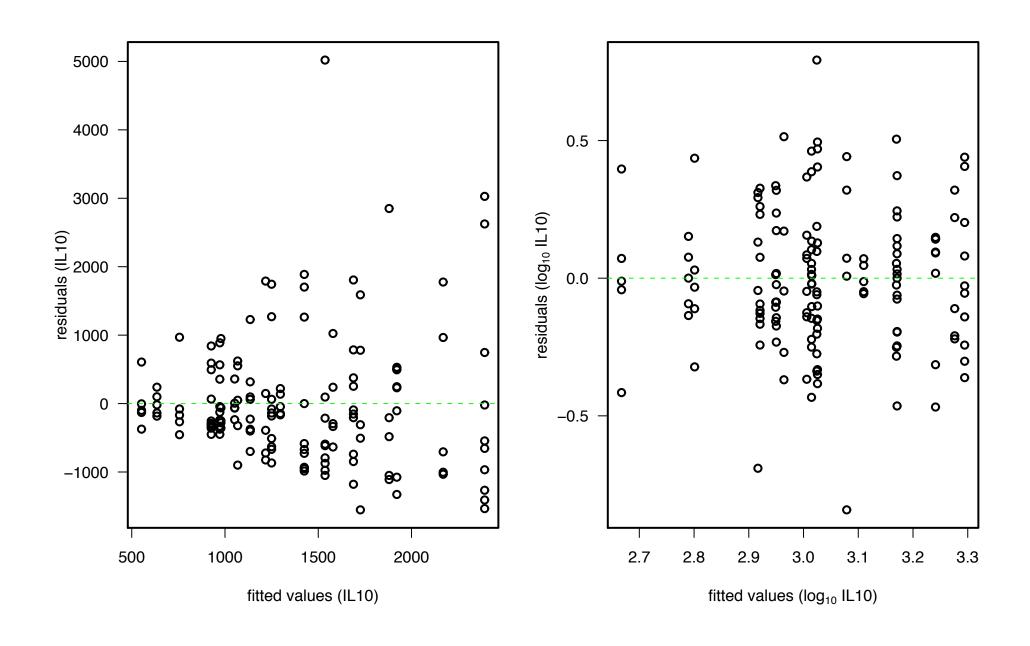
#### Residuals



# QQ plots of all residuals



#### Residuals vs fitted values



### SDs vs means

