Linear regression an ANOVA

February 11, 2014

Aims

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- Look at analysis of variance ANOVA

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- Apply these methods using R

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- Look at analysis of variance ANOVA
- Apply these methods using R
- Look at how to apply these methods to genetic data

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- The best way to explain this method is through an example

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- We can display this data in a scatterplot

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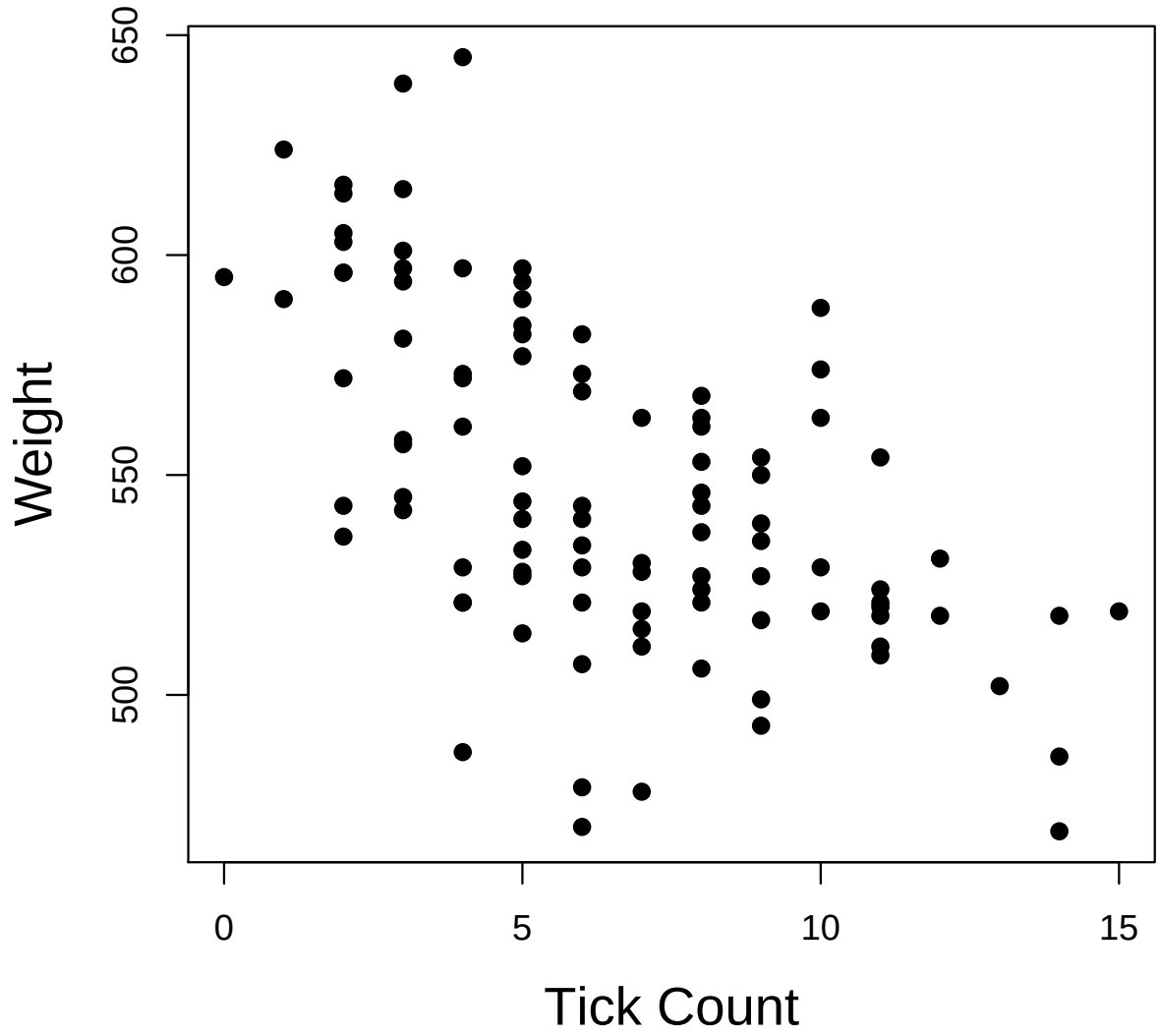

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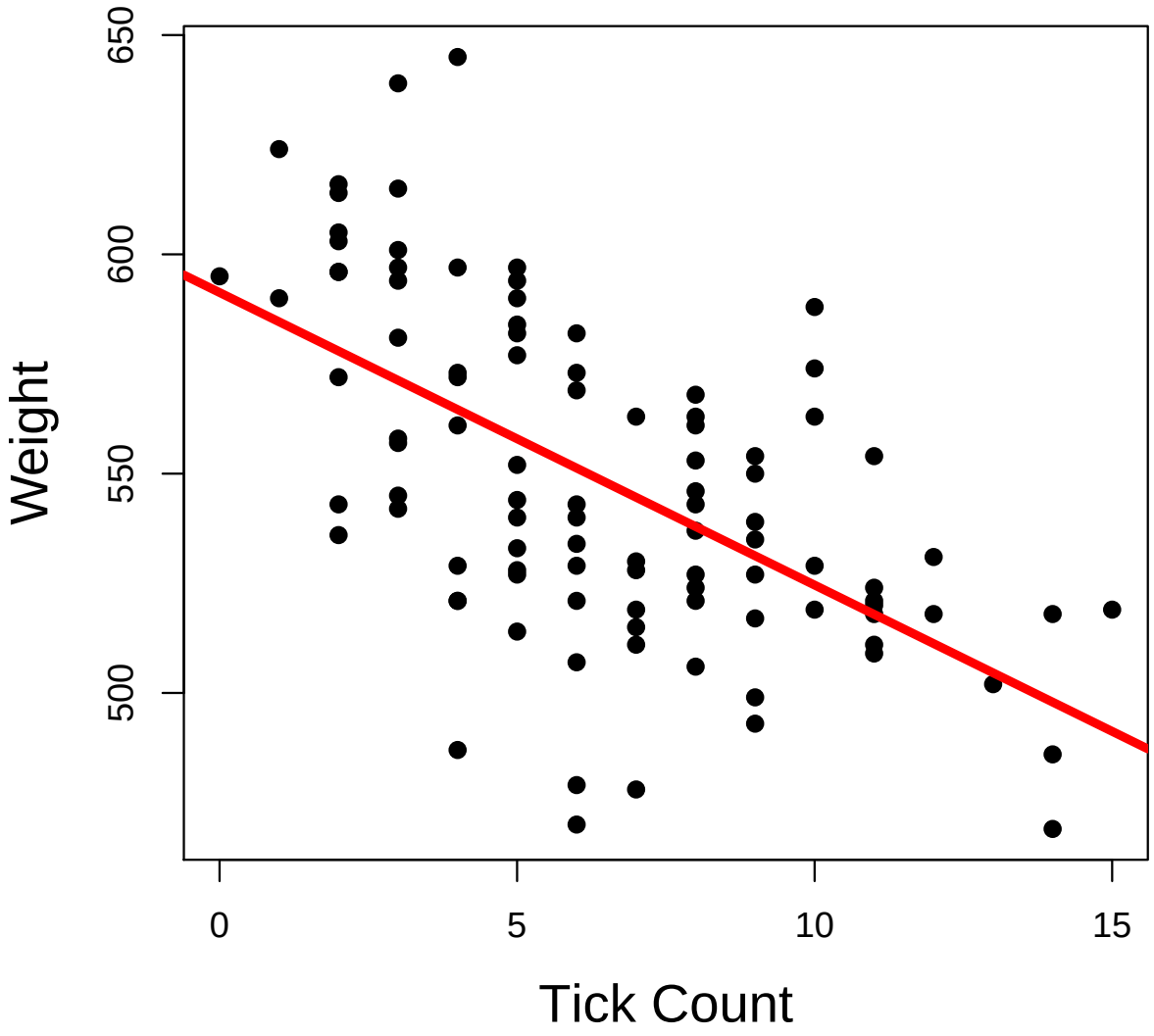

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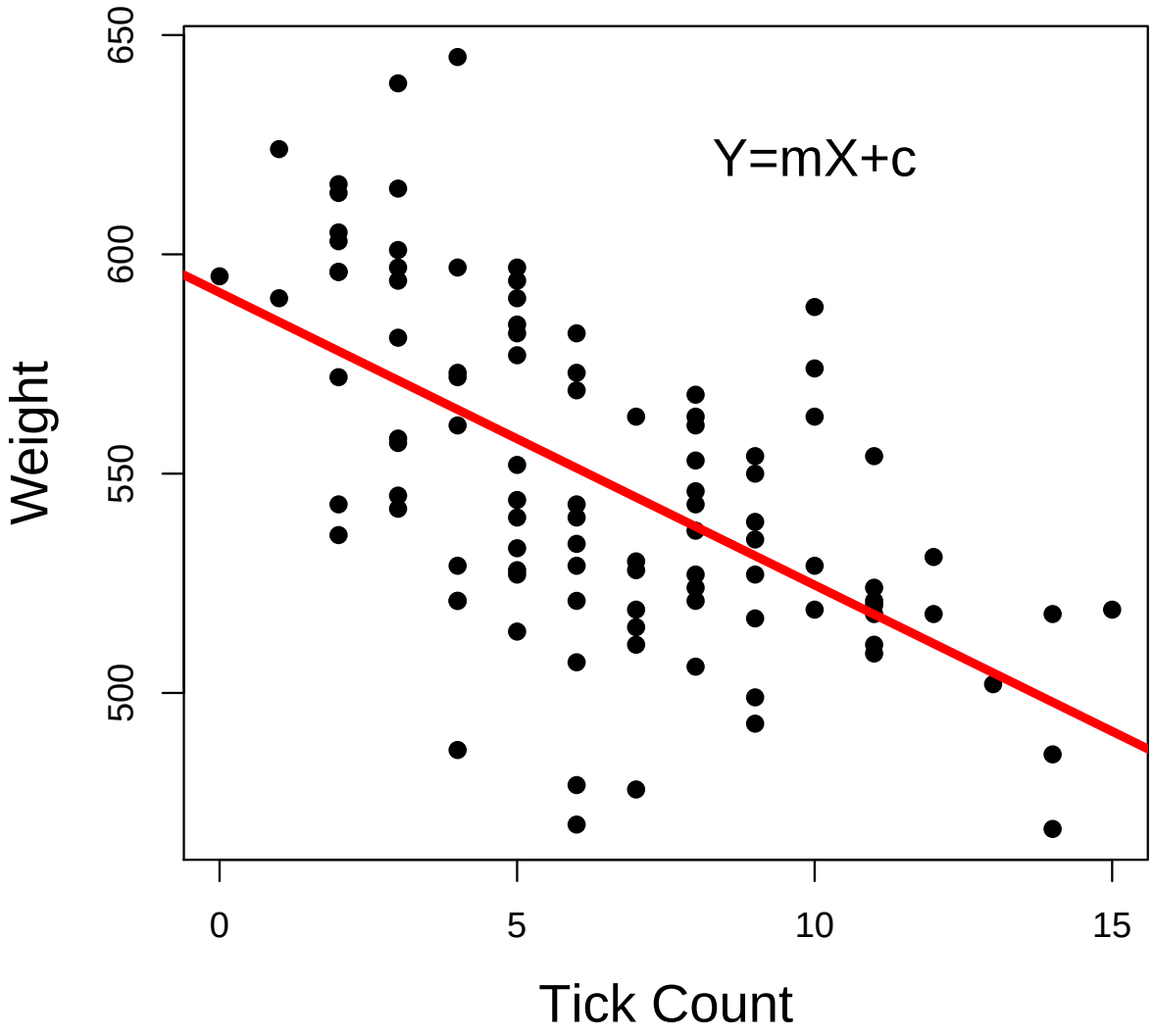

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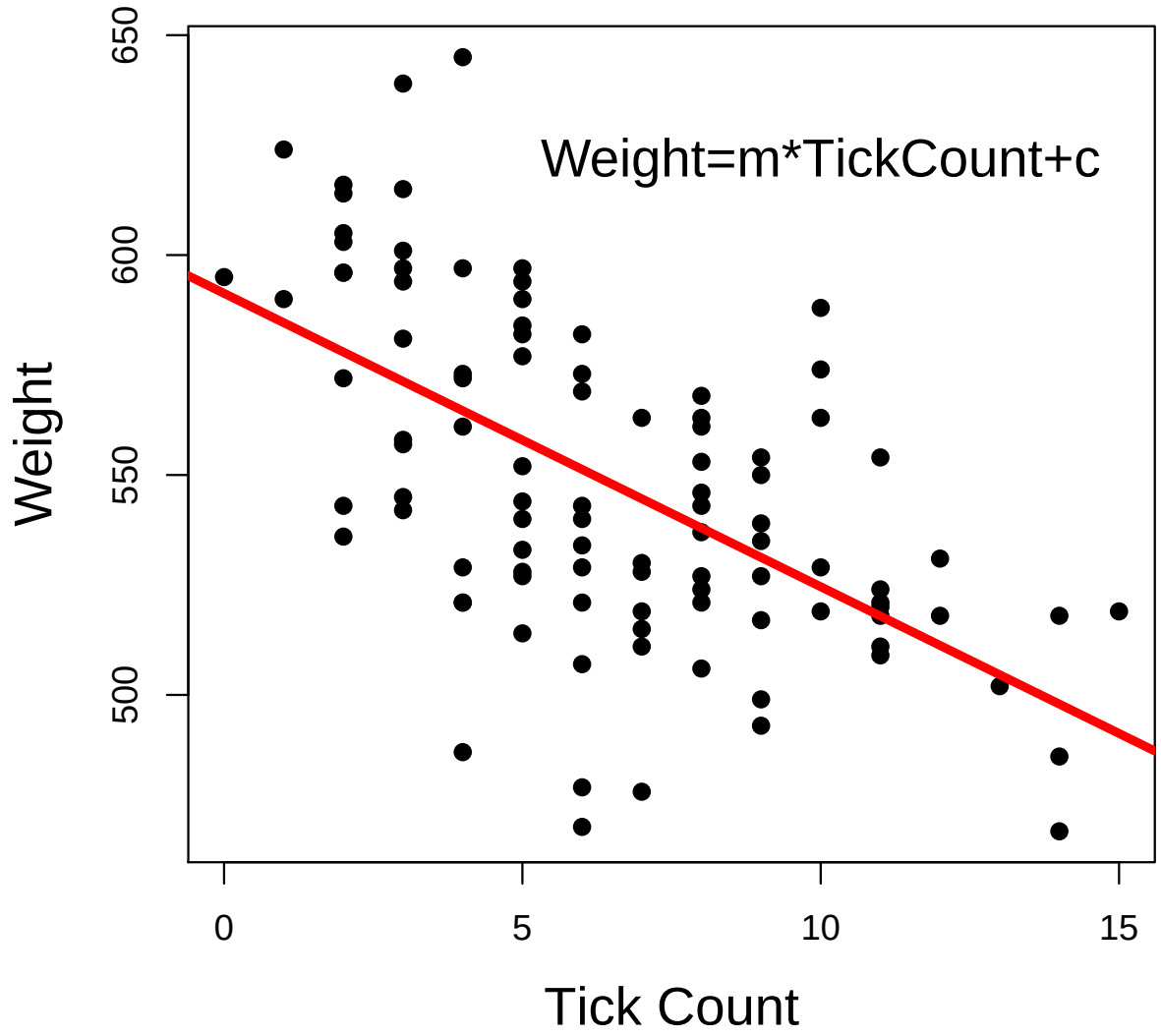

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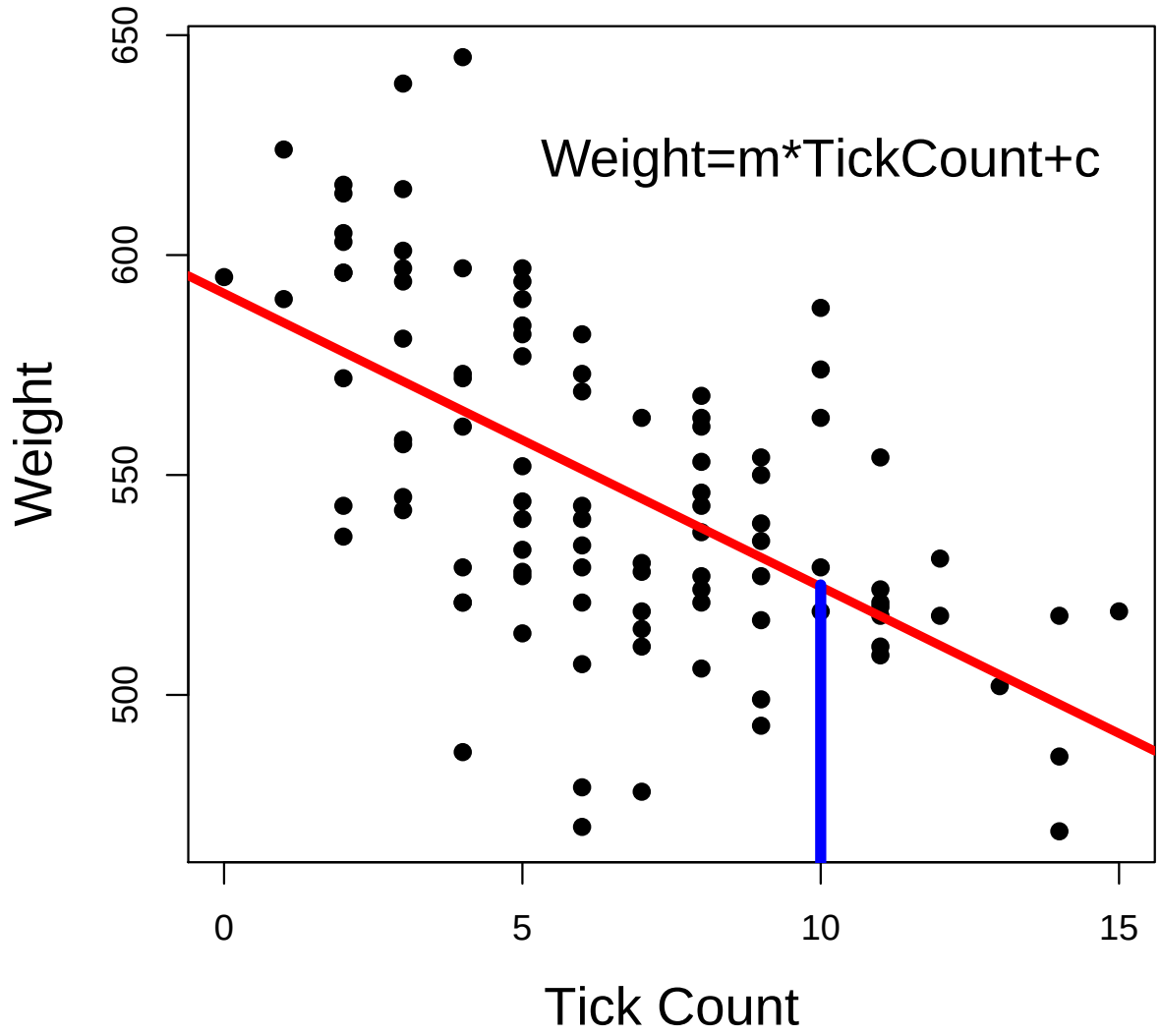

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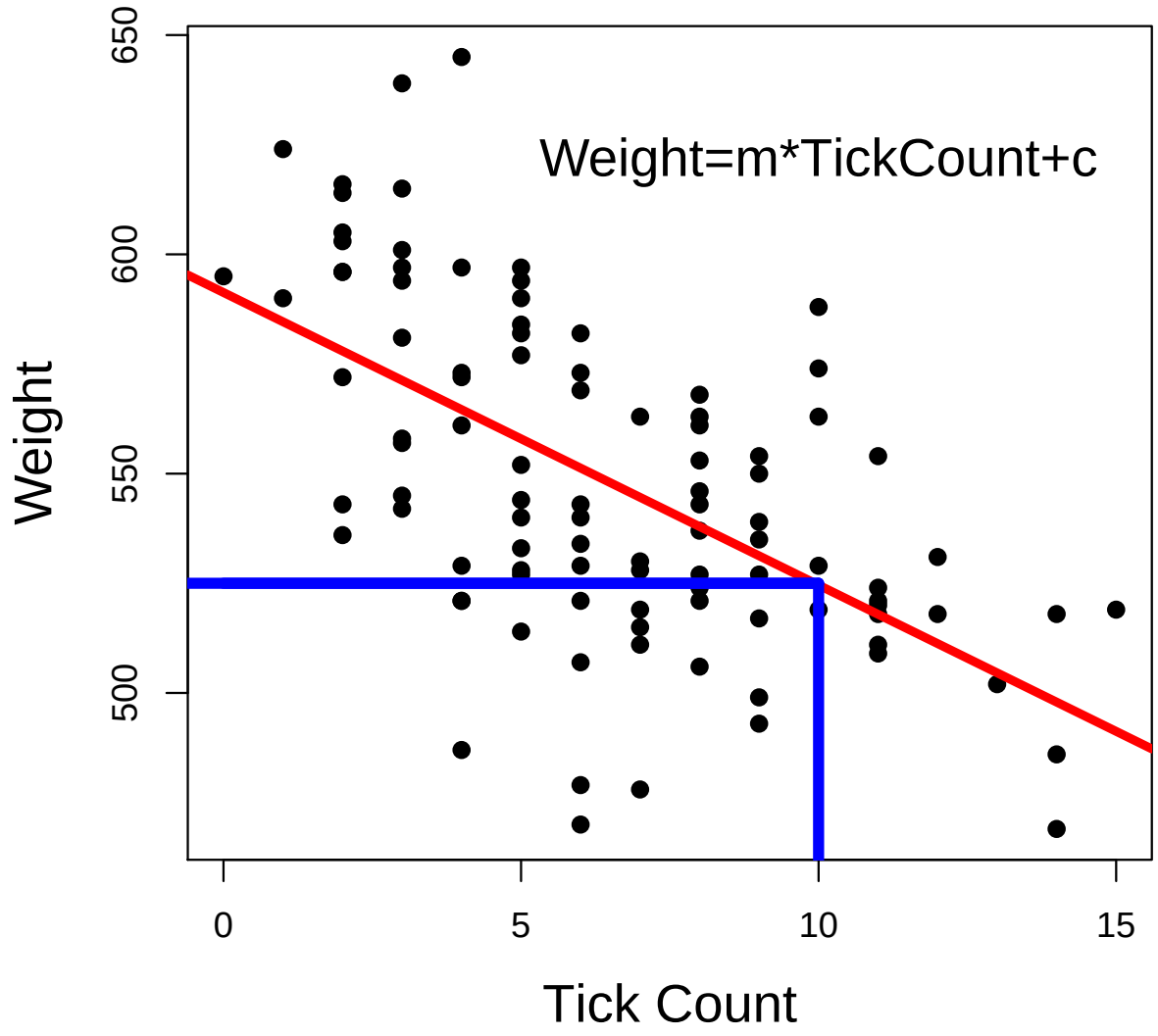

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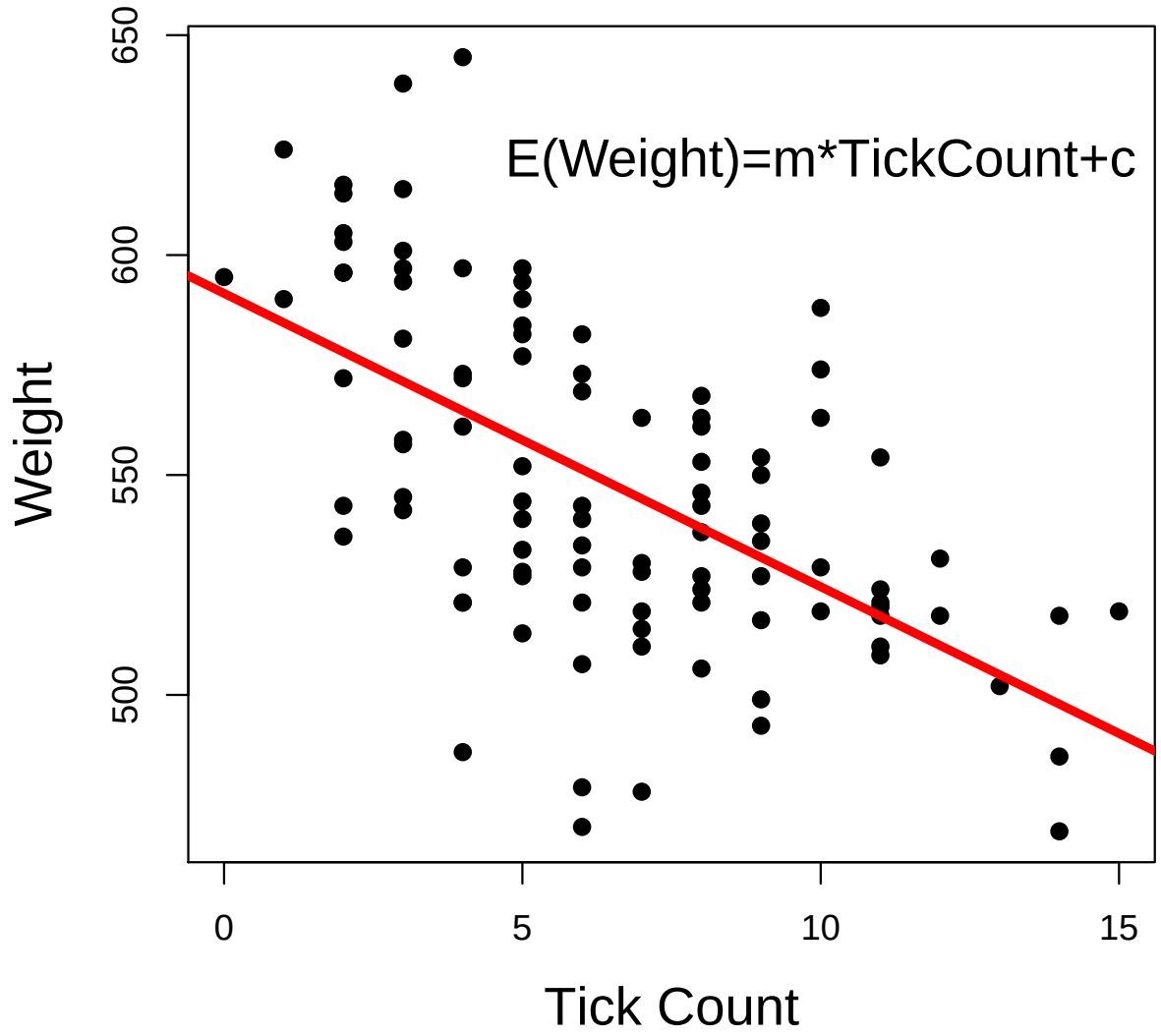

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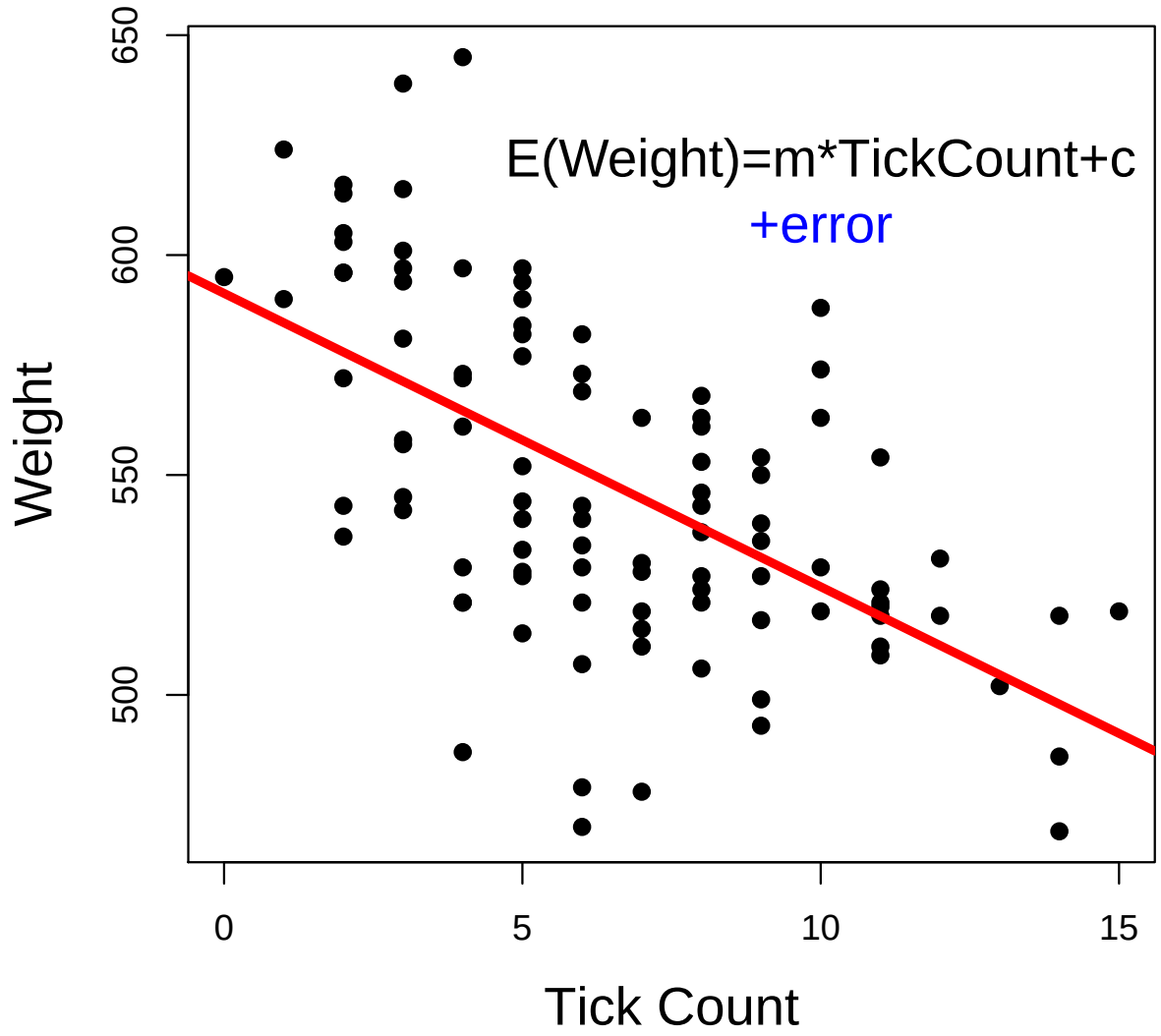

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- There is a function in R which can do this.
- But most statistical test make some assumptions about data
- If we want to use a function in R, then we always need to make sure the data meet the assumptions

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- The more common and powerful statistical tools make distributional assumptions
- The most common distribution is the normal distribution
- It assumes the data are centered around some mean value with some level or variation

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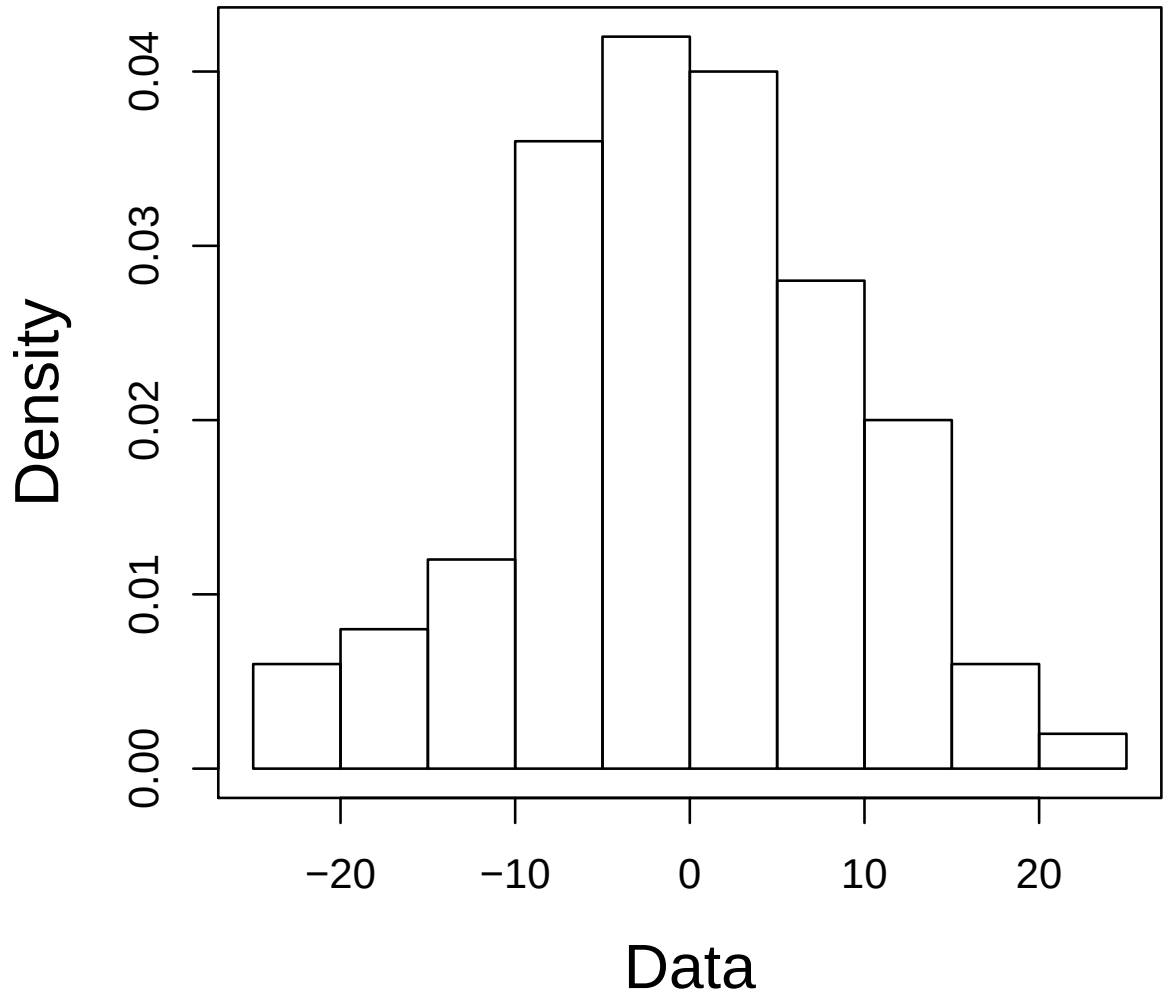

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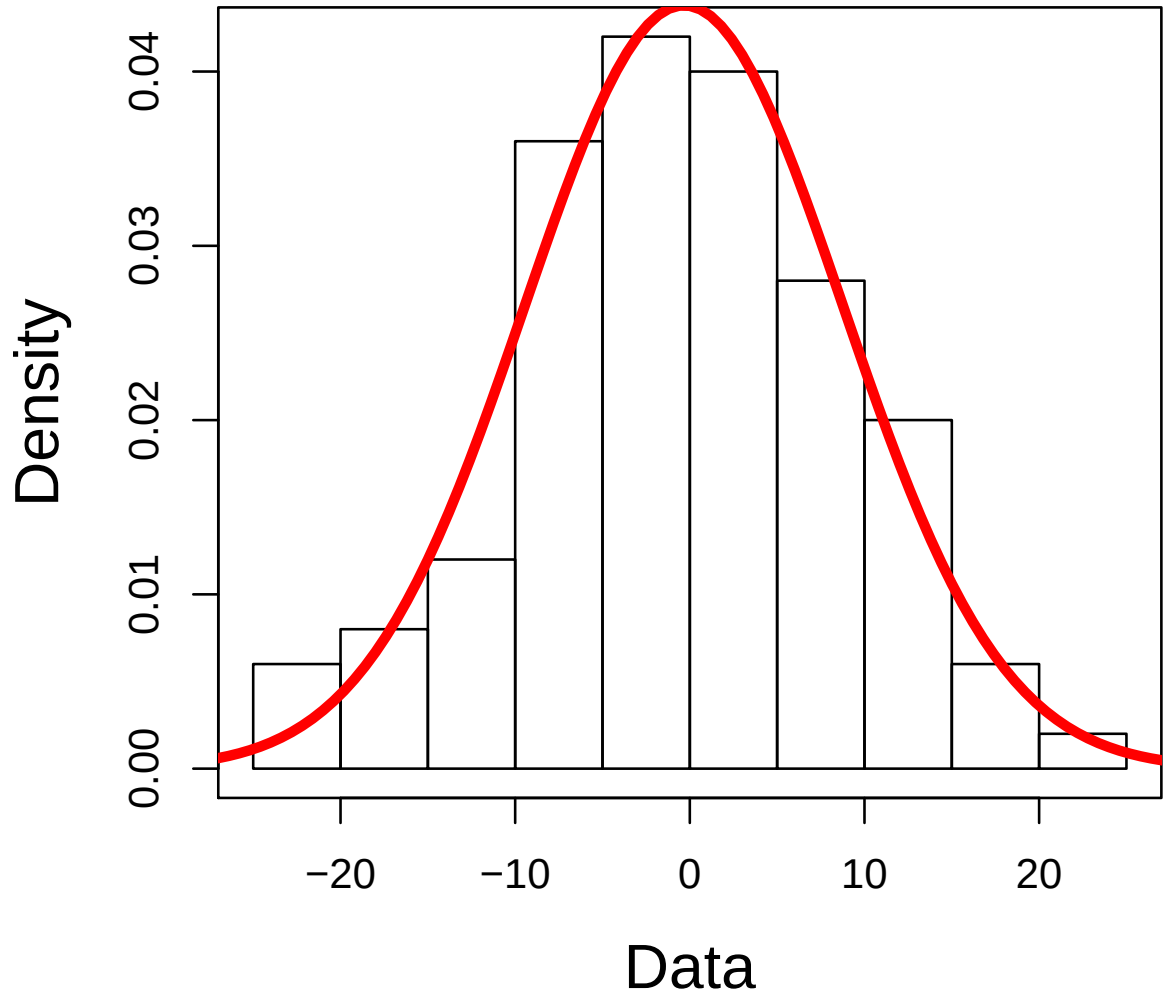

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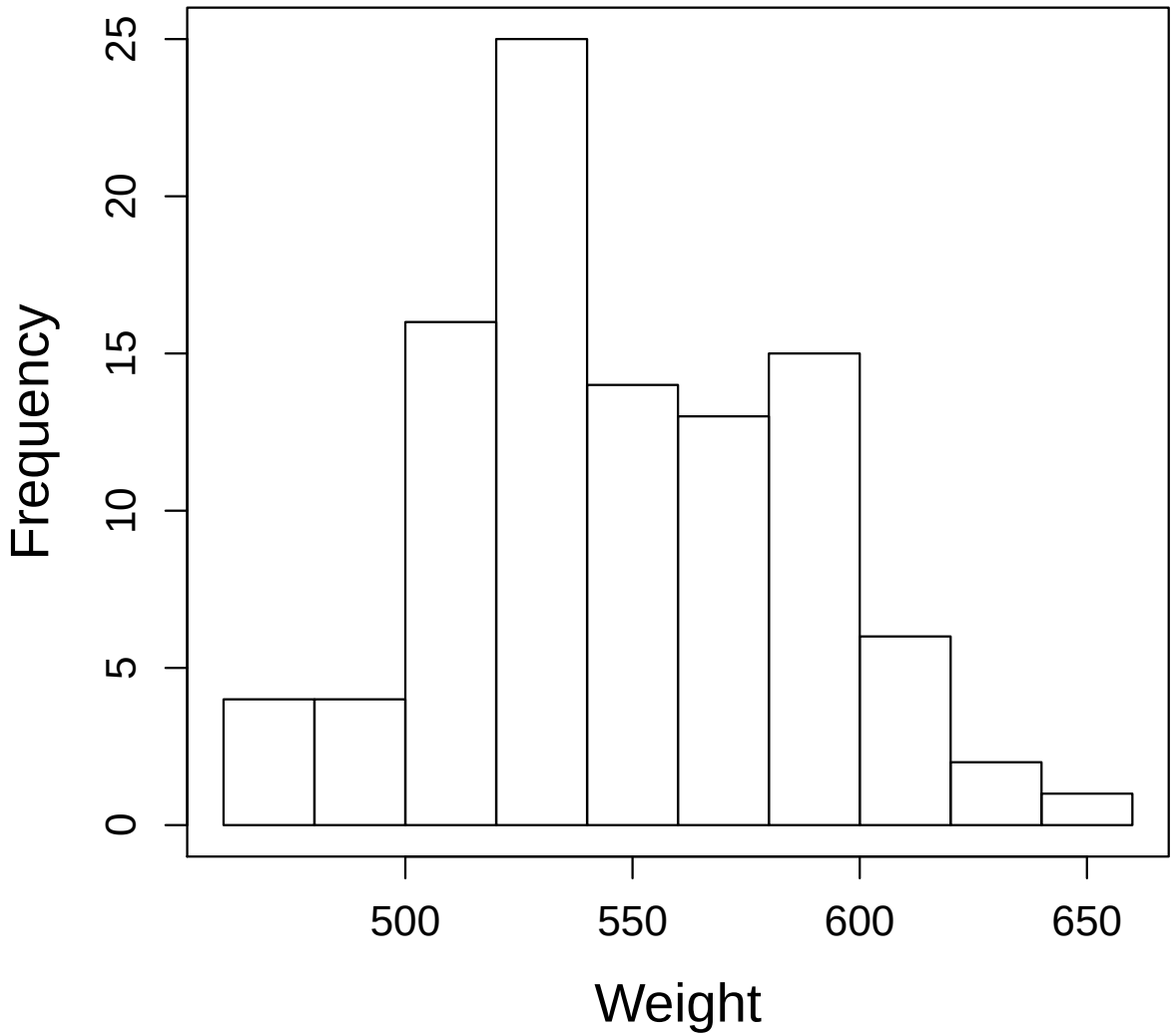

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Coefficients:

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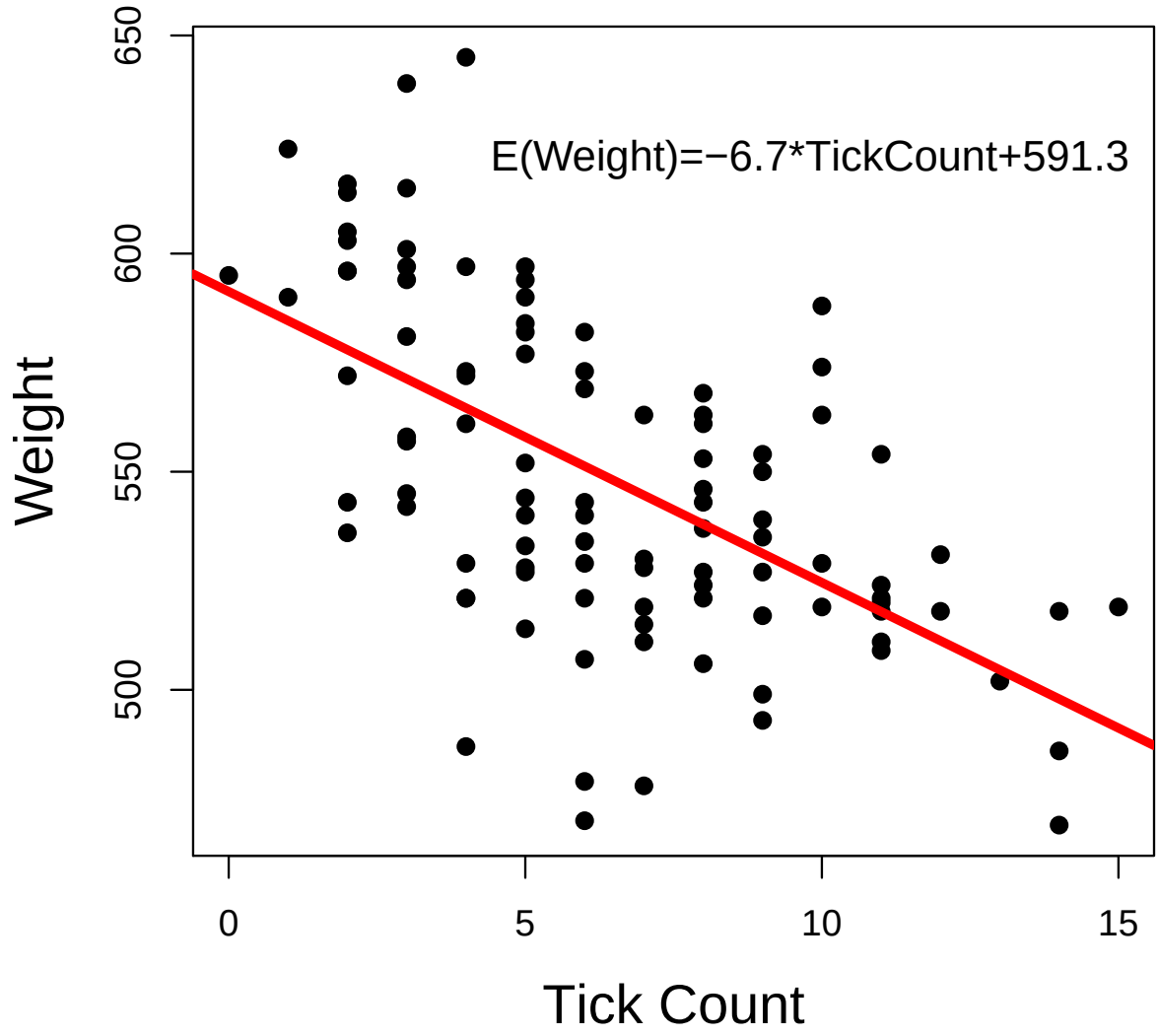

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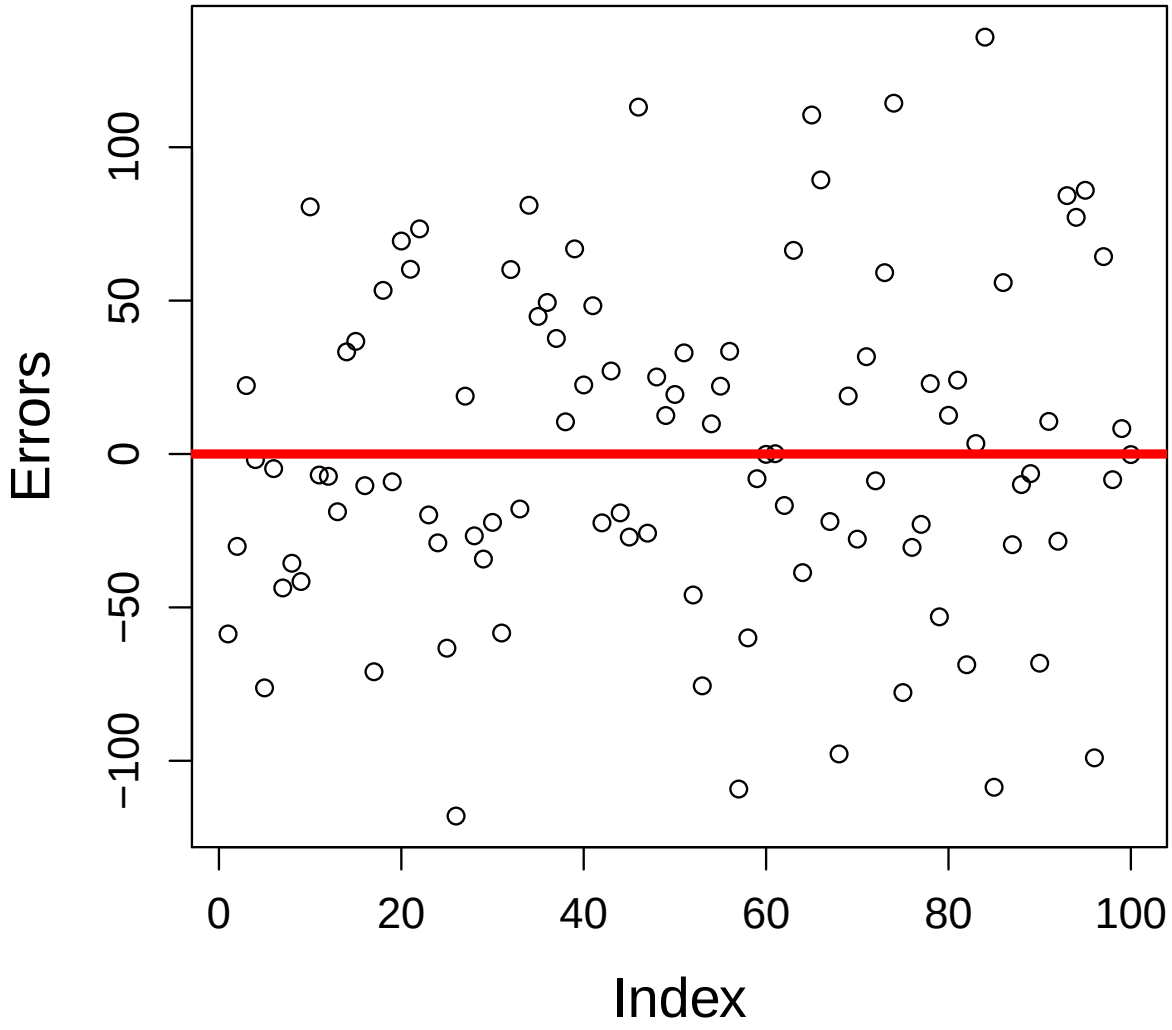

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- If the parameter m was equal to zero, then there would be no relationship between tick count and weight

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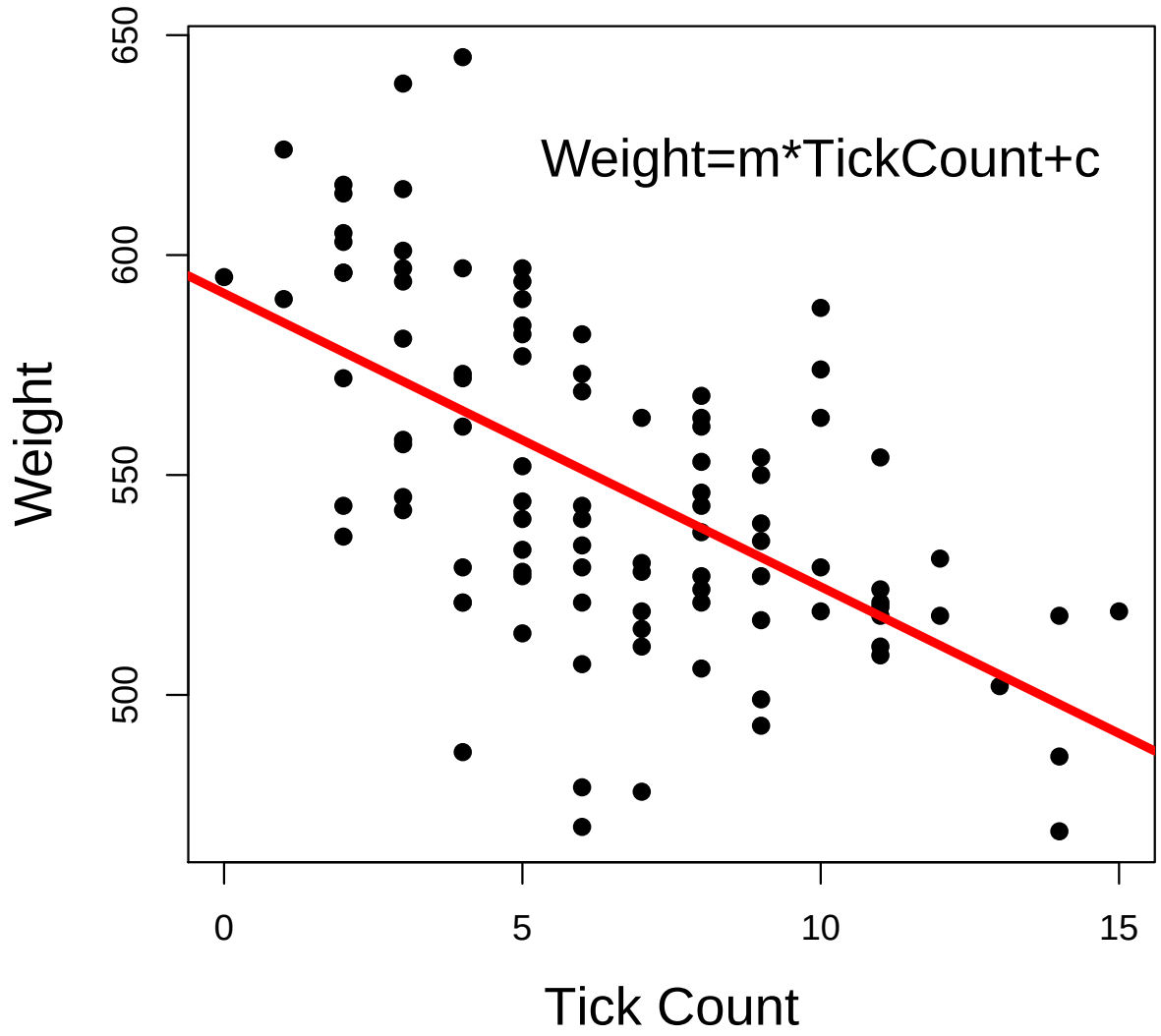

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- This is normally called the significance level of the test.

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$$Weight = c + m_1 TickCount + m_2 Breed + m_3 Housing + \ldots + error$$

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3. The ANOVA is used to see if there is a difference in some response variable between different groups
4. It does this by assessing the amount of variation within groups compared to the amount of variation between groups
5. There is a function in R which does anova.

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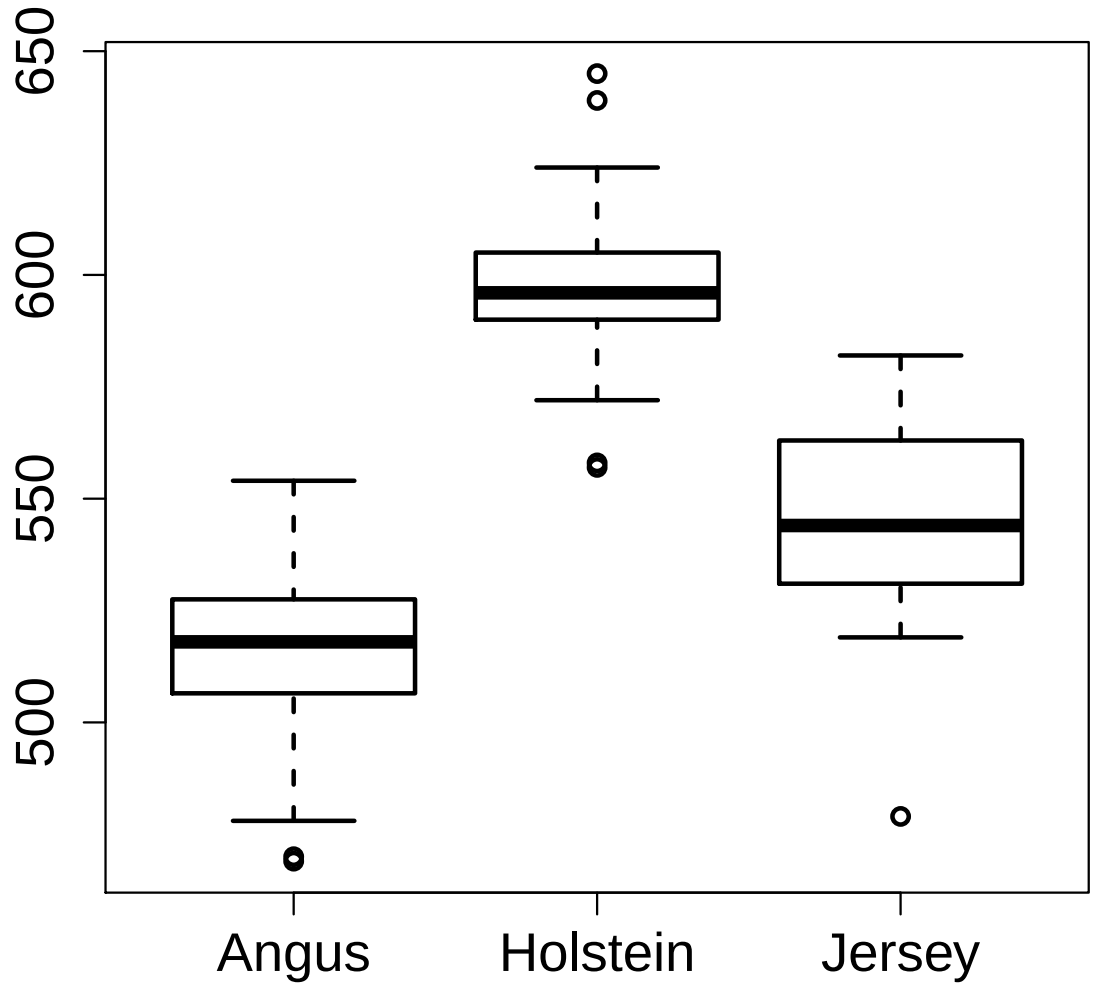
5. Again, we can look at the data graphically.

ANOVA



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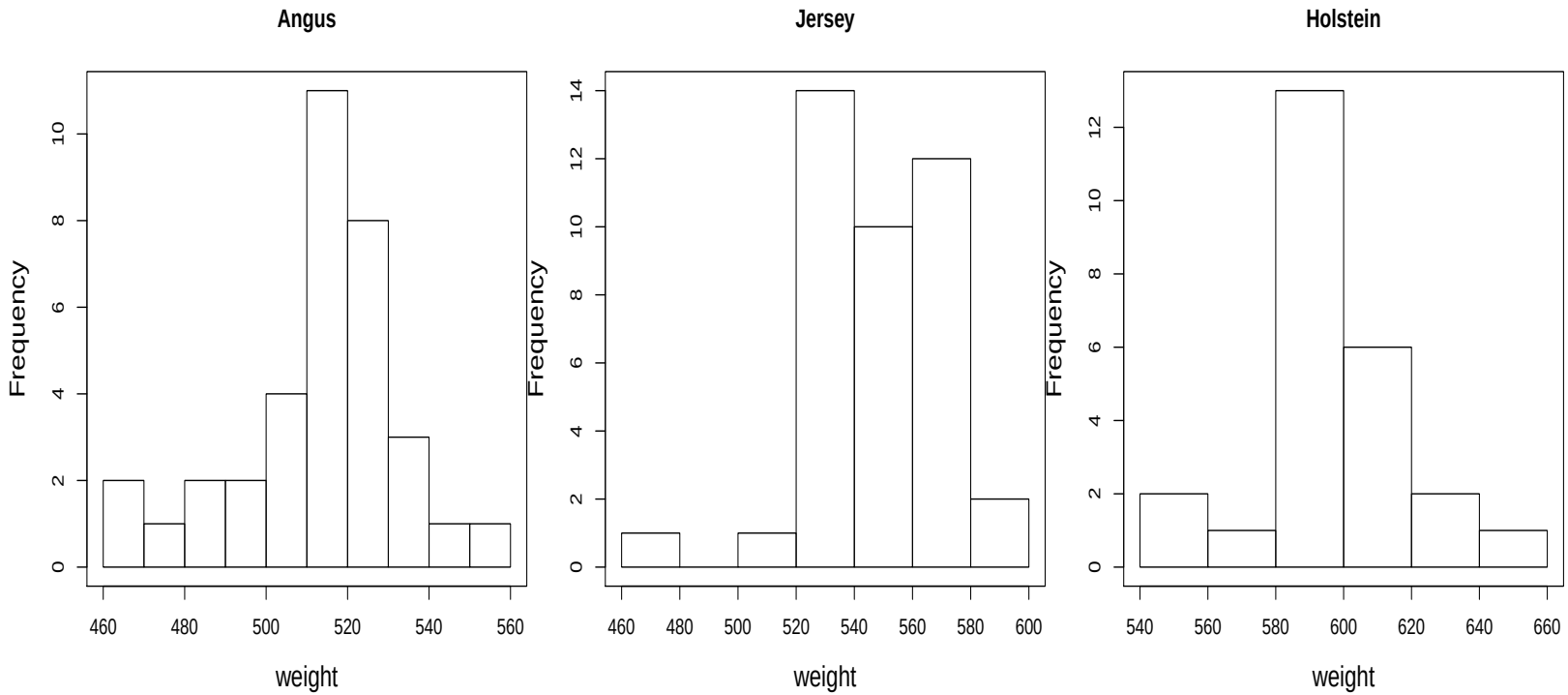
  - Look at histograms of each group separately to see if they look normal
- The three groups have similar variances
  - Look at the spreads of the histograms and boxplots to see if they look the same
  - Use the *var()* function in R for each of the three groups and see if they are around the same.

ANOVA


Angus
Frequency
0
2
4
6
8
10
460
480
500
520
540
560
weight
Jersey
Frequency
0
2
4
6
8
10
12
14
460
480
500
520
540
560
580
600
weight
Holstein
Frequency
0
2
4
6
8
10
12
540
560
580
600
620
640
660
weight

(a) (b) (c)

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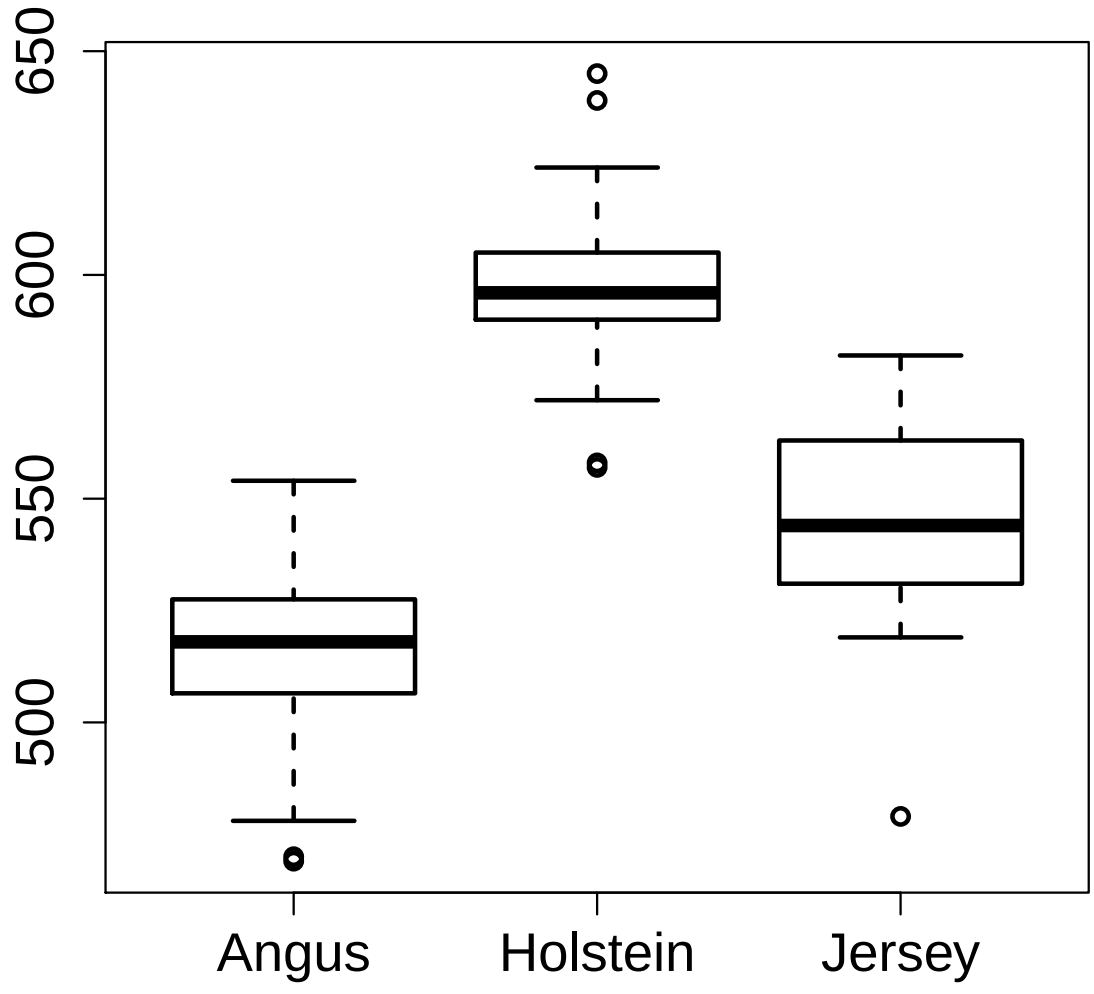

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The mean weight from Angus = the mean weight from Holstein = mean weight from Jersey

- If we reject this hypothesis, then we only know that there is at least one difference between the three breeds and not where the differences lie.
- We can do this in R using the *aov* function

ANOVA

$aov(weight \sim breed)$

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breed	2	101768	50884	116.9	$< 2e-16$	$***$
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Example

Suppose with have height measurements from 1000 people and we have data from one locus with two alleles A and B. We want to test if this locus is associated with height.

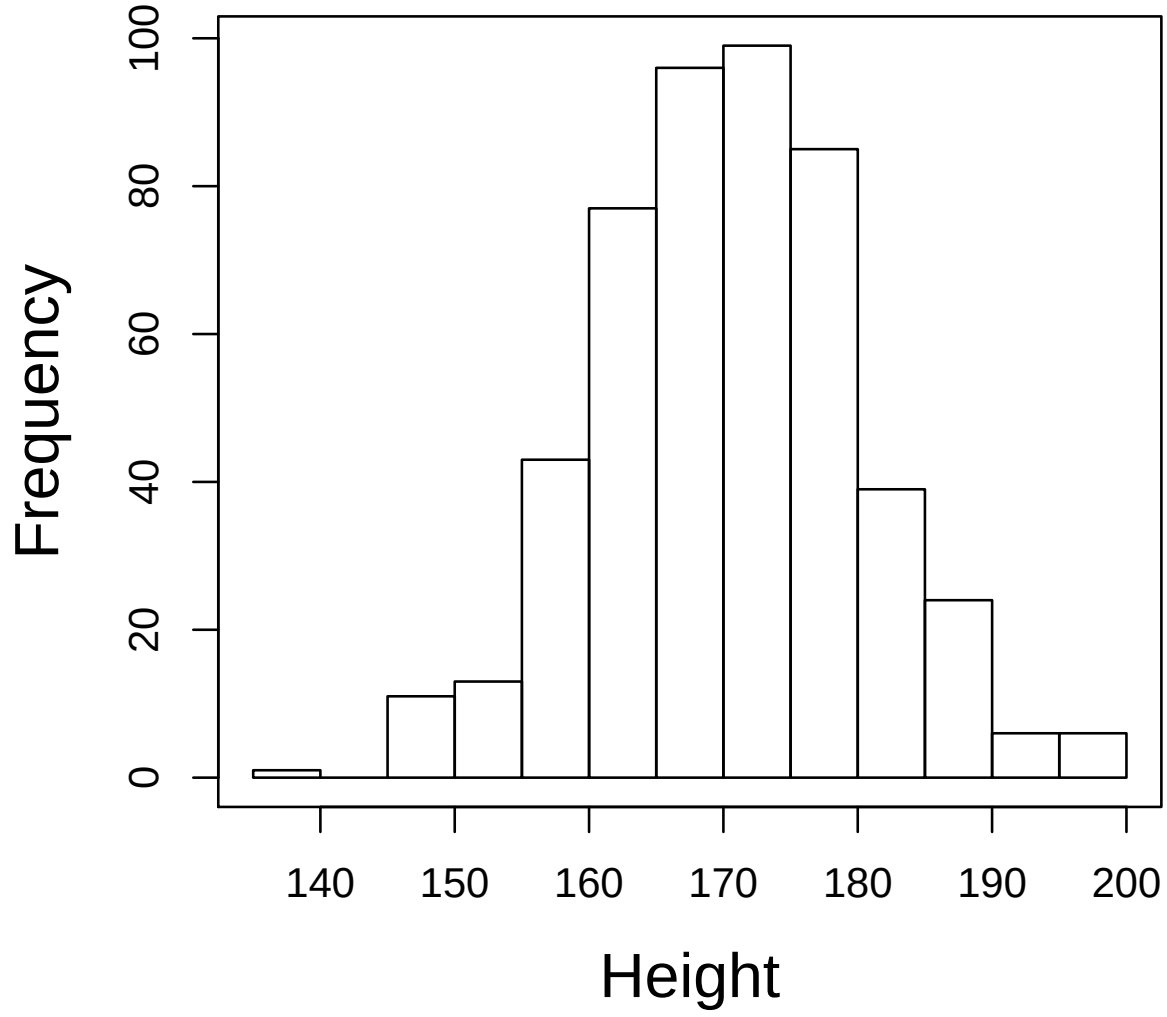
ID	Height	Genotype
1	150	AB
2	161	AA
3	145	BB
4	189	AA
5	141	BA
⋮	⋮	⋮

Example

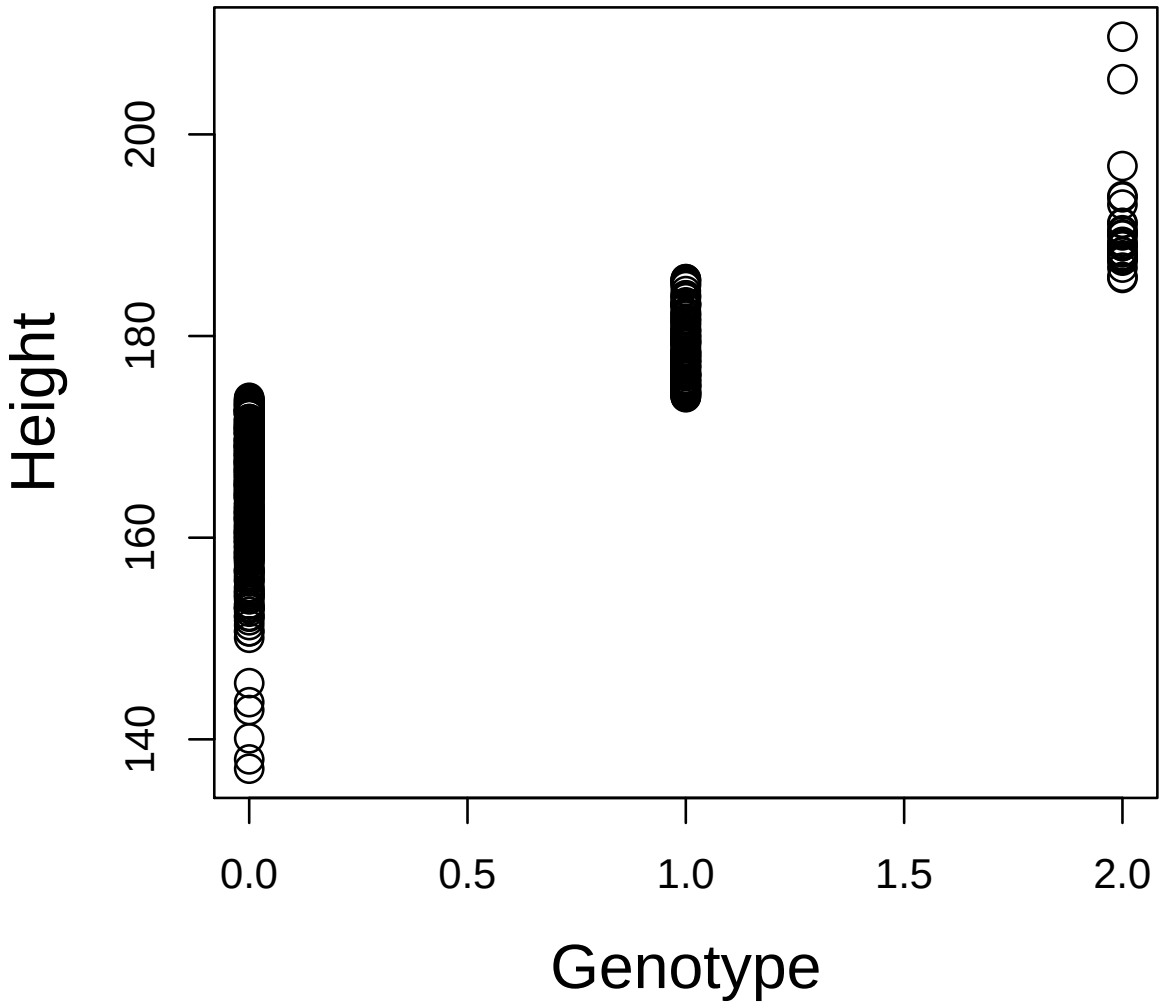
Suppose with have height measurements from 1000 people and we have data from one locus with two alleles A and B. We want to test if this locus is associated with height.

ID	Height	Genotype
1	150	1
2	161	0
3	145	2
4	189	0
5	141	1
⋮	⋮	⋮

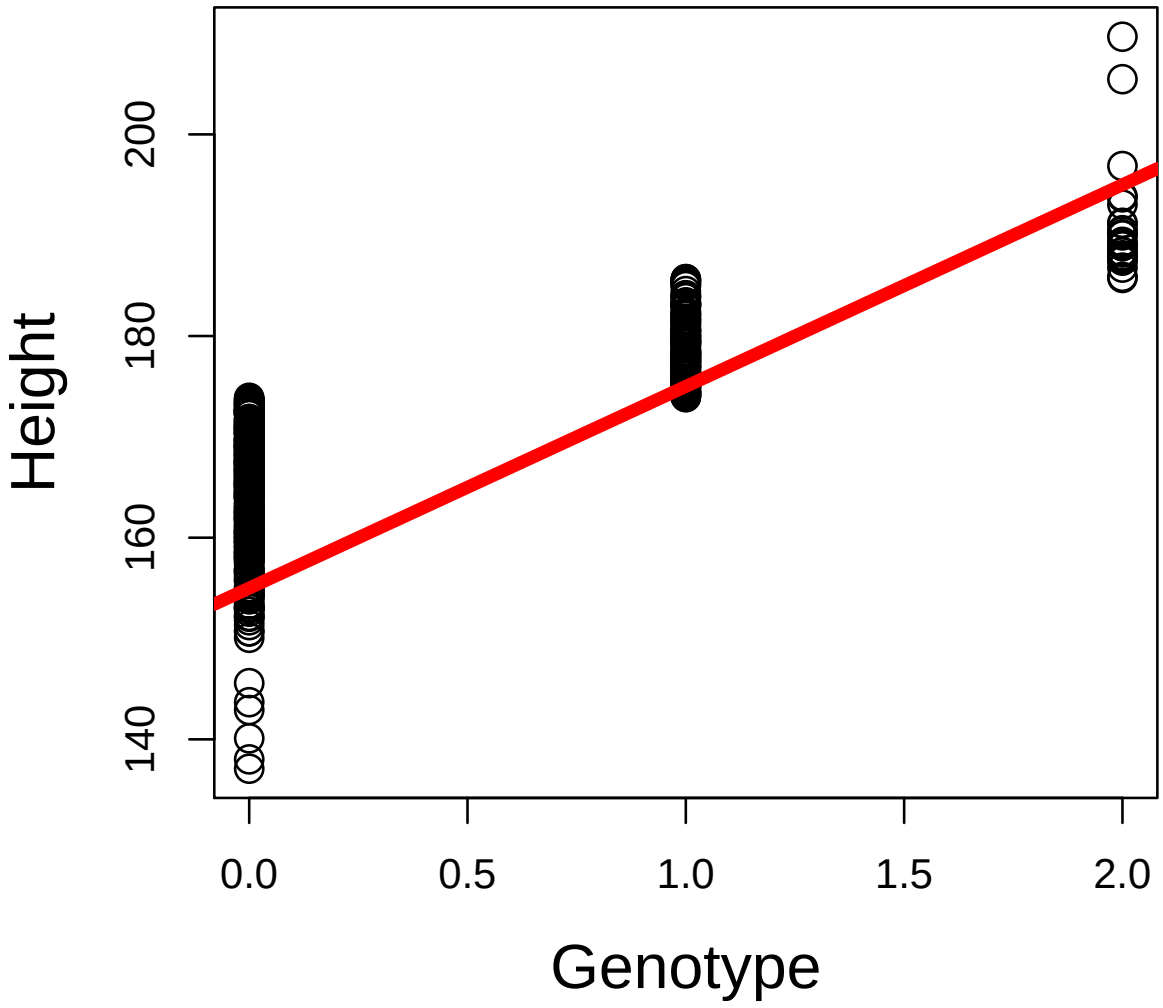
Example



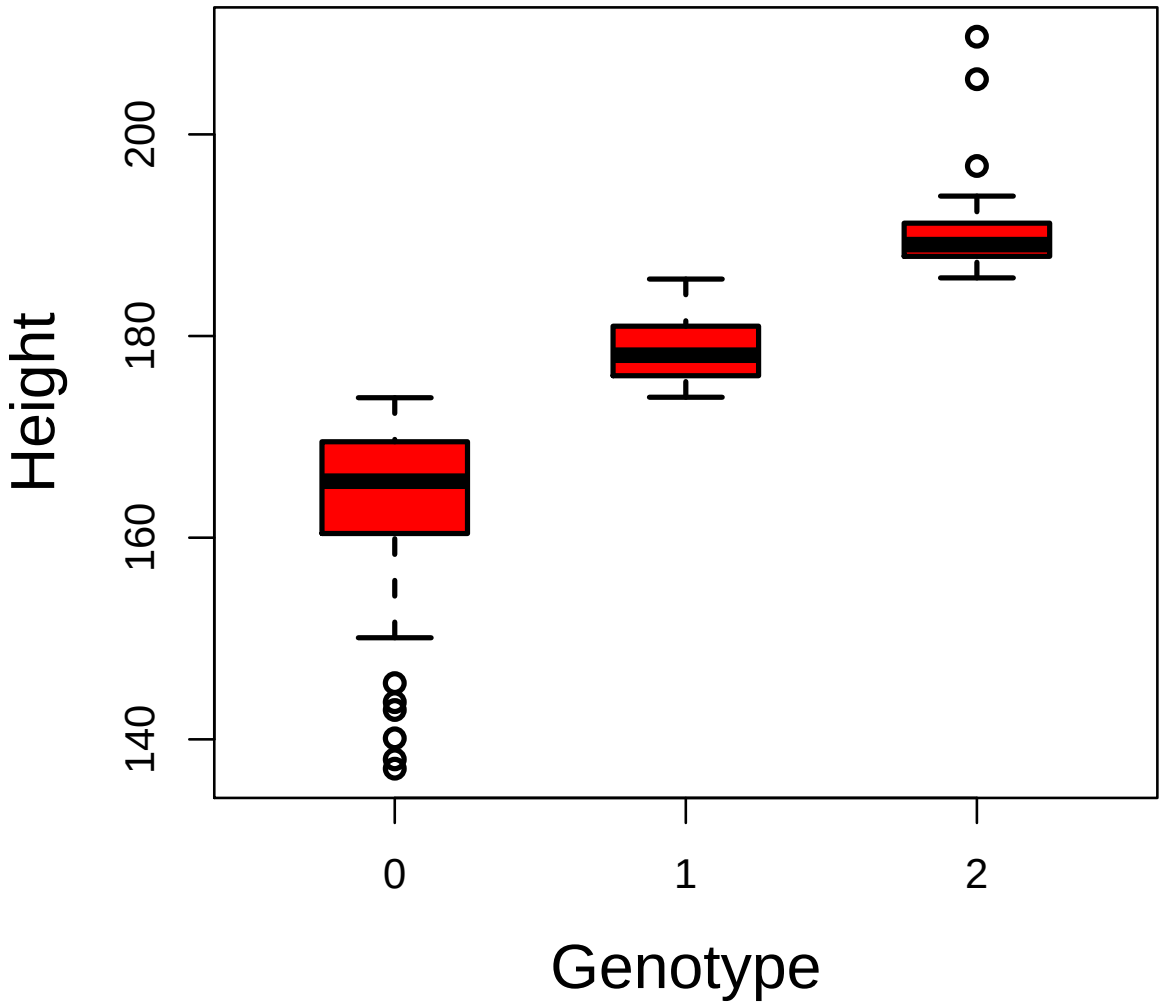
Example



Example - Linear regression



Example - ANOVA



Example - Linear regression

Call:
lm(formula = height ~ genotype)

Residuals:

Min	*1Q*	*Median*	*3Q*	*Max*
−27.4684	−3.3333	0.3393	4.4179	17.8228

Coefficients:

	Estimate	*Std.Error*	*tvalue*	*Pr(>|t|)*	
(*Intercept*)	164.5621	0.3090	532.5	$< 2e-16$	***
genotype	13.6526	0.4433	30.8	$< 2e-16$	***

*Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1*

Residual standard error: 5.831 on 498 degrees of freedom Multiple R-squared: 0.6558, Adjusted R-squared: 0.6551 F-statistic: 948.6 on 1 and 498 DF, p-value: ¡ 2.2e-16

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Example - ANOVA

$aov(height \sim genotype)$

Terms:

	Df	*SumSq*	*MeanSq*	*Fvalue*	$Pr(>F)$	
genotype	1	32257	32257	948.6	$< 2e-16$	$***$
Residuals	498	16934	34			

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