

ANOVA assumptions

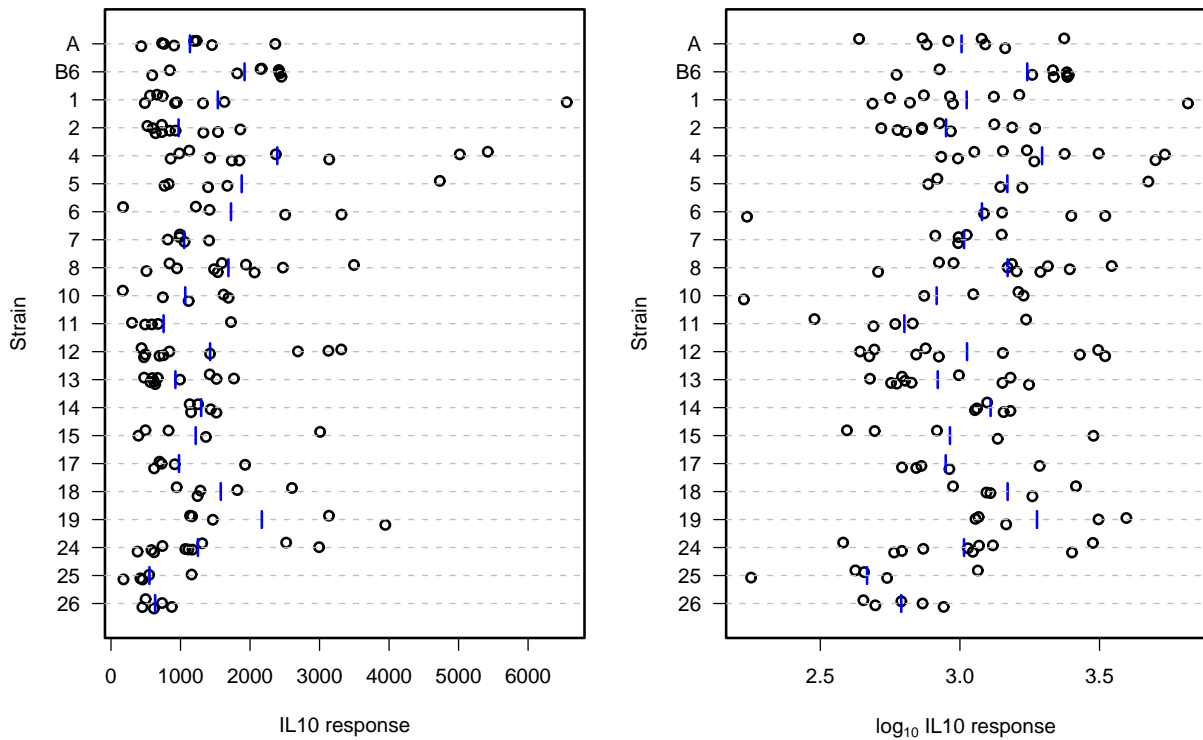
- Data in each group are a random sample from some population.
- Observations within groups are independent.
- Samples are independent.
- Underlying populations normally distributed.
- Underlying populations have the same variance.

Diagnostics

- QQ plot within each group
- QQ plot of all residuals, $y_{ti} - \bar{y}_t$.
- Plot residuals, $y_{ti} - \bar{y}_t$, against fitted values, \bar{y}_t .
- Plot SD versus mean for each group.

- Plot the residuals against other factors.
(e.g., order of measurements, weight or age of mouse).

Example



ANOVA Tables

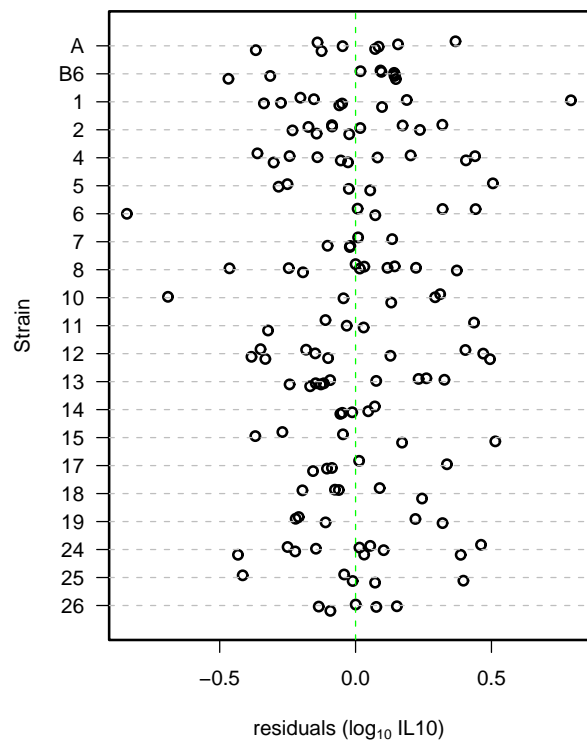
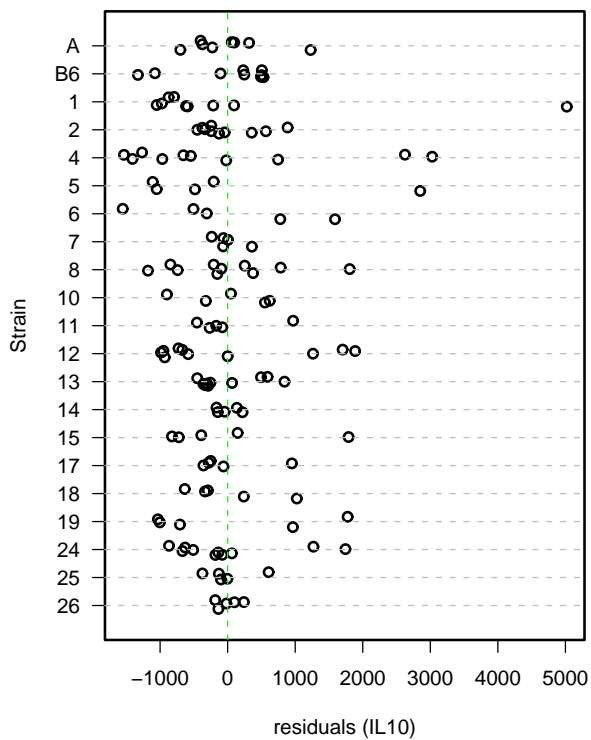
Original scale / 1000:

source	SS	df	MS	F	P-value
between strains	33	20	1.69	1.70	0.042
within strains	124	125	0.99		
total	157	145			

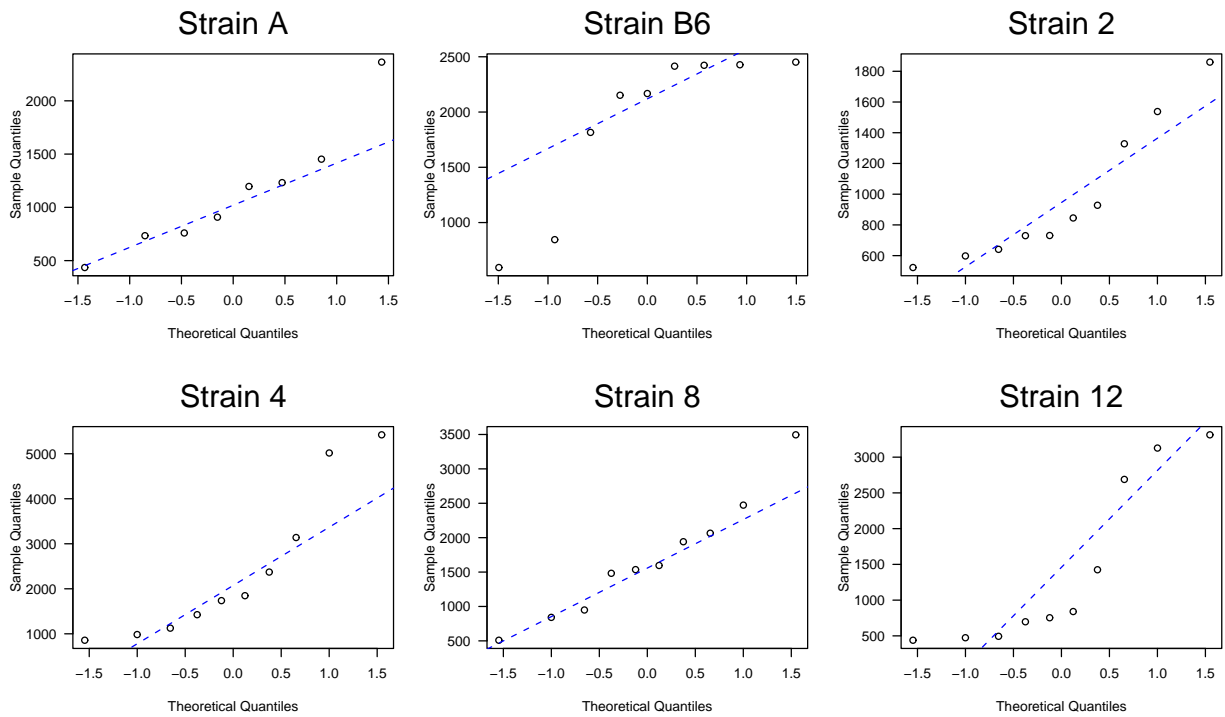
log₁₀ scale:

source	SS	df	MS	F	P
between strains	3.35	20	0.167	2.25	0.0036
within strains	9.29	125	0.074		
total	12.63	145			

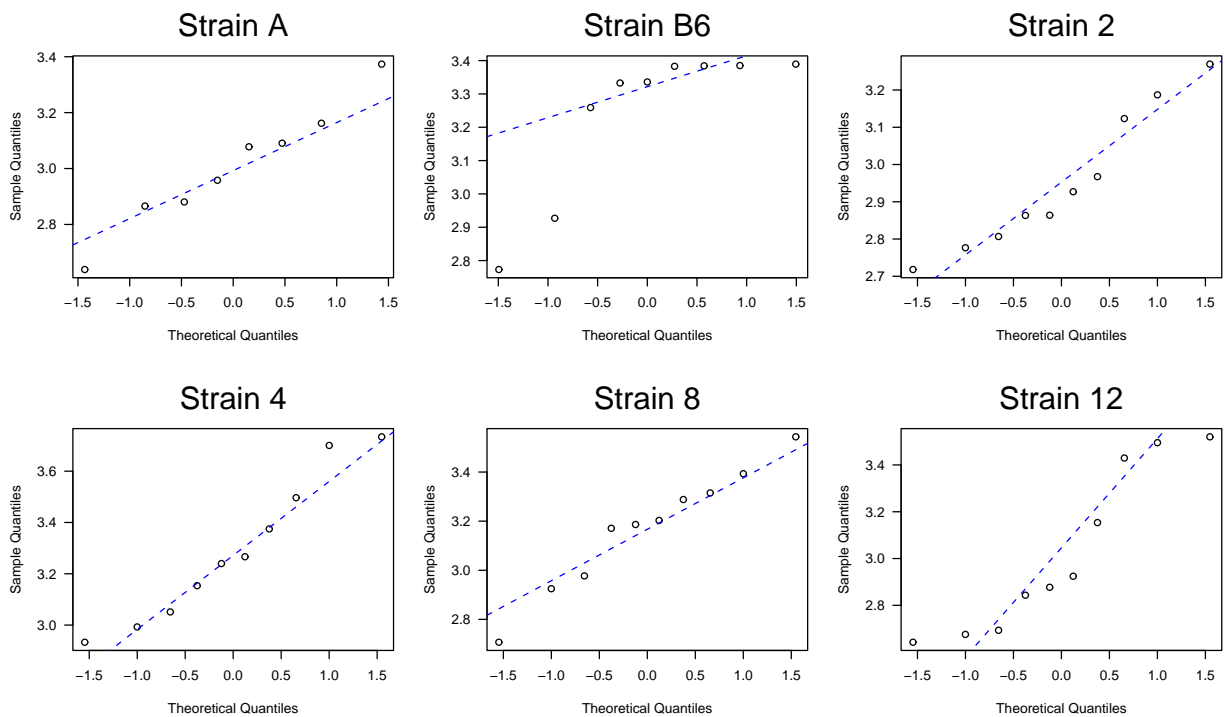
Residuals



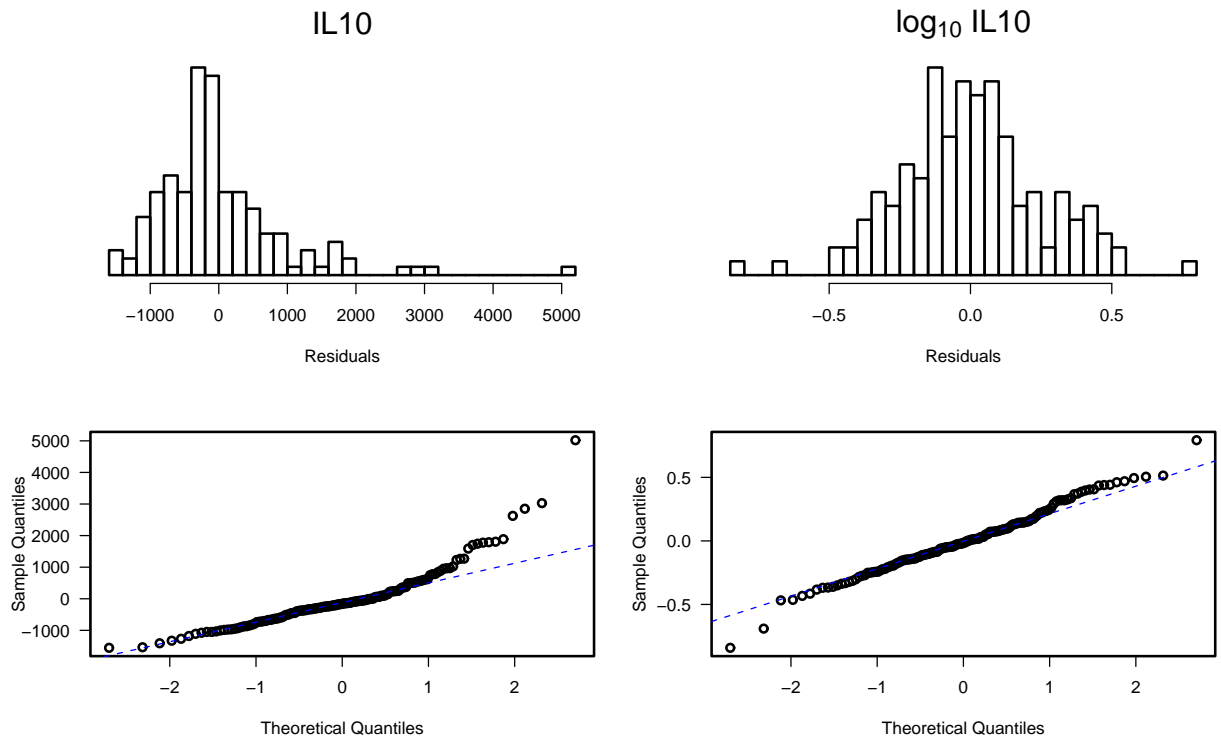
Within-group QQ-plots : IL10



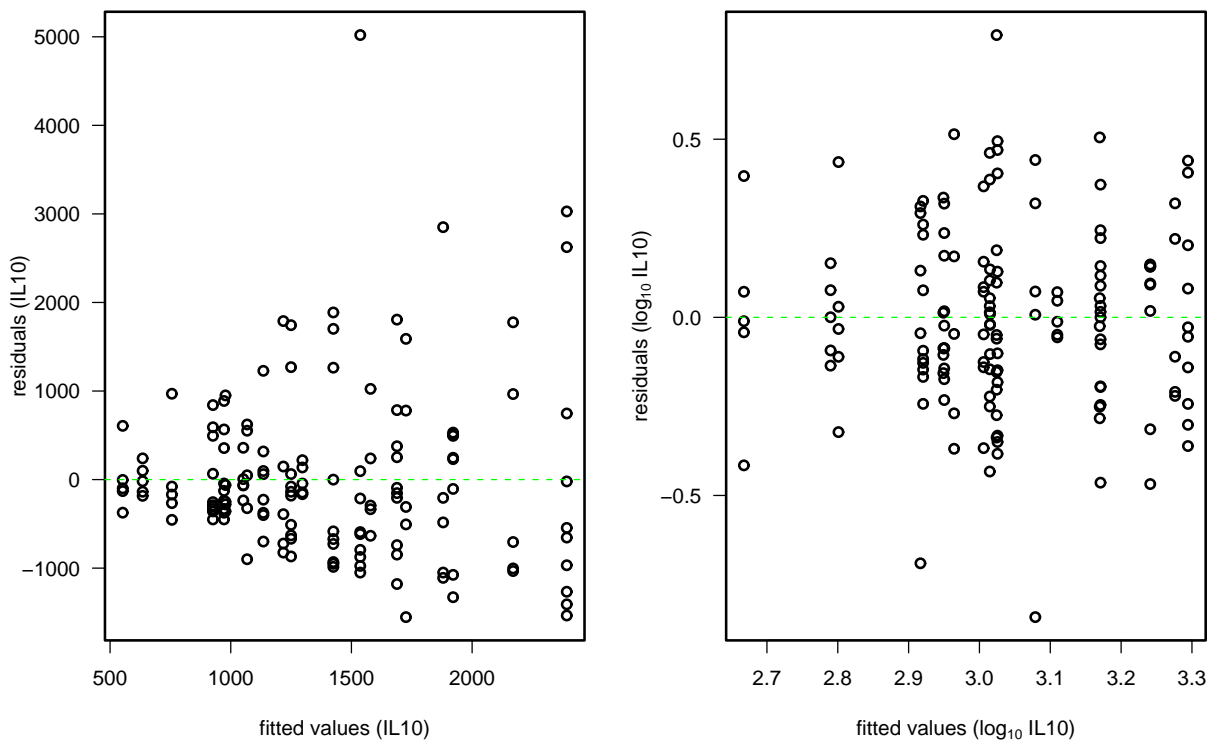
Within-group QQ-plots : \log_{10} IL10



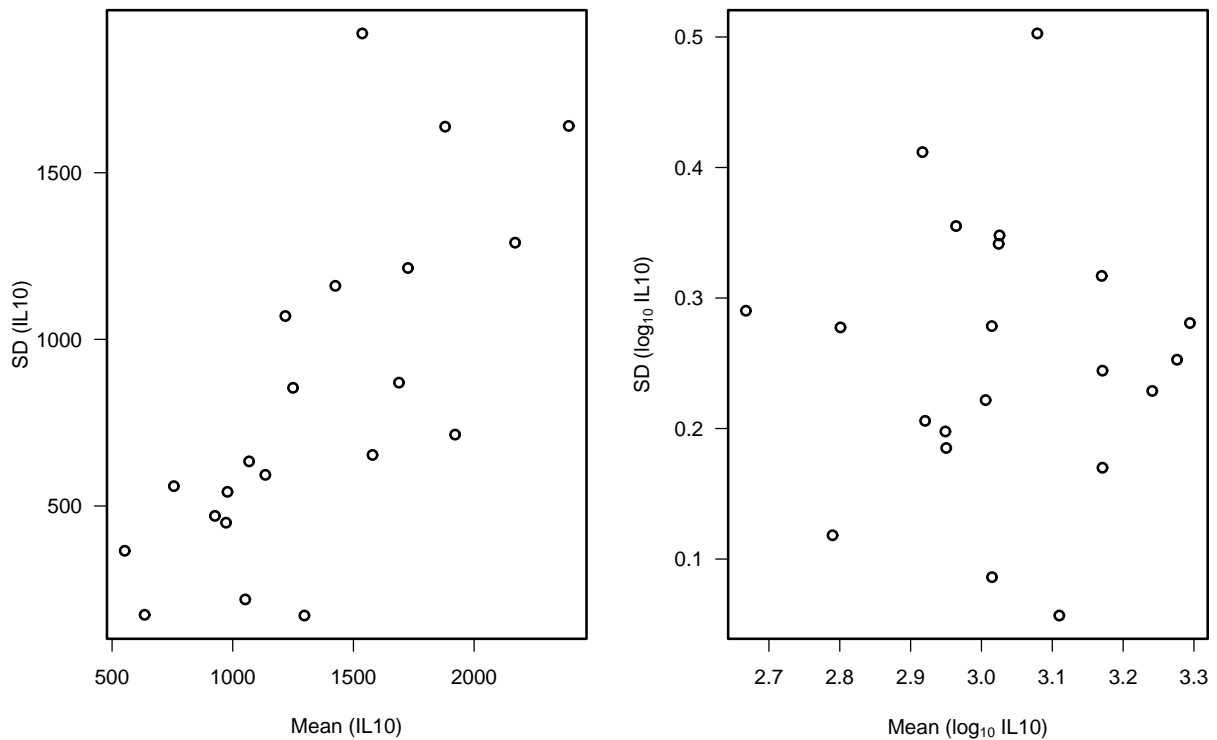
QQ plots of all residuals



Residuals vs fitted values



SDs vs means



Homogeneity of variances

One of the ANOVA assumptions was homogeneity of the group variances. This can formally be tested with [Bartlett's test](#).

Assume we have k treatment groups.

n_t number of cases in treatment group t .

N number of cases (overall).

Y_{ti} response i in treatment group t .

\bar{Y}_t average response in treatment group t .

S_t^2 the sample variance in treatment group t .

Bartlett's test

We want to test $H_0 : \sigma_1^2 = \dots = \sigma_k^2$ versus $H_a : H_0$ is false.

- Calculate the pooled sample variance:

$$S^2 = \frac{\sum_t (n_t - 1) \times S_t^2}{\sum_t (n_t - 1)} = \frac{\sum_t (n_t - 1) \times S_t^2}{N - k}$$

- Calculate the test statistic

$$X^2 = (N - k) \times \log(S^2) - \sum_t (n_t - 1) \times \log(S_t^2)$$

- Calculate the following correction factor:

$$C = 1 + \frac{1}{3(k-1)} \left[\sum_t \frac{1}{n_t - 1} - \frac{1}{\sum_t (n_t - 1)} \right]$$

If H_0 is true, then

$$X^2/C \sim \chi^2(\text{df}=k-1)$$

Example

- For the example data, there are 21 strains with between 5 and 10 observations per strain.
- The pooled sample variance on original scale / 1000 is 0.99.
- The pooled sample variance on \log_{10} scale is 0.074.
- The test statistics were 79.9 and 34.0.
- The correction factor ended up being 1.07.
- Thus we look at the values $79.9 / 1.07 = 74.8$ and $34.0 / 1.07 = 31.8$.
- Since there are 21 strains, we refer to the $\chi^2(\text{df} = 20)$ distribution.
- We end up with P-values of 2.9×10^{-8} and 0.045.

The R function `bartlett.test()` can be used to do these calculations.

Hartley's F-max test

In case that the number of observations are the same in every treatment group, there is a quick and dirty alternative to Bartlett's test, called **Hartley's F-max test**. For this test, simply compute

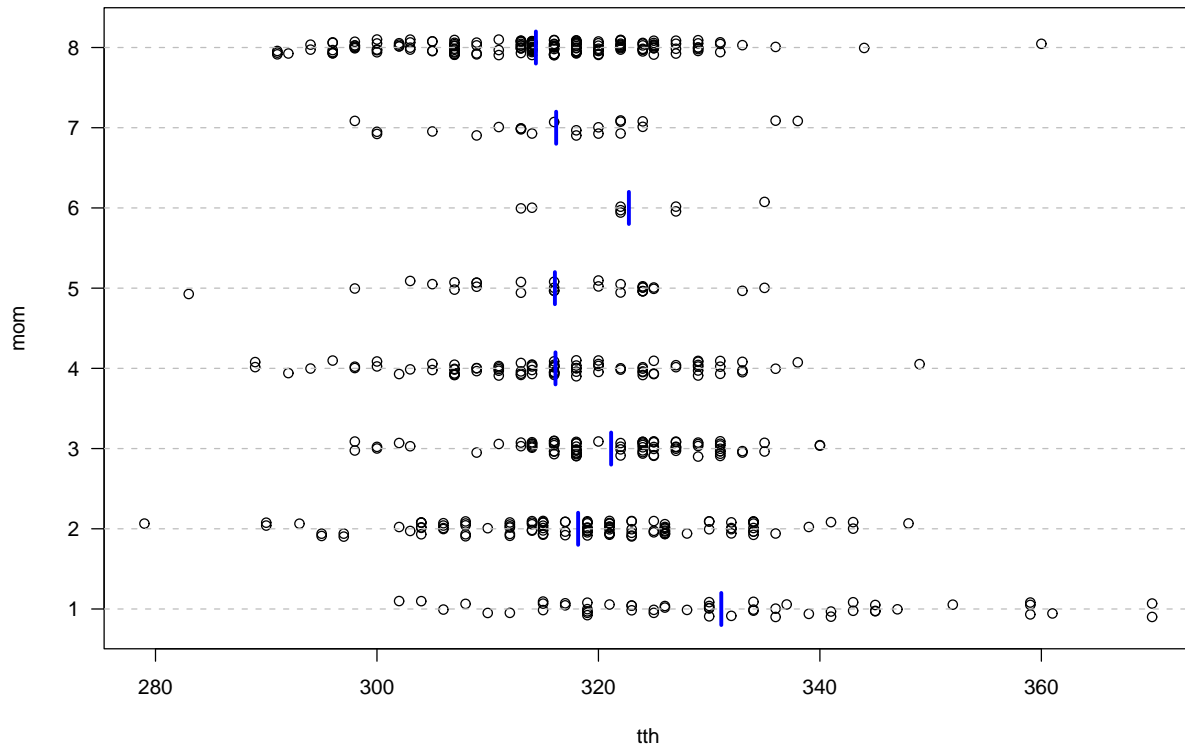
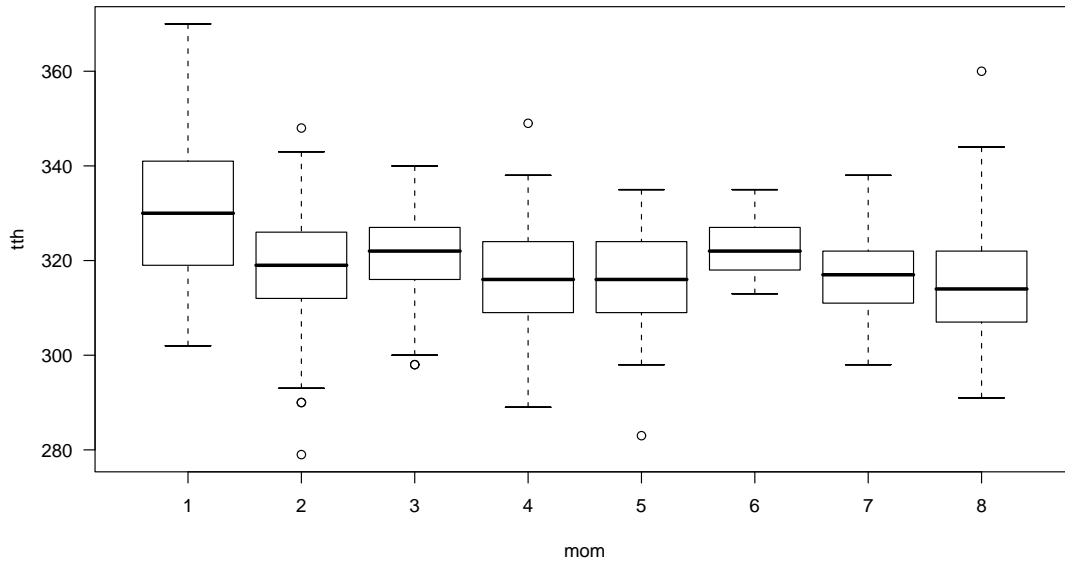
$$F_{\max} = \frac{\max(S_t^2)}{\min(S_t^2)}$$

There is a look-up table with critical values for F_{\max} , using the number of treatment groups (k) and the degrees of freedom associated with each of the group variances ($n_t - 1$).

Df	α	Number of treatment groups										
		2	3	4	5	6	7	8	9	10	11	12
2	0.05	39	87.5	142	202	266	333	403	475	550	626	704
	0.01	199	448	729	1036	1362	1705	2063	2432	2813	3204	3605
3	0.05	15.4	27.8	39.2	50.7	62	72.9	83.5	93.9	104	114	124
	0.01	47.5	85	120	151	184	216	249	281	310	337	361
4	0.05	9.6	15.5	20.6	25.2	29.5	33.6	37.5	41.4	44.6	48	51.4
	0.01	23.2	37	49	59	69	79	89	97	106	113	120
5	0.05	7.15	10.8	13.7	16.3	18.7	20.8	22.9	24.7	26.5	28.2	29.9
	0.01	14.9	22	28	33	38	42	46	50	54	57	60
6	0.05	5.82	8.38	10.4	12.1	13.7	15	16.3	17.5	18.6	19.7	20.7
	0.01	11.1	15.5	19.1	22	25	27	30	32	34	36	37
7	0.05	4.99	6.94	8.44	9.7	10.8	11.8	12.7	13.5	14.3	15.1	15.8
	0.01	8.89	12.1	14.5	16.5	18.4	20	22	23	24	26	27
8	0.05	4.43	6	7.18	8.12	9.03	9.8	10.5	11.1	11.7	12.2	12.7
	0.01	7.5	9.9	11.7	13.2	14.5	15.8	16.9	17.9	18.9	19.8	21
9	0.05	4.03	5.34	6.31	7.11	7.8	8.41	8.95	9.45	9.91	10.3	10.7
	0.01	6.54	8.5	9.9	11.1	12.1	13.1	13.9	14.7	15.3	16	16.6
10	0.05	3.72	4.85	5.67	6.34	6.92	7.42	7.87	8.28	8.66	9.01	9.34
	0.01	5.85	7.4	8.6	9.6	10.4	11.1	11.8	12.4	12.9	13.4	13.9
12	0.05	3.23	4.16	4.79	5.2	5.72	6.22	6.69	7.12	7.51	7.85	8.16
	0.01	5.25	6.8	7.8	8.6	9.3	10.0	10.6	11.1	11.5	12.0	12.4

Another example

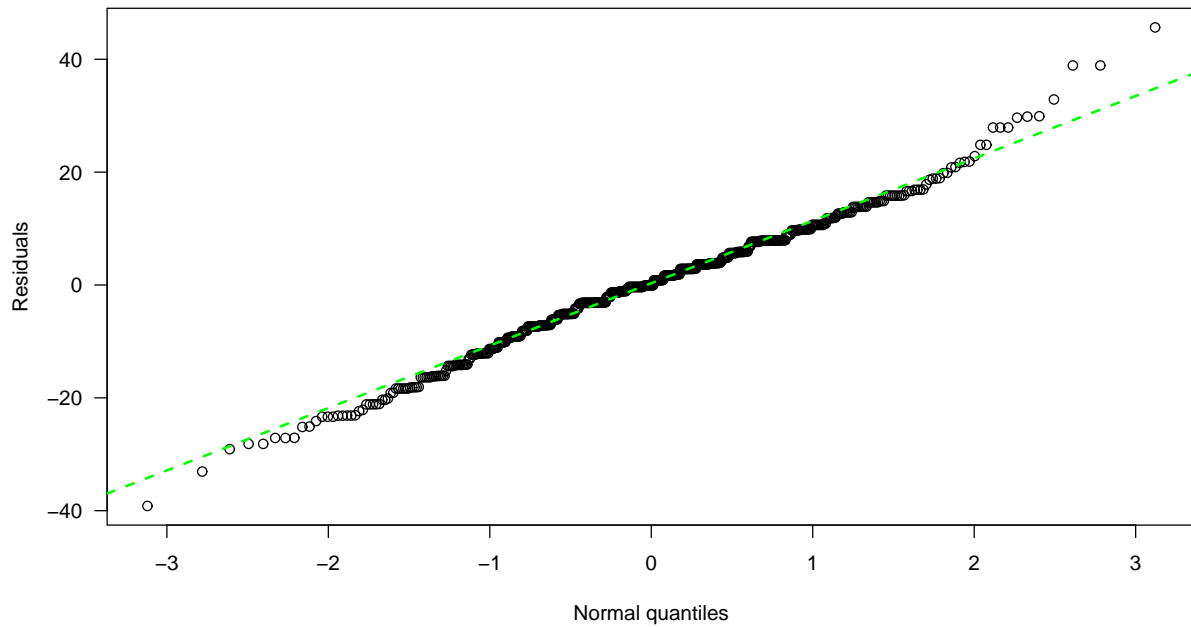
Rate of growth in fish eggs from different mothers



ANOVA Table

source	SS	df	MS	F	P-value
between moms	12757	7	1822	13.5	4e-16
within moms	73510	546	135		
total	86267	553			

QQ plot of all residuals



QQ plots within each group

