

LARVAL MEASUREMENT SUMMARY

treatment	replicate	larva	arm length (μm)
pH 7.8	A	1	405.6
pH 7.8	A	2	403.5
pH 7.8	A	3	423.1
pH 7.8	A	4	358.4
pH 7.8	A	5	487.8
pH 7.8	B	1	458.7
pH 7.8	B	2	486.7
pH 7.8	B	3	472
pH 7.8	B	4	450
pH 7.8	B	5	487.2
pH 7.8	C	1	485.4
pH 7.8	C	2	440.6
pH 7.8	C	3	543.2
pH 7.8	C	4	390.5
pH 7.8	C	5	487.6
pH 8.1	A	1	520.2
pH 8.1	A	2	531.1
pH 8.1	A	3	545.6
pH 8.1	A	4	586
pH 8.1	A	5	524.4
pH 8.1	B	1	499.7
pH 8.1	B	2	557.1
pH 8.1	B	3	547.6
pH 8.1	B	4	549.7
pH 8.1	B	5	492.4
pH 8.1	C	1	554.3
pH 8.1	C	2	577.6
pH 8.1	C	3	507.9
pH 8.1	C	4	517.9
pH 8.1	C	5	517.7

LARVAL MEASUREMENT SUMMARY

treatment	replicate	larva	arm length (μm)
pH 7.8	A	1	405.6
pH 7.8	A	2	403.5
pH 7.8	A	3	423.1
pH 7.8	A	4	358.4
pH 7.8	A	5	487.8
pH 7.8	B	1	458.7
pH 7.8	B	2	486.7
pH 7.8	B	3	472
pH 7.8	B	4	450
pH 7.8	B	5	487.2
pH 7.8	C	1	485.4
pH 7.8	C	2	440.6
pH 7.8	C	3	543.2
pH 7.8	C	4	390.5
pH 7.8	C	5	487.6
pH 8.1	A	1	520.2
pH 8.1	A	2	531.1
pH 8.1	A	3	545.6
pH 8.1	A	4	586
pH 8.1	A	5	524.4
pH 8.1	B	1	499.7
pH 8.1	B	2	557.1
pH 8.1	B	3	547.6
pH 8.1	B	4	549.7
pH 8.1	B	5	492.4
pH 8.1	C	1	554.3
pH 8.1	C	2	577.6
pH 8.1	C	3	507.9
pH 8.1	C	4	517.9
pH 8.1	C	5	517.7

REPLICATE MEANS

treatment	rep	mean arm length (μm)
pH 7.8	A	415.7
pH 7.8	B	470.9
pH 7.8	C	469.5
pH 8.1	A	541.5
pH 8.1	B	529.3
pH 8.1	C	535.1

TREATMENT MEANS

treatment	mean arm length (μm)	standard deviation	standard error of the mean
pH 7.8	452.0	48.5	28.0
pH 8.1	535.3	27.4	15.8

Standard deviation is a calculation of variation around the mean.

More info on standard deviation and how to calculate it:

<http://udel.edu/~mcdonald/statdispersion.html#stddev>

Standard error is another measure of variance around the mean, and is the standard deviation divided by the square root of the sample size.

(The sample size in our data is 3, since that is the number of replicate samples)

	pH 7.7	pH 8.1
repA	405.6	520.2
	403.5	531.1
	423.1	545.6
	358.4	586
	487.8	524.4
repB	458.7	499.7
	486.7	557.1
	472	547.6
	450	549.7
	487.2	492.4
repC	485.4	554.3
	440.6	577.6
	543.2	507.9
	390.5	517.9
	487.6	517.7

"rep" = replicate

Anova: Two-Factor With Replication *

SUMMARY	pH 7.7	pH 8.1	Total
<i>repA</i>			
Count	5	5	10
Sum	2078.4	2707.3	4785.7
Average	415.68	541.46	478.57
Variance	2196.827	712.828	5687.793
<i>repB</i>			
Count	5	5	10
Sum	2354.6	2646.5	5001.1
Average	470.92	529.3	500.11
Variance	275.547	940.415	1487.157
<i>repC</i>			
Count	5	5	10
Sum	2347.3	2675.4	5022.7
Average	469.46	535.08	502.27
Variance	3272.078	878.332	3040.733
<i>Total</i>			
Count	15	15	
Sum	6780.3	8029.2	
Average	452.02	535.28	
Variance	2349.115	749.7331	

ANOVA

Source of Variation	SS	df	MS	F	P-value	F crit
Replicate	3434.424	2	1717.212	1.244954	0.3058930	3.4028261
Treatment	51991.71	1	51991.71	37.69324	0.0000024	4.2596773
Interaction	6845.336	2	3422.668	2.481385	0.1048223	3.4028261
Within	33104.11	24	1379.338			
Total	95375.58	29				

* An ANOVA (or "Analysis of Variance") is a series of statistics used to compare the amount and sources of variation in a set of data. The simplest use of ANOVA is to compare the means of two or more groups (or treatments). In our case, we are comparing the mean arm length in larvae reared in two pH conditions.

The reason why we are using an ANOVA rather than a student t-test, is that the design of our experiment involves multiple individuals (5) within each replicate (3 jars) for both treatments (pH 7.7 and 8.1). T-tests can only be performed on comparisons between the means of two samples.

The ANOVA also lets us look at various possible sources of variation in our data, including variation within and among replicates, as well as interaction effects across replicates between treatments. And, of course, we can look at the treatments themselves as a sources of variation.

See also:

<http://udel.edu/~mcdonald/statnested.html>

Therefore, the two treatments (pH 7.7 and 8.1) are different from another with a p-value of **p<0.00001**