



The ANOVA table									
 The ana 	lysis i	s usually l	aid out in a	a table					
 For a one-way layout (where the response is assumed to vary according to grouping on one factor): 									
•									
Source	df	55	MS	F	p-val				
Source Treatment	df k-1	SS Σ(m _i -m)²	MS SST/(k-1)	F MST/MSE	p-val *				
Source Treatment Error	df k-1 n-k	$\frac{SS}{\Sigma(m_i-m)^2}$ $\frac{\Sigma(y_{ij}-m_i)^2}{\Sigma(y_i-m_i)^2}$	MS SST/(k-1) SSE/(n-k)	F MST/MSE	p-val *				















One-Way ANOVA Total degrees of freedom: N-1 Subdivided into df_B = g - 1 and df_W = N - g This gives the test statistic F F = B/W * N-g/g-1







- Why not start off doing separate (z or t) tests for each pair of samples? ...
- Testing the assumptions
- Which mean(s) is/are not equal
 - can do *post hoc* testing (pairwise *t*-tests, for example)
- Multiple comparisons (multiple testing)
- 'Data snooping'





- 2 experimental factors you randomize treatments to each unit
- 2 observational factors you cross-classify your populations into groups and get a sample from each population
- 1 experimental and 1 observational factor you get a sample of units from each population, then use randomization to assign levels of the experimental factor (treatments), separately within each sample





















More on model formulas

- The generic form is response ~ predictors
- The predictors can be numeric or factor
- Other symbols to create formulas with combinations of variables (e.g. interactions)
 - + to add more variables
 - to *leave out* variables
 - : to introduce *interactions* between two terms
 - * to include both interactions and the terms
 - (a*b is the same as a+b+a:b)
 - \mathbf{n} adds all terms including interactions up to order \mathbf{n}
 - I () treats what's in () as a *mathematical expression*

Interpreting R output								
> chicks.aov	<- a	aov(Weigl	nt ~ Hou	se + Prot	tein*LP*LS)		
> summary(chic	cks	.aov)						
	Df	Sum Sq	Mean Sq	F value	Pr(>F)			
House	1	708297	708297	15.8153	0.0021705	**		
Protein	1	373751	373751	8.3454	0.0147366	*		
LP	2	636283	318141	7.1037	0.0104535	*		
LS	1	1421553	1421553	31.7414	0.0001524	* * *		
Protein:LP	2	858158	429079	9.5808	0.0038964	**		
Protein:LS	1	7176	7176	0.1602	0.6966078			
LP:LS	2	308888	154444	3.4485	0.0687641	•		
Protein:LP:LS	2	50128	25064	0.5596	0.5868633			
Residuals	11	492640	44785					
Signif. codes:	0	***' 0.0	01 `**' 0	.01 `*' 0	.05 `.' 0.1	°'1		

Num ables d	er of g	ICO grou	ul a up n	nd gra neans:	phi	cal	analy	ysis
.0-	Lev	Level of protein		Groundnut 6676 6893	Soy 7 6	rbean 452 961	Mean 7064 7927	
-	Me	an	2	6719 6763	6	624 012	6671 6887	9 17
		G	-nut	Soy	Level of p		otein	Mean
Level o fish	of (6	537 989	6752 7273	0 6750 7379	$ \begin{array}{r} 1 \\ 6595 \\ 7259 \end{array} $	$ \begin{array}{r} 2 \\ 6588 \\ 6755 \end{array} $	6644 7131
Mean		6	763	7012	7064	6927	6671	6887







Typical deviations from straight line patterns

- Outliers
- Curvature at both ends (long or short tails)
- Convex/concave curvature (asymmetry)
- Horizontal segments, plateaus, gaps















