

Analysis of Variance (ANOVA)

Review: Two-Sample T-Test

- Comparison between two groups
 - ✓ (**two groups** in a categorical variable like Female/Male or Hispanic/non-Hispanic)
- Observed samples from each population
- Assume **underlying normality** in each population
- Use rank-based methods when not normal

Notes:

- Analysis of Variance (ANOVA) is an **extension** of the two-sample t-test.

Limitations of T-Test

- **Single** classification variable with only **two groups**
 - ✓ What if there are more than two groups?
 - ✓ What about the case of more than one categorical variable?

Notes:

- ANOVA enables testing with more than one **categorical variable** and more than two **groups**
 - Example: With ANOVA, we can study the effect of gender and race on salary at the **same** time.
- ANOVA enables you to compare the **mean** values for more than 3 levels

When do we use ANOVA model?

- Setting: **Continuous response & Categorical (grouping) variables**
- **Goal: Analyze the difference among groups and study the behaviors of response variable depending on grouping variable**
(E.g.) we are interested in blood sugar (continuous);
- Variable1: treatment (placebo/ treatment1/ treatment2)
- Variable2: diet (vegetarian/ vegan/ else)
- Variable3: exercise (<1 hr/ between 1 and 3 hrs/ >3 hrs)

Want to answer:

- Does type of treatment (or diet or exercise) affect **blood sugar**?
- If so, which treatment is the most efficient?
- Does diet help to decrease blood sugar?

Notes:

- **Continuous response** = variable of interest (ex. Salary, Blood Sugar)
- **Categorical Variables** = grouping variables (ex. Race / Gender, Treatment / Diet / Exercise)

ANOVA model

Kind of extension of **two-sample t-test**

- Compare means of two groups
- T-test can be applied only when **both** groups follow **normal** (parametric test)
- Two types of t-test under equal variance or unequal variance assumption



Similar in **ANOVA** test

- Can compare means from more than three groups
- Assumptions for classic ANOVA (again, parametric test):
 - ****Normality** for all groups, **equal variances**, **iid** sample**
- More specific statement at slide 11
- Modified test when groups have different variances (**welch's ANOVA**)

Notes:

- iid = independent samples
- Follows normal distribution? = **Classic ANOVA** | Doesn't follow normal distribution? = **Welch's ANOVA**

Definitions

- **One-way analysis of variance:** ANOVA based on a single categorical predictor variable
- **Two-way analysis of variance:** based on 2 independent categorical predictor variables
- **N-way analysis of variance:** based on n independent categorical variables

Notes:

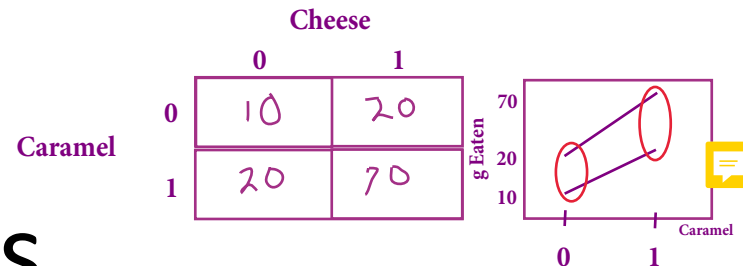
- One-way ANOVA = Salary based on Race
- Two-way ANOVA = Salary based on Gender and Race
- N-way ANOVA = Salary based on Gender, Race, and Age

Interaction (Synergy) Effect Example: Combination of Caramel and Cheese variables

- **Response:** How much popcorn that gets eaten (g / oz)
- **Cheese:** No cheese (Level 0) | Cheese (Level 1)
- **Caramel:** No caramel (Level 0) | Caramel (Level 1)

*Effect of one variable depends on the level of the other variable

* Parallel lines = no interaction = one variable does NOT depend on level of other variable



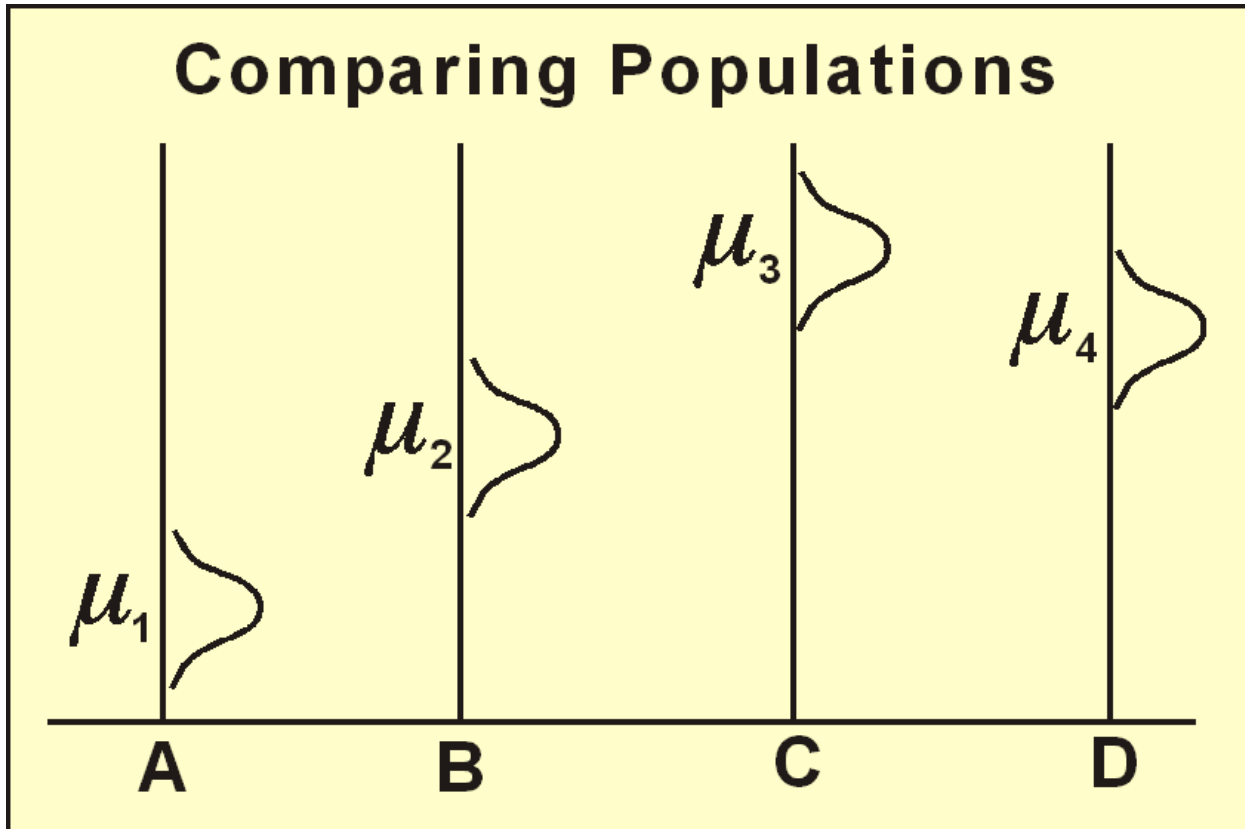
Definitions

- **Main effect:** effect of single categorical predictor
- **Interaction:** the combined effect of combination of categorical predictors -> **for example, synergy effect**
- **First-order interaction:** an interaction between two categorical predictors
- **N-th order interaction:** interaction of a categorical predictor with n other categorical predictors
 - **hard interpretation or potential overfitting issue. In practice, include them only when needed**
- **Balanced data:** data with an equal number of observations in each cell
- **Unbalanced data:** at least one cell has different number of observations

Notes:

- Salary Example:
 - Gender **main effect** or Race **main effect** (they effect salary **separately** depending on the level of Gender or Race)
 - Gender and Race **combined** effect on Salary (interaction effect)

ANOVA assumption overview



ANOVA Hypotheses

- Null Hypothesis: There are no mean differences between the groups on response
 - **H0: $\mu_1 = \mu_2 = \dots = \mu_g$,**
where g is the number of groups.
 - E.g., means of salary are same regardless of different education levels
- Alternate Hypothesis:
 - **H1: At least ONE of the group means is significantly different from the others in the population**
 - NOTE: But we do not know which group has larger or smaller mean

ANOVA Hypotheses

- For **the interactions**:
(for multi-way ANOVA like 2-way, 3-way)

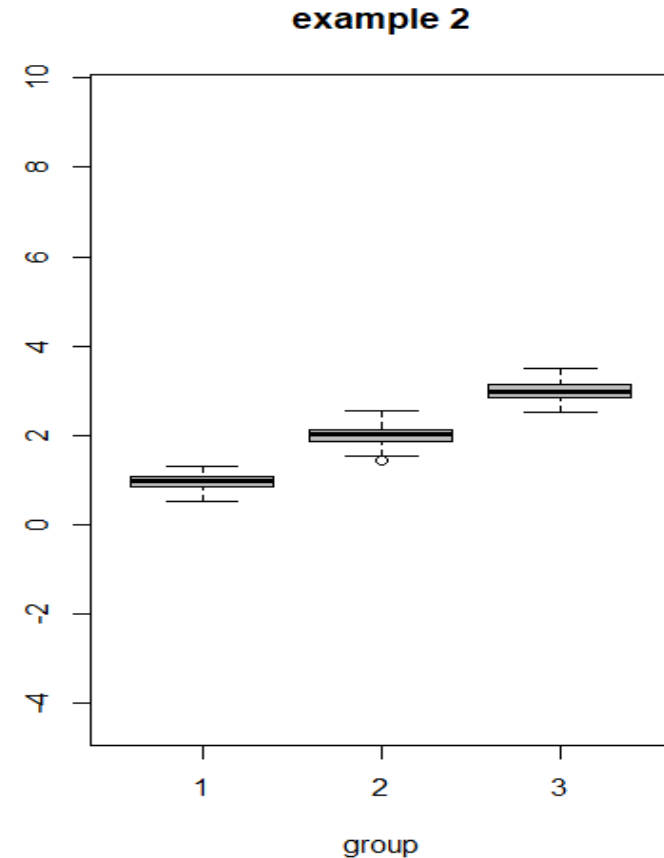
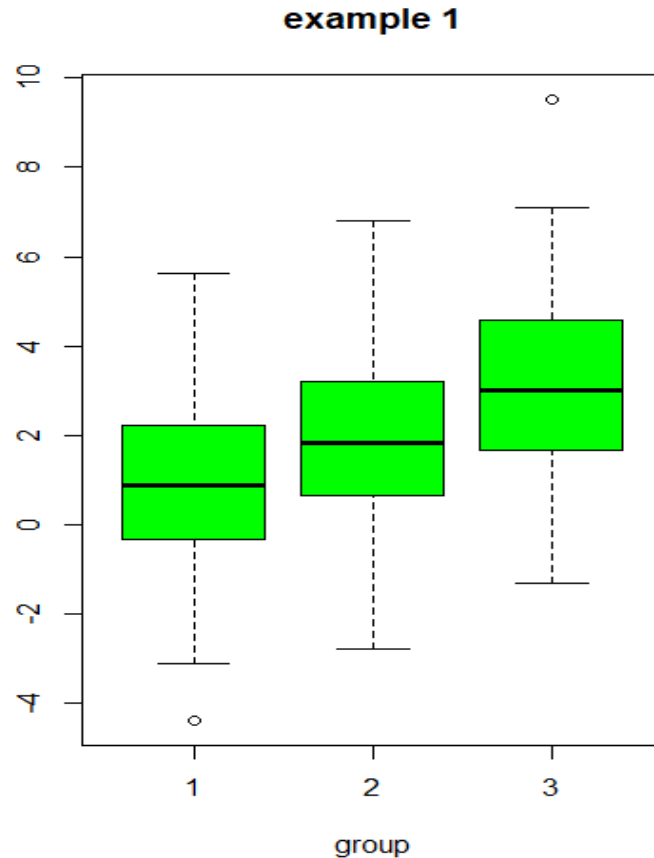
We can also test the null hypothesis for interactions.

- Null hypothesis:
H0: There is **no interaction** between independent variables in the population.
- Alternative hypothesis:
H1: There is **an interaction** between independent variables in the population.

Assumptions of ANOVA

- 1) The response (dependent) variable is **continuous**
- 2) Populations from which samples were drawn **follow normal distribution**
 - i.e., Each group should be normally distributed
 - ✓ Note: ANOVA relatively *robust* to violations of normality
- 3) Populations from which samples were drawn must have **equal variances** (Homogeneity of Variance)
 - ✓ Need to perform equal variance test before applying ANOVA
- 4) Observations must be **independent of one another**

The F test



- **Between group mean variation (differences)** are same for both examples
- How about **within group variation**?

The F test

- Use **F-test** when all assumptions are satisfied
- The F test uses the F statistic to determine if there are any significant main effects or interactions
- Formula and Intuition:
$$F = \text{Between groups variation} / \text{Within group variation}$$
- Make a conclusion based on p-values of F-test

The F test

- If the F-statistic is NOT statistically significant, then you are done and there is no reason to conduct additional analyses. No difference among groups is found.
- If the F-statistic is statistically significant:
 - All you know now is that there is **at least one mean that differs from the another**.
 - ✓ To determine which mean(s) differ, you need to conduct post-hoc test
 - ✓ Able to get the information which group has significantly larger of smaller mean value

Example: ToothGrowth

- Response: Tooth length (continuous variable)
- **Supplement: VC or OJ**
- **Dose: 0.5, 1 or 2**
 - ✓ Should be coded as a **factor** not as a numeric

Example: One-way ANOVA

- Install package “car”
- Perform analysis of variance of **Toothlength** as a function of **Dose**
 - I. Check balanced or unbalanced
 - II. Run one-way ANOVA with **aov()** or possibly, **lm()**
 - III. Check equal variance assumption – levene’s test
 - H_0 : all groups have the same variances vs.
Ha: at least one group has different variance
 - Could use Welch adjustment if equal variance assumption is not valid
 - IV. Check Normality assumption - check diagnostics plot
 - qq plot and residual plot
 - V. What is conclusion?

Example: One-way ANOVA

- ANOVA table interpretation
- R-Square value for predictive power of the model
- Significance of **Dose** as a predictive variable
- Conclusion about impact of **Dose** on tooth growth

One-way ANOVA example:

```
tooth$Dose= as.factor(tooth$Dose)
str(tooth)
```

```
## 'data.frame':    60 obs. of  3 variables:
## $ Toothlength: num  4.2 11.5 7.3 5.8 6.4 10 11.2 11.2 5.
2 7 ...
## $ Supplement : Factor w/ 2 levels "OJ","VC": 2 2 2 2 2 2
2 2 2 2 ...
## $ Dose       : Factor w/ 3 levels "0.5","1","2": 1 1 1 1
1 1 1 1 1 1 ...
```

- Balance or Unbalanced?

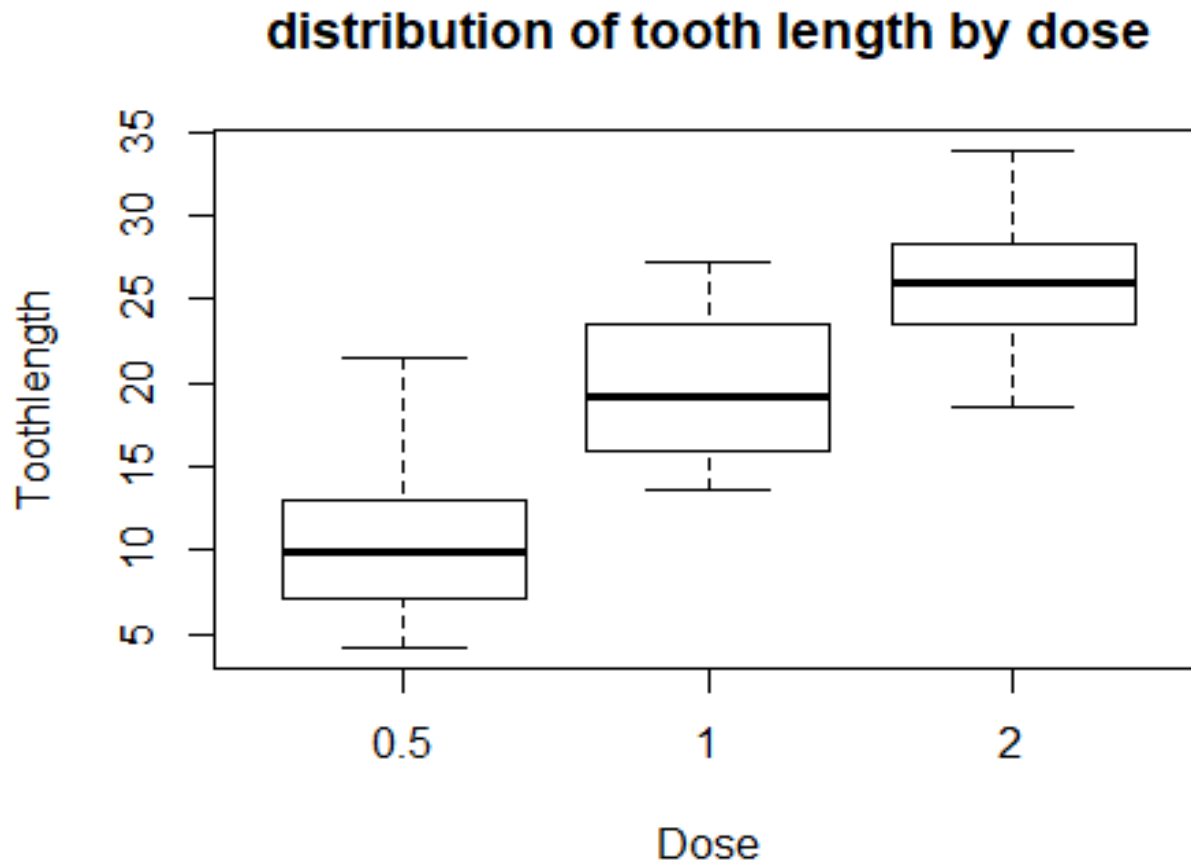
```
table(tooth$Dose); table(tooth$Supplement)
```

```
##
## 0.5    1    2
## 20   20   20
```

```
##
## OJ VC
## 30 30
```

One-way ANOVA example:

```
boxplot(Toothlength ~ Dose, data=tooth, main="distribution of tooth length by dose")
```




One-way ANOVA example:

```
aov.res= aov(Toothlength~Dose, data=tooth)
```

```
summary(aov.res)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Dose           2   2426    1213    67.42 9.53e-16 ***
## Residuals     57   1026      18
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Total sum of squares (3452)

(variation of Toothlength)

= sum of squares by Dose (2426)

(variation of Toothlength explained by Dose)

+ sum of squares by Error (1026)

(variation of Toothlength not be explained by the model)

H0: Dose has no effect on tooth growth
($\mu_{0.5} = \mu_1 = \mu_2$)

Ha: Does has an effect on tooth growth
(at least one group in Dose has different mean of tooth length)

One-way ANOVA example:

- To calculate **R-square**, need to run anova with **lm()**
- Results from **lm()** and **aov()** are exactly identical

```
lm.res= lm(Toothlength ~ Dose, data=tooth)
```

```
anova(lm.res)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Toothlength
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## Dose        2 2426.4  1213.2   67.416 9.533e-16 ***
```

```
## Residuals  57 1025.8    18.0
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(lm.res)$r.squared
```

```
## [1] 0.7028642
```

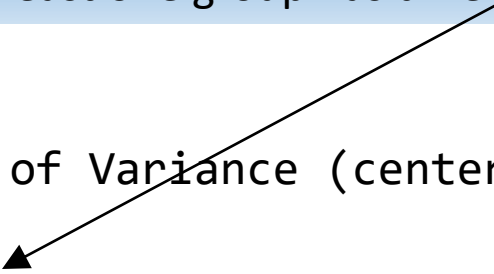
R-square: percentage of variation in a response variable that is explained by the model (Dose)

One-way ANOVA example:

H0: all groups in Dose have the same variance
Ha: at least one group has different variance

```
leveneTest(aov.res)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group    2  0.6457 0.5281
##           57
```



Welch's ANOVA – when homogeneity assumption is violated

```
oneway.test(Toothlength ~ Dose, data=tooth, var.equal=FALSE)

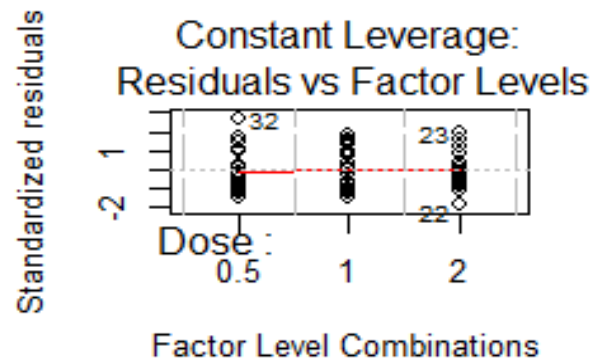
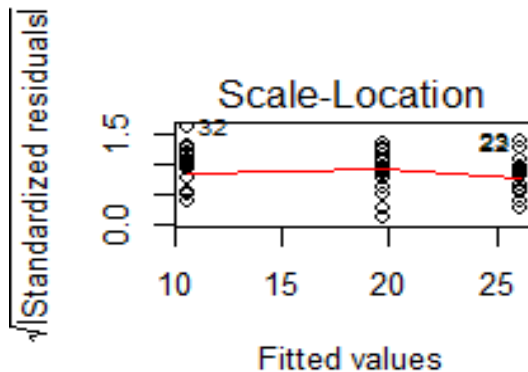
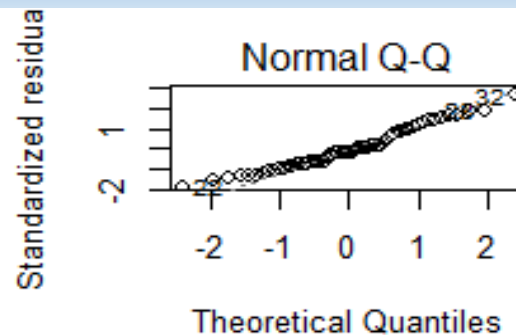
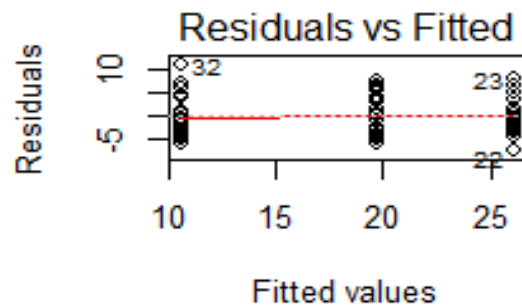
##
## One-way analysis of means (not assuming equal variances)
##
## data:  Toothlength and Dose
## F = 68.401, num df = 2.000, denom df = 37.743, p-value = 2.81
2e-13
```

One-way ANOVA example:

- Normality check – use diagnostics plot instead of rigorous shapiro test by group

```
par(mfrow=c(2,2))  
plot(aov.res)
```

If normal qq plot shows almost straight line, It supports normality assumption.



Multiple Comparisons

- Pairwise comparison with two-sample t-test
 - If there are 3 groups, there will be total 3 comparisons
 - (group1 vs. group2), (group1 vs. group3) and (group2 vs. group3)
- Making many comparisons at once!!
- Need to account for increased probability of making wrong decision
- Need correction in calculating p-value from t-test
 - **Scheffe method, Tukey's Method, etc.**
- **Should know how to interpret the result. What is null hypothesis and what kind of conclusion can we make?**

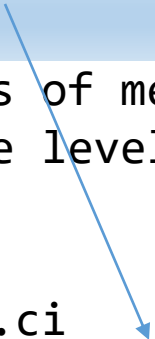
One-way ANOVA example:

```
ScheffeTest(aov.res)
```

Pairwise t-test with modified p-values:

$H_0: \mu_1 = \mu_{0.5}$ vs. $H_1: \mu_1 \neq \mu_{0.5}$

```
##
##   Posthoc multiple comparisons of means: Scheffe Test
##     95% family-wise confidence level
##
## $Dose
##           diff      lwr.ci      upr.ci      pval
## 1-0.5    9.130    5.758155  12.501845  4.3e-08 ***
## 2-0.5   15.495   12.123155  18.866845  1.2e-15 ***
## 2-1      6.365    2.993155   9.736845  7.6e-05 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Able to get information which pairs are significantly different

Final conclusion:

All three different Dose have different effect on tooth length and specifically, Dose 2 > Dose 1 > Dose 0.5

One-way ANOVA example:

```
TukeyHSD(aov.res)
```

```
##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = Toothlength ~ Dose, data = tooth)
##
## $Dose
##           diff           lwr           upr          p adj
## 1-0.5   9.130   5.901805 12.358195 0.00e+00
## 2-0.5  15.495  12.266805 18.723195 0.00e+00
## 2-1     6.365   3.136805  9.593195 4.25e-05
```

- Different method but we can interpret the output in the same way
- In practice, Scheffe and Tukey are popular

Example: Two-way ANOVA

- Two main effects (**Dose, Supplement**) and their interaction
- Interpret significance of model, terms, etc.
- Model validity check (check assumptions)
- Interpretation of Post-hoc test result

Two-way ANOVA example:

```
aov.res2 <- aov(Toothlength ~ Dose * Supplement , data = too  
th)
```

H0: Supplement has no effect on tooth growth

$$(\mu_{OJ} = \mu_{VC})$$

Ha: Supplement has an effect on tooth growth
(at least one group in supplement has
different mean of tooth length; $\mu_{OJ} \neq \mu_{VC}$)

```
summary(aov.res2)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
## Dose	2	2426.4	1213.2	92.000	< 2e-16	***
## Supplement	1	205.4	205.4	15.572	0.000231	***
## Dose:Supplement	2	108.3	54.2	4.107	0.021860	*
## Residuals	54	712.1	13.2			
## ---						
## Signif. codes:	0	'***'	0.001	'**'	0.01	'*' 0.05 '.' 0.1
' ' 1						

H0: no interaction between type and supplement

Ha: exist an interaction between type and supplement

Two-way ANOVA example:

```
leveneTest(aov.res2)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
```

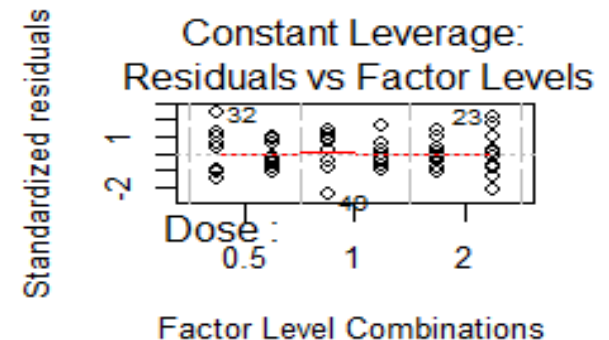
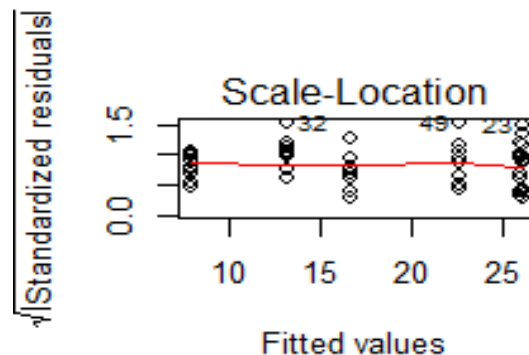
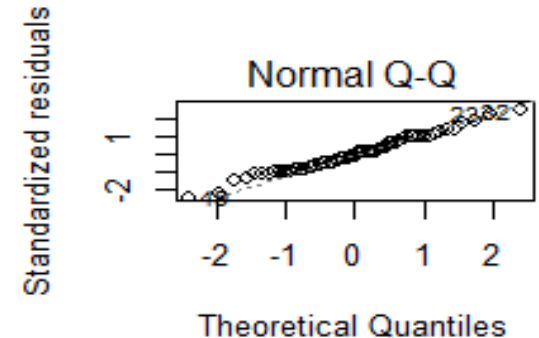
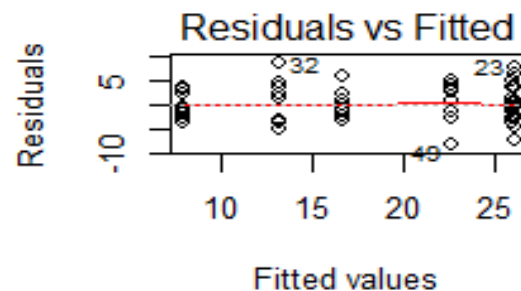
```
##           Df F value Pr(>F)
```

```
## group    5  1.7086 0.1484
```

```
##           54
```

```
par(mfrow=c(2,2))
```

```
plot(aov.res2)
```



Model validity check

- Homogeneity of variance?
- Normality?

Two-way ANOVA example:

```
lm.res2= lm(Toothlength ~ Dose * Supplement, data=tooth)
summary(lm.res2)$r.squared # R-square
## [1] 0.7937246
```

- Compare R-square from one-way ANOVA model (Dose)
- R-square always increases as the model gets bigger (larger number of independent variables)

Two-way ANOVA example:

```
ScheffeTest(aov.res2)
```

```
##
## Posthoc multiple comparisons of means: Scheffe Test
## 95% family-wise confidence level
##
## $Dose
##      diff      lwr.ci      upr.ci      pval
## 1-0.5  9.130    5.16355  13.09645  3.8e-08 *
## 2-0.5 15.495   11.52855  19.46145  3.9e-16 *
## 2-1     6.365    2.39855  10.33145  0.00014 *
##
## $Supplement
##      diff      lwr.ci      upr.ci      pval
## VC-OJ  -3.7   -6.938593  -0.4614069  0.0153 *
##
## $`Dose:Supplement`
##      diff      lwr.ci      upr.ci      pval
## 1:OJ-0.5:OJ  9.47    3.860592  15.0794079  5.5e-05 ***
..... (omitted)
```

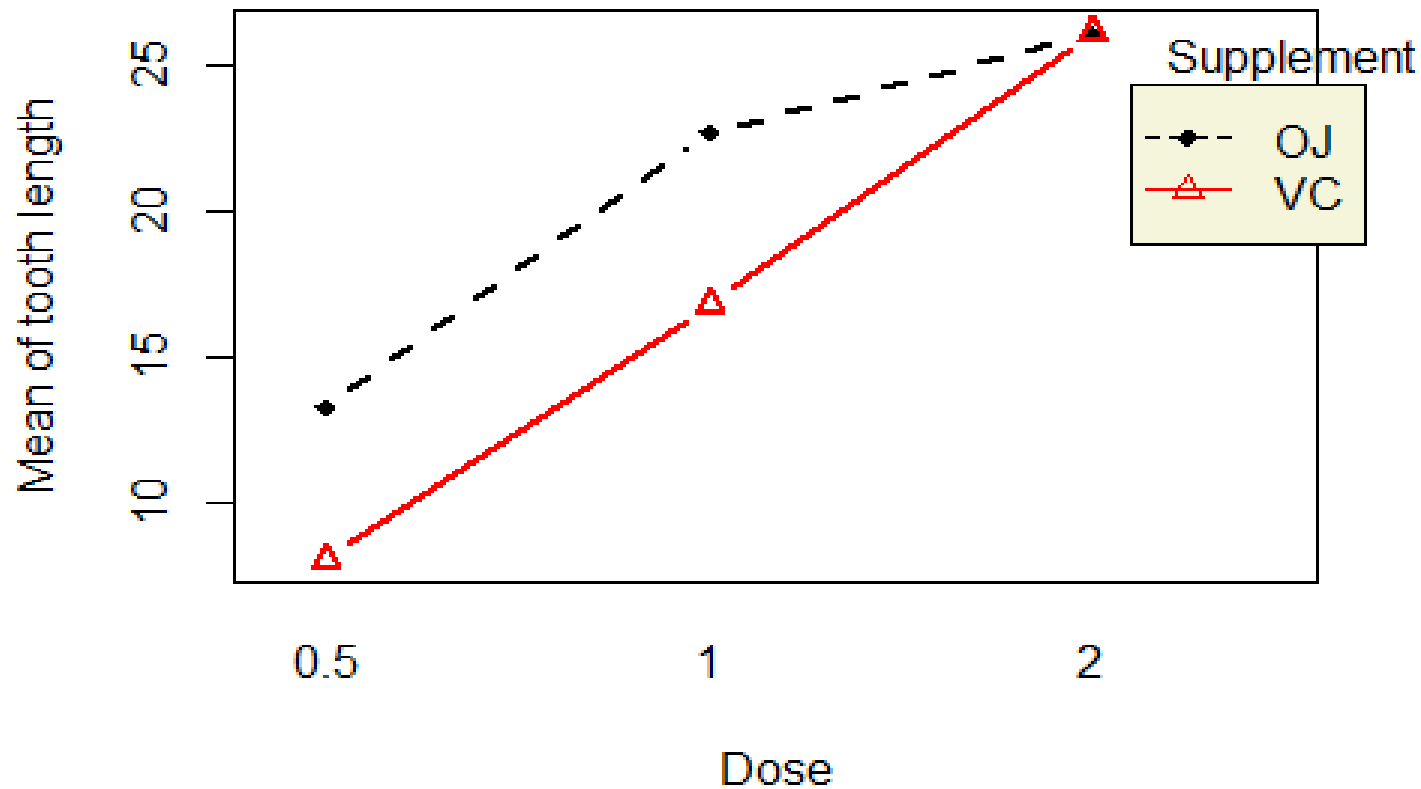
Focus on post-hoc analysis for main effects

Dose effect:
Dose2>Dose1>Dose0.5

Supplement effect:
VC < OJ

Two-way ANOVA example:

Interaction plot



Some notes:

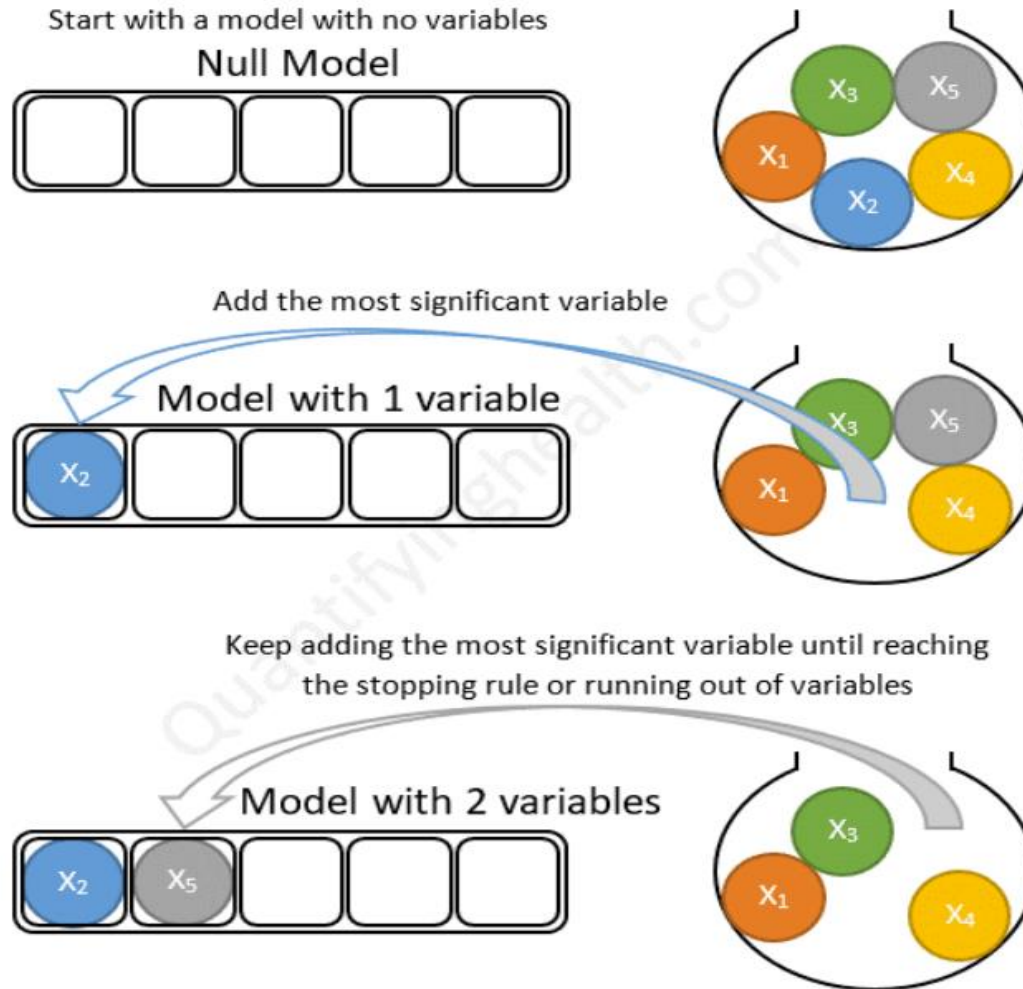
- Significance of model \leftrightarrow R-square
(0 or not) (prediction power)
- Model with higher R-square is always better?
 - What about the model with R-square = 100%?
 - What is the goal of the analysis?
- In post-hoc analysis, it can happen e.g.,
 $\mu_{0.5} = \mu_1$ and $\mu_{0.5} = \mu_2$ but $\mu_1 \neq \mu_2$
 - Why it happens and how can we make a conclusion?

Model Selection

- For the case of n-way ANOVA, the largest model with all possible interactions has $(2^n - 1)$ terms
- How to choose the best model?
 - Forward selection/ Backward elimination
 - Stepwise selection (Backward + Forward)

Forward selection

Forward stepwise selection example with 5 variables:



Forward selection

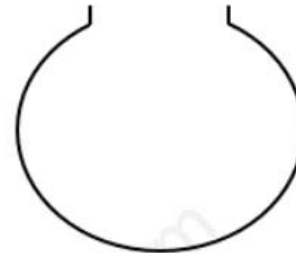
1. Begins with a model that contains no variables (called the Null Model)
 2. Then starts adding the most significant variables one after the other
 3. Until a pre-specified stopping rule is reached; Specifically, until there is no more variable which has p-value smaller than significance level (in general 0.05, but not necessarily)
- Once a variable is entered, there is no chance to be out
 - Final model may include insignificant variables

Backward elimination

Backward stepwise selection example with 5 variables:

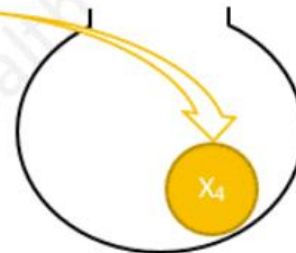
Start with a model that contains all the variables

Full Model



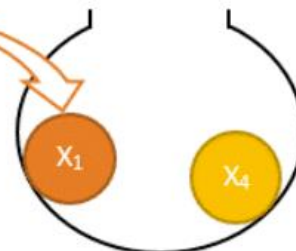
Remove the least significant variable

Model with 4 variables



Keep removing the least significant variable until reaching the stopping rule or running out of variables

Model with 3 variables



Backward elimination

1. Begins with a model that contains all variables under consideration (called the *Full Model*)
 2. Then starts removing the least significant variables one after the other
 3. Until a pre-specified stopping rule is reached – no more variable with p-value greater than significance level (0.05 but not necessarily)
- Once a variable is eliminated, there is no chance to be in
 - All variables in the final model are always significant

Model Selection

- What should we do if interaction term ($X1*X2$) is significant but main effect ($X1$ or $X2$) is not?
 - In practice, if main effects are not significant, we do not include interaction between them even if it is significant
 1. Forward/ backward/ stepwise selection on main effect model first
 2. Test interaction among significant main effects
- Use package “MASS” in R
 - Use AIC criteria instead of p-value, but idea is the same
 - AIC will be covered in linear regression

Practice

- Using the **grass.csv** , let's start with a model that includes **Method**, **Variety**, and **Group** as independent variables and **Yield** as the response variable.
- Perform model selection
 - Backward elimination manually
 - Forward selection manually
 - Stepwise selection using `stepAIC()` in package “MASS”
- Find the final model from each approach