

STAT021 Statistical Methods II

Lecture 5 One-way ANOVA Model

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Review: statistical modeling

- Variability
- ▶ How to quantify variability
- Standard deviation (SD)
 - Sample standard deviation
 - Degree of freedom
- Variance
- Sampling variability of statistics
 - Definition
 - Standard error (SE)
 - Example
 - Sample size

Outline

One-way ANOVA

▶ Data example: Fruit flies



- **▶** CHOOSE
 - Exploratory data analysis
 - Null and alternative model
- FIT
 - Parameter estimation
- ▶ ASSESS model
 - Triple decomposition
 - Sum of squares and degrees of freedom
 - Mean square
 - F statistic

Example: Fruit flies

Increased reproduction leads to shorter life spans for female fruit flies. But the question remained whether an increase in sexual activity would also reduce the life spans of male fruit flies. The researchers designed an experiment to answer this question. They randomly assigned 75 male fruit flies to one of the following three groups:

▶ 8 virgins: Each male fruit fly was assigned to live with 8 virgin female fruit flies.



▶ 1 virgin: Each male fruit fly was assigned to live with 1 virgin female fruit fly.



None: Each male fruit fly lived alone.



Example: Fruit flies

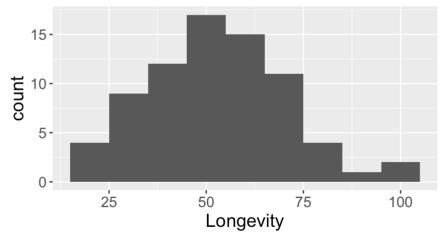
Questions of interest

- Is there statistically significant difference in life span (*Longevity*) of fruit flies among the three groups (*Treatment*)?
 - t tests are for two-group problems only
 - One-way ANOVA compares more than two population means
- ▶ If yes, which group(s) is(are) statistically significantly different?
 - Multiple pairwise comparisons

- ▶ **Response variable**: *Longevity*, quantitative; Mean: 53.0 days; SD: 17.9 days.
- **Explanatory variable**: *Treatment*, categorical; $n_1 = n_2 = n_3 = 25$

```
# install.packages("ggplot2") # install the package
library(ggplot2) # make the pacakge available
theme_update(text=element_text(size=15)) # set font size
ggplot(data=fly, aes(Longevity))+ # specify dataset and variable
geom_histogram(binwidth=10)+ # plot histogram
ggtitle("Histogram of Longevity") # main title
```

Histogram of Longevity



Relationship between Longevity and Treatment

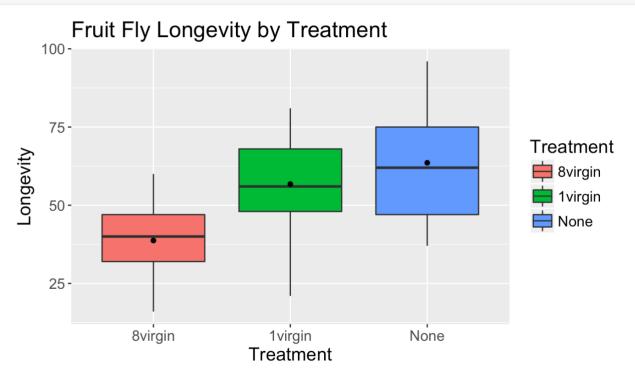
```
# define my own function to calcuate mean, sd and n at once
mysummary <- function(x){ c(mean=mean(x), sd=sd(x), n=length(x))}
# apply the function on Longevity by Treatment
aggregate(Longevity ~ Treatment, data=fly, FUN=mysummary)

## Treatment Longevity.mean Longevity.sd Longevity.n</pre>
```

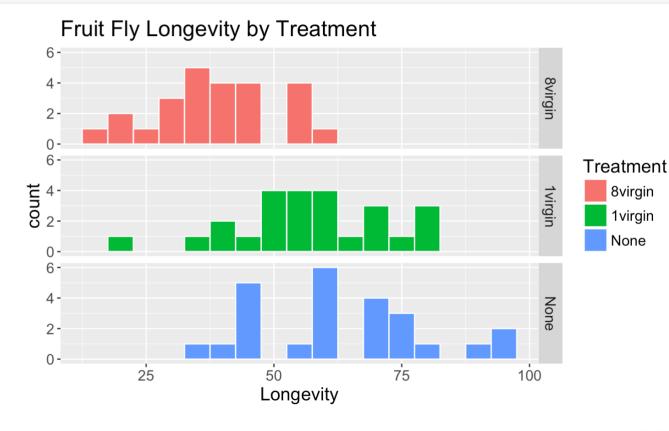
## 2 lvirgin 56.76000 14.92838 25.000	##		Treatment	Longevity.mean	Longevity.sa	ronderity.u
3	##	1	8virgin	38.72000	12.10207	25.00000
## 3 None 63.56000 16.45215 25.000	##	2	1virgin	56.76000	14.92838	25.00000
	##	3	None	63.56000	16.45215	25.00000

Treatment	Size	Mean	SD
8virgin	$n_1 = 25$	$\bar{y}_1 = 38.7$	$s_1 = 12.1$
1virgin	$n_2 = 25$	$\bar{y}_2 = 56.8$	$s_2 = 14.9$
None	$n_3 = 25$	$\bar{y}_3 = 63.6$	$s_3 = 16.5$
Overall	n = 75	$\bar{y} = 53.0$	s = 17.9

```
ggplot(fly, aes(x=Treatment, y=Longevity))+
  geom_boxplot(aes(fill=Treatment))+ # color by Treatment
  stat_summary(fun.y=mean, geom="point")+ # add the points of mean
  ggtitle("Fruit Fly Longevity by Treatment")
```



```
ggplot(fly, aes(Longevity))+
  geom histogram(binwidth=5, aes(fill=Treatment), color="white")+
  facet grid(Treatment ~ .)+ # plot histogram by Treatment
  ggtitle("Fruit Fly Longevity by Treatment")
```



- Based on exploratory data analysis, it seems that the three groups do have different means.
- Let's verify it using one-way ANOVA

8virgin

1virgin

None

Denote *Longevity* as *Y*

ANOVA model: each group has a unique population mean.

Data = Model + Error
$$Y = \mu_1 + \epsilon \text{ for the 8virgin group}$$

$$Y = \mu_2 + \epsilon \text{ for the 1virgin group}$$

$$Y = \mu_3 + \epsilon \text{ for the None group}$$

or in general

Data = Model + Error

$$Y = \mu_k + \epsilon$$
 for $k = 1, 2, 3$

- μ_k is the **group mean** of the *k*th group, where k = 1, 2, 3.
- $\epsilon \sim N(0, \sigma)$.

ANOVA model: each group has a unique population mean.

Data = Model + Error

$$Y = \mu_k + \epsilon$$

 $Y = \mu + \alpha_k + \epsilon$ for $k = 1, 2, 3$

- μ_k : **group mean** of the kth group. $\mu_k = \mu + \alpha_k$.
 - μ : **grand mean** of Y.
 - α_k : **group effect** of the *k*th group.

We are interested in whether

- $\mu_1 = \mu_2 = \mu_3 = \mu$, which is equivalent to
- $\alpha_1 = \alpha_2 = \alpha_3 = 0.$

ANOVA model: each group has a unique population mean.

Data = Model + Error

$$Y = \mu_k + \epsilon$$

 $Y = \mu + \alpha_k + \epsilon$ for $k = 1, 2, 3$ and $\epsilon \stackrel{iid}{\sim} N(0, \sigma)$

Model assumptions for the error term ϵ :

- \blacktriangleright Zero mean: mean of ϵ is 0.
- Equal variance: $Var(\epsilon) = \sigma^2$ is the same for all groups.
- Normal distribution: $\epsilon \sim N(0, \sigma)$.
- Independence: errors are independent of each other $\epsilon \stackrel{iid}{\sim} N(0, \sigma)$
 - \sim \overset{iid} {\sim}: independently and identically distributed.

We will compare the **ANOVA model** (each group has a unique population mean)

Data = Model + Error

$$Y = \mu_k + \epsilon$$

 $Y = \mu + \alpha_k + \epsilon$ for $k = 1, 2, 3$ and $\epsilon \stackrel{iid}{\sim} N(0, \sigma)$

to the **simpler/null model** (every group has the same population mean)

Data = Model + Error

$$Y = \mu + \epsilon \text{ for } \epsilon \stackrel{iid}{\sim} N(0, \sigma)$$

Null and alternative hypotheses of one-way ANOVA:

- $H_0: \alpha_1 = \alpha_2 = \alpha_3 = 0.$
- H_a : at least one $\alpha \neq 0$.

One-way ANOVA Model

One-Way Analysis of Variance Model

The **ANOVA model** for a quantitative response variable and one categorical explanatory variable with K values is

Data = Grand Mean + Group Effect + Error

$$Y = \mu + \alpha_k + \epsilon$$

where k refers to the specific category of the explanatory variable and $k = 1, 2, \dots, K$, and $\epsilon \stackrel{iid}{\sim} N(0, \sigma)$.

The null and alternative hypotheses for the ANOVA model are

$$H_0: \alpha_1 = \alpha_2 = \cdots = \alpha_K = 0;$$

 H_a : at least one $\alpha_k \neq 0$.

Null model:

$$Y = \mu + \epsilon \quad \text{for } \epsilon \stackrel{iid}{\sim} N(0, \sigma)$$

• Parameters: μ and σ .

ANOVA model:

$$Y = \mu_k + \epsilon$$

 $Y = \mu + \alpha_k + \epsilon \text{ for } k = 1, 2, 3 \text{ and } \epsilon \stackrel{iid}{\sim} N(0, \sigma)$

- Parameters: μ , α_k and σ .
 - Note: μ_k is also a parameter. Estimating μ and α_k is equivalent to estimating μ_k .

Data = Model + Error

Population:
$$Y = \mu_k + \epsilon$$
 for $\epsilon \stackrel{iid}{\sim} N(0, \sigma)$

Sample: $y = \bar{y}_k + \epsilon$

- *y*: observed values of *Y* (*Longevity*)
- \bar{y}_k : sample mean of *Y* (*Longevity*) for the *k*th group
- Residual $e = y \bar{y}_k$; standard deviation of e is the estimate of σ .

Null model:

$$Y = \mu + \epsilon \quad \text{for } \epsilon \stackrel{iid}{\sim} N(0, \sigma)$$

 $y = \bar{y} + e$

Residual $e = y - \bar{y}$; standard deviation of e is the estimate of σ .

Null model:

$$Y = \mu + \epsilon \text{ for } e \stackrel{iid}{\sim} N(0, \sigma)$$

 $y = \bar{y} + e$
 $y = \bar{y} + y - \bar{y}$
 $61 = 53.0 + 61 - 53.0$
 $53 = 53.0 + 53 - 53.0$
 $33 = 53.0 + 33 - 53.0$
...

- $\bar{y} = 53.0$
- ▶ SD of e = SD of $y \bar{y} = 17.9$
- Here we consider \bar{y} as the **predicted value of** y, which is usually denoted as \hat{y} . So in the null model, $\hat{y} = \bar{y}$.

ANOVA model:

$$Y = \mu_k + \epsilon \quad \text{for } k = 1, 2, \dots, K \text{ and } \epsilon \stackrel{iid}{\sim} N(0, \sigma)$$
 $Y = \mu + \alpha_k + \epsilon$
 $y = \bar{y}_k + \epsilon$
 $y = \bar{y} + \bar{y}_k - \bar{y} + y - \bar{y}_k$

- The estimate of μ is sample mean \bar{y}
- The estimate of α_k is sample group effect $\bar{y}_k \bar{y}$
- $e = y \bar{y}_k$
- In the ANOVA model, $\hat{y} = \bar{y}_k$.

ANOVA model:

$$Y = \mu_k + \epsilon \quad \text{for } k = 1, 2, \dots, K \text{ and } \epsilon \stackrel{iid}{\sim} N(0, \sigma)$$
 $Y = \mu + \alpha_k + \epsilon$
 $y = \bar{y}_k + \epsilon$
 $y = \bar{y} + \bar{y}_k - \bar{y} + y - \bar{y}_k$

- Froup mean: $\bar{y}_1 = 63.6$, $\bar{y}_2 = 56.8$, $\bar{y}_3 = 38.7$
- Grand mean: $\bar{y} = 53.0$
- Froup effect: $\bar{y}_1 \bar{y} = 10.6$, $\bar{y}_2 \bar{y} = 13.8$, $\bar{y}_3 \bar{y} = -14.3$

Null model

ANOVA model

		$Y = \mu$	$Y = \mu + \epsilon$		$Y = \mu + \alpha_k + \epsilon$		
Treatment	Observed	Predicted	Residual	Predicted	Residual		
Treatment	У	$\hat{y} = \bar{y}$	$e = y - \bar{y}$	$\hat{y} = \bar{y}_k$	$e = y - \bar{y}_k$		
8virgin	33	53.0	-20.0	38.7	-5.7		
8virgin	26	53.0	-27.0	38.7	-12.7		
1virgin	53	53.0	0.0	56.8	-3.8		
1virgin	60	53.0	7.0	56.8	3.2		
None	61	53.0	8.0	63.6	-2.6		
None	71	53.0	18.0	63.6	7.4		
•••	•••	•••	•••	•••	•••		

In general, the ANOVA model has smaller residuals (in absolute value) than the null model.

Data	=	Grand Mean	+	Group Effect	+	Error
Y	=	μ	+	$lpha_k$	+	ϵ
У	=	\bar{y}	+	$\bar{y}_k - \bar{y}$	+	$y - \bar{y}_k$
33	=	53.0	+	-14.3	+	-5.7
26	=	53.0	+	-14.3	+	-12.7
53	=	53.0	+	3.8	+	-3.8
60	=	53.0	+	3.8	+	3.2
61	=	53.0	+	10.6	+	-2.6
71	=	53.0	+	10.6	+	7.4
• • •		↑		↑		↑
	,	No variability	Variability between groups		Variability within groups	

Total variability in data

Variability of the null model residuals

Variability from the group effects

Variability explained by the ANOVA model

Variability in the residuals

Variability left in the ANOVA model residuals

- ▶ Thus, the ANOVA method analyzes the variability in the data and measures how it can be explained by the explanatory variable.
- ▶ Specifically, the ANOVA method compares the average variability explained by the model to the average variability left in the residuals.
 - If the ratio is large, the ANOVA model explained a lot variability that was left in the null model residuals. ANOVA model is better than the null model.
 - If the ratio is small, the ANOVA model still cannot explain the variability that was left in the null model residuals. ANOVA model is no better than the null model.
- ▶ How to quantify the *average* variability?
- It involves the concept of **degree of freedom**: the number of values in the final calculation of a statistic that are free to vary.

Data

$$y - \bar{y} = \bar{y}_k - \bar{y} + y - \bar{y}_k$$

Sum of squares

$$SSTotal = SSGroup + SSE$$

$$\sum (y - \bar{y})^2 = \sum (\bar{y}_k - \bar{y})^2 + \sum (y - \bar{y}_k)^2$$

Degrees of freedom

$$df_{Total} = df_{Group} + df_{Error}$$

of $y - 1 = \#$ of groups $-1 + \#$ of $y - \#$ of groups $n - 1 = K - 1 + n - K$
 $75 - 1 = 3 - 1 + 75 - 3$

ASSESS model: Mean square

Average variability: Mean square

Mean Square =
$$\frac{\text{Sum of Squares}}{\text{Degree of Freedom}}$$

$$MSGroup = \frac{SSGroup}{df_{Group}} = \frac{\sum (\bar{y}_k - \bar{y})^2}{K - 1}$$

$$MSE = \frac{SSE}{df_{Error}} = \frac{\sum (y - \bar{y}_k)^2}{n - K}$$

- MSE, mean square error, is the estimate of σ^2 (or \sqrt{MSE} is the estimate of σ)
- We denote the estimate of σ as $\hat{\sigma}$.

ASSESS model: F statistic

The ANOVA method compares the average variability explained by the model to the average variability left in the residuals using the *F* statistic

$$F = \frac{MSGroups}{MSE}$$

- F is large: the ANOVA model is better than the null model. The groups have significantly different means.
- F is small: the ANOVA model is NOT better than the null model. The group means are not that different.
- For our fruit fly example, F = 19.31. Do you consider it to be large enough for us to say the ANOVA model is better than the null?

Summary

- Data example: Fruit flies
- **▶** CHOOSE
 - Exploratory data analysis
 - Null and alternative model $Y = \mu + \epsilon$ vs. $Y = \mu + \alpha_k + \epsilon$
- FIT
 - Parameter estimation
- ▶ ASSESS model
 - Triple decomposition
 - Sum of squares and degrees of freedom
 - Mean square
 - F statistic