

ANOVA Pairwise Comparisons

Stat 120

May 18 2022

Post-ANOVA

- Inference **AFTER** doing **ANOVA** to compare means for several groups:
 - Confidence interval for a single mean
 - Confidence interval for a difference in two means
 - Pairwise t-test for a difference in two means

ANOVA for Difference in Means

- **Data:** Random samples of size n_1, n_2, \dots, n_k from each of k populations (or groups)
- **Summary statistics:**
 - Sample mean for each group
 - Std. dev. for each group
 - Mean and std. dev. for all values

ANOVA for Difference in Means

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$$

H_a : at least one μ_i is different

- **Conditions:** Similar variability AND either sample sizes in each group are large (each $n_i \geq 30$) OR the data are relatively normally distributed

Cuckoo Birds

- Cuckoo birds lay their eggs in the nests of other birds
- When the cuckoo baby hatches, it kicks out all the original eggs/babies
- If the cuckoo is lucky, the mother will raise the cuckoo as if it were her own
 - Do cuckoo bird eggs found in nests of different species differ in size?



Cuckoo bird in nest

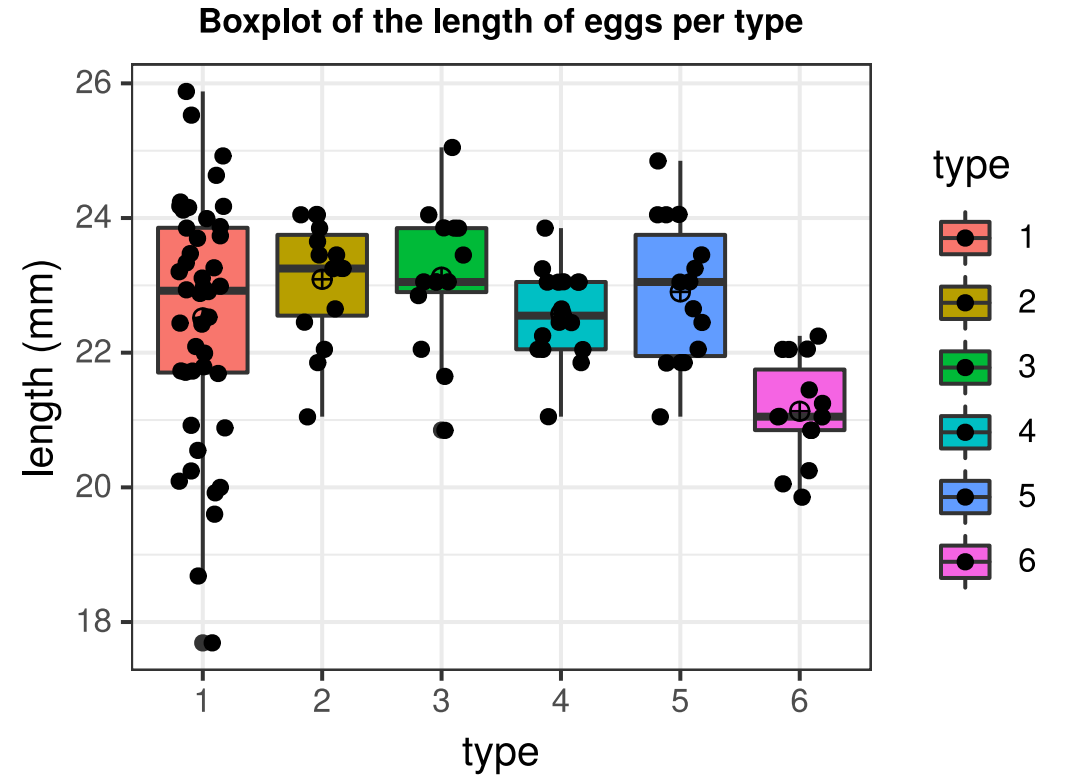
Cuckoo Dataset

- **cuckoo** dataset contains information on 120 Cuckoo eggs, obtained from randomly selected "foster" nests.
- researchers have measured the **length** (in mm) and established the **type** (species) of foster parent.

- **type=1**: Meadow pipit
- **type=2**: Tree pipit
- **type=3**: Dunnock
- **type=4**: European robin
- **type=5**: White wagtail
- **type=6**: Eurasian wren

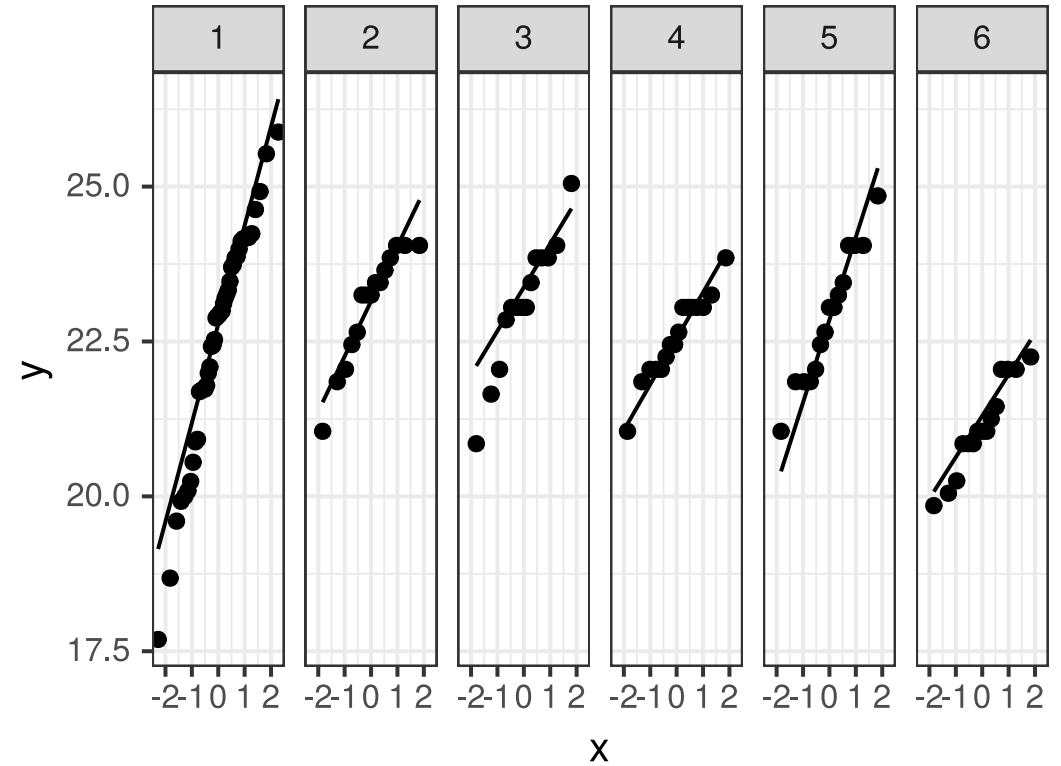
Side-by-side Boxplot (1a)

```
cuckoo %>%
  ggplot(aes(x=type,y=length,fill=type)) +
  theme_bw() +
  geom_boxplot() +
  geom_jitter(width = 0.2) +
  labs(title = "Boxplot of the length of eggs per type",
       y = "length (mm)",
       x = "type") +
  stat_summary(fun=mean, geom="point", shape=10,
              size=2, color="black", fill="black") +
  theme(plot.title = element_text(hjust=0.5, size=9,
                                  face='bold'))
```



Approximate normality in groups (1b)

```
cuckoo %>%  
  ggplot(aes(sample=length)) +  
  geom_qq() +  
  geom_qq_line() +  
  facet_grid(~type) +  
  theme_bw()
```



Fitting ANOVA (1c)

```
fit_anova <- aov(length~type, cuckoo)
summary(fit_anova)
```

```
              Df Sum Sq Mean Sq F value    Pr(>F)
type              5   41.12    8.223     4.713 0.000602 ***
Residuals       113  197.18    1.745
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Since the **p-value** is very small, at the significance level of 5%, we have sufficient evidence to conclude that the mean egg length for at least one bird type is **different** from the mean egg length in at least one other bird type.

But which of the species are different?

Inference after ANOVA

- Compute a CI for any μ_i
- Compute a CI for $\mu_i - \mu_j$
- Pairwise t-test for difference in means

$$H_0 : \mu_i = \mu_j \text{ vs. } H_a : \mu_i \neq \mu_j$$

- Use the usual procedures except:
 - Estimate any σ with the pooled standard deviation: \sqrt{MSE}
 - Use the error degrees of freedom for any t-values

Inference after ANOVA

Compute a CI for any μ_i

- The usual procedure:

$$\bar{x}_i \pm t^* \frac{s_i}{\sqrt{n_i}}$$

- **BUT** after **ANOVA**, estimate any σ with the pooled standard deviation:

$$\bar{x}_i \pm t^* \frac{\sqrt{MSE}}{\sqrt{n_i}}$$

- the corresponding $df=n-k$

Cuckoo Eggs (1d)

Find a 95% confidence interval for the mean cuckoo egg length in European robin nests (Type = 4).

```
MSE <- 1.745  
summary(fit_anova)
```

```
          Df Sum Sq Mean Sq F value    Pr(>F)  
type         5   41.12    8.223    4.713 0.000602 ***  
Residuals   113  197.18    1.745  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
```

Type	mean	sd	n
1	22.51636	1.8058292	44
2	23.09000	0.9014274	15
3	23.12143	1.0687365	14
4	22.57500	0.6845923	16
5	22.90333	1.0676186	15
6	21.13000	0.7437357	15

$$\bar{x}_i \pm t^* \frac{\sqrt{MSE}}{\sqrt{n_i}}, \text{ df} = n - k$$

Inferences after ANOVA

Compute a CI for any $\mu_i - \mu_j$

- The usual procedure:

$$(\bar{x}_i - \bar{x}_j) \pm t^* \sqrt{\frac{s_i^2}{n_i} + \frac{s_j^2}{n_j}}$$

- BUT after ANOVA, estimate any σ with the pooled standard deviation:

$$(\bar{x}_i - \bar{x}_j) \pm t^* \sqrt{MSE \left(\frac{1}{n_i} + \frac{1}{n_j} \right)}$$

- the corresponding $df=n-k$

Cuckoo Eggs (1e)

Find a 95% CI for the difference in mean egg length between European robin(type = 4) and Eurasian wren(type = 6) nests.

```
          Df Sum Sq Mean Sq F value    Pr(>F)
type          5   41.12    8.223    4.713 0.000602 ***
Residuals    113  197.18    1.745
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Type	mean	sd	n
1	22.51636	1.8058292	44
2	23.09000	0.9014274	15
3	23.12143	1.0687365	14
4	22.57500	0.6845923	16
5	22.90333	1.0676186	15
6	21.13000	0.7437357	15

$$(22.575 - 21.130) \pm 1.981 \cdot \sqrt{1.745 \left(\frac{1}{16} + \frac{1}{15} \right)} = (0.50, 2.39)$$

```
(stat[4,2] - stat[6,2]) + c(-1,1)* (qt(1-0.05/2, df=113))* sqrt(MSE*(1/stat[4,4] + 1/stat[6,4]))
[1] 0.5044174 2.3855826
```

Why is it important that the interval contains only positive values?

Cuckoo Eggs (1f)

Find a 95% CI for the difference in mean egg length between **Dunnock** (type = 3) and **European robin** (type = 4) nests.

```
          Df Sum Sq Mean Sq F value    Pr(>F)
type         5   41.12    8.223     4.713 0.000602 ***
Residuals  113  197.18    1.745
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Type	mean	sd	n
1	22.51636	1.8058292	44
2	23.09000	0.9014274	15
3	23.12143	1.0687365	14
4	22.57500	0.6845923	16
5	22.90333	1.0676186	15
6	21.13000	0.7437357	15

```
(stat[3,2] - stat[4,2]) + c(-1,1)* (qt(1-0.05/2, df=113))*sqrt(MSE*(1/stat[3,4] + 1/stat[4,4]))
[1] -0.4113351  1.5041922
```

$$(23.121 - 22.575) \pm 1.981 \cdot \sqrt{1.188 \left(\frac{1}{14} + \frac{1}{16} \right)} = (-0.41, 1.50)$$

What does it mean if the interval contains 0?

Multiple Comparisons

- Often, doing pairwise comparisons after ANOVA involves many tests
 - e.g. k groups/categories, then we have $\frac{k(k-1)}{2}$ comparisons
 - $k = 6$ bird species then 15 pairwise tests.
- If each test has an α chance of a Type I error (finding a difference between a pair that aren't different), the overall Type I error rate can be much higher.
 - Use a smaller α for each pairwise test (Bonferroni)
 - $\alpha^* = \frac{\alpha}{k}$
 - e.g $\alpha = 0.05$ and $k = 6$, then $\alpha^* = 0.05/6 = 0.0083$

Cuckoo Eggs (1g)

- Which means are “different” at a 5% significance level?

```
pairwise.t.test(cuckoo$length, cuckoo$type, p.adjust.method = "bonferroni")
```

Pairwise comparisons using t tests with pooled SD

data: cuckoo\$length and cuckoo\$type

	1	2	3	4	5
2	1.0000	-	-	-	-
3	1.0000	1.0000	-	-	-
4	1.0000	1.0000	1.0000	-	-
5	1.0000	1.0000	1.0000	1.0000	-
6	0.0097	0.0013	0.0014	0.0436	0.0055

P value adjustment method: bonferroni

Multiple Comparisons (1h)

```
library(multcomp, quietly = TRUE)
fit <- lm(length~type, cuckoo)
mcp <- glht(fit, linfct = mcp(type =
summary(mcp)
```

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: `lm(formula = length ~ type, data = cuckoo)`

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t)	
2 - 1 == 0	0.57364	0.39495	1.452	0.68900	
3 - 1 == 0	0.60506	0.40534	1.493	0.66348	
4 - 1 == 0	0.05864	0.38564	0.152	0.99999	
5 - 1 == 0	0.38697	0.39495	0.980	0.92128	
6 - 1 == 0	-1.38636	0.39495	-3.510	0.00813	**
3 - 2 == 0	0.03143	0.49089	0.064	1.00000	
4 - 2 == 0	-0.51500	0.47475	-1.085	0.88349	
5 - 2 == 0	-0.18667	0.48235	-0.387	0.99880	
6 - 2 == 0	-1.96000	0.48235	-4.063	0.00124	**
4 - 3 == 0	-0.54643	0.48342	-1.130	0.86433	
5 - 3 == 0	-0.21810	0.49089	-0.444	0.99768	
6 - 3 == 0	-1.99143	0.49089	-4.057	0.00122	**
5 - 4 == 0	0.32833	0.47475	0.692	0.98196	
6 - 4 == 0	-1.44500	0.47475	-3.044	0.03291	*
6 - 5 == 0	-1.77333	0.48235	-3.676	0.00469	**

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

Your Turn 1

05:00



- Go over to the in class activity file
- Complete the remaining activity