Post-ANOVA

Stat 120

May 21 2023

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*
- *Multiple comparisons*

ANOVA for Difference in Means

Data: Random samples of size $n_1, n_2, \cdots, n_k$ 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

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

$$H_a : \text{at least one } \mu_i \text{ is different}$$

- ***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***

Cuckoo bird in nest

Do cuckoo bird eggs found in nests of different species differ in size?

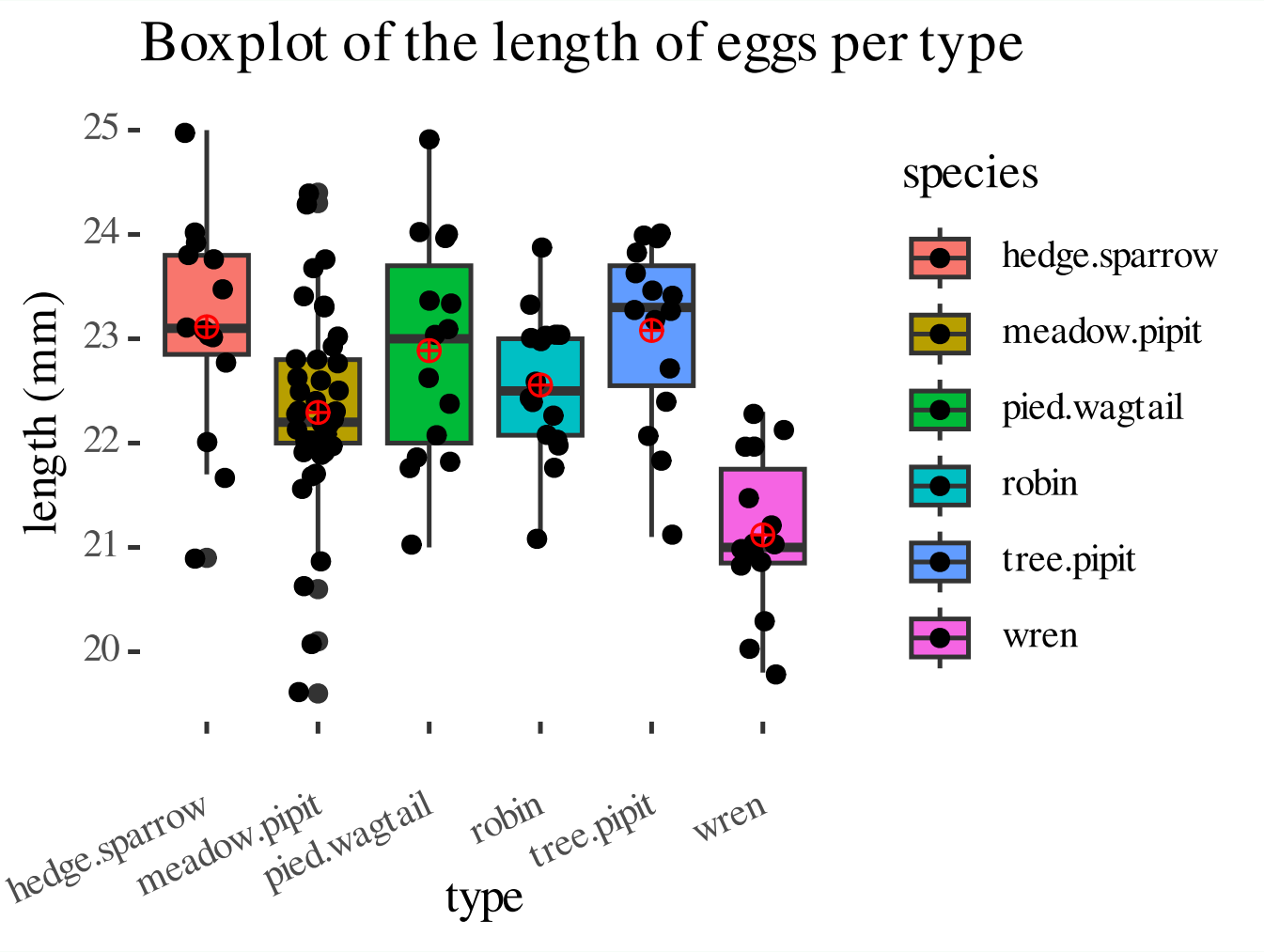
Cuckoo Dataset

- *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.*

- Species=1: Hedge Sparrow
- Species=2: Meadow Pit
- Species=3: Pied Wagtail
- Species=4: European Robin
- Species=5: Tree Pipit
- Species=6: Eurasian Wren

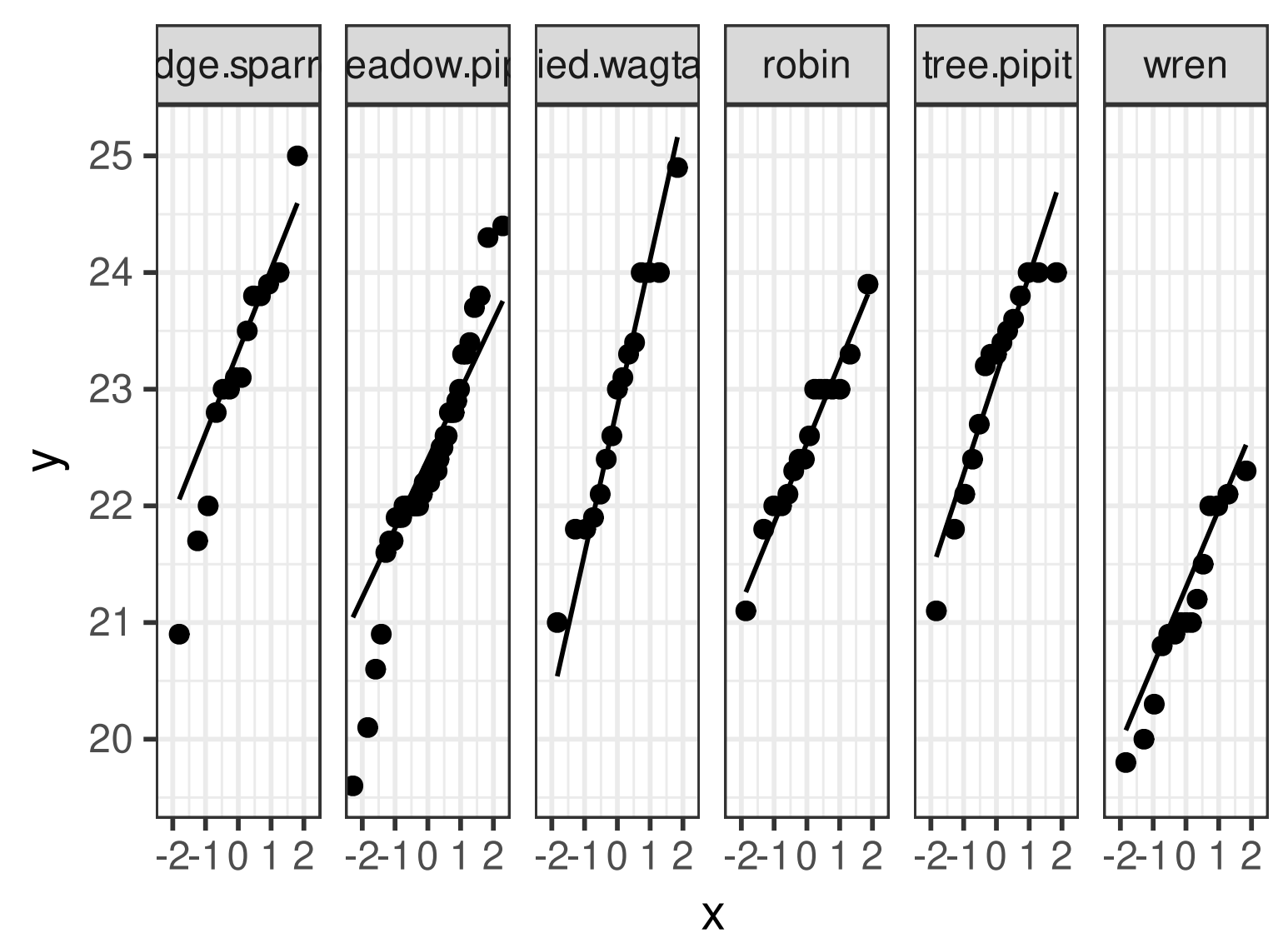
Side-by-side Boxplot (1a)

```
Cuckoo %>%
  ggplot(aes(x=species,y=length,fill=spe
  theme_bw() +
  geom_boxplot() +
  geom_jitter(width = 0.2) +
  labs(title ="Boxplot of the length of
       y = "length (mm)",
       x = "type") +
  stat_summary(fun=mean, geom="point", s
               size=2, color="red", fill
  ggthemes::theme_tufte() +
  theme(axis.text.x = element_text(angle
```



Approximate normality in groups (1b)

```
Cuckoo %>%
  ggplot(aes(sample=length))
  geom_qq() +
  geom_qq_line() +
  facet_grid(~species) +
  theme(strip.text.x = elemen
  theme_bw()
```



Fitting ANOVA (1c)

```
library(broom)
fit_anova <- aov(length~species, Cuckoo)
knitr::kable(tidy(fit_anova))
```

term	df	sumsq	meansq	statistic	p.value
species	5	42.81015	8.5620298	10.44934	0
Residuals	114	93.40985	0.8193847	NA	NA

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

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

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 <- 0.8193847
knitr::kable(tidy(fit_anova))
```

term	df	sumsq	meansq	statistic	p.value
species	5	42.81015	8.5620298	10.44934	0
Residuals	114	93.40985	0.8193847	NA	NA

type	mean	sd	n
hedge.sparrow	23.11429	1.0494373	14
meadow.pipit	22.29333	0.9195849	45
pied.wagtail	22.88667	1.0722917	15
robin	22.55625	0.6821229	16
tree.pipit	23.08000	0.8800974	15
wren	21.12000	0.7542262	15

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

Inference after ANOVA

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

Compute a CI for $\mu_i - \mu_j$

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

Use the usual procedures except estimate any σ with the pooled standard deviation: $\sqrt{MSE}$ and use the error degrees of freedom, df=n-k, for any t-values

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

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.

term	df	sumsq	meansq	statistic	p.value
species	5	42.81015	8.5620298	10.44934	0
Residuals	114	93.40985	0.8193847	NA	NA

type	mean	sd	n
hedge.sparrow	23.11429	1.0494373	14
meadow.pipit	22.29333	0.9195849	45
pied.wagtail	22.88667	1.0722917	15
robin	22.55625	0.6821229	16
tree.pipit	23.08000	0.8800974	15
wren	21.12000	0.7542262	15

$$(22.556 - 21.120) \pm 1.981 \cdot \sqrt{0.8194\left(\frac{1}{16} + \frac{1}{15}\right)} = (0.792, 2.081)$$

```
(stat[4,2] - stat[6,2]) + c(-1,1)* (qt(1-0.05/2, df=114))* sqrt(MSE*(1/stat[4,4] + 1/stat[6,4]))
[1] 0.7917811 2.0807189
```

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 Pied Wagtail (type = 3) and European robin(type = 4) nests.

term	df	sumsq	meansq	statistic	p.value
species	5	42.81015	8.5620298	10.44934	0
Residuals	114	93.40985	0.8193847	NA	NA

$$(22.887 - 22.556) \pm 1.981 \cdot \sqrt{0.8194\left(\frac{1}{15} + \frac{1}{16}\right)} = (-0.314, 0.975)$$

type	mean	sd	n
hedge.sparrow	23.11429	1.0494373	14
meadow.pipit	22.29333	0.9195849	45
pied.wagtail	22.88667	1.0722917	15
robin	22.55625	0.6821229	16
tree.pipit	23.08000	0.8800974	15
wren	21.12000	0.7542262	15

```
(stat[3,2] - stat[4,2]) + c(-1,1)* (qt(1-0.05/2, df=114))*sqrt(MSE*(1/stat[3,4] + 1/stat[4,4]))
[1] -0.3140522  0.9748855
```

What does it mean if the interval contains 0?

Mutiple 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.*

Mutiple Comparisons

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)

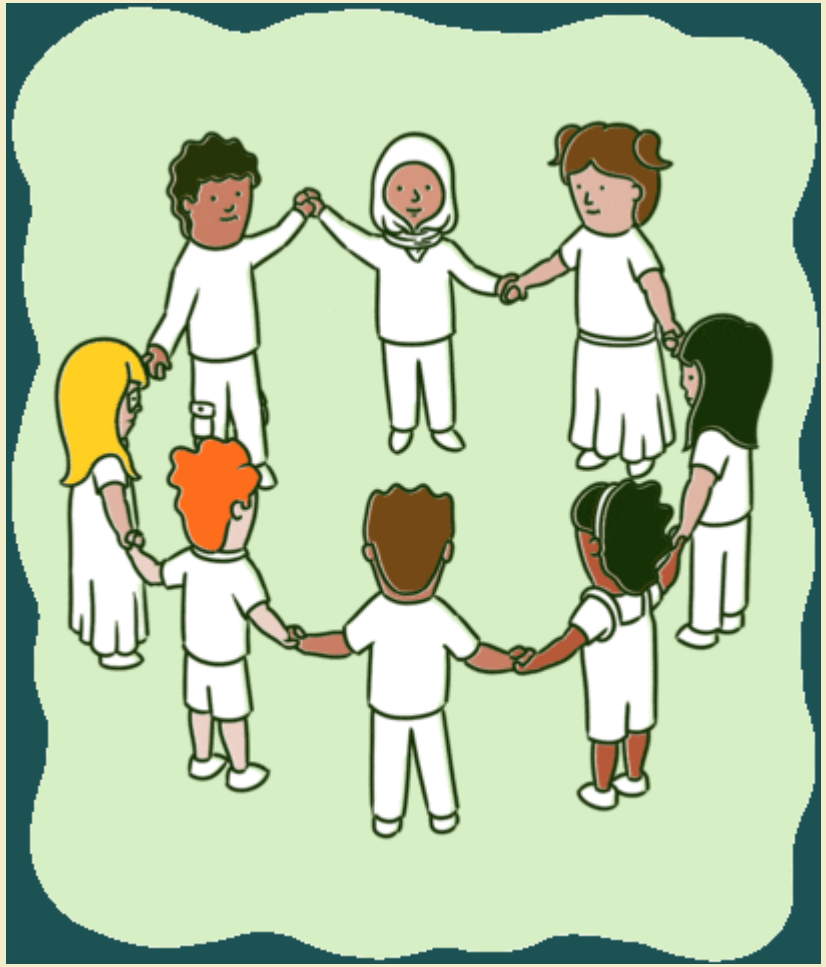
Which means are "different" at a 5% significance level?

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

```
    Pairwise comparisons using t tests with pooled SD

data:  Cuckoo$length and Cuckoo$species

             hedge.sparrow meadow.pipit pied.wagtail robin   tree.pipit
meadow.pipit 0.05554       -            -           -       -
pied.wagtail 1.00000       0.44898      -           -       -
robin        1.00000       1.00000      1.00000     -       -
tree.pipit   1.00000       0.06426      1.00000     1.00000 -
wren         5e-07         0.00045      7e-06       0.00035 5e-07

P value adjustment method: bonferroni
```

YOUR TURN 1

10:00



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