

# **Lecture 03b – One-way ANOVA**

ENVX2001 Applied Statistical Methods

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Feb 2026

**Why ANOVA?**

## The problem with multiple $t$ -tests

Suppose we want to compare weight gain of chicks fed on **4 different diets**.

With  $t$ -tests, we'd need  $\binom{4}{2} = 6$  pairwise comparisons:

1-2, 1-3, 1-4, 2-3, 2-4, 3-4

Even if there are no true differences, each test has a 5% chance of incorrectly finding significance. How does that add up?

```
prob_all_correct ← 0.95^6  
prob_all_correct
```

```
[1] 0.7350919
```

We have a **26.5%** chance that at least one test result will be incorrect!

## We need a better method

The **problem of multiple comparisons** requires a technique that considers **all** treatments at once.

## ANOVA – Analysis of Variance

Before deciding *which* treatments differ, we first consider:

1. Differences **between** the treatment groups – **between-treatment effects**
2. Differences **within** each treatment group – **within-treatment effects**
  - due to random environmental fluctuations, genetics, experimental error

## Chick weight data

## The experiment



- 20 chicks
- 4 diets
- 5 replicates per diet
- Response: weight gain (g)

```
chicks_wide ← read.csv("data/chicks.csv")  
chicks_wide
```

	Diet.1	Diet.2	Diet.3	Diet.4
1	99	61	42	169
2	88	112	97	137
3	76	30	81	169
4	38	89	95	85
5	94	63	92	154

## Reshaping the data

```
chicks <- read.csv("data/chicks.csv") |>
  pivot_longer(
    cols = starts_with("Diet"),
    names_to = "diet",
    values_to = "weight"
  ) |>
  mutate(diet = as.factor(diet))
```

chicks

```
# A tibble: 20 × 2
  diet    weight
  <fct>   <int>
1 Diet.1     99
2 Diet.2     61
3 Diet.3     42
4 Diet.4    169
5 Diet.1     88
```

6	Diet.2	112
7	Diet.3	97
8	Diet.4	137
9	Diet.1	76
10	Diet.2	30
11	Diet.3	81
12	Diet.4	169
13	Diet.1	38
14	Diet.2	89
15	Diet.3	95
16	Diet.4	85
17	Diet.1	94
18	Diet.2	63
19	Diet.3	92
20	Diet.4	154



# **ANOVA concepts**

## Terminology

- **Factor** (or treatment): the categorical variable of interest (here: diet)
- **Levels**: the categories within a factor (here: Diet 1, Diet 2, Diet 3, Diet 4)
- **Replicates**: the number of observations per level (here:  $r = 5$ )
- $t$  = number of treatments;  $N$  = total observations =  $r \times t = 20$

This is a **one-way** (or one-factor) ANOVA because there is only one factor (diet).

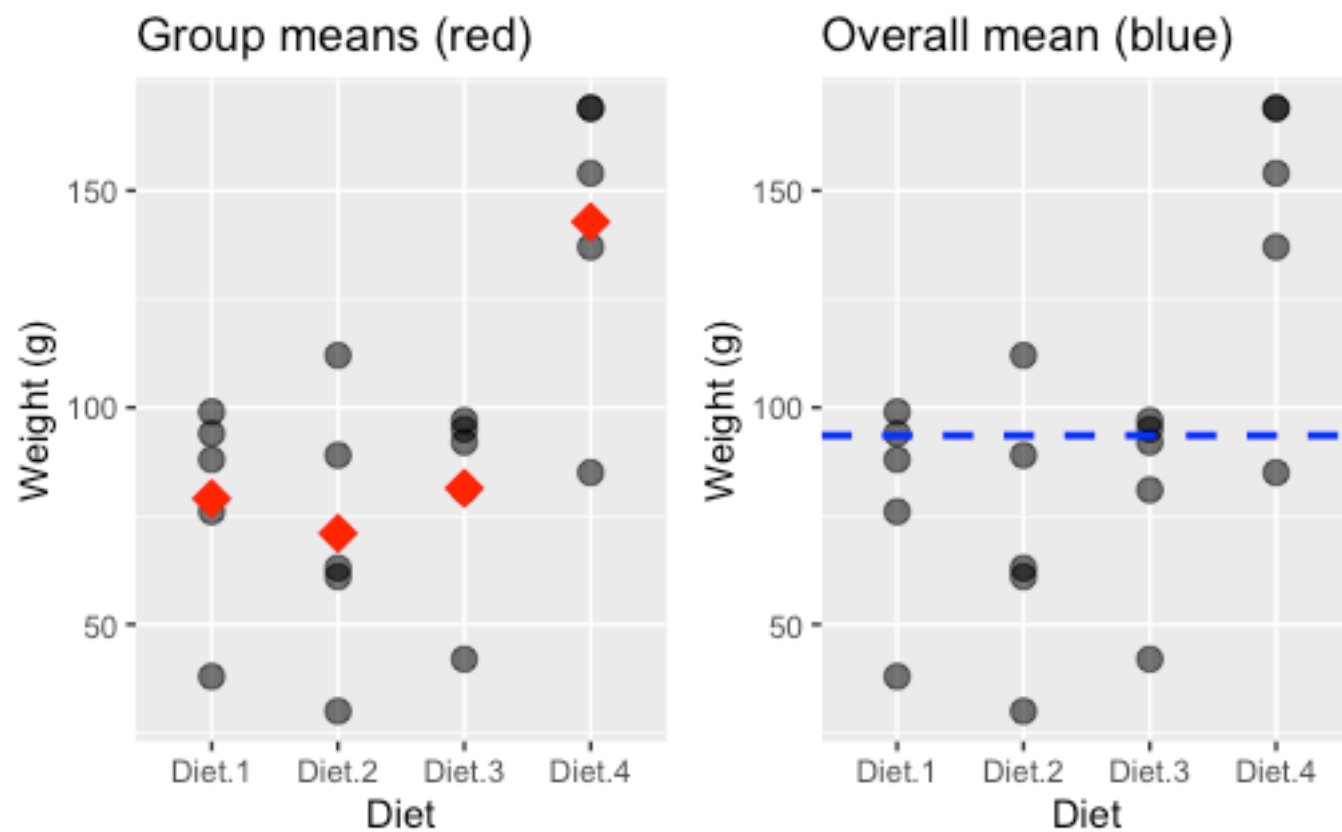
## Which model best describes the data?

```
overall_mean ← mean(chicks$weight)
group_means ← chicks |>
  group_by(diet) |>
  summarise(mean_wt = mean(weight))

p1 ← ggplot(chicks, aes(diet, weight)) +
  geom_point(size = 3, alpha = 0.6) +
  geom_point(data = group_means, aes(diet, mean_wt),
    shape = 18, size = 5, colour = "red") +
  labs(title = "Group means (red)", x = "Diet", y = "Weight (g)")

p2 ← ggplot(chicks, aes(diet, weight)) +
  geom_point(size = 3, alpha = 0.6) +
  geom_hline(yintercept = overall_mean, colour = "blue",
    linewidth = 1, linetype = "dashed") +
  labs(title = "Overall mean (blue)", x = "Diet", y = "Weight (g)")

library(patchwork)
p1 + p2
```



Does the **group means model** (left) explain the data better than the **overall mean model** (right)?

**Model equation**

## Same form as the $t$ -test

$$y_{ij} = \mu_i + \varepsilon_{ij}$$

- $i = 1, 2, \dots, t$  (treatment);  $j = 1, 2, \dots, n_i$  (replicate)

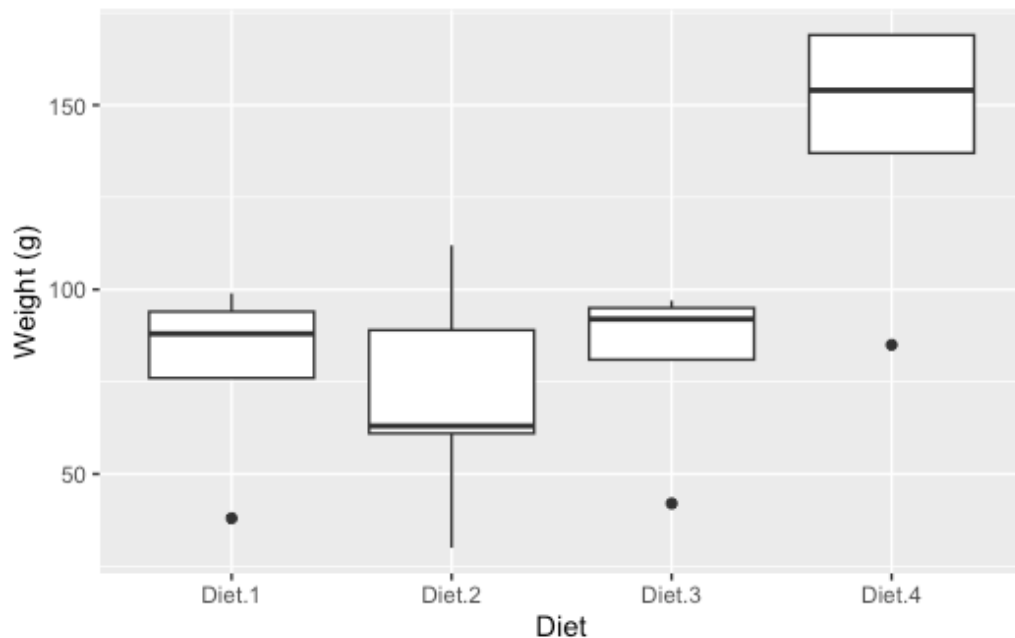
In the chick example:

- $y_{ij}$  = observed weight gain for the  $j$ th chick on Diet  $i$
- $\mu_i$  = mean weight gain for chicks on Diet  $i$
- $\varepsilon_{ij}$  = random error (residual)

# Assumptions

## Checking normality

```
ggplot(chicks, aes(diet, weight)) +  
  geom_boxplot() +  
  labs(x = "Diet", y = "Weight (g)")
```



```
shapiro.test(chicks$weight)
```

Shapiro-Wilk normality test

data: chicks\$weight  
W = 0.93272, p-value = 0.1742

$p > 0.05$ : we can assume normality.



## Checking equal variances

- $\sigma_1^2 = \sigma_2^2 = \dots = \sigma_t^2$
- General guide:  $\frac{\text{largest SD}}{\text{smallest SD}} < 2.0$
- Alternatively, use **Bartlett's test** of homogeneity of variance:

```
bartlett.test(weight ~ diet, data = chicks)
```

Bartlett test of homogeneity of variances

data: weight by diet

Bartlett's K-squared = 0.85164, df = 3, p-value = 0.8371

### Warning

Bartlett's test is **sensitive to non-normality**. Only use it when normality is reasonable.

# Hypothesis test

## Hypotheses

- **Null hypothesis:**  $H_0 : \mu_1 = \mu_2 = \dots = \mu_t$
- **Alternative hypothesis:**  $H_1$ : not all  $\mu_i$  are equal

! Important

ANOVA only tells us that **at least two** group means are different – not *which* ones.

## The concept: partition variability

Partition the total variability into components:

$$SS_{\text{total}} = SS_{\text{treatment}} + SS_{\text{residual}}$$

- $SS_{\text{treatment}}$ : variation **between** groups (due to diet)
- $SS_{\text{residual}}$ : variation **within** groups (random error)

If the treatment has a real effect,  $SS_{\text{treatment}}$  should be **large** relative to  $SS_{\text{residual}}$ .

# Variance partitioning

**Total sum of squares:**  $SS_{\text{total}}$

$$SS_{\text{total}} = \sum (y_{ij} - \bar{y})^2$$

```
overall_mean ← mean(chicks$weight)
ss_total ← sum((chicks$weight - overall_mean)^2)
ss_total
```

```
[1] 29678.95
```

## Treatment sum of squares: $SS_{\text{treatment}}$

$$SS_{\text{treatment}} = \sum n_i \times (\bar{y}_i - \bar{y})^2$$

```
group_means <- chicks |>
  group_by(diet) |>
  summarise(grp_mean = mean(weight))

ss_trt <- sum(5 * (group_means$grp_mean - overall_mean)^2)
ss_trt
```

```
[1] 16466.95
```

## Residual sum of squares: $SS_{\text{residual}}$

$$SS_{\text{residual}} = \sum (y_{ij} - \bar{y}_i)^2$$

```
chicks_with_means <- chicks |>
  left_join(group_means, by = "diet")

ss_res <- sum((chicks_with_means$weight - chicks_with_means$grp_mean)^2)
ss_res
```

```
[1] 13212
```

**Check:**  $SS_{\text{total}} = SS_{\text{treatment}} + SS_{\text{residual}}$

```
c(ss_total, ss_trt + ss_res)
```

```
[1] 29678.95 29678.95
```



## **ANOVA table**

## Structure

Source	df	SS	MS	F
Treatment	$t - 1$	$SS_{\text{trt}}$	$SS_{\text{trt}} / (t - 1)$	$MS_{\text{trt}} / MS_{\text{res}}$
Residual	$N - t$	$SS_{\text{res}}$	$SS_{\text{res}} / (N - t)$	
<b>Total</b>	$N - 1$	$SS_{\text{total}}$		

- $N$  = total observations,  $t$  = number of treatment levels
- **Mean Squares** (MS) standardise SS so they are comparable
- The larger the ratio  $MS_{\text{trt}} / MS_{\text{res}}$ , the stronger the treatment effect

## Using `aov()` in R

```
model ← aov(weight ~ diet, data = chicks)
summary(model)
```

```
          Df Sum Sq Mean Sq F value Pr(>F)
diet         3  16467     5489   6.647  0.004 **
Residuals    16  13212      826
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Interpreting the results

- $F = 6.65$  with  $df = 3, 16$
- $p = 0.004$  which is  $< 0.05$ , so we **reject**  $H_0$
- There are **significant differences** in mean weight gain amongst the 4 diets

## How much variability is explained?

$$\frac{SS_{\text{treatment}}}{SS_{\text{total}}} = \frac{1.6467 \times 10^4}{2.9679 \times 10^4} = 55.5\%$$

The diets explain about 55% of the total variability in chick weight gain.

**Post-hoc: which groups differ?**

## Confidence intervals for group means

We can examine 95% CIs for each treatment mean:

$$95\% \text{ CI} = \bar{y}_i \pm t_{N-t}^{0.025} \times SE(\bar{y}_i)$$

where  $SE(\bar{y}_i) = \sqrt{MS_{\text{res}}/n_i}$

## Using emmeans

```
library(emmeans)
emm ← emmeans(model, "diet")
emm
```

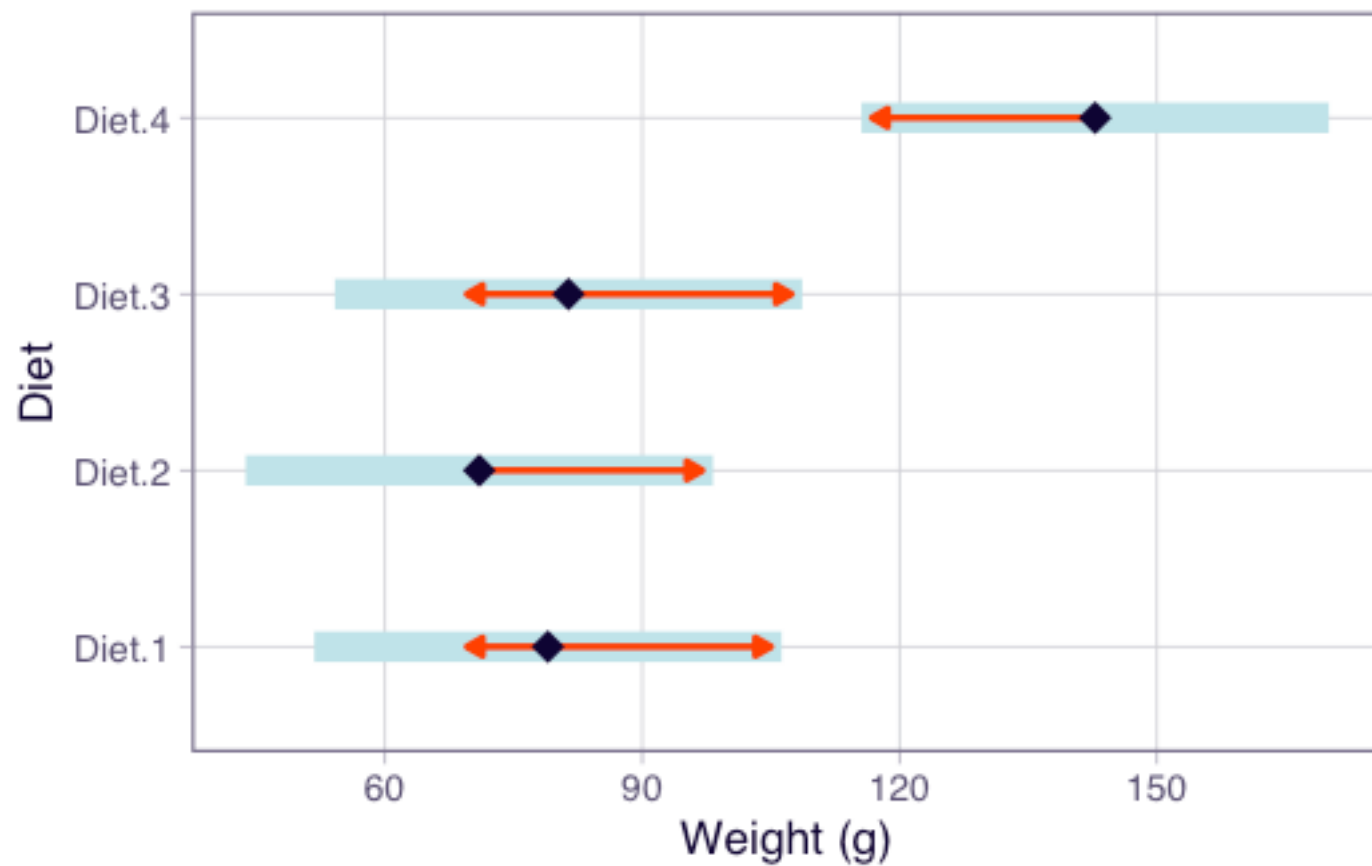
diet	emmean	SE	df	lower.CL	upper.CL
Diet.1	79.0	12.9	16	51.8	106.2
Diet.2	71.0	12.9	16	43.8	98.2
Diet.3	81.4	12.9	16	54.2	108.6
Diet.4	142.8	12.9	16	115.6	170.0

Confidence level used: 0.95

## Visualising group comparisons

```
plot(emm, comparisons = TRUE) +  
  labs(x = "Weight (g)", y = "Diet")
```





Groups with **overlapping** arrows are **not** significantly different from each other.

# Summary

## $t$ -test vs ANOVA

- $t$ -test: compares means of **2** groups
- ANOVA: compares means of **2 or more** groups simultaneously
- ANOVA avoids the inflated Type I error rate from multiple  $t$ -tests
- The ANOVA  $F$ -test tells us *if* differences exist, but not *where*
- Post-hoc methods (e.g. `emmeans`) identify *which* pairs differ

## Next week

- How to better identify which pairs are significantly different
- How to test and interpret model assumptions using **residual diagnostics**

## References

- Quinn & Keough (2002), Chapter 7: Section 7.1
- Mead et al. (2002), Chapter 18: Sections 18.1–18.3

**Thanks!**

**Questions?**

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