Session #2: Additive vs Multiplicative Models

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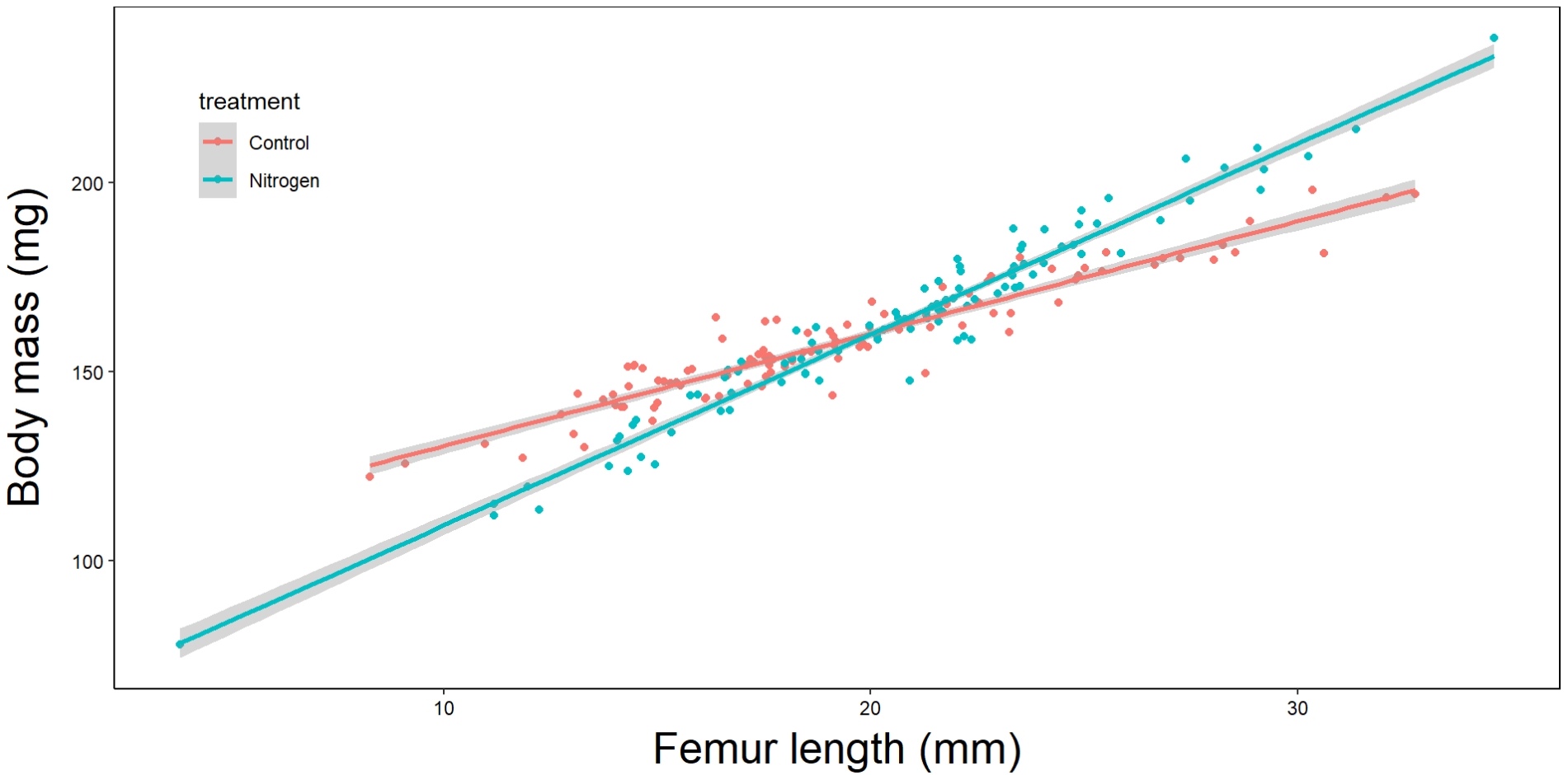
Additive vs multiplicative models

- So far, we have only looked at linear models with a single predictor (X) variable.
  - However, we can include two or more variables into our models
  - When we do this, we can fit these models as *additive* or *multiplicative* models
    - They make different assumptions and test different hypotheses
    - Need to be very sure we know which model we want

An extended example

Let's reconsider the `femurLength` and `bodyMass` example, and assume we reared half the insects on stock plants (`Control`) and the other half on nitrogen-enriched plants (`Nitrogen`) (hereafter `treatment`)



Additive model - fitting

- Hypothesis: Is there a diet `treatment` effect on `bodyMass` after controlling for `femurLength`?
- Tests for a difference in means between `treatment` groups

```
# Fit additive model
mod_add <- glm(
  data = df,
  family = gaussian(link = "identity"),
  bodyMass ~ 1 + femurLength + treatment
)
```

Additive model - LRT

```
Analysis of Deviance Table (Type II tests)

Response: bodyMass
             LR Chisq Df Pr(>Chisq)
femurLength  1409.75  1     <2e-16 ***
treatment       0.04  1     0.8456
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is no statistical support for a difference in `bodyMass` between insects reared on stock plants versus nitrogen-enriched plants (X2 = 0.04, df = 1, *P* = 0.846).

Additive model - beta

```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment, family = gaussian(link =
"identity"),
    data = df)

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        81.6551     2.1568  37.860   <2e-16 ***
femurLength         3.9654     0.1056  37.547   <2e-16 ***
treatmentNitrogen  -0.2036     1.0455  -0.195    0.846
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 53.29987)
```

- (Intercept) = 81.65
  - Population mean `bodyMass` when `femurLength` = 0 (averaged across treatments)

Additive model - beta

```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment, family = gaussian(link =
"identity"),
    data = df)

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        81.6551     2.1568  37.860   <2e-16 ***
femurLength         3.9654     0.1056  37.547   <2e-16 ***
treatmentNitrogen  -0.2036     1.0455  -0.195    0.846
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 53.29987)
```

- Beta `femurLength` = 3.96
  - As `femurLength` in the `Control` treatment increases by 1mm, `bodyMass` increases by 3.96mg

Additive model - beta

```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment, family = gaussian(link =
"identity"),
    data = df)

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        81.6551     2.1568  37.860   <2e-16 ***
femurLength         3.9654     0.1056  37.547   <2e-16 ***
treatmentNitrogen  -0.2036     1.0455  -0.195    0.846
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 53.29987)
```

Multiplicative model - fitting

- Hypothesis: Is the relationship between `bodyMass` and `femurLength` comparable between stock and nitrogen-enriched plants (`treatment`)?
- Tests for a difference in slopes between `treatment` groups
- This is often called and *interaction term model* or *slopes model*

```
# Fit multiplicative model
mod_mlt <- glm(
  data = df,
  family = gaussian(link = "identity"),
  bodyMass ~ 1 + femurLength + treatment + femurLength:treatment
)
```

Multiplicative - LRT

```
Analysis of Deviance Table (Type II tests)

Response: bodyMass
                     LR Chisq Df Pr(>Chisq)
femurLength             2747.79  1     <2e-16 ***
treatment                  0.07  1     0.7857
femurLength:treatment    187.98  1     <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The `femurLength:treatment` term indicates statistical support for an interactive/multiplicative effect of `femurLength` on `bodyMass` (X2 = 187.79, df = 1, $P < 0.001$).
  - I.e. The relationship between `femurLength` and `bodyMass` **depends on** whether the insect was reared on stock plants or nitrogen-enriched plants

Multiplicative model - intercept

```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment + femurLength:treatment,
    family = gaussian(link = "identity"), data = df)

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                 100.7075     2.0779   48.47   <2e-16 ***
femurLength                   2.9739     0.1047   28.42   <2e-16 ***
treatmentNitrogen           -41.7941     3.1245  -13.38   <2e-16 ***
femurLength:treatmentNitrogen   2.0764     0.1514   13.71   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 27.34541)
```

- (Intercept) = 81.65
  - Mean `bodyMass` when `femurLength` = 0 in the `Control` group

Multiplicative model - beta

```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment + femurLength:treatment,
    family = gaussian(link = "identity"), data = df)

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                 100.7075     2.0779   48.47   <2e-16 ***
femurLength                   2.9739     0.1047   28.42   <2e-16 ***
treatmentNitrogen           -41.7941     3.1245  -13.38   <2e-16 ***
femurLength:treatmentNitrogen   2.0764     0.1514   13.71   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 27.34541)
```

- Beta `femurLength` = 2.97
  - As `femurLength` in the `Control` treatment increases by 1mm, `bodyMass` increases by 2.97mg, on average

Multiplicative model - beta

```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment + femurLength:treatment,
    family = gaussian(link = "identity"), data = df)

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                 100.7075     2.0779   48.47   <2e-16 ***
femurLength                   2.9739     0.1047   28.42   <2e-16 ***
treatmentNitrogen           -41.7941     3.1245  -13.38   <2e-16 ***
femurLength:treatmentNitrogen   2.0764     0.1514   13.71   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 27.34541)
```

- Beta `treatmentNitrogen` = -41.79
  - Mean `bodyMass` when `femurLength` = 0 in the `Nitrogen` group is 41.79mg less than in the `Control` group

Multiplicative model - beta

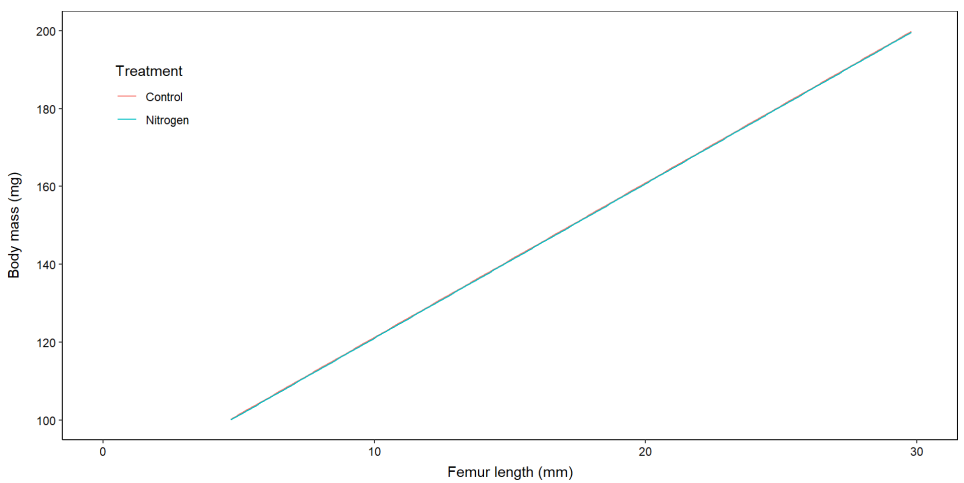
```
Call:
glm(formula = bodyMass ~ 1 + femurLength + treatment + femurLength:treatment,
    family = gaussian(link = "identity"), data = df)

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                 100.7075     2.0779   48.47   <2e-16 ***
femurLength                   2.9739     0.1047   28.42   <2e-16 ***
treatmentNitrogen           -41.7941     3.1245  -13.38   <2e-16 ***
femurLength:treatmentNitrogen   2.0764     0.1514   13.71   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 27.34541)
```

- Beta `femurLength:treatmentNitrogen` = 2.07
  - As `femurLength` increases by 1mm, `bodyMass` increases by 2.07mg more, on average, than for a 1mm increase in the `Control` treatment

Additive vs multiplicative

1. Additive model: Tests for a difference in means between treatments

```r
# Fit additive model
mod_add <- glm(
  data = df,
  family = gaussian(link = "identity"),
  bodyMass ~ 1 + femurLength + treatment
)
```



2. Multiplicative model: Tests for a difference in slopes between treatments

```r
# Fit multiplicative model
mod_mlt <- glm(
  data = df,
  family = gaussian(link = "identity"),
  bodyMass ~ 1 + femurLength + treatment
)
```