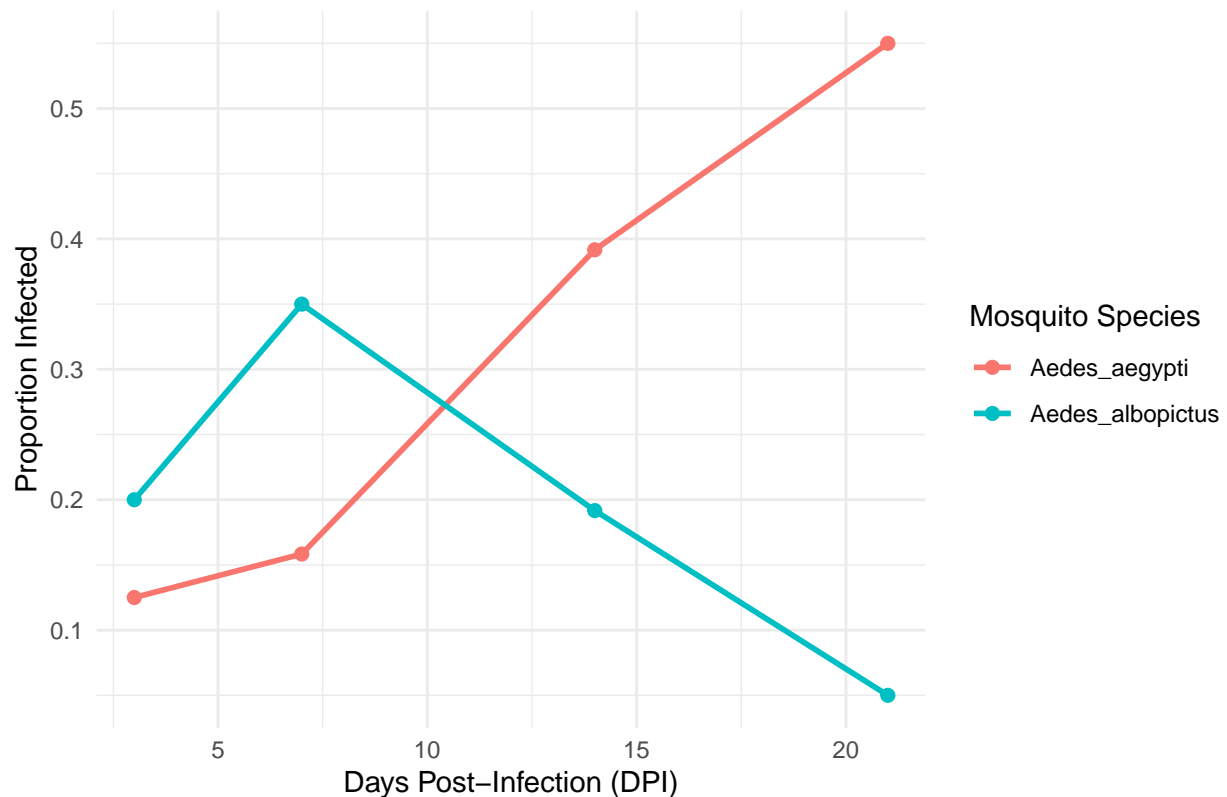


Statistical Test for Detecting Differences Between Two Time Trends

1. Exploratory Overview of the Experiment

This dataset originates from a vector competence experiment and investigating whether two mosquito species:
1. *Aedes aegypti* and 2. *Aedes albopictus* can become infected with and transmit a virus over time.

Infection Rate Over Time by Mosquito Species



Experimental Design Summary

- *Mosquito species*: *Aedes aegypti*, *Aedes albopictus*.
- *Time points*: 3, 7, 14, and 21 days post-infection (dpi)
- *Replicates*: 2 biological replicates
- **Tissue types sampled**:
 - **Body**: assesses infection
 - **Legs**: assesses dissemination
 - **Saliva**: assesses transmission
- **Virus detection method**: qRT-PCR
 - Binary outcome: Pos (positive) or Neg (negative)

Variables of Interest

- **Predictors**: mosquito species (`Mosquito_specie`), days post-infection (`dpi`)

- **Outcomes:**
 - **Infection** – determined by qRT-PCR result from **Body**
 - **Dissemination** – determined by qRT-PCR result from **Legs**
 - **Transmission** – determined by qRT-PCR result from **Saliva**

Main Research Question

Do the temporal trends of infection, dissemination, and transmission significantly differ between *Aedes aegypti* and *Aedes albopictus*?

2. Statistical Modeling

2.1 Logistic Regression for Infection

To evaluate the effect of mosquito species and dpi on infection status, we fit a logistic regression model.

Hypotheses

- **Null hypothesis (H_0):** The effect of dpi on infection probability is the same for both species.
- **Alternative hypothesis (H_1):** The effect of dpi on infection probability differs between species.

Model Formula

We model the log-odds of infection using the logistic regression model:

$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 \cdot \text{Species} + \beta_2 \cdot \text{dpi} + \beta_3 \cdot (\text{Species} \times \text{dpi})$$

- where p is the probability of infection (i.e., positive qRT-PCR result for body tissue).

2.2 Mixed-Effects Logistic Regression for Infection

To consider for experimental replication, we extend the previous model by fitting a mixed-effects logistic regression model. This allows us to model infection probability while adjusting for potential variation between biological replicates.

Hypotheses:

- Null hypothesis (H_0): The effect of dpi on infection probability is the same for both species, and replicates do not influence the results.
- Alternative hypothesis (H_1): The effect of dpi on infection probability differs between species, after adjusting for replicate-level variability.

2.3 Bayesian Logistic Regression for Infection

We fit a Bayesian logistic regression model. This approach allows estimating the probability that infection rates differ by species and time, using Bayesian inference.

Hypotheses:

- Null hypothesis (H_0): There is no effect of dpi, species, or their interaction on infection probability.
- Alternative hypothesis (H_1): There is an effect of at least one predictor on infection probability, with uncertainty expressed via posterior distributions.