

# Stochastic simulations

## Today's agenda:

- Discuss simulations
- Do some simple simulations

# What are simulations?

Experimentation with the help of a model

- We choose (or build) a model, select parameters, and see what happens

# Uses of simulations

- Theory development (what happens when I add a new feature?)
- Model design (does this model capture the intended dynamics?)
- Study design (how many replicates do I need?)
- Methods development (does this metric tell us what we want?)

# How to simulate?

- 1) Select a model
- 2) Choose one or more sets of parameters
- 3) Simulate using the model and parameters
- 4) Examine the output
- 5) Revise 1 and repeat as needed (optionally)

# Simple linear function with normal error

- Let's pick a simple line as our model ( $y = a + bx$ )
- For our parameters:
  - $A = 2$
  - $B = 1$
  - $X = 1:20$

```
a <- 2
```

```
b <- 1
```

```
x <- 1:20
```

```
y_det <- a + b * x
```

```
plot(x = x, y = y_det)
```

# Simple linear function with normal error

- Let's make it a bit more realistic by adding some uncertainty

```
a <- 2
```

```
b <- 1
```

```
x <- 1:20
```

```
y_det <- a + b * x
```

```
y_stoch <- rnorm(n = 20, mean = y_det, sd = 2)
```

```
plot(x=x, y=y_stoch)
```

# Simple linear function with normal error

- Try re-running these lines a few times and see what happens

```
y_stoch <- rnorm(n = 20, mean = y_det, sd = 2)  
plot(x=x, y=y_stoch)
```

# Simple linear function with normal error

Each time you re-run `rnorm()` you get a different set of points

- A random draw from a normal distribution
- Each draw represents a different possible outcome for the same model/parms



# Simple linear function with correlated error

What if the variation increases with mean?

- E.g., variation in body size might increase with mean body size

```
a <- 2
```

```
b <- 1
```

```
x <- 1:20
```

```
sd_multiplier <- 0.3
```

```
y_det <- a + b * x
```

```
y_stoch <- rnorm(n = 20, mean = y_det, sd = y_det*sd_multiplier)
```

```
plot(x=x, y=y_stoch)
```

# Simple linear function with correlated error

Do a few more replicates, comparing them with the deterministic bit

```
y_det <- a + b * x  
y_stoch <- rnorm(n = 20, mean = y_det, sd = y_det*sd_multiplier)  
  
plot(x = x, y = y_stoch)  
points(x, y_det, col = "blue")
```

# Hyperbolic function with negative binomial error

Model:  $y = a \cdot b / (b + x)$

Error: negative binomial

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```
a <- 20  
b <- 1  
k <- 5  
x <- runif(50, min=0, max=5) #How does this differ from x <- 0:5?  
  
y_det <- a/(b+x)  
  
plot(x = x, y = y_det)
```

**What is the shape of the plotted line?**

**Why doesn't a normal error term make sense?**

# Hyperbolic function with negative binomial error

Adding the negative binomial error:

```
y <- rnbinom(n = 50, mu = y_det, size = k)
plot(x = x, y = y)
```

Run these a few times to get a sense of the variation

What does the mu parameter control?

# Categorical differences

Model:  $y = a*b/(b+x)$

Adding multiple categories:

- Assume species differ in  $a$  and  $b$  parameters
- Assume they have the same error size parameter

# Categorical differences

Model:  $y = a \cdot b / (b + x)$

Adding multiple categories:

- Assume species differ in  $a$  and  $b$  parameters
- Assume they have the same error size parameter

We need different parameters and a way of accessing them

# Categorical differences

Create a grouping variable:

```
g <- factor(rep(1:2, each = 25))
```

This will be used to divide up the 50 observations into 2 groups



# Categorical differences

Specify parameters as vectors

```
a <- c(20,10)
```

```
b <- c(1,2)
```

Define y\_det with the different variables:

```
y_det <- a[g]/(b[g]+x)
```

Which values will apply to group 2? Why?

(Hint: try a[1] or a[2] to see what happens)

# Categorical differences

Plot the two sets of variables:

```
plot(x = x, y = y_det)
```

# Categorical differences

Now add in the variation and plot again:

```
y <- rbinom(n = 50, size = k, mu = y_det)
plot(x = x, y = y)
```

Does that look right?

# Categorical differences

```
plot(x = x, y = y)
```

Difficult to tell the clusters apart

Need to improve the plot

`pch` controls plot symbols

`col` controls plot colors

Both are designed to work with numbers

# Categorical differences

We can have R give each group a different color

```
plot(x = x, y = y, col = g)
```

Try this out!

pch works in the same way, give it a shot!

Also try having both pch and col correspond to the group

# Using simulations

Once we have the simulated data we can, e.g. :

- Compare to expectations/existing data
- Compare to data with other parameter values
- Check whether groups can be differentiated
- Check whether downstream analyses do what we expect

# Using simulations

For our categorical trait simulation:

- Try changing  $a$  and  $b$  for one or both groups
- Can you find parameter values where the two groups seem very different?
- Or where they seem identical?
- Are there some parameter values where they overlap in some regions but not in others?

# Adding more

Simulations and models can range from very simple to very complex

- Simpler models are easier to validate and debug
- More complex models add more realism
- Start simple and add parameters as needed

See 5.2.2.2 in the book for a more complex example



## **Before next class:**

- Read 5.3 (especially important to understand if you plan experiments!)