R Programming For Natural Resource Professionals

Week 14
Simulations: resampling/bootstrapping

The week ahead...

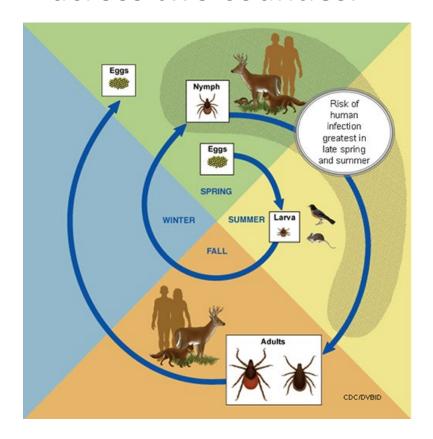
Learning objectives for this week

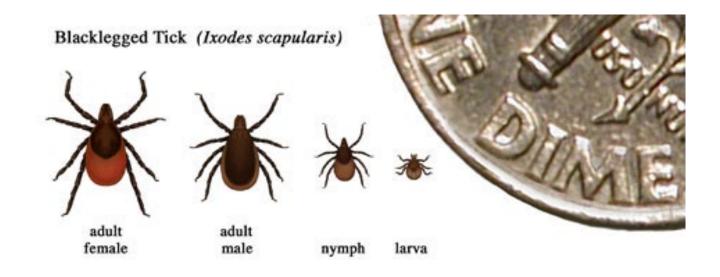
- 1. Understand motivators for simulation-based hypothesis testing.
- 2. Understand two simulation-based hypothesis testing algorithms.
- 3. Use a 'tidy' approach to permutation testing and bootstrapping

Rationale for simulation-based hypothesis testing

- Goal: Estimate the probability of the observed data
 - "How likely is the observed data to have occurred by random chance?"
- Simulation techniques make no assumptions about residual distributions
- Two approaches we'll discuss
 - Permutation: Best for estimating a null distribution.
 - "Does variable A depend on variable B?"
 - Bootstrapping: Best for determining confidence intervals
 - "How confident am I in the relationship between variables?"

• Compare the number of blacklegged ticks found on harvested deer across two counties.



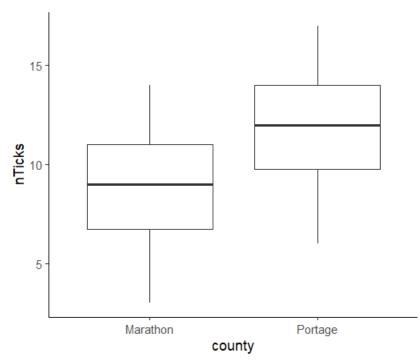


 Compare the number of blacklegged ticks found on harvested deer across two counties.

• On average, a Marathon County deer had 3.03 ticks fewer than a Portage

County deer





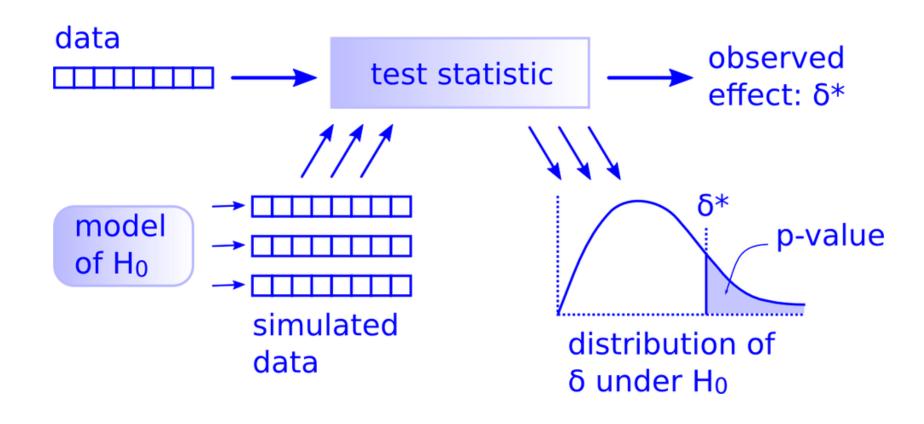
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• Test by:

- 1. Removing the "county" designation from deer's tick count.
- 2. Re-assign "county" designations to each value by drawing from the pooled values without replacement.
- 3. Calculate the difference in mean tick values per county.
- 4. Repeat many times.
- 5. Compare observed statistic to the generated distribution of the statistic.

Overview of permutation test routine



- 1. specify(): allows you to specify the variable, or relationship between variables, that you're interested in
- 2. hypothesize() allows you to declare the null hypothesis
- 3. generate() allows you to generate data reflecting the null hypothesis
- 4. calculate() allows you to calculate a distribution of statistics from the generated data to form the null distribution





Data %>%

specify() %>%

hypothesize() %>%

generate() %>%

calculate()



specify(): allows you to specify the variable, or relationship between variables, that you're interested in.

State the model's formula in the usual R syntax

- Response ~ predictor
- Response ~ predictor1 + predictor2
- Etc.



hypothesize() allows you to declare the null hypothesis

Two supported options: "point" and "independence"

- Point: Does the distribution differ from a point estimate (1 sample t-test)
- Independence: Are the variables related to one another?



generate() allows you to generate data reflecting the null hypothesis

Reps: Number of replicates to generate

Type: "permute" or "bootstrap"



calculate() allows you to calculate a distribution of statistics from the generated data to form the null distribution

Stat: "mean", "median", "sum", "sd", "prop", "count", "diff in means", "diff in medians", "diff in props", "Chisq" (or "chisq"), "F" (or "f"), "t", "z", "ratio of props", "slope", "odds ratio", or "correlation".

Order: How to order variables for the calculation. E.g., c("var1", "var2")

Bootstrapping

- Purpose: Determine confidence of a parameter estimate
- There are a variety of bootstrap methods, but at their core is a common process:
 - 1. Begin with an observed sample of size N
 - 2. Generate a simulated sample of size N by drawing observations from your observed sample independently and with replacement.
 - 3. Compute and save the statistic of interest
 - 4. Repeat this process many times (e.g. 1,000)
 - 5. Treat the distribution of your estimated statistics of interest as an estimate of the population distribution of that statistic.

Bootstrapping

```
modelr
```

```
Data %>%
    specify() %>%
    generate(type = "bootstrap") %>%
    calculate() %>%
    get_confidence_interval()
```