

Owen et al. - Figure 4

This script will reproduce Figure 4 from *Owen et al. - Sample size planning for insect critical thermal limits studies*.

Load required packages

```
if (!require("pacman")) install.packages("pacman")
pacman::p_load(tidyverse,
               tidyr,
               readr,
               data.table,
               viridis,
               here)

# Load ThermalSampleR package
# To download on first use, remove # from line below
# devtools::install_github("CJMvS/ThermalSampleR")
library(ThermalSampleR)
```

Set ggplot theme (makes nice plots)

```
theme_set(theme_classic() +
           theme(panel.border = element_rect(colour = "black", fill = NA),
                 axis.text = element_text(colour = "black"),
                 axis.title.x = element_text(margin = unit(c(2, 0, 0, 0), "mm")),
                 axis.title.y = element_text(margin = unit(c(0, 4, 0, 0), "mm")),
                 legend.position = "none"))
```

Load raw thermal limits data

```
# Also, load raw data (without CI's)
raw_data <- readr::read_csv(here::here("./data_clean/ct_min_data_clean.csv"))

# Make insect_sp column into a factor
raw_data <- raw_data %>%
  dplyr::mutate(col = as.factor(insect_sp))
```

Perform analysis

Here, let's subset the data to only the first 15 individuals tested per *Eccritotarsus* species, perform bootstrap re-sampling of the data, and calculate summary statistics to evaluate whether testing additional individuals is required for this experiment.

Keep in mind that the aim of this experiment was to evaluate if *Eccritotarsus eichhorniae* has a lower CTmin than *Eccritotarsus catarinensis*, as *E. eichhorniae* needs to be able to tolerate the cold temperatures at inland sites, where the current biocontrol agent (*E. catarinensis*) performs sub-optimally.

```
# Subset data
raw_data_ex <- raw_data %>%
  dplyr::filter(insect_sp %in% c("Eccritotarsus catarinensis_QTG",
                                "Eccritotarsus eichhorniae_QTG"))

# Let's assume we only had the first 15 samples (n = 15), for each species
raw_data_ex <- raw_data_ex %>%
  dplyr::filter(between(sample_size, 1, 15))

# Check subset worked (n = 15 per species)
raw_data_ex %>% dplyr::count(insect_sp)
```

```
## # A tibble: 2 x 2
##   insect_sp          n
## * <chr>          <int>
## 1 Eccritotarsus catarinensis_QTG    15
## 2 Eccritotarsus eichhorniae_QTG    15
```

Use ThermalSampleR to evaluate sample size required

```
# Set reproducible seed
set.seed(2012)

# Perform bootstrap re-sampling
sims_15 <- ThermalSampleR::boot_two(
  # Data frame containing raw thermal limits data
  data = raw_data_ex,
  # Column name containing species ID's
  groups_col = col,
  # Name of first species
  group1 = "Eccritotarsus catarinensis_QTG",
  # Name of second species
  group2 = "Eccritotarsus eichhorniae_QTG",
  # Column name of thermal limits data
  response = ct_val,
  # Sample size to extrapolate towards
  n_max = 50,
  # Number of bootstrap iterations
  iter = 499)
```

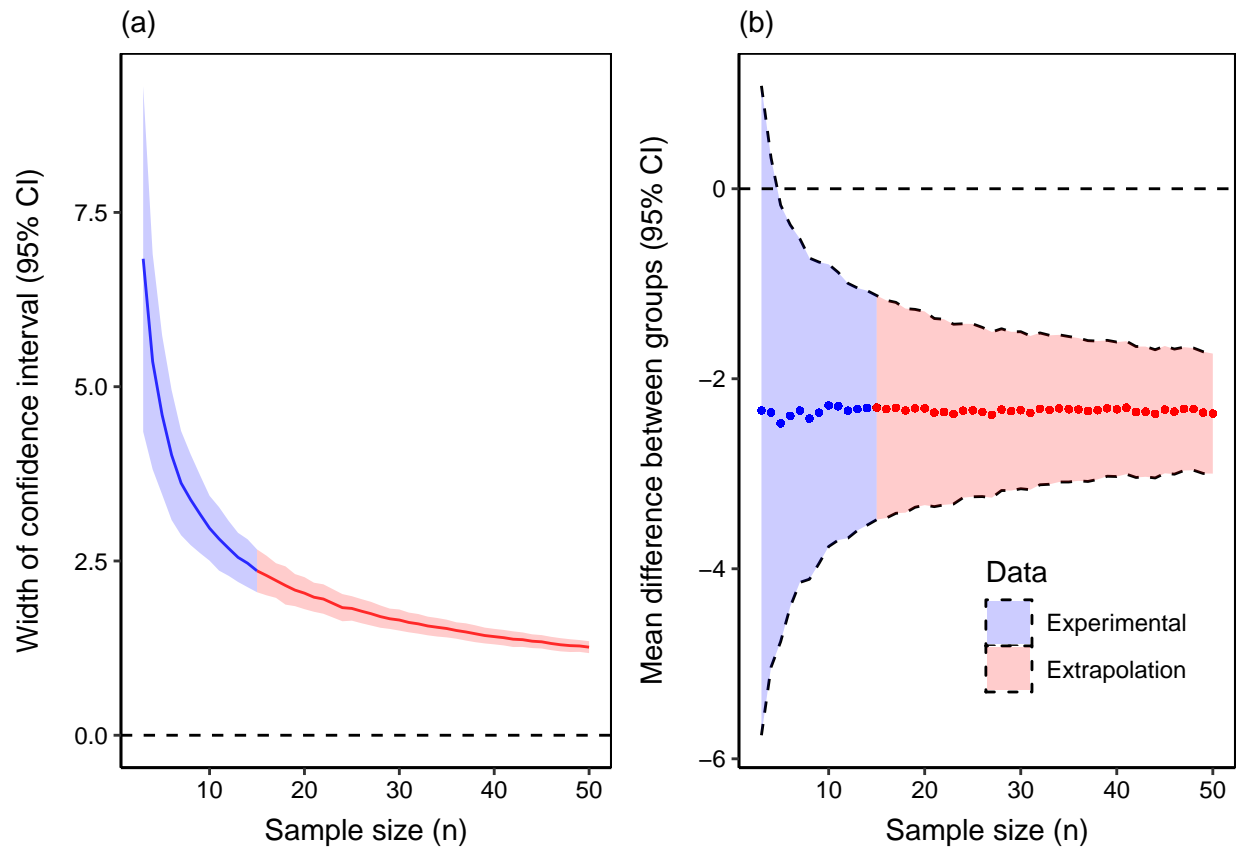
Make figure

```
# Plot bootstrap samples
fig4 <- ThermalSampleR::plot_two_groups(
  # Data frame containing bootstrap re-samples
  x = sims_15,
```

```

# Minimum number of samples to evaluate
n_min = 3,
# How many individuals were tested?
n_max = 15,
legend.position = c(0.7, 0.2))
fig4

```



Save figure to PC

```

# Save figure to file
ggplot2::ggsave(here::here("./figures/figure_4.png"),
                width = 8,
                height = 5)

```