

Owen et al. - Figure 3

This script will reproduce Figure 3 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)
```

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 bootstrap data

We have already drawn our bootstrap samples, load that data. This is the output from script-01.

```
# Load raw data (with CI's)
boot_tci <- readr::read_csv(here::here("./data_clean/ct_min_bootstrap_with_ci.csv"))

##
## -- Column specification -----
## cols(
##   insect_sp = col_character(),
##   sample_size = col_double(),
##   iter = col_double(),
##   mean = col_double(),
##   sd = col_double(),
##   median_pop_val = col_double(),
##   std_error = col_double(),
##   error = col_double(),
```

```
## lower_ci = col_double(),
## upper_ci = col_double()
## )

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

Plot width of CI

```
# Add width of CI to bootstrapped data
ci_width_bs <- boot_tci %>%
  dplyr::mutate(
    # Calculate 95% CI width
    w_ci = upper_ci - lower_ci) %>%
  # Summarise mean values across each species and sample size
  dplyr::group_by(insect_sp, sample_size) %>%
  dplyr::summarise(
    # Calculate mean 95% CI width
    ci_mean = mean(w_ci, na.rm = TRUE),
    # Calculate standard deviation of 95% CI width
    ci_sd = sd(w_ci, na.rm = TRUE),
    # Calculate standard error of 95% CI width
    ci_se = ci_mean/sqrt(sample_size),
    # Calculate mean - 1 se of 95% CI width
    lower_se = mean(ci_mean - ci_se),
    # Calculate mean + 1 se of 95% CI width
    upper_se = mean(ci_mean + ci_se)) %>%
  # Keep a single row per insect_sp + sample_size
  dplyr::slice(1) %>%
  dplyr::ungroup() %>%
  # Now average over all species
  dplyr::group_by(sample_size) %>%
  dplyr::summarise(ci_mean = mean(ci_mean),
    ci_sd = mean(ci_sd),
    lower_se = mean(lower_se),
    upper_se = mean(upper_se))
```

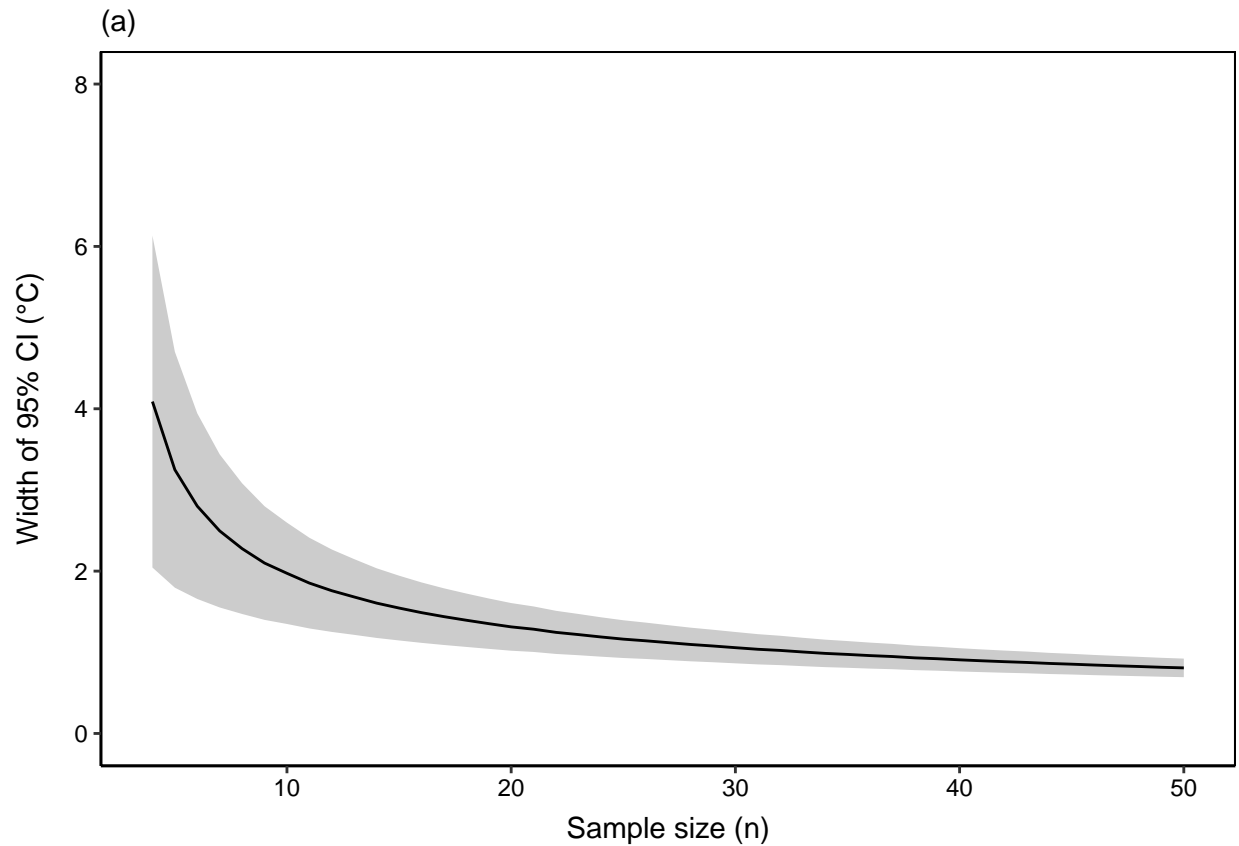
'summarise()' has grouped output by 'insect_sp', 'sample_size'. You can override using the '.groups'

```
# Plot relationship - averaged across species (focused y axis)
fig_3a <- ci_width_bs %>%
  # Remove n = 3 for visualisation (when mean > 2, R removes the entire line)
  dplyr::filter(sample_size > 3) %>%
  ggplot(data = ., aes(x = sample_size,
    y = ci_mean)) +
  geom_ribbon(aes(ymin = lower_se,
    ymax = upper_se),
    fill = "gray80") +
  geom_line() +
  scale_y_continuous(breaks = seq(0, 8, 2),
```

```

limits = c(0, 8)) +
labs(x = "Sample size (n)",
     subtitle = "(a)",
     y = "Width of 95% CI (°C)")
fig_3a

```



Perform analysis

Here, we calculate the change in the width of the 95% confidence interval (CI) of the CTmin estimate for each species, and then average over all species in our dataset.

Make figure

```

# Calculate change in width of CI, averaged across all species
ci_width_change <- boot_tci %>%
  dplyr::mutate(
    # Calculate 95% CI width
    w_ci = upper_ci - lower_ci,
    # Calculate the change in 95% CI width
    ci_change = abs(w_ci-lag(w_ci))) %>%
    # Summarise mean values across each species and sample size
    dplyr::group_by(insect_sp, sample_size) %>%

```

```

dplyr::summarise(
  # Calculate mean 95% CI change
  ci_change_mean = mean(ci_change, na.rm = TRUE),
  # Calculate standard deviation of 95% CI change
  ci_change_sd   = sd(w_ci, na.rm = TRUE),
  # Calculate standard error of 95% CI change
  ci_change_se   = ci_change_mean/sqrt(sample_size),
  # Calculate mean - 1 se of 95% CI change
  lower_se       = mean(ci_change_mean - ci_change_se),
  # Calculate mean + 1 se of 95% CI change
  upper_se       = mean(ci_change_mean + ci_change_se)) %>%
# Keep a single row per insect_sp + sample_size
dplyr::slice(1) %>%
dplyr::ungroup() %>%
# Now average over all species
dplyr::group_by(sample_size) %>%
dplyr::summarise(ci_change_mean = mean(ci_change_mean),
                  ci_change_sd   = mean(ci_change_sd),
                  lower_se       = mean(lower_se),
                  upper_se       = mean(upper_se))

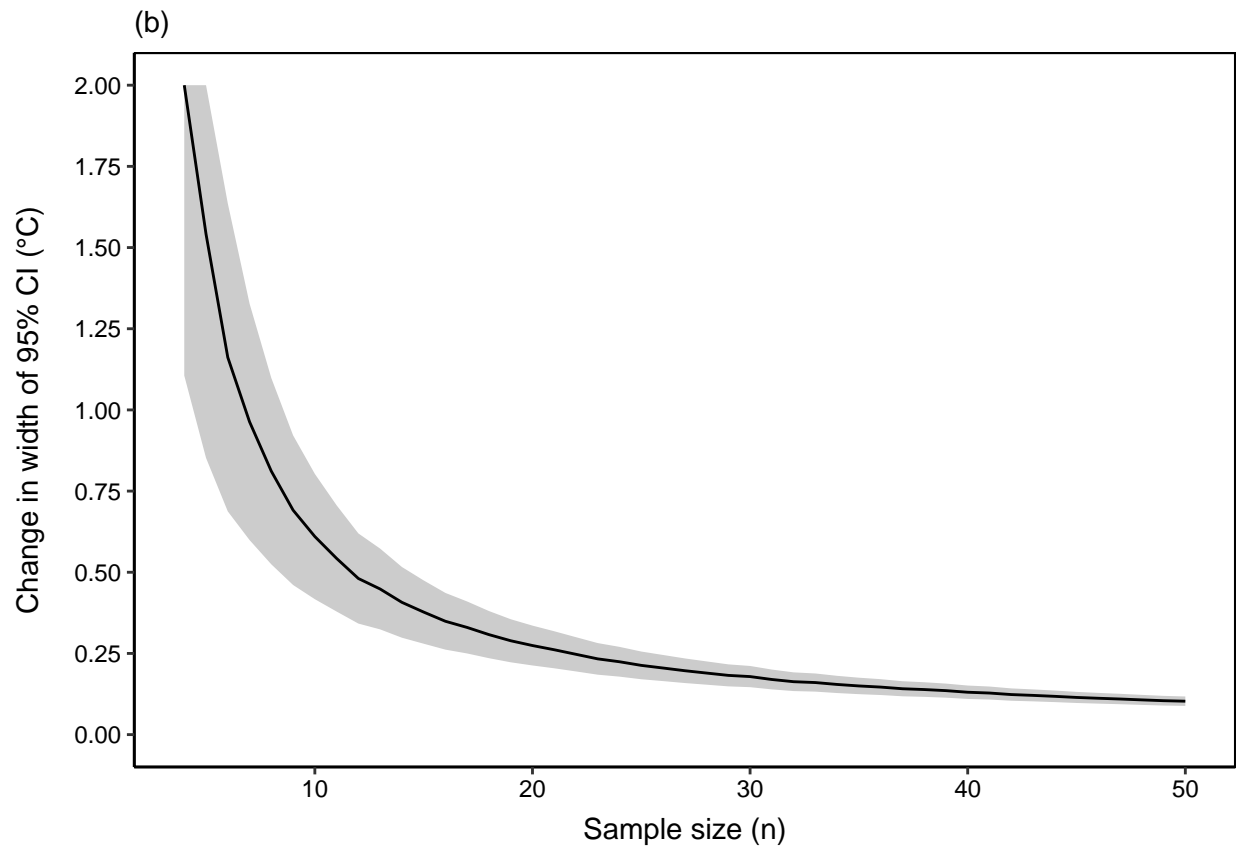
```

'summarise()' has grouped output by 'insect_sp', 'sample_size'. You can override using the '.groups'

```

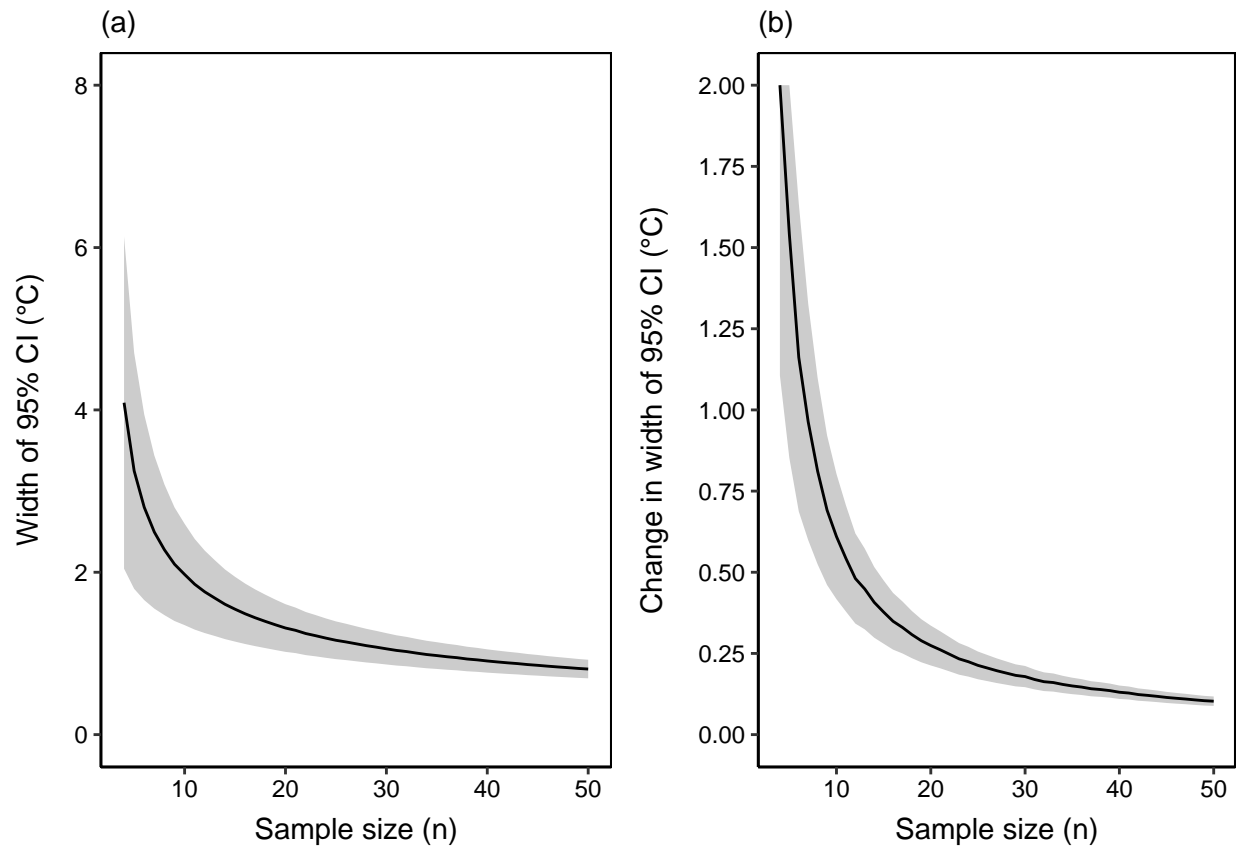
# Plot relationship - averaged across species (focused y axis)
fig_3b <- ci_width_change %>%
  # Set mean and upper se upper limit to 2 for ease of visualisation
  dplyr::mutate(upper_se = dplyr::if_else(upper_se > 2,
                                          2,
                                          upper_se)) %>%
  dplyr::mutate(ci_change_mean = dplyr::if_else(ci_change_mean > 2,
                                                2,
                                                ci_change_mean)) %>%
  # Remove n = 3 for visualisation (when mean > 2, R removes the entire line)
  dplyr::filter(sample_size > 3) %>%
  ggplot(data = ., aes(x = sample_size,
                      y = ci_change_mean)) +
  geom_ribbon(aes(ymin = lower_se,
                 ymax = upper_se),
             fill = "gray80") +
  geom_line() +
  scale_y_continuous(breaks = seq(0, 2, 0.25),
                    limits = c(0, 2)) +
  labs(x = "Sample size (n)",
       subtitle = "(b)",
       y = "Change in width of 95% CI (°C)")
fig_3b

```



Put the two plots together in one graph

```
# Put together  
fig3 <- cowplot::plot_grid(fig_3a,  
                             fig_3b,  
                             ncol = 2)  
fig3
```



```
# Save figure to file
ggplot2::ggsave(here::here("./figures/figure_3.png"),
  width = 8,
  height = 5)
```