

Figure 3 and supplements

NSMR

```
library(readr)
library(ggplot2)
library(ggrepel)
library(ggpubr)
library(cowplot)

##
## Attaching package: 'cowplot'
## The following object is masked from 'package:ggpubr':
##
##   get_legend
Now we'll load up the data, change iteration/phylo_hypothesis to factor type data
df_cragi <- readr::read_csv("CRAGI_tidy_corr.csv")

## Parsed with column specification:
## cols(
##   node = col_character(),
##   taxon = col_character(),
##   species = col_character(),
##   random = col_character(),
##   block_id = col_double(),
##   iteration = col_double(),
##   density = col_double(),
##   acc_ls = col_character(),
##   total_density = col_double(),
##   density_ratio = col_double(),
##   multi_sp = col_double(),
##   para = col_character(),
##   block_corr = col_double()
## )
df_calmi <- readr::read_csv("CALMI_tidy_corr.csv")

## Parsed with column specification:
## cols(
##   node = col_character(),
##   taxon = col_character(),
##   species = col_character(),
##   random = col_character(),
##   block_id = col_double(),
##   iteration = col_double(),
##   density = col_double(),
##   acc_ls = col_character(),
##   total_density = col_double(),
```

```
## density_ratio = col_double(),
## multi_sp = col_double(),
## para = col_character(),
## block_corr = col_double()
## )
```

```
df_musmu <- readr::read_csv("MUSMU_tidy_corr.csv")
```

```
## Parsed with column specification:
## cols(
##   node = col_character(),
##   taxon = col_character(),
##   species = col_character(),
##   random = col_character(),
##   block_id = col_double(),
##   iteration = col_double(),
##   density = col_double(),
##   acc_ls = col_character(),
##   total_density = col_double(),
##   density_ratio = col_double(),
##   multi_sp = col_double(),
##   para = col_character(),
##   block_corr = col_double()
## )
```

```
df_mizye <- readr::read_csv("MIZYE_tidy_corr.csv")
```

```
## Parsed with column specification:
## cols(
##   node = col_character(),
##   taxon = col_character(),
##   species = col_character(),
##   random = col_character(),
##   block_id = col_double(),
##   iteration = col_double(),
##   density = col_double(),
##   acc_ls = col_character(),
##   total_density = col_double(),
##   density_ratio = col_double(),
##   multi_sp = col_double(),
##   para = col_character(),
##   block_corr = col_double()
## )
```

```
df_sacko <- readr::read_csv("SACKO_tidy_corr.csv")
```

```
## Parsed with column specification:
## cols(
##   node = col_character(),
##   taxon = col_character(),
##   species = col_character(),
##   random = col_character(),
##   block_id = col_double(),
##   iteration = col_double(),
##   density = col_double(),
##   acc_ls = col_character(),
```

```

## total_density = col_double(),
## density_ratio = col_double(),
## multi_sp = col_double(),
## para = col_character(),
## block_corr = col_double()
## )

df_strpu <- readr::read_csv("STRPU_tidy_corr.csv")

## Parsed with column specification:
## cols(
##   node = col_character(),
##   taxon = col_character(),
##   species = col_character(),
##   random = col_character(),
##   block_id = col_double(),
##   iteration = col_double(),
##   density = col_double(),
##   acc_ls = col_character(),
##   total_density = col_double(),
##   density_ratio = col_double(),
##   multi_sp = col_double(),
##   para = col_character(),
##   block_corr = col_double()
## )

map_signif_level <- c(`****` = 1e-04, `***` = 0.001, `**` = 0.01, `*` = 0.05, ns = 1)

make_plot <- function(tbl,
  key = "observed",
  comparisons = list(c("observed", "random")),
  bracket_y = NULL,
  ylims = c(-0.5, 1.5)) {

  if(is.null(bracket_y)) {
    h = ylims[2] - ylims[1]
    bracket_y = c(.9,.825,.75)*h + ylims[1]
  }

  size.summary <- tbl %>% dplyr::filter(random == "observed") %>% dplyr::group_by(node, para) %>% dplyr
  ggplot(tbl, aes_string(x = 'random', y = 'block_corr', fill = 'random')) +
    #geom_violin(draw_quantiles = c(0.25, 0.5, 0.75)) +
    geom_boxplot(outlier.shape=NA) +
    facet_grid(para ~ node) +
    theme_cowplot(font_size = 6) +
    geom_signif(comparisons = list(c("observed", "random")),
      test = "wilcox.test", test.args = list(paired = FALSE, exact = FALSE), na.rm = TRUE,
      map_signif_level = map_signif_level,
      color="black", tip_length = 0.01, size = .25, textsize = 1,
      y_position = bracket_y, data = NULL) +
    scale_y_continuous(name = "Block correlation", limits = c(-0.5, 1.5)) +
    theme(legend.title = element_blank(),
      plot.margin = unit(c(1,0,0,0), units='cm'),
      legend.position = 'bottom',
      legend.justification = 'center',

```

```

    strip.text = element_text(size = 6, margin = margin(5,0,5,0,'pt')),
    axis.ticks.x = element_blank(),
    axis.title.y = element_text(size = 7),
    axis.text = element_text(size = 6)) +
  geom_text(data = size.summary, aes(x=1, y= 1.2,hjust=0.4,label=label), inherit.aes=F, size = 1)
}

```

Make boxplots

```

p_calmi <- make_plot(df_calmi)

## `summarise()` regrouping output by 'node' (override with `.groups` argument)
p_cragi <- make_plot(df_cragi)

## `summarise()` regrouping output by 'node' (override with `.groups` argument)
p_mizye <- make_plot(df_mizye)

## `summarise()` regrouping output by 'node' (override with `.groups` argument)
p_musmu <- make_plot(df_musmu)

## `summarise()` regrouping output by 'node' (override with `.groups` argument)
p_sacko <- make_plot(df_sacko)

## `summarise()` regrouping output by 'node' (override with `.groups` argument)
p_strpu <- make_plot(df_strpu)

## `summarise()` regrouping output by 'node' (override with `.groups` argument)
ggsave(filename = 'SF7A_calmi_corr_boxplots.pdf',
        plot = p_calmi,
        units = 'cm',
        width = 13,
        height = 7)

## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
ggsave(filename = 'SF7B_cragi_corr_boxplots.pdf',
        plot = p_cragi,
        units = 'cm',
        width = 13,
        height = 7)

ggsave(filename = 'SF7C_mizye_corr_boxplots.pdf',
        plot = p_mizye,
        units = 'cm',
        width = 13,
        height = 7)

ggsave(filename = 'SF7D_musmu_corr_boxplots.pdf',
        plot = p_musmu,
        units = 'cm',
        width = 13,
        height = 7)

```

```
ggsave(filename = 'SF7E_sacko_corr_boxplots.pdf',
        plot = p_sacko,
        units = 'cm',
        width = 13,
        height = 7)

ggsave(filename = 'SF7F_strpu_corr_boxplots.pdf',
        plot = p_strpu,
        units = 'cm',
        width = 13,
        height = 7)
```

```
## Warning: Removed 7 rows containing non-finite values (stat_boxplot).
```