SF10 hox and wnt boxplots

NSMR

```
library(readr)
library(ggplot2)
library(gridExtra)
library(grid)
library(ggpubr)
library(cowplot)
##
## Attaching package: 'cowplot'
## The following object is masked from 'package:ggpubr':
##
##
       get_legend
library(RColorBrewer)
Now we'll load up the data, change iteration/phylo_hypothesis to factor type data
df_wnt <- readr::read_csv("wnt.tidydf.csv")</pre>
## 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_character(),
##
     para = col_character()
df_hox <- readr::read_csv("hox.tidydf.csv")</pre>
## 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_character(),
##
     para = col_character()
## )
Here we define a function to make boxplots of the supp figure.
map signif level <-c(***** = 1e-04, **** = 0.001, *** = 0.01, ** = 0.05, ns = 1)
make_plot <- function(tbl,</pre>
                      key = "observed",
                      comparisons = list(c("observed", "random")),
                      bracket y = NULL,
                      ylims = c(-2.5, 2.5)) {
  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(taxon) %>% dplyr::si
  ggplot(tbl, aes_string(x = 'random', y = 'log10_density_ratio', fill = 'random')) +
    geom_boxplot(outlier.shape = NA) +
    facet_grid(~ taxon) +
    theme cowplot() +
    theme(axis.title.x = element blank(), axis.text.x = element blank()) +
    geom_signif(comparisons = comparisons,
                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 = .5, textsize = 2,
                y_position = bracket_y, data = NULL) +
    scale_y_continuous(name = "log10(Density ratio)", limits = c(-2.5, 2.5)) +
    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, angle = 90, 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=2.2,hjust = 0.5,label = label), size = 2, inherit.aes=F)
}
Modify data format to make it easy to use
df_wnt$taxon <- factor(df_wnt$taxon, levels=c('Poriferan','Ctenophore','Placozoan','Cnidarian', 'Acoel'
df_wnt$node <- as.factor(df_wnt$node)</pre>
df wnt$random <- as.factor(df wnt$random)</pre>
df_wnt$species <- as.factor(df_wnt$species)</pre>
df_wnt$log10_density_ratio <- log10(df_wnt$density_ratio)</pre>
df_hox$taxon <- factor(df_hox$taxon, levels=c('Poriferan', 'Ctenophore', 'Placozoan', 'Cnidarian', 'Acoel
df_hox$node <- as.factor(df_hox$node)</pre>
df_hox$random <- as.factor(df_hox$random)</pre>
```

```
df_hox$species <- as.factor(df_hox$species)</pre>
df_hox$log10_density_ratio <- log10(df_hox$density_ratio)</pre>
Make the plots and save them
hox_p <- make_plot(df_hox)</pre>
## `summarise()` ungrouping output (override with `.groups` argument)
wnt_p <- make_plot(df_wnt)</pre>
## `summarise()` ungrouping output (override with `.groups` argument)
gridplot <- gridExtra::grid.arrange(grobs = list(hox_p,wnt_p), ncol = 2)</pre>
                                       Cephalochordate
                                                                                                       Cephalochordate
                        Lophotrochozoan
                               Ambulacrarian
               Ecdysozoan
                                                      Vertebrate
                                                                            Ecdysozoan
        Cnidarian
                                                                                                                Vertebrate
                                               Tunicate
                     n=9...
                                                                                   n=3<sub>*</sub>
             n=11...
   2
log10(Density ratio)
                                                          log10(Density ratio)
  -2
                                                             -2
                                                                          observed = random
ggsave(plot = gridplot,
         filename = 'hox_wnt.pdf',
         unit = 'cm',
         width = 15,
         height = 12)
```