

Forestplot with Shannon, Chao1 and Simpson indexes

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To run this code, you must already have run the scripts of each index (difference_shannon.Rmd, difference_chao1.Rmd, difference_simpson.Rmd) to have the data frame test_shannon, test_chao1, test_simpson.

```
load("forestplot_environment.RData")
library(metafor)
library(forestplot)
library(ggplot2)
library(grid)

grid.newpage()
layout(matrix(1:3,1,3))
page.layout <- grid.layout(nrow = 1, ncol = 40,
  widths = unit(c(1.2), "cm"),
  heights = unit(c(1), "null"),
  default.units = "null",
  respect = FALSE,
  just = "centre")
pushViewport(viewport(layout = page.layout))
pushViewport(viewport(layout.pos.col = 1:25))
col_no <- grep("coef", colnames(test_shannon))
row_names <-
  ↪ list(c("Disease",rep("Asthma",3),"",rep("Asthma",5),"",rep("Asthma",2),"", "", "", rep("COPD",2),
  ↪ "",rep("COPD",6),"", "", rep("CF",6),"", "", "", "NCFB", "", "" ),
  ↪ c("Sample",rep("BAL",3),"BAL summary","Sputum",rep("Sputum
  ↪ (induced)",4),"Sputum (induced) summary","UA","UA","UA
  ↪ summary","", "", rep("BAL",2),"BAL summary",
  ↪ "LA","LA","Sputum","Sputum","Sputum
  ↪ (induced)","UA","", "", "LA",rep("Sputum",5),"Sputum summary",
  ↪ "", "", "BAL", "", "" ),
  ↪ c("Study","Goleva et al. 2013","Denner et al. 2016","Sverrild et al.
  ↪ 2017","", "Liu et al. 2020","Li et al. 2017","Marri et al. 2013","Huang et
  ↪ al. 2020","Munck et al. 2016","", "Park et al. 2014","Lee et al.
  ↪ 2018","", "Asthma summary","", "Erb-Downward et al. 2011","Pragman et al.
  ↪ 2012","", "Einarsson et al. 2016","Kim et al. 2017","Feigelman et al.
  ↪ 2017","Millares et al. 2015","Wang et al. 2020","Park et al. 2014","COPD
  ↪ summary","", "Pletcher et al. 2019","Soret et al. 2020","Narayanamurthy et
  ↪ al. 2017","Filkins et al. 2012","Coburn et al. 2015","Carmody et al.
  ↪ 2013","", "CF summary","", "Byun et al. 2017","", "Summary"))

coef <- with(test_shannon, cbind(coef1,coef3,coef4,coef2))
low <- with(test_shannon, cbind(low1,low3,low4,low2))
high <- with(test_shannon, cbind(high1,high3,high4,high2))
```

```

forestplot(row_names,
  coef, low, high,
  hrzl_lines = list("2" = gpar(lty = 1),"16" = gpar(lty = 2),"27" = gpar(lty = 2),"36" =
    ↪ gpar(lty = 2),"38" = gpar(lty = 1)),
  title = "
    ↪ Difference of mean Shannon index",
  pos.title = "right",
  boxsize = 0.2,
  col = fpColors(
    box = c("royalblue", "orange","green","red"),
    line = c("royalblue", "orange","green","red"),
    summary = c("royalblue", "orange","green","red")
  ),
  vertices = TRUE,
  is.summary =
    ↪ c(TRUE,rep(FALSE,3),TRUE,rep(FALSE,5),TRUE,rep(FALSE,2),TRUE,TRUE,rep(FALSE,3),TRUE,
      rep(FALSE,6),TRUE,rep(FALSE,7),TRUE,TRUE,rep(FALSE,3),TRUE),
  xlab = "Difference of mean Shannon index",
  new_page = FALSE,
  legend = c("Healthy/Stable","Healthy/Diseased","Stable/Exacerbated","Healthy/Exacerbated"),
  legend_args = fpLegend(
    #pos = list("topright","inset" =unit(1, "npc"),"align"="horizontal"),
    pos = list("topright","inset" =unit(21.5, "cm"),"align"="vertical"),
    title = "Difference",
    r = unit(0, "npc"),
    gp = NULL
  )
)
)

popViewport()
pushViewport(viewport(layout.pos.col = 26:33))
col_no <- grep("coef", colnames(test_chao1))
row_names <-
  ↪ list(c("Disease",rep("Asthma",3),"",rep("Asthma",5),"",rep("Asthma",2),"", "", "", rep("COPD",2),
    "", rep("COPD",6), "", "", rep("CF",6), "", "", "", "NCFB", "", "" ),
    c("Sample",rep("BAL",3),"BAL summary","Sputum",rep("Sputum
      ↪ (induced)",4),"Sputum (induced) summary","UA","UA","UA
      ↪ summary","", "", rep("BAL",2),"BAL summary",
      ↪ "LA","LA","Sputum","Sputum","Sputum
      ↪ (induced)","UA","", "", "LA",rep("Sputum",5),"Sputum summary",
      ↪ "", "", "BAL", "", "" ),
    c("Study","Goleva et al. 2013","Denner et al. 2016","Sverrild et al.
      ↪ 2017","", "Liu et al. 2020","Li et al. 2017","Marri et al. 2013","Huang et
      ↪ al. 2020","Munck et al. 2016","", "Park et al. 2014","Lee et al.
      ↪ 2018","", "Asthma summary","", "Erb-Downward et al. 2011","Pragman et al.
      ↪ 2012","", "Einarsson et al. 2016","Kim et al. 2017","Feigelman et al.
      ↪ 2017","Millares et al. 2015","Wang et al. 2020","Park et al. 2014","COPD
      ↪ summary","", "Pletcher et al. 2019","Soret et al. 2020","Narayanamurthy et
      ↪ al. 2017","Filkins et al. 2012","Coburn et al. 2015","Carmody et al.
      ↪ 2013","", "CF summary","", "Byun et al. 2017","", "Summary"))

coef <- with(test_chao1, cbind(coef1,coef3,coef4,coef2))
low <- with(test_chao1, cbind(low1,low3,low4,low2))

```

```

high <- with(test_chao1, cbind(high1,high3,high4,high2))
forestplot(rep(NA,39),
  coef, low, high,
  hrzl_lines = list("2" = gpar(lty = 1),"16" = gpar(lty = 2),"27" = gpar(lty = 2),"36" =
    ↪ gpar(lty = 2),"38" = gpar(lty = 1)),
  title = "Difference of mean Chao1 index",
  boxsize = 0.2,
  col = fpColors(
    box = c("royalblue", "orange","green","red"),
    line = c("royalblue", "orange","green","red"),
    summary = c("royalblue", "orange","green","red")
  ),
  vertices = TRUE,
  is.summary =
    ↪ c(TRUE,rep(FALSE,3),TRUE,rep(FALSE,5),TRUE,rep(FALSE,2),TRUE,TRUE,rep(FALSE,3),TRUE,
      rep(FALSE,6),TRUE,rep(FALSE,7),TRUE,TRUE,rep(FALSE,3),TRUE),
  xlab = "Difference of mean Chao1 index",
  new_page = FALSE,
  #legend = c("Healthy/Stable","Stable/Exacerbated","Healthy/Exacerbated"),
  #legend_args = fpLegend(
    # pos = list(x = 0.87, y = 0.85),
    # title = "Difference",
    # r = unit(.1, "npc"),
    # gp = gpar(col = "#CCCCC", lwd = 1.5)
    #)
)

popViewport()
pushViewport(viewport(layout.pos.col = 34:40))
col_no <- grep("coef", colnames(test_simpson))
row_names <-
  ↪ list(c("Disease",rep("Asthma",3),"",rep("Asthma",5),"",rep("Asthma",2),"", "", "", rep("COPD",2),
    "",rep("COPD",6),"", "",rep("CF",6),"", "", "", "NCFB", "", ""),
    c("Sample",rep("BAL",3),"BAL summary","Sputum",rep("Sputum
      ↪ (induced)",4),"Sputum (induced) summary","UA","UA","UA
      ↪ summary","", "",rep("BAL",2),"BAL summary",
      ↪ "LA","LA","Sputum","Sputum","Sputum
      ↪ (induced)","UA","", "", "LA",rep("Sputum",5),"Sputum summary",
      ↪ "", "", "BAL", "", "")),
    c("Study","Goleva et al. 2013","Denner et al. 2016","Sverrild et al.
      ↪ 2017","", "Liu et al. 2020","Li et al. 2017","Marri et al. 2013","Huang et
      ↪ al. 2020","Munck et al. 2016","", "Park et al. 2014","Lee et al.
      ↪ 2018","", "Asthma summary","", "Erb-Downward et al. 2011","Pragman et al.
      ↪ 2012","", "Einarsson et al. 2016","Kim et al. 2017","Feigelman et al.
      ↪ 2017","Millares et al. 2015","Wang et al. 2020","Park et al. 2014","COPD
      ↪ summary","", "Pletcher et al. 2019","Soret et al. 2020","Narayanamurthy et
      ↪ al. 2017","Filkins et al. 2012","Coburn et al. 2015","Carmody et al.
      ↪ 2013","", "CF summary","", "Byun et al. 2017","", "Summary"))

coef <- with(test_simpson, cbind(coef1,coef3,coef4,coef2))
low <- with(test_simpson, cbind(low1,low3,low4,low2))
high <- with(test_simpson, cbind(high1,high3,high4,high2))
forestplot(rep(NA,39),

```

```

coef, low, high,
hrzl_lines = list("2" = gpar(lty = 1), "16" = gpar(lty = 2), "27" = gpar(lty = 2), "36" =
  ↪ gpar(lty = 2), "38" = gpar(lty = 1)),
title = "Difference of mean Simpson index",
boxsize = 0.2,
col = fpColors(
  box = c("royalblue", "orange", "green", "red"),
  line = c("royalblue", "orange", "green", "red"),
  summary = c("royalblue", "orange", "green", "red")
),
vertices = TRUE,
is.summary =
  ↪ c(TRUE, rep(FALSE, 3), TRUE, rep(FALSE, 5), TRUE, rep(FALSE, 2), TRUE, TRUE, rep(FALSE, 3), TRUE,
    rep(FALSE, 6), TRUE, rep(FALSE, 7), TRUE, TRUE, rep(FALSE, 3), TRUE),
xlab = "Difference of mean Simpson index",
new_page = FALSE,
#legend = c("Healthy/Stable", "Healthy/Diseased", "Stable/Exacerbated", "Healthy/Exacerbated"),
#legend_args = fpLegend(
#  pos = list(x = 0, y = 0.87),
#  title = "Difference",
#  r = unit(.1, "snpc"),
#  gp = gpar(col = "#CCCCCC", lwd = 1.5)
#)
)

popViewport(2)

dev.off()

```