



View(varroa)

library(tidyverse)

library(ggpubr)

library(rstatix)

set.seed(1234)

varroa %>% sample\_n\_by("Region", size=415)

varroa = varroa %>%

 reorder\_levels("Region", order = c("South", "HI", "UT"))

varroa %>%

 group\_by("Regions") %>%

 get\_summary\_stats("Mites", type = "common")

ggboxplot(varroa, x="Region", y="Mites")

res.kruskal=kruskal\_test(varroa, Mites~Region); res.kruskal

varroa %>% kruskal.test(Mites~Region)

varroa %>% kruskal\_effsize(Mites~Region)

pwc= varroa %>% dunn\_test(Mites~Region, p.adjust.method = "bonferroni");pwc

D2= varroa %>% wilcox\_test(Mites~Region, p.adjust.method=("bonferroni"));D

pwc= pwc %>% add\_xy\_position(x="Region");pwc

ggboxplot(varroa, x="Region", y="Mites") +

 stat\_pvalue\_manual(pwc, hide.ns= TRUE) +

 labs(

 subtitle = get\_test\_label(res.kruskal, detailed = TRUE),

 caption = get\_pwc\_label(pwc)

 )

set.seed(1234)

varroa %>% sample\_n\_by("Source", size=415)

varroa = varroa %>%

 reorder\_levels("Source", order = c("M", "F", "S"))

varroa %>%

 group\_by("Source") %>%

 get\_summary\_stats("Mites", type = "common")

ggboxplot(varroa, x="Source", y="Mites")

res.kruskal=kruskal\_test(varroa, Mites~Source); res.kruskal

varroa %>% kruskal.test(Mites~Source)

varroa %>% kruskal\_effsize(Mites~Source)

pwc= varroa %>% dunn\_test(Mites~Region, p.adjust.method = "bonferroni");pwc

D2= varroa %>% wilcox\_test(Mites~Region, p.adjust.method=("bonferroni"));D

pwc= pwc %>% add\_xy\_position(x="Region");pwc

ggboxplot(varroa, x="Source", y="Mites") +

 stat\_pvalue\_manual(pwc, hide.ns= TRUE) +

 labs(

 subtitle = get\_test\_label(res.kruskal, detailed = TRUE),

 caption = get\_pwc\_label(pwc)

 )

set.seed(1234)

varroa %>% sample\_n\_by("Lineage", size=415)

varroa = varroa %>%

 reorder\_levels("Lineage", order = c("A", "C", "M", "O"))

varroa %>%

 group\_by("Lineage") %>%

 get\_summary\_stats("Mites", type = "common")

ggboxplot(varroa, x="Lineage", y="Mites")

res.kruskal=kruskal\_test(varroa, Mites~Lineage); res.kruskal

varroa %>% kruskal.test(Mites~Lineage)

varroa %>% kruskal\_effsize(Mites~Lineage)

pwc= varroa %>% dunn\_test(Mites~Lineage, p.adjust.method = "bonferroni");pwc

D2= varroa %>% wilcox\_test(Mites~Region, p.adjust.method=("bonferroni"));D

pwc= pwc %>% add\_xy\_position(x="Lineage");pwc

ggboxplot(varroa, x="Lineage", y="Mites") +

 stat\_pvalue\_manual(pwc, hide.ns= TRUE) +

 labs(

 subtitle = get\_test\_label(res.kruskal, detailed = TRUE),

 caption = get\_pwc\_label(pwc)

 )