In-field assays

2023-04-10

```
source(here::here("setup.R"))
```

```
Skipping install of 'drcData' from a github remote, the SHA1 (09f9da30) has not changed since
  Use `force = TRUE` to force installation

Skipping install of 'drc' from a github remote, the SHA1 (8719d43a) has not changed since las
  Use `force = TRUE` to force installation

Skipping install of 'medrc' from a github remote, the SHA1 (bc36df51) has not changed since l
  Use `force = TRUE` to force installation

[conflicted] Will prefer dplyr::filter over any other package.
[conflicted] Will prefer dplyr::select over any other package.
```

```
library(lme4)
theme_set(theme_bw(base_size=12))
```

```
dat <- rio::import("data/field.csv") %>%
  mutate_at(vars(fungicide, season, tree), as.factor) %>%
  mutate(fungicide=fct_relevel(fungicide, "Control"))
str(dat)
```

```
'data.frame':   60 obs. of  5 variables:
 $ fungicide: Factor w/ 3 levels "Control","Bellis",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ season   : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...
 $ tree     : Factor w/ 10 levels "1","2","3","4",..: 1 2 3 4 5 6 7 8 9 10 ...
 $ leaves   : int  250 250 250 250 250 250 250 250 250 250 ...
 $ diseased : int  27 19 26 30 16 40 27 22 19 8 ...
```

Data scheme

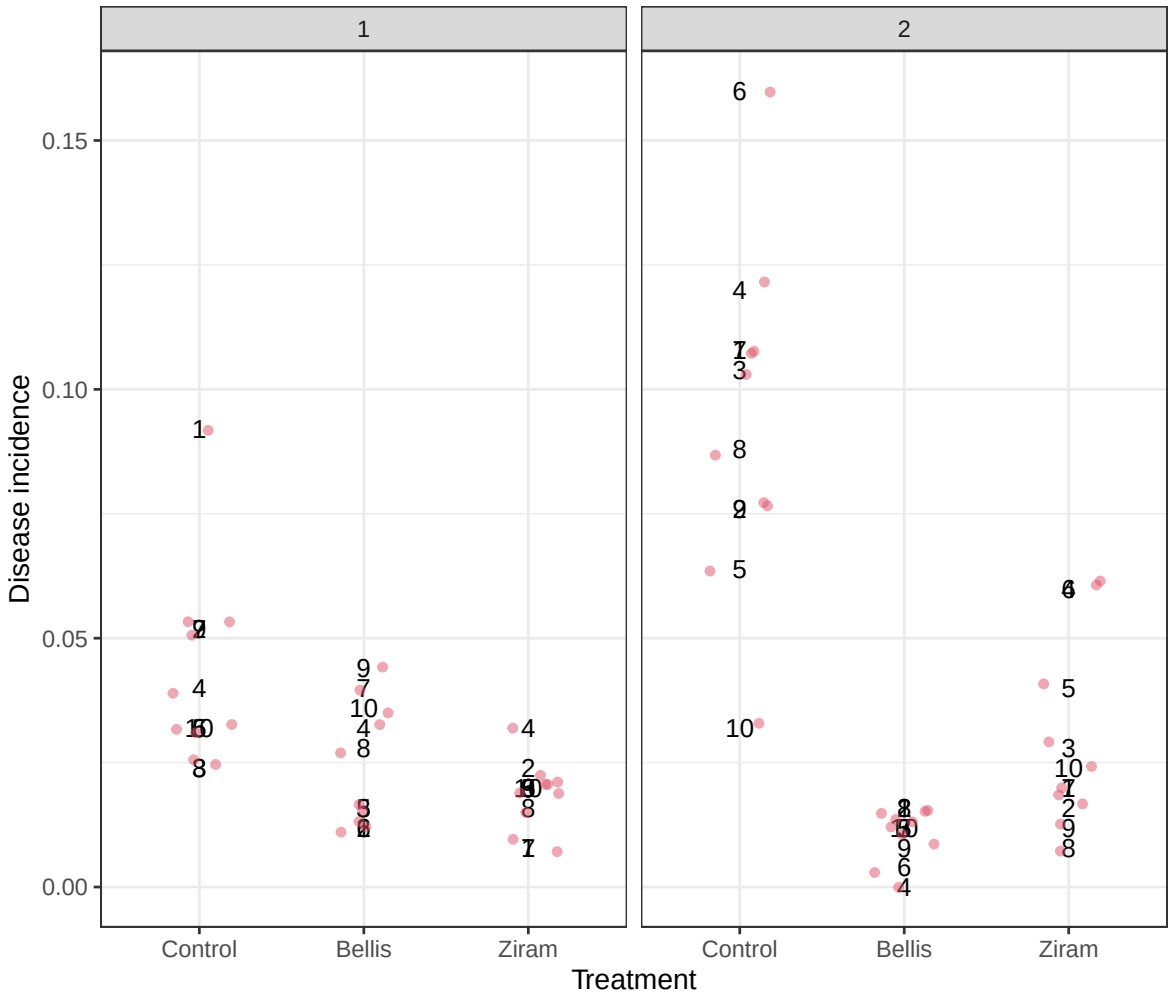
```
ftable(xtabs(~ fungicide + tree + season, dat))
```

```
              season 1 2
fungicide tree
Control   1           1 1
          2           1 1
          3           1 1
          4           1 1
          5           1 1
          6           1 1
          7           1 1
          8           1 1
          9           1 1
          10          1 1
Bellis    1           1 1
          2           1 1
          3           1 1
          4           1 1
          5           1 1
          6           1 1
          7           1 1
          8           1 1
          9           1 1
          10          1 1
Ziram     1           1 1
          2           1 1
          3           1 1
          4           1 1
          5           1 1
          6           1 1
          7           1 1
          8           1 1
          9           1 1
          10          1 1
```

Model

```
dat %>%
  ggplot() +
```

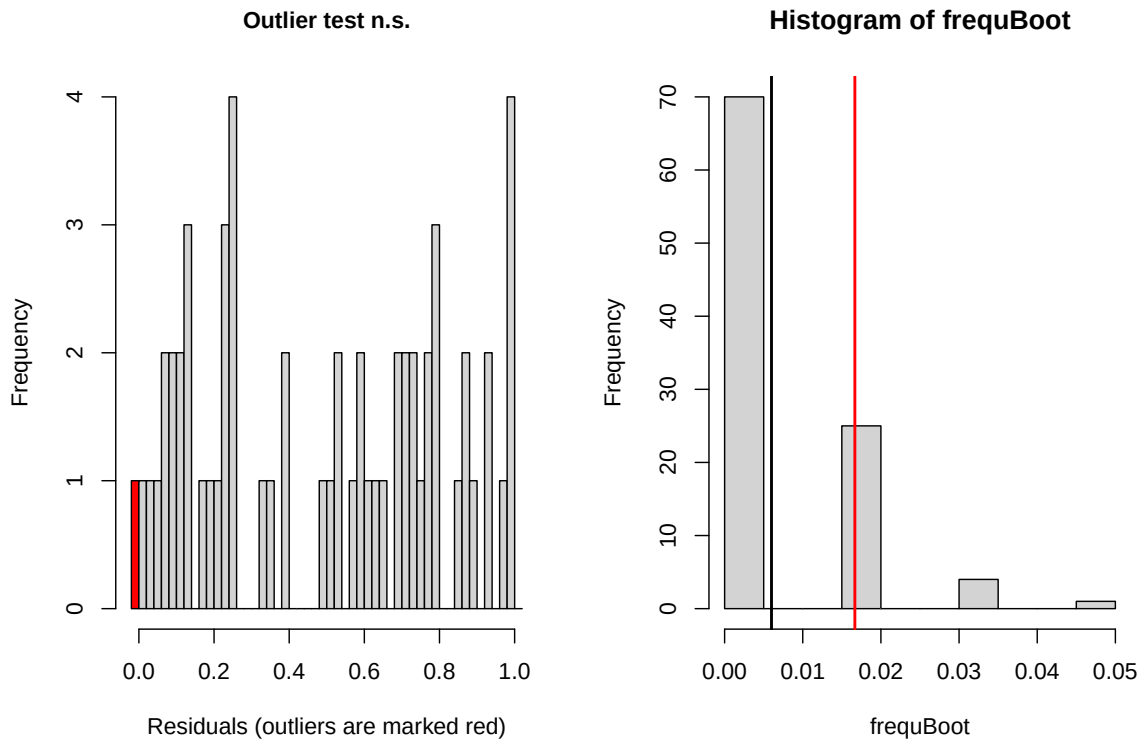
```
  aes(x=fungicide, y=diseased/leaves) +
  # geom_boxplot(width=.5) +
  geom_text(aes(label=tree))+
  geom_jitter(width=.2, col=2, alpha=.5) +
  labs(x="Treatment", y="Disease incidence") +
  facet_wrap("season")
```




```
mod <- glmer(diseased/leaves ~ fungicide * season + (1|tree),
             weights=leaves, family=binomial, dat)
```

Goodness of fit

```
simulateResiduals(mod) %>% testResiduals()
```




```
car::Anova(mod)
```

Chisq	Df	Pr(>Chisq)
161	2	1.35e-35
25.2	1	5.11e-07
41.1	2	1.18e-09

Means comparison test

```
emm <- emmeans(mod, ~ fungicide|season, type="response")
res <- cld(emm, alpha=0.05, Letters=letters,  type="response") %>%
   mutate(`%Control`=abs((prob/dplyr::filter(.,fungicide=="Control")%>% pull(prob)-1)*100)
  tibble
```

```
res %>%
  rename(Season="season") %>%
  ggplot()+
  aes(x=fungicide, y =prob)+
  geom_pointrange(aes(ymin=asymp.LCL , ymax=asymp.UCL))+
  facet_wrap("Season", labeller = label_both) + geom_text(aes(label=str_squish(.group)), a
  geom_jitter(data=dat%>%rename(Season="season") , aes(y=diseased/leaves), alpha=.2, width
```