

In-field assays

2023-04-14

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

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

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

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

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

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

```
v Setting active project to 'C:/Users/tudela.alumine/Documents/github_alu/Chemical_control_o
```

```
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

```
fctable(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

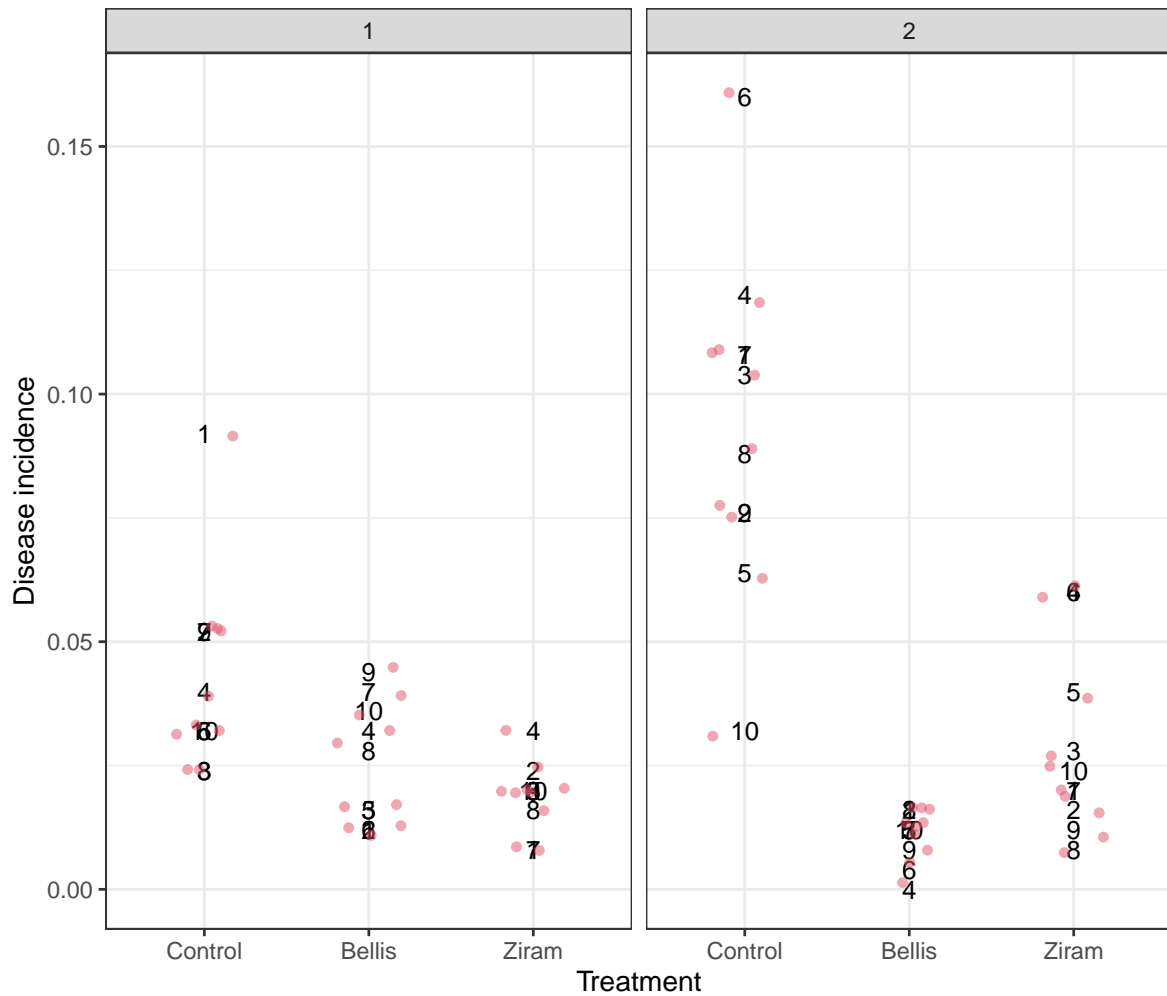
Model

```
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")

```



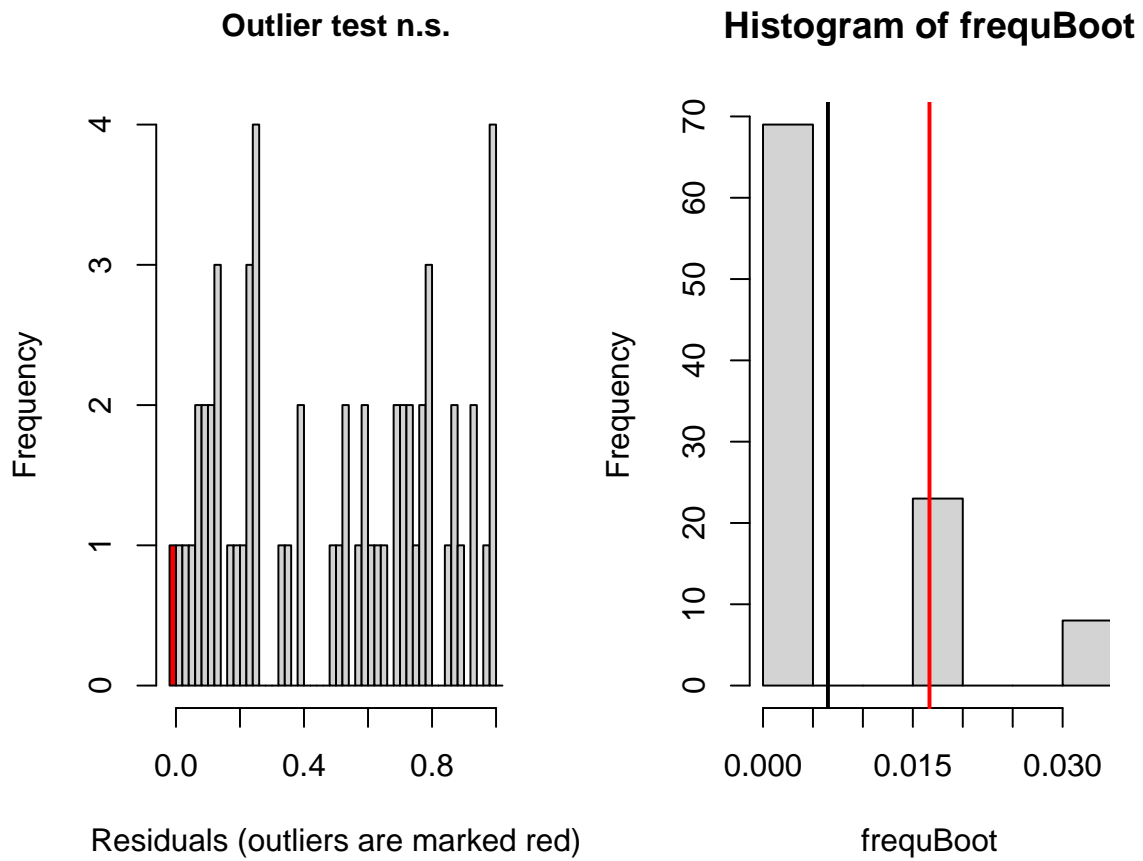
```

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=asyp.LCL , ymax=asyp.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

```

