

In vitro experiments

2023-04-14

Mycelial growth

```
raw <- rio::import("data/mycelial_growth.csv", dec=",")

dat <- raw %>%
  mutate_at(vars(dose, colony_diameter), as.numeric) %>%
  mutate_at(vars(fungicide, strain, experiment, plate), as.factor) %>%
  # mutate(dose_decimal = format(dose, scientific = FALSE) %>% str_squish()) %>%
  # mutate(dose = as.numeric(dose_decimal)) %>%
  mutate(curve_id = interaction(fungicide:strain:experiment))
```

Data scheme

```
dat %>% str
```

```
'data.frame':  756 obs. of  7 variables:
 $ fungicide      : Factor w/ 4 levels "Bellis","Merpan",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ strain         : Factor w/ 3 levels "S20","S23","S8": 2 2 2 1 1 1 3 3 3 2 ...
 $ experiment     : Factor w/ 3 levels "1","2","3": 1 1 1 1 1 1 1 1 1 1 ...
 $ dose          : num  0 0 0 0 0 0 0 0 0 100 ...
 $ plate         : Factor w/ 3 levels "1","2","3": 1 2 3 1 2 3 1 2 3 1 ...
 $ colony_diameter: num  53 55 56 52 53 52 51 51 52 0 ...
 $ curve_id      : Factor w/ 36 levels "Bellis:S20:1",...: 4 4 4 1 1 1 7 7 7 4 ...
```

```
ftable(xtabs(~ fungicide + strain + experiment + dose, dat))
```

```
                                dose 0 0.01 0.1 0.5 1 10 50 100 500 1000
fungicide strain experiment
```

Bellis	S20	1	3	3	3	0	3	3	3	3	0	0
		2	3	3	3	0	3	3	3	3	0	0
		3	3	3	3	0	3	3	3	3	0	0
	S23	1	3	3	3	0	3	3	3	3	0	0
		2	3	3	3	0	3	3	3	3	0	0
		3	3	3	3	0	3	3	3	3	0	0
	S8	1	3	3	3	0	3	3	3	3	0	0
		2	3	3	3	0	3	3	3	3	0	0
		3	3	3	3	0	3	3	3	3	0	0
Merpan	S20	1	3	0	3	0	3	3	0	3	3	3
		2	3	0	3	0	3	3	0	3	3	3
		3	3	0	3	0	3	3	0	3	3	3
	S23	1	3	0	3	0	3	3	0	3	3	3
		2	3	0	3	0	3	3	0	3	3	3
		3	3	0	3	0	3	3	0	3	3	3
	S8	1	3	0	3	0	3	3	0	3	3	3
		2	3	0	3	0	3	3	0	3	3	3
		3	3	0	3	0	3	3	0	3	3	3
Timorex	S20	1	3	0	3	0	3	3	0	3	3	3
		2	3	0	3	0	3	3	0	3	3	3
		3	3	0	3	0	3	3	0	3	3	3
	S23	1	3	0	3	0	3	3	0	3	3	3
		2	3	0	3	0	3	3	0	3	3	3
		3	3	0	3	0	3	3	0	3	3	3
	S8	1	3	0	3	0	3	3	0	3	3	3
		2	3	0	3	0	3	3	0	3	3	3
		3	3	0	3	0	3	3	0	3	3	3
Ziram	S20	1	3	0	3	3	3	3	3	3	0	0
		2	3	0	3	3	3	3	3	3	0	0
		3	3	0	3	3	3	3	3	3	0	0
	S23	1	3	0	3	3	3	3	3	3	0	0
		2	3	0	3	3	3	3	3	3	0	0
		3	3	0	3	3	3	3	3	3	0	0
	S8	1	3	0	3	3	3	3	3	3	0	0
		2	3	0	3	3	3	3	3	3	0	0
		3	3	0	3	3	3	3	3	3	0	0

```
# per fungicide / strain
```

```
dat %>%
```

```
  nest(data = c(dose, colony_diameter)) %>%
```

```
  mutate(mod = map(data, ~broom::tidy(drm(colony_diameter~dose, fct = LL.3(), data = .))))
```

```
  unnest(c(mod))%>%
```

```

tibble()

# per fungicide
dat %>%
  nest(data = c(-fungicide)) %>%
  mutate(mod = map(data, ~broom::tidy(drm(colony_diameter~dose, fct = LL.3(), data = .))))
  unnest(c(mod)) %>%
  tibble()

```

Meta-analysis approach

```

mod_mg <- metadrm(colony_diameter ~ dose,
                  data=dat,
                  fct=LL.3(),
                  ind=curve_id,
                  cid2=fungicide,
                  struct="UN")
summary(mod_mg)

```

Two-stage meta-analysis dose-response model

Model fitted: Log-logistic (ED50 as parameter) with lower limit at 0

Call:

```
metadrm(formula = colony_diameter ~ dose, fct = LL.3(), ind = curve_id,
        data = dat, cid2 = fungicide, struct = "UN")
```

Variance estimates:

	estim	sqrt
tau^2.1	0.0023	0.0481
tau^2.2	8.1930	2.8623
tau^2.3	0.0001	0.0076

	rho.b:(I	rho.d:(I	rho.e:(I
b:(Intercept)	1	-0.0949	0.9136
d:(Intercept)	-0.0949	1	-0.4915
e:(Intercept)	0.9136	-0.4915	1

Coefficients:

Estimate	Std.Err	t value	Pr(> t)
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```

b:Bellis 5.7954e-01 1.8249e-02 31.7572 < 2.2e-16 ***
b:Merpan 3.6118e-01 1.8337e-02 19.6968 < 2.2e-16 ***
b:Timorex 3.4904e-01 3.2449e-02 10.7565 < 2.2e-16 ***
b:Ziram 3.9270e-01 2.0238e-02 19.4040 < 2.2e-16 ***
d:Bellis 5.1375e+01 9.8903e-01 51.9446 < 2.2e-16 ***
d:Merpan 5.2514e+01 1.0668e+00 49.2274 < 2.2e-16 ***
d:Timorex 4.9987e+01 1.3972e+00 35.7759 < 2.2e-16 ***
d:Ziram 5.3064e+01 1.1219e+00 47.3004 < 2.2e-16 ***
e:Bellis 2.9754e-02 2.7299e-03 10.8994 < 2.2e-16 ***
e:Merpan 2.4515e+01 1.6200e+00 15.1327 < 2.2e-16 ***
e:Timorex 1.1284e+02 2.2168e+01 5.0901 1.779e-06 ***
e:Ziram 6.4556e+00 6.1620e-01 10.4764 < 2.2e-16 ***

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Estimates

```
ec50s <- ED(mod_mg, respLev=c(50)) %>% as.data.frame()
```

Estimated effective doses

```

              Estimate Std. Error
e:Bellis:50 2.9754e-02 2.7299e-03
e:Merpan:50 2.4515e+01 1.6200e+00
e:Timorex:50 1.1284e+02 2.2168e+01
e:Ziram:50 6.4556e+00 6.1620e-01

```

```

# coef_mod_mg <- summary(mod_mg) %>% data.frame %>%
#   rownames_to_column("param") %>%
#   separate(param, c("param", "fungicide"))
# ec50s <- coef_mod_mg %>% filter(param=="e")
# ec50s

```

Comparing effective dose levels for meta analysis

```

ed_comp <- EDcomp(mod_mg,
  percVec=c(50),
  percMat=rbind(c(1,1,1,1)),
  interval="fieller") %>%
  data.frame %>%

```

```
rownames_to_column("comp") %>%
rowwise() %>%
mutate(relative_to_one = f(Lower, Upper, 1)) # %>%
```

Estimated ratios of effect doses

	Estimate	Lower	Upper
Bellis/Merpan:50/50	1.2137e-03	9.5935e-04	1.5105e-03
Bellis/Timorex:50/50	2.6369e-04	1.7897e-04	4.4300e-04
Bellis/Ziram:50/50	4.6091e-03	3.5352e-03	6.0262e-03
Merpan/Timorex:50/50	2.1726e-01	1.5163e-01	3.6084e-01
Merpan/Ziram:50/50	3.7976e+00	3.0366e+00	4.8414e+00
Timorex/Ziram:50/50	1.7479e+01	1.0384e+01	2.5875e+01

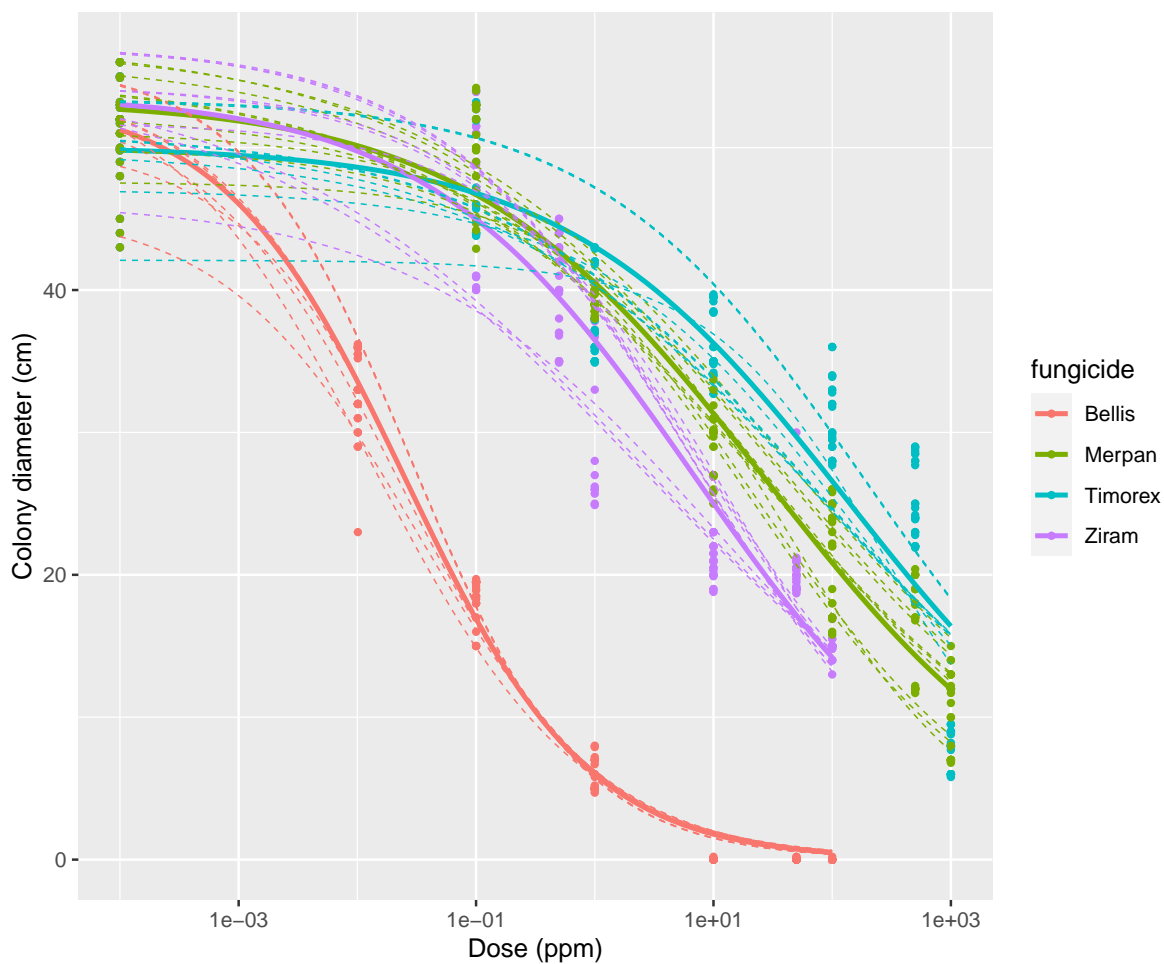
```
# as_huxtable() %>%
# set_number_format(1)
```

As we compare EC50 ratios between fungicides, if the confidence interval does not contain 1, fungicides differ among them:

```
ed_comp %>%
ggplot()+
aes(x=comp, y=Estimate) +
geom_pointrange(aes(ymin = Lower, ymax = Upper, col=relative_to_one))+
geom_hline(yintercept = 1, linetype=2)+
# scale_y_log10()+
coord_flip() +
labs(col="Relative to 1")
```

```
dat %>%
ggplot()+
aes(x=dose+0.0001, y=colony_diameter, col=fungicide) +
geom_point(size=1) +
geom_smooth(method = drm,
             method.args = list(fct = L.3(), se = F) +
             geom_smooth(aes(group=curve_id), size=.3, linetype=2,
                           method = drm,
                           method.args = list(fct = L.3(), se = F) +
             labs(title= "", x = "Dose (ppm)", y = "Colony diameter (cm)") +
```

```
scale_x_log10()
```



Spore germination

```
germi_raw <- rio::import("data/germination.csv", dec=",")
germi_dat <- germi_raw %>%
  mutate_at(vars(dose), as.numeric) %>%
  mutate_at(vars(fungicide, strain, repetition, replicate), as.factor) %>%
  mutate(curve_id = interaction(fungicide:strain:repetition)) %>%
  mutate(dose_ = dose+0.0001)
```

Data scheme

```
germi_dat %>% str
```

```
'data.frame':  468 obs. of  12 variables:
 $ fungicide      : Factor w/  4 levels "Bellis","Merpan",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ strain         : Factor w/  3 levels "S20","S23","S8": 2 2 2 1 1 1 3 3 3 2 ...
 $ repetition     : Factor w/  2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
 $ replicate      : Factor w/  3 levels "1","2","3": 1 2 3 1 2 3 1 2 3 1 ...
 $ dose           : num  100 100 100 100 100 100 100 100 100 50 ...
 $ germinated_conidia : int  0 0 0 0 0 0 0 0 0 0 ...
 $ total_conida    : int  100 100 100 100 100 100 100 100 100 100 ...
 $ non_germinated_conidia: int  100 100 100 100 100 100 100 100 100 100 ...
 $ inhibition_perc : int  100 100 100 100 100 100 100 100 100 100 ...
 $ germination_percent : int  0 0 0 0 0 0 0 0 0 0 ...
 $ curve_id       : Factor w/ 24 levels "Bellis:S20:1",...: 3 3 3 1 1 1 5 5 5 3 ...
 $ dose_          : num  100 100 100 100 100 ...
```

```
ftable(xtabs(complete.cases(germination_percent)~fungicide+dose, data=germi_dat))
```

	dose	0	0.1	1	10	50	100	500	1000
fungicide									
Bellis		18	18	18	18	18	18	0	0
Merpan		18	18	18	18	0	18	18	18
Timorex		18	18	18	18	0	18	18	18
Ziram		18	18	18	18	18	18	0	0

```
ftable(xtabs(complete.cases(germination_percent)~fungicide+dose+strain , data=germi_dat))
```

		strain	S20	S23	S8
fungicide	dose				
Bellis	0		6	6	6
	0.1		6	6	6
	1		6	6	6
	10		6	6	6
	50		6	6	6
	100		6	6	6
	500		0	0	0
	1000		0	0	0

Merpan	0	6	6	6
	0.1	6	6	6
	1	6	6	6
	10	6	6	6
	50	0	0	0
	100	6	6	6
	500	6	6	6
	1000	6	6	6
Timorex	0	6	6	6
	0.1	6	6	6
	1	6	6	6
	10	6	6	6
	50	0	0	0
	100	6	6	6
	500	6	6	6
	1000	6	6	6
Ziram	0	6	6	6
	0.1	6	6	6
	1	6	6	6
	10	6	6	6
	50	6	6	6
	100	6	6	6
	500	0	0	0
	1000	0	0	0

Meta-analysis

```
mod_germ <- metadrm(germination_percent ~ dose_,
  data=germi_dat,
  fct=LL.3(),
  ind=curve_id,
  cid2=fungicide,
  struct="UN")
summary(mod_germ)
```

Two-stage meta-analysis dose-response model

Model fitted: Log-logistic (ED50 as parameter) with lower limit at 0

Call:

```
metadrm(formula = germination_percent ~ dose_, fct = LL.3(),
  ind = curve_id, data = germi_dat, cid2 = fungicide, struct = "UN")
```


Variance estimates:

	estim	sqrt
tau^2.1	0.0024	0.0494
tau^2.2	0.0063	0.0792
tau^2.3	0.0001	0.0090

	rho.b:(I	rho.d:(I	rho.e:(I
b:(Intercept)	1	1.0000	1.0000
d:(Intercept)	1.0000	1	1.0000
e:(Intercept)	1.0000	1.0000	1

Coefficients:

	Estimate	Std.Err	t value	Pr(> t)
b:Bellis	1.0899e+00	8.5417e-02	12.7594	< 2.2e-16 ***
b:Merpan	1.3070e+00	5.6028e-02	23.3286	< 2.2e-16 ***
b:Timorex	1.0750e+00	1.2498e-01	8.6014	4.650e-12 ***
b:Ziram	6.1460e-01	4.1545e-02	14.7935	< 2.2e-16 ***
d:Bellis	9.9899e+01	2.3603e-01	423.2484	< 2.2e-16 ***
d:Merpan	9.7988e+01	5.3055e-01	184.6913	< 2.2e-16 ***
d:Timorex	9.7660e+01	1.7236e+00	56.6592	< 2.2e-16 ***
d:Ziram	9.9054e+01	2.0387e+00	48.5862	< 2.2e-16 ***
e:Bellis	2.3170e-02	5.1014e-03	4.5419	2.744e-05 ***
e:Merpan	1.1356e+00	2.4159e-02	47.0036	< 2.2e-16 ***
e:Timorex	2.8903e+02	3.4065e+01	8.4846	7.338e-12 ***
e:Ziram	1.5577e-01	2.7043e-02	5.7600	3.080e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Estimates

```
ec50s_g <- ED(mod_germ, respLev=c(50)) %>% as.data.frame()
```

Estimated effective doses

	Estimate	Std. Error
e:Bellis:50	2.3170e-02	5.1014e-03
e:Merpan:50	1.1356e+00	2.4159e-02
e:Timorex:50	2.8903e+02	3.4065e+01
e:Ziram:50	1.5577e-01	2.7043e-02

ec50s_g

Estimate	Std. Error
0.0232	0.0051
1.14	0.0242
289	34.1
0.156	0.027

```
germ_comp <- EDcomp(mod_germ,
  percVec=c(50),
  percMat=rbind(c(1,1,1,1)),
  interval="fieller") %>%
  data.frame %>%
  rownames_to_column("comp") %>%
  rowwise() %>%
  mutate(relative_to_one = f(Lower, Upper, 1))
```

Estimated ratios of effect doses

	Estimate	Lower	Upper
Bellis/Merpan:50/50	2.0404e-02	1.1405e-02	2.9477e-02
Bellis/Timorex:50/50	8.0165e-05	4.3407e-05	1.2636e-04
Bellis/Ziram:50/50	1.4875e-01	7.7874e-02	2.6041e-01
Merpan/Timorex:50/50	3.9289e-03	3.1644e-03	5.1559e-03
Merpan/Ziram:50/50	7.2900e+00	5.3920e+00	1.1188e+01
Timorex/Ziram:50/50	1.8555e+03	1.2413e+03	2.9785e+03

```
# germ_comp
```

```
coef_mod_germ <- summary(mod_germ) %>% data.frame %>%
  rownames_to_column("param") %>%
  separate(param, c("param", "fungicide"))
```

Two-stage meta-analysis dose-response model

Model fitted: Log-logistic (ED50 as parameter) with lower limit at 0

Call:

```
metadrm(formula = germination_percent ~ dose_, fct = LL.3(),
        ind = curve_id, data = germi_dat, cid2 = fungicide, struct = "UN")
```

Variance estimates:

	estim	sqrt
tau^2.1	0.0024	0.0494
tau^2.2	0.0063	0.0792
tau^2.3	0.0001	0.0090

	rho.b:(I	rho.d:(I	rho.e:(I
b:(Intercept)	1	1.0000	1.0000
d:(Intercept)	1.0000	1	1.0000
e:(Intercept)	1.0000	1.0000	1

Coefficients:

	Estimate	Std.Err	t value	Pr(> t)
b:Bellis	1.0899e+00	8.5417e-02	12.7594	< 2.2e-16 ***
b:Merpan	1.3070e+00	5.6028e-02	23.3286	< 2.2e-16 ***
b:Timorex	1.0750e+00	1.2498e-01	8.6014	4.650e-12 ***
b:Ziram	6.1460e-01	4.1545e-02	14.7935	< 2.2e-16 ***
d:Bellis	9.9899e+01	2.3603e-01	423.2484	< 2.2e-16 ***
d:Merpan	9.7988e+01	5.3055e-01	184.6913	< 2.2e-16 ***
d:Timorex	9.7660e+01	1.7236e+00	56.6592	< 2.2e-16 ***
d:Ziram	9.9054e+01	2.0387e+00	48.5862	< 2.2e-16 ***
e:Bellis	2.3170e-02	5.1014e-03	4.5419	2.744e-05 ***
e:Merpan	1.1356e+00	2.4159e-02	47.0036	< 2.2e-16 ***
e:Timorex	2.8903e+02	3.4065e+01	8.4846	7.338e-12 ***
e:Ziram	1.5577e-01	2.7043e-02	5.7600	3.080e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
# ec50_germ <- coef_mod_germ %>% filter(param=="e")
# ec50_germ
```

```
germ_comp %>%
  ggplot()+
  aes(x=comp, y=Estimate) +
```

```

geom_pointrange(aes(ymin = Lower, ymax = Upper, col=relative_to_one))+
geom_hline(yintercept = 1, linetype=2)+
coord_flip() +
labs(col="Relative to 1")

germi_dat %>%
  ggplot()+
  aes(x=dose+0.0001, y=germination_percent, col=fungicide) +
  scale_x_log10() +
  geom_point(size=1) +
  geom_smooth(method = drm,
              method.args = list(fct = L.3()), se = F) +
  geom_smooth(aes(group=curve_id), size=.3, linetype=2,
              method = drm,
              method.args = list(fct = L.3()), se = F) +
  labs(title= "", x = "Dose (ppm)", y = "Germination (%)", col= "Fungicide")

```

