analysis

```
library(MASS)
library(broom)
library(tidyverse)
options(pillar.sigfig=4)
```

Data import

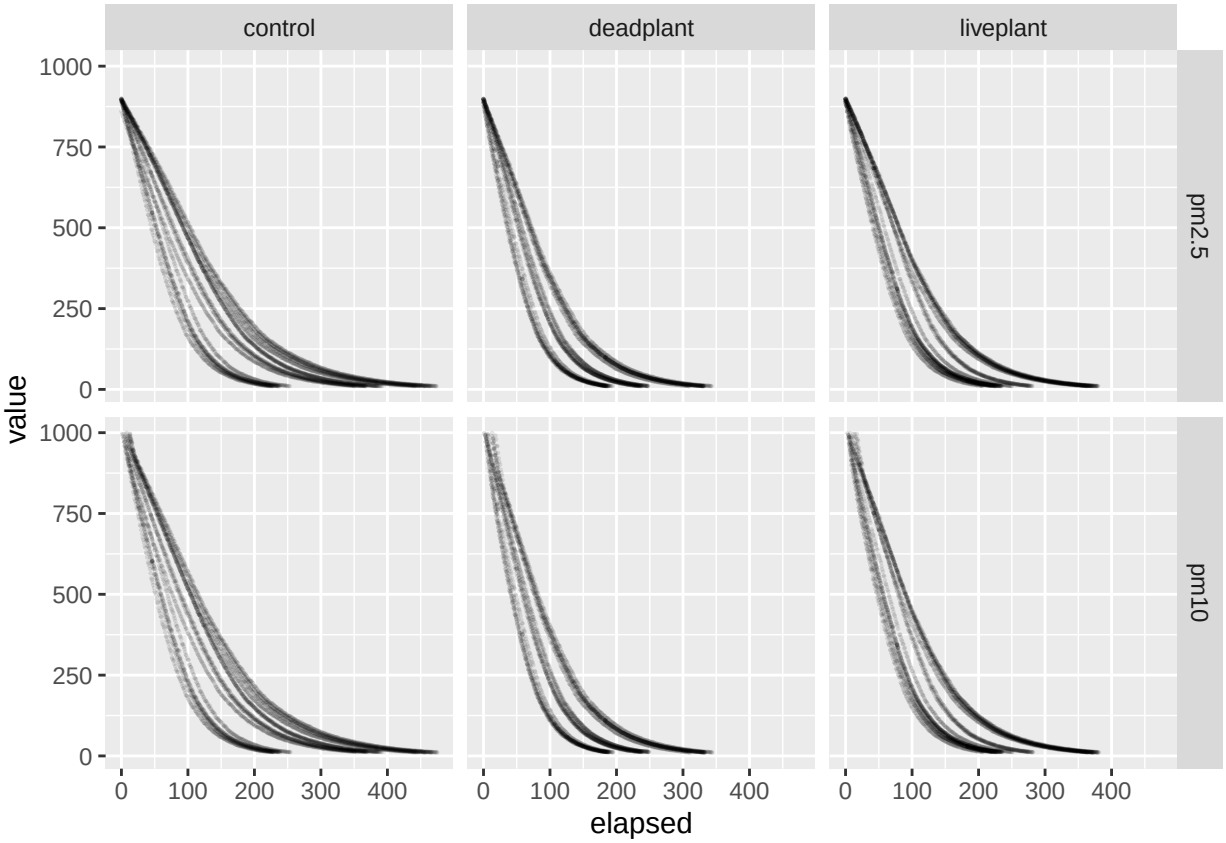
```
csv2tibble <- function(fn, show_plot = FALSE) {

  # Determine the condition of this trial
  if (grepl("-nothing", fn)) {
    condition <- "control"
  } else if (grepl("-plant", fn)) {
    condition <- "liveplant"
  } else if (grepl("-deadplant", fn)) {
    condition <- "deadplant"
  # } else if (grepl("-soil", fn)) {
  #   condition <- "soil"
  } else {
    stop("Cannot infer condition for file ", fn)
  }

  # Determine the enclosure/sensor of this trial
  if (grepl("1a", fn)) {
    sensor <- "A"
  } else if (grepl("2b", fn)) {
    sensor <- "B"
  } else if (grepl("3d", fn)) {
    sensor  <- "C"
  } else {
    stop("Cannot infer enclosure/sensor for file ", fn)
  }

  tib <- fn %>%
    { suppressMessages(
      read_csv(., col_names = c("datetime", "type", "value"))) } %>%
    # obs of type "comment" are not used
    filter(type %in% c("pm2.5", "pm10")) %>%
    mutate(value=as.numeric(value)) %>%
    mutate(
      condition=condition, sensor=sensor, fn=fn,
      has_area=condition %in% c("deadplant", "liveplant"),
      has_bio=condition == "liveplant")

  # Experiment starts when PM2.5 first drops below 900.
```

```
  first_pm2.5_999.99 <- tib %>%
    filter(type == "pm2.5" & value == 999.9) %>%
    .$datetime %>%
    last()
  first_pm2.5_sub900 <- tib %>%
    filter(datetime > first_pm2.5_999.99) %>%
    filter(type == "pm2.5" & value <= 900) %>%
    .$datetime %>%
    first()

  # Experiment ends when PM2.5/PM10 first drops below 10.
  first_sub10 <- tib %>%
    filter(datetime > first_pm2.5_sub900 & value < 10) %>%
    .$datetime %>%
    first()

  if (show_plot) {
    g <- ggplot(tib, aes(x=datetime, y=value, colour=type)) +
      geom_point() +
      geom_hline(yintercept = c(900, 999.9)) +
      geom_vline(xintercept = c(
        first_pm2.5_999.99, first_pm2.5_sub900, first_sub10))
    print(g)
  }

  tib <- filter(tib, between(datetime, first_pm2.5_sub900, first_sub10)) %>%
    # PM sensor not specified to measure PM10 > 999.9
    filter(!(type == "pm10" & value > 999.9)) %>%
    # use minutes instead of seconds, otherwise will get Inf on exp later
    mutate(elapsed=as.numeric(datetime-first_pm2.5_sub900)/60)

  tib
}

# Make a list of two tibbles, one for PM2.5, the other for PM10.
data <- list.files("05-analysis-proper/", "*.csv") %>%
  Filter(function(x) !grepl("-soil", x), .) %>%
  paste0("05-analysis-proper/", .) %>%
  lapply(csv2tibble) %>%
  do.call(bind_rows, .) %>%
  mutate(
    condition=
      factor(condition, levels=c("control", "deadplant", "liveplant")),
    type=factor(type, levels=c("pm2.5", "pm10"))) %>%
  {list(
    pm2.5 = filter(., type=="pm2.5"),
    pm10 = filter(., type=="pm10")
  )}
```

Note that we omit the soil controls because 5 of 15 of those trials suffer from systematic errors, likely due to a leaky seal on the enclosure.

Sanity check:

```r
do.call(bind_rows, data) %>%
  filter(value > 10) %>%
  ggplot(aes(x=elapsed, y=value)) +
  geom_point(size=.1, alpha=.1) +
  facet_grid(type~condition)
```



Model selection

Stepwise BIC optimisation reports a complex model to be most suitable for both PM2.5 and PM10.

```r
model_full <- (
  value ~ elapsed*sensor + elapsed*has_area + elapsed*has_bio)
glm_bare <- glm(value ~ 1, family=Gamma("log"), data=data$pm2.5)
glm_full <- glm(model_full, family=Gamma("log"), data=data$pm2.5)
stepAIC(
  glm_bare, scope=list(lower=glm_bare, upper=glm_full),
  direction="both", trace = FALSE,
  k=log(nrow(data$pm2.5)))
```

```
##
## Call:  glm(formula = value ~ elapsed + sensor + has_area + has_bio +
##     elapsed:sensor + elapsed:has_area + elapsed:has_bio, family = Gamma("log"),
##     data = data$pm2.5)
##
## Coefficients:
##          (Intercept)               elapsed               sensorB
```

```
##             7.117660             -0.012917              0.059531
##              sensorC          has_areaTRUE           has_bioTRUE
##             0.115783             -0.094929              0.050745
##      elapsed:sensorB       elapsed:sensorC  elapsed:has_areaTRUE
##            -0.006360              0.002730             -0.004514
##  elapsed:has_bioTRUE
##             0.001663
##
## Degrees of Freedom: 12916 Total (i.e. Null);  12907 Residual
## Null Deviance:       19600
## Residual Deviance: 555.6     AIC: 120000
```

```
glm_bare <- glm(value ~ 1, family=Gamma("log"), data=data$pm10)
glm_full <- glm(model_full, family=Gamma("log"), data=data$pm10)
stepAIC(
  glm_bare, scope=list(lower=glm_bare, upper=glm_full),
  direction="both", trace = FALSE,
  k=log(nrow(data$pm10)))
```

```
##
## Call:  glm(formula = value ~ elapsed + sensor + has_area + has_bio +
##     elapsed:sensor + elapsed:has_area + elapsed:has_bio, family = Gamma("log"),
##     data = data$pm10)
##
## Coefficients:
##          (Intercept)               elapsed               sensorB
##             7.229400             -0.012919              0.068170
##              sensorC          has_areaTRUE           has_bioTRUE
##             0.158966             -0.089328              0.051289
##      elapsed:sensorB       elapsed:sensorC  elapsed:has_areaTRUE
##            -0.006443              0.002545             -0.004595
##  elapsed:has_bioTRUE
##             0.001675
##
## Degrees of Freedom: 12561 Total (i.e. Null);  12552 Residual
## Null Deviance:       18770
## Residual Deviance: 497   AIC: 116800
```

However, we will opt for a simpler model instead, which has comparable BIC:

```
model_simpler <- (
  value ~ elapsed*sensor + elapsed:has_area + elapsed:has_bio)
tibble(
  pm2.5_simpler = BIC(glm(model_simpler, family=Gamma("log"), data=data$pm2.5)),
  pm2.5_full = BIC(glm(model_full, family=Gamma("log"), data=data$pm2.5)),
  pm10_simpler = BIC(glm(model_simpler, family=Gamma("log"), data=data$pm10)),
  pm10_full = BIC(glm(model_full, family=Gamma("log"), data=data$pm10))
)
```

```
## # A tibble: 1 x 4
##   pm2.5_simpler pm2.5_full pm10_simpler pm10_full
##           <dbl>      <dbl>        <dbl>     <dbl>
## 1       120148.    120042.      116992.   116901.
```

Regression

For PM2.5

```
fits <- list()
fits$pm2.5 <- data$pm2.5 %>%
  glm(model_simpler, family=Gamma(link="log"), data=.)
summary(fits$pm2.5)
```

```
##
## Call:
## glm(formula = model_simpler, family = Gamma(link = "log"), data = .)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.93346  -0.14335   0.00321   0.12225   0.48891
##
## Coefficients:
##                          Estimate Std. Error  t value Pr(>|t|)
## (Intercept)             7.077e+00  5.820e-03 1215.896  < 2e-16 ***
## elapsed                -1.276e-02  3.211e-05 -397.467  < 2e-16 ***
## sensorB                 5.400e-02  9.023e-03    5.984 2.23e-09 ***
## sensorC                 1.127e-01  7.823e-03   14.411  < 2e-16 ***
## elapsed:sensorB        -6.306e-03  6.374e-05  -98.930  < 2e-16 ***
## elapsed:sensorC         2.750e-03  3.990e-05   68.925  < 2e-16 ***
## elapsed:has_areaTRUE -4.961e-03  2.515e-05 -197.256  < 2e-16 ***
## elapsed:has_bioTRUE   1.932e-03  2.704e-05   71.450  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0402728)
##
##     Null deviance: 19600.52  on 12916  degrees of freedom
## Residual deviance:   560.99  on 12909  degrees of freedom
## AIC: 120081
##
## Number of Fisher Scoring iterations: 6
```

For PM10

```
fits$pm10 <- data$pm10 %>%
  glm(model_simpler, family=Gamma(link="log"), data=.)
summary(fits$pm10)
```

```
##
## Call:
## glm(formula = model_simpler, family = Gamma(link = "log"), data = .)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.84576  -0.13568  -0.00035   0.11556   0.46944
##
## Coefficients:
##                          Estimate Std. Error  t value Pr(>|t|)
```

```
## (Intercept)           7.192e+00  5.814e-03 1236.939   <2e-16 ***
## elapsed              -1.278e-02  3.167e-05 -403.440   <2e-16 ***
## sensorB               6.364e-02  9.038e-03    7.042    2e-12 ***
## sensorC               1.576e-01  7.910e-03   19.924   <2e-16 ***
## elapsed:sensorB      -6.396e-03  6.318e-05 -101.245   <2e-16 ***
## elapsed:sensorC       2.558e-03  3.965e-05   64.498   <2e-16 ***
## elapsed:has_areaTRUE -5.015e-03  2.421e-05 -207.111   <2e-16 ***
## elapsed:has_bioTRUE   1.944e-03  2.596e-05   74.880   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.03708203)
##
##     Null deviance: 18773.99  on 12561  degrees of freedom
## Residual deviance:   501.37  on 12554  degrees of freedom
## AIC: 116926
##
## Number of Fisher Scoring iterations: 6
```

Confidence interval for estimates

Since the p-values are all non-informatively small, we report the confidence intervals instead.

```
coeffs <- lapply(names(fits), function(pm) {
    tidy(fits[[pm]]) %>% mutate(pm=pm)
  })
names(coeffs) <- names(fits)  # was erased
cis <- lapply(fits, confint)
```

```
## Waiting for profiling to be done...
## Waiting for profiling to be done...
```

```
stopifnot(all(coeffs$pm2.5$term == rownames(cis$pm2.5)))
stopifnot(all(coeffs$pm10$term == rownames(cis$pm10)))
stopifnot(all(names(coeffs) == names(cis)))  # in the same order

bind_cols(
  do.call(bind_rows, coeffs),
  do.call(bind_rows, lapply(cis, as_tibble))) %>%
  dplyr::select(pm, term, `2.5 %`, estimate, `97.5 %`)
```

```
## # A tibble: 16 x 5
##    pm    term                   `2.5 %`  estimate  `97.5 %`
##    <chr> <chr>                    <dbl>     <dbl>     <dbl>
##  1 pm2.5 (Intercept)           7.066     7.077     7.088
##  2 pm2.5 elapsed              -0.01283  -0.01276  -0.01270
##  3 pm2.5 sensorB               0.03603   0.05400   0.07197
##  4 pm2.5 sensorC               0.09716   0.1127    0.1283
##  5 pm2.5 elapsed:sensorB      -0.006435 -0.006306 -0.006177
##  6 pm2.5 elapsed:sensorC       0.002670  0.002750  0.002830
##  7 pm2.5 elapsed:has_areaTRUE -0.005011 -0.004961 -0.004910
##  8 pm2.5 elapsed:has_bioTRUE   0.001879  0.001932  0.001985
##  9 pm10  (Intercept)           7.181     7.192     7.203
## 10 pm10  elapsed              -0.01284  -0.01278  -0.01272
## 11 pm10  sensorB               0.04578   0.06364   0.08151
## 12 pm10  sensorC               0.1419    0.1576    0.1733
```

```
## 13 pm10  elapsed:sensorB      -0.006523 -0.006396 -0.006270
## 14 pm10  elapsed:sensorC       0.002479  0.002558  0.002637
## 15 pm10  elapsed:has_areaTRUE -0.005063 -0.005015 -0.004967
## 16 pm10  elapsed:has_bioTRUE   0.001893  0.001944  0.001995
```

Effect on half-life

Let λ_1 be the coefficient of time t under some first condition, and λ_2 the same coefficient under a different second condition. We can identify the marginal multiplicative effect of the second condition over the first on the half-life as follows:

$$\begin{aligned}\frac{t_{1/2,\,2}}{t_{1/2,\,1}} &= \frac{\ln 2/\lambda_2}{\ln 2/\lambda_1} \\ &= \frac{\lambda_1}{\lambda_2},\end{aligned}$$

where $t_{1/2,\,1}$ is the half-life under the first condition, and $t_{1/2,\,2}$ under the second.

Note that since the half-life is a ratio of coefficient sets of a conditions, there is no easy way to factorise out the coefficients associated with the control variables. So, we report the marginal percentage change in half-life by presence of surface area and then biological activity, once for each sensor.

```
diff_hl <- function(c2, c1, pm) {
  stopifnot(pm %in% c("pm2.5", "pm10"))
  coeff <- coeffs[[pm]]
  ci <- cis[[pm]]
  stopifnot(all(c1 %in% rownames(ci)))
  stopifnot(all(c2 %in% rownames(ci)))

  lambda1s <- c1 %>%
    sapply(function(c) {
      lower <- ci[c, 1]
      est <- filter(coeff, term == c) %>% pull(estimate)
      upper  <- ci[c, 2]
      c(lower, est, upper)
    }) %>%
    t()

  lambda2s <- c2 %>%
    sapply(function(c) {
      lower <- ci[c, 1]
      est <- filter(coeff, term == c) %>% pull(estimate)
      upper  <- ci[c, 2]
      c(lower, est, upper)
    }) %>%
    t()

  apply(lambda1s, 2, sum) / apply(lambda2s, 2, sum)
}

hl_design <- tibble(
  pm = c(rep("pm2.5", 6), rep("pm10", 6)),
  effect_of = rep(c(rep("area", 3), rep("bio", 3)), 2),
  sensor = rep(c("A", "B", "C"), 4)
)
hl_effects <- apply(hl_design, 1, function(row) {
```

```
    pm <- row[1];  effect_of <- row[2];  sensor <- row[3]
    stopifnot(pm %in% c("pm2.5", "pm10"))
    stopifnot(effect_of %in% c("area", "bio"))
    stopifnot(sensor %in% c("A", "B", "C"))

    # Construct c1
    c1 <- "elapsed"
    if (sensor == "B") c1 <- c(c1, "elapsed:sensorB")
    if (sensor == "C") c1 <- c(c1, "elapsed:sensorC")
    if (effect_of == "bio") c1 <- c(c1, "elapsed:has_areaTRUE")

    # Construct c2
    if (effect_of == "area") c2 <- c(c1, "elapsed:has_areaTRUE")
    if (effect_of == "bio") c2 <- c(c1, "elapsed:has_bioTRUE")

    diff_hl(c2, c1, pm)
  }) %>%
  t() %>%
  as.data.frame()

bind_cols(hl_design, hl_effects) %>%
  mutate(lower=V1, estimate=V2, upper=V3) %>%
  dplyr::select(-V1, -V2, -V3)
```

```
## # A tibble: 12 x 6
##    pm    effect_of sensor  lower estimate  upper
##    <chr> <chr>     <chr>   <dbl>    <dbl>  <dbl>
##  1 pm2.5 area      A      0.7191   0.7201 0.7212
##  2 pm2.5 area      B      0.7936   0.7936 0.7936
##  3 pm2.5 area      C      0.6697   0.6687 0.6678
##  4 pm2.5 bio       A      1.118    1.122  1.127
##  5 pm2.5 bio       B      1.084    1.087  1.091
##  6 pm2.5 bio       C      1.141    1.148  1.155
##  7 pm10  area      A      0.7172   0.7182 0.7192
##  8 pm10  area      B      0.7927   0.7927 0.7927
##  9 pm10  area      C      0.6718   0.6709 0.6699
## 10 pm10  bio       A      1.118    1.123  1.127
## 11 pm10  bio       B      1.084    1.087  1.091
## 12 pm10  bio       C      1.140    1.146  1.153
```

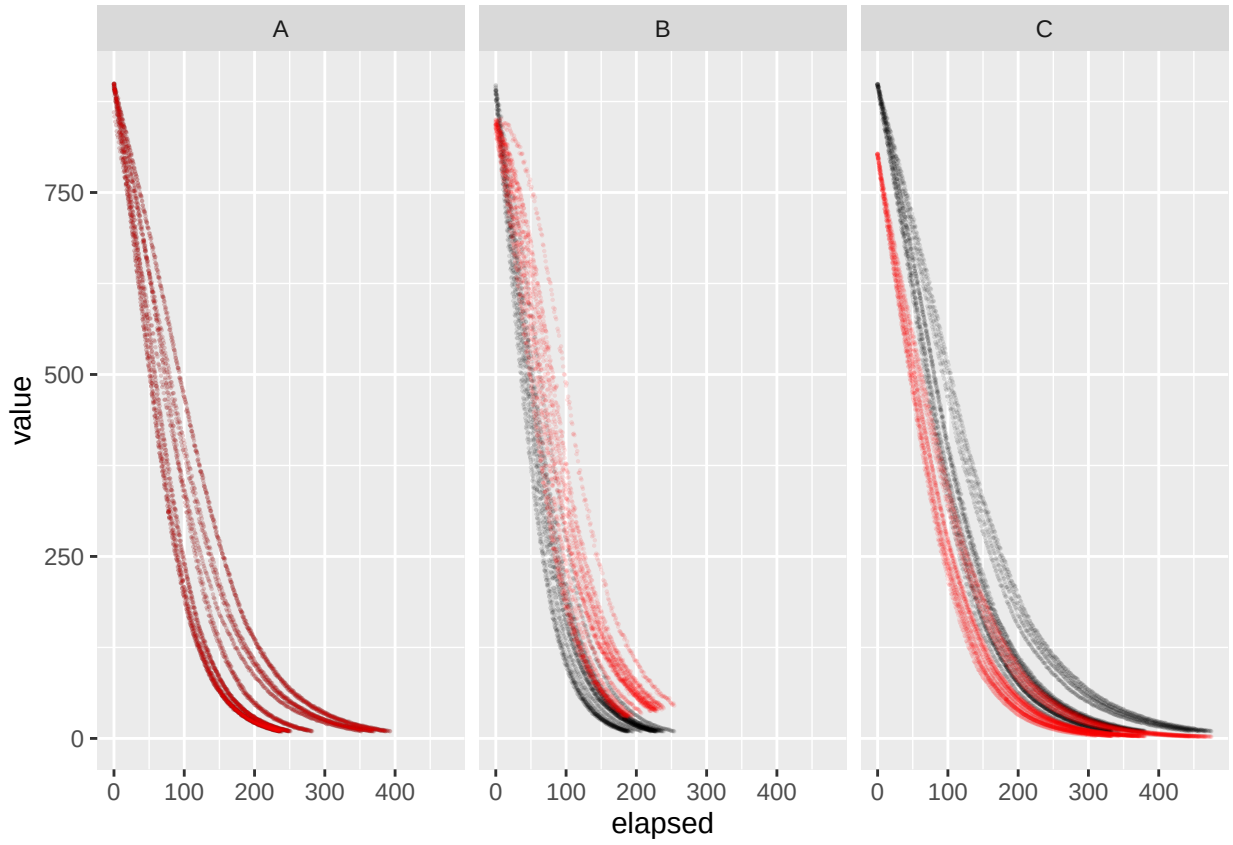
Visualisation

Pre-computation

For the purpose of visualization, we first 'normalize' readings by factoring out sensor effects. The resulting value is named the \texttt{sc_value}, as in sensor-normalized value.

```
pm2.5_glm.tb <- tidy(fits$pm2.5)

sensorB_coeff <- pm2.5_glm.tb %>%
  filter(term == "sensorB") %>%
  .$estimate
sensorC_coeff <- pm2.5_glm.tb %>%
  filter(term == "sensorC") %>%
```

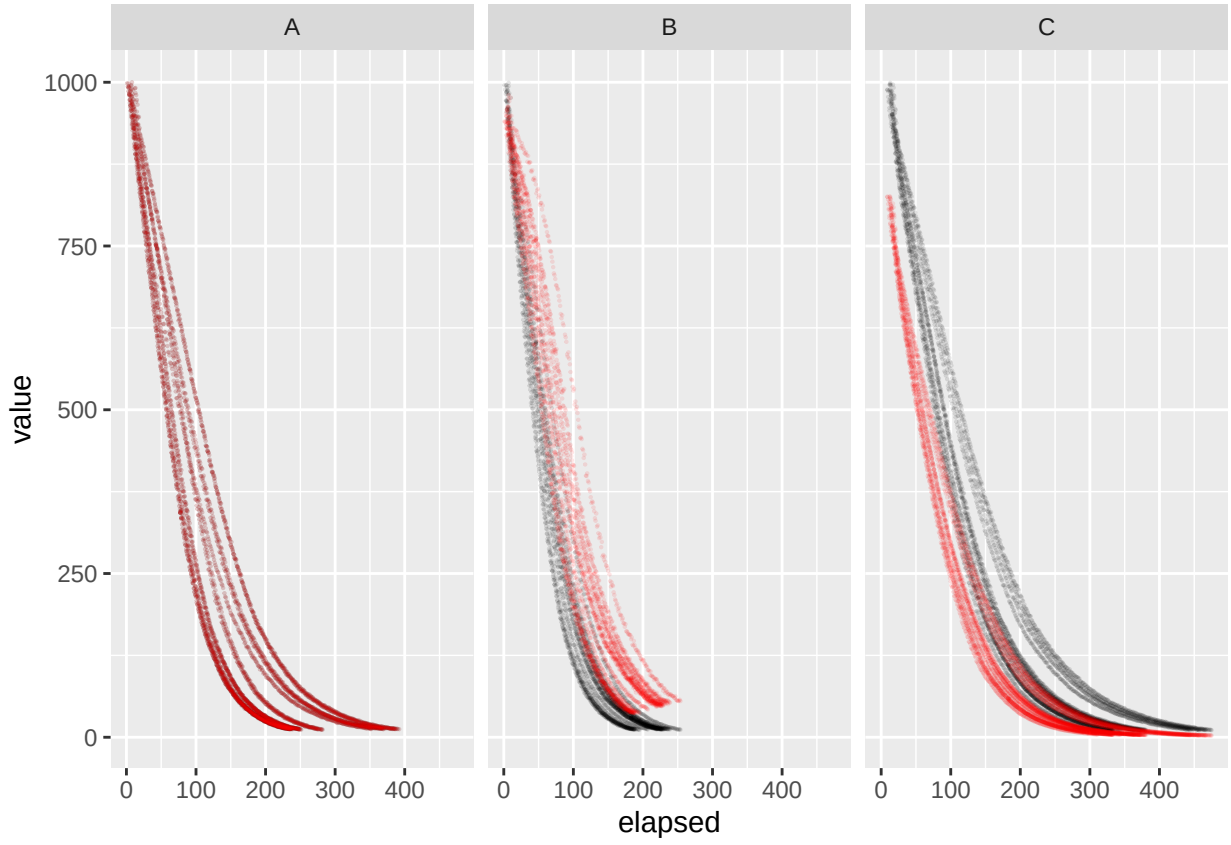
```
  .$estimate
sensorB_int_coeff <- pm2.5_glm.tb %>%
  filter(term == "elapsed:sensorB") %>%
  .$estimate
sensorC_int_coeff <- pm2.5_glm.tb %>%
  filter(term == "elapsed:sensorC") %>%
  .$estimate

data$pm2.5 <- data$pm2.5 %>%
  mutate(sc_value=recode(
    sensor,
    A=value,
    B=value / exp(sensorB_coeff + sensorB_int_coeff*elapsed),
    C=value / exp(sensorC_coeff + sensorC_int_coeff*elapsed)
  ))

data$pm2.5 %>%
  ggplot(aes(x=elapsed)) +
  geom_point(aes(y=value), size=.1, alpha=.1) +
  geom_point(aes(y=sc_value), size=.1, alpha=.1, colour="red") +
  facet_grid(~sensor)
```



Repeat for PM10.

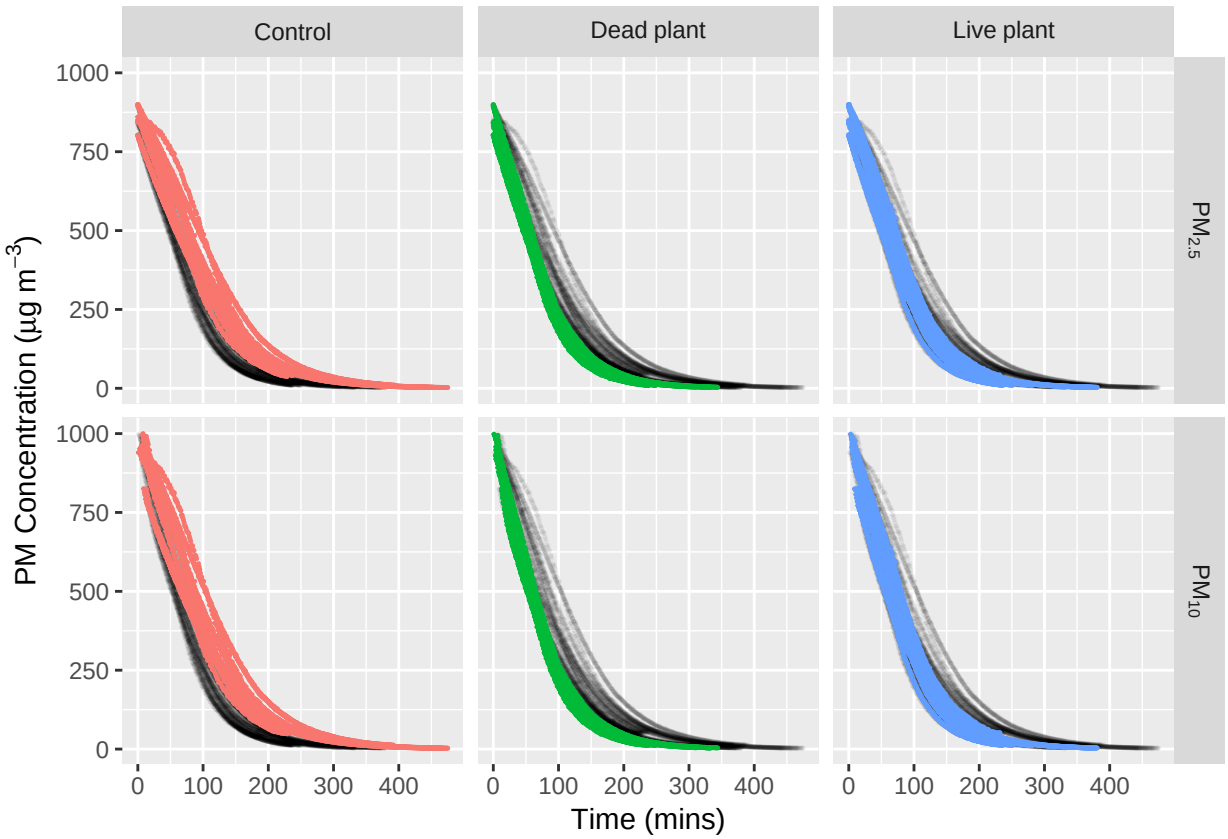
```
pm10_glm.tb <- tidy(fits$pm10)

sensorB_coeff <- pm10_glm.tb %>%
```

```
  filter(term == "sensorB") %>%
  .$estimate
sensorC_coeff <- pm10_glm.tb %>%
  filter(term == "sensorC") %>%
  .$estimate
sensorB_int_coeff <- pm10_glm.tb %>%
  filter(term == "elapsed:sensorB") %>%
  .$estimate
sensorC_int_coeff <- pm10_glm.tb %>%
  filter(term == "elapsed:sensorC") %>%
  .$estimate

data$pm10 <- data$pm10 %>%
  mutate(sc_value=recode(
    sensor,
    A=value,
    B=value / exp(sensorB_coeff + sensorB_int_coeff*elapsed),
    C=value / exp(sensorC_coeff + sensorC_int_coeff*elapsed)
  ))

data$pm10 %>%
  ggplot(aes(x=elapsed)) +
  geom_point(aes(y=value), size=.1, alpha=.1) +
  geom_point(aes(y=sc_value), size=.1, alpha=.1, colour="red") +
  facet_grid(~sensor)
```



Final graph

```
data %>%
  do.call(bind_rows, .) %>%
  mutate(
    type=factor(
      ifelse(type == "pm2.5", "PM[2.5]", "PM[10]"),
      levels=c("PM[2.5]", "PM[10]")),
    # `~` represent spaces when parsed by ggplot:label_parsed
    condition=recode(
      condition,
      control = "Control",
      deadplant = "Dead~plant",
      liveplant = "Live~plant"
    )) %>%
  ggplot(aes(x=elapsed, y=sc_value)) +
  geom_point(
    data=bind_rows(data) %>%
      dplyr::select(-condition) %>%
      mutate(type=factor(
        ifelse(type == "pm2.5", "PM[2.5]", "PM[10]"),
        levels=c("PM[2.5]", "PM[10]"))),
    aes(x=elapsed, y=sc_value),
    size=.2, alpha=.05
  ) +
  geom_point(aes(fill=condition, colour=condition), size=.2, shape=21) +
  facet_grid(type ~ condition, labeller=label_parsed) +
  theme(legend.position = "none") +
  ylab(expression("PM Concentration ("*mu*"g m"^-3*")")) +
  xlab(expression("Time (mins)"))
```




```
ggsave("concentration-time.eps", device=cairo_ps, width=9, height=6, units="in")
```