Supplementary material 1: The R code for fitting multiple survival curves (data for multiple seed lots) and hypothesis testing.

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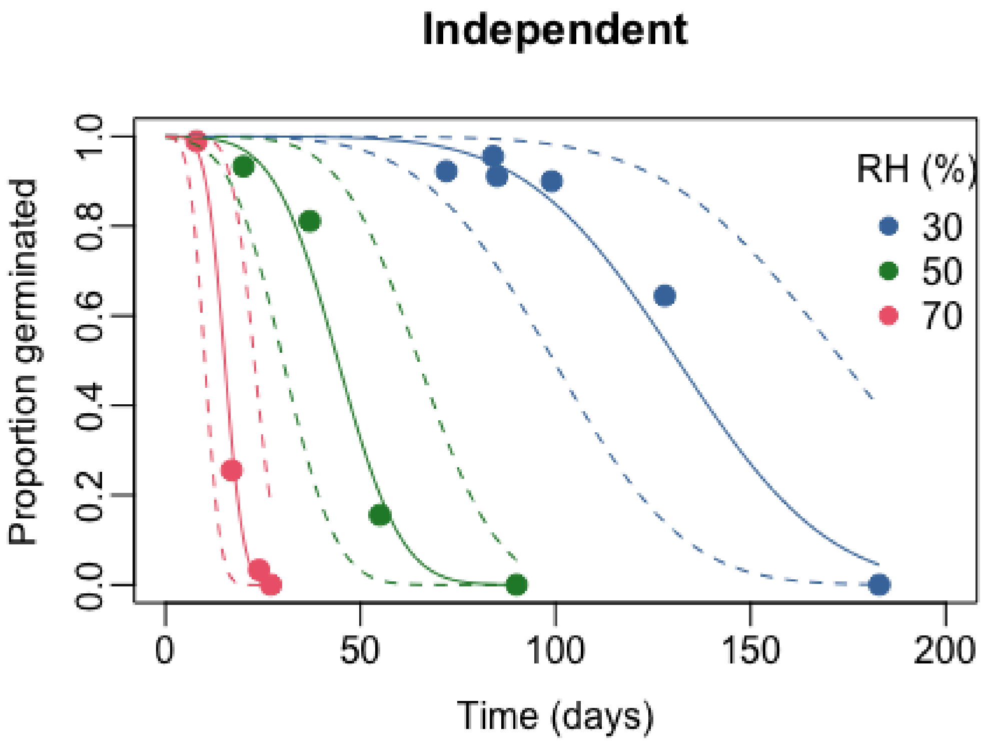
This supplementary material demontrates how to analyze seed longevity in R to fit the viability equation. Original data is from Rezaei *et al*. (2023).

```
# load libraries
library(tidyverse) # usefull for all manor of data manipulation and
visualizartion

## ── Attaching core tidyverse packages ──────────────────────── tidyverse
2.0.0 ──
## ✓ dplyr     1.1.4     ✓ readr     2.1.5
## ✓ forcats   1.0.0     ✓ stringr   1.5.1
## ✓ ggplot2   3.5.0     ✓ tibble    3.2.1
## ✓ lubridate 1.9.3     ✓ tidyr     1.3.1
## ✓ purrr     1.0.2
## ── Conflicts ──────────────────────────────────────────
tidyverse_conflicts() ──
## ✕ dplyr::filter() masks stats::filter()
## ✕ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all
conflicts to become errors

library(MASS) # the dose.p() function used to calculate P50 and P85

##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select

library(knitr) # used to make tables in R Markdown

# set working directory
#setwd("my/file/path")



# Read in data
# brna short for the study organism, Brassica napus
```

```
brna <- read.csv("Rezaei_etal_2023_SSR.csv", header = TRUE)
glimpse(brna)

## Rows: 117
## Columns: 10
## $ Treatment    <chr> "Desorption 170", "Desorption 170", "Desorption 170",
"De…
## $ MC           <dbl> 9.141008, 9.141008, 9.141008, 9.141008, 8.000368,
8.00036…
## $ storage.RH   <dbl> 66.91, 66.91, 66.91, 66.91, 60.95, 60.95, 60.95,
60.95, 5…
## $ period       <int> 8, 17, 24, 27, 13, 24, 31, 41, 20, 37, 55, 90, 50,
59, 65…
## $ sown         <int> 90, 90, 90, 90, 87, 90, 90, 90, 90, 90, 90, 90, 90,
90, 9…
## $ germinated   <int> 89, 23, 3, 0, 83, 28, 10, 0, 84, 73, 14, 0, 73, 57,
51, 3…
## $ germ.percent <dbl> 98.888889, 25.555556, 3.333333, 0.000000, 95.402299,
31.1…
## $ sorption     <chr> "Desorption", "Desorption", "Desorption",
"Desorption", "…
## $ chamber.RH   <int> 70, 70, 70, 70, 60, 60, 60, 60, 50, 50, 50, 50, 40,
40, 4…
## $ cycle        <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, …

# citation for dataset;
# Rezaei, S., Buitink, J. & Hay, F.R. (2023) Contrasting seed moisture
sorption
# behaviour between two species and the implication for seed longevity.
# Seed Science Research, 1-9. https://doi.org/10.1017/ S0960258523000156

# Tell R which variables are factors
brna <- brna |>
  mutate(Treatment = as.factor(Treatment),
         sorption = as.factor(sorption),
         chamber.RH = as.factor(chamber.RH),
         cycle = as.factor(cycle))
glimpse(brna)

## Rows: 117
## Columns: 10
## $ Treatment    <fct> Desorption 170, Desorption 170, Desorption 170,
Desorptio…
## $ MC           <dbl> 9.141008, 9.141008, 9.141008, 9.141008, 8.000368,
8.00036…
## $ storage.RH   <dbl> 66.91, 66.91, 66.91, 66.91, 60.95, 60.95, 60.95,
60.95, 5…
## $ period       <int> 8, 17, 24, 27, 13, 24, 31, 41, 20, 37, 55, 90, 50,
59, 65…
```

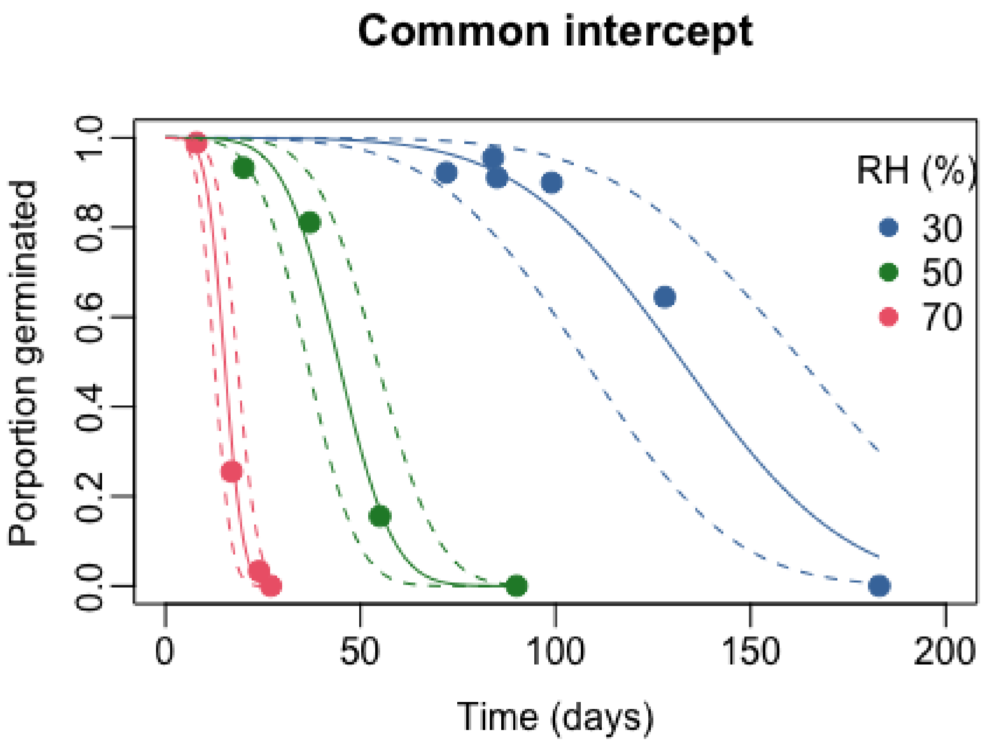
```
## $ sown         <int> 90, 90, 90, 90, 87, 90, 90, 90, 90, 90, 90, 90, 90,
90, 9…
## $ germinated   <int> 89, 23, 3, 0, 83, 28, 10, 0, 84, 73, 14, 0, 73, 57,
51, 3…
## $ germ.percent <dbl> 98.888889, 25.555556, 3.333333, 0.000000, 95.402299,
31.1…
## $ sorption     <fct> Desorption, Desorption, Desorption, Desorption,
Desorptio…
## $ chamber.RH   <fct> 70, 70, 70, 70, 60, 60, 60, 60, 50, 50, 50, 50, 40,
40, 4…
## $ cycle        <fct> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, …

### analysis and plotting with three different Treatments ###

# subset desorption, cycle 1, and 3 RHs (30, 50, 70%)
des<-droplevels(subset(brna, sorption == "Desorption" &  cycle == "1"))
des<-droplevels(subset(des, chamber.RH == "30" |chamber.RH == "50" |
chamber.RH == "70"))

### Independent (independent Ki and -sigma^-1)
independent <- glm(formula = cbind(germinated, sown-germinated) ~ Treatment +
Treatment:period -1 , family = binomial(link = "probit"),  data = des)
summary(independent)

##
## Call:
## glm(formula = cbind(germinated, sown - germinated) ~ Treatment +
##     Treatment:period - 1, family = binomial(link = "probit"),
##     data = des)
##
## Coefficients:
##                                 Estimate Std. Error z value Pr(>|z|)
## TreatmentDesorption 130         4.315944   0.281077  15.355   <2e-16 ***
## TreatmentDesorption 150         3.433957   0.344167   9.978   <2e-16 ***
## TreatmentDesorption 170         3.978369   0.427873   9.298   <2e-16 ***
## TreatmentDesorption 130:period -0.032867   0.002419 -13.585   <2e-16 ***
## TreatmentDesorption 150:period -0.077701   0.007848  -9.900   <2e-16 ***
## TreatmentDesorption 170:period -0.261960   0.025678 -10.202   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1086.437  on 14  degrees of freedom
## Residual deviance:   36.411  on  8  degrees of freedom
## AIC: 90.036
##
## Number of Fisher Scoring iterations: 6
```

```
#generating coefficient and confidence intervals for plotting
coefficients.for.plotting1<- cbind(summary(independent)$coef[,c(1)],
confint(independent, level = 0.95)) # level can be modified. Because few
datapoints, intervals are large. Could use eg 75.

## Waiting for profiling to be done...

plot(des$period, des$germinated/des$sown, xlab="Time (days)",
ylab="Proportion germinated", xlim=c(0,200), ylim=c(0,1), mgp=c(2,.5,0),
pch=19, cex=1.2,
col=c("#4477AA","#228833","#EE6677")[unclass(des$Treatment)])
curve(pnorm(coefficients.for.plotting1[1] + coefficients.for.plotting1[4]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=1,lwd=1, col = "#4477AA")
curve(pnorm(coefficients.for.plotting1[2]  +
coefficients.for.plotting1[5]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=1,lwd=1, col = "#228833")
curve(pnorm(coefficients.for.plotting1[3]  +
coefficients.for.plotting1[6]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=1,lwd=1, col = "#EE6677")

### If confidence intervals are to be shown see below code ###

curve(pnorm(coefficients.for.plotting1[1,2] +
coefficients.for.plotting1[4,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=2,lwd=1, col = "#4477AA")
curve(pnorm(coefficients.for.plotting1[1,3] +
coefficients.for.plotting1[4,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=2,lwd=1, col = "#4477AA")

curve(pnorm(coefficients.for.plotting1[2,2] +
coefficients.for.plotting1[5,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=2,lwd=1, col = "#228833")
curve(pnorm(coefficients.for.plotting1[2,3] +
coefficients.for.plotting1[5,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=2,lwd=1, col = "#228833")

curve(pnorm(coefficients.for.plotting1[3,2] +
coefficients.for.plotting1[6,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=2,lwd=1, col = "#EE6677")
curve(pnorm(coefficients.for.plotting1[3,3] +
coefficients.for.plotting1[6,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=2,lwd=1, col = "#EE6677")

legend(175, 1, title = "RH (%)",
rev(unique(des$chamber.RH)),col=c("#4477AA","#228833","#EE6677"), pch=19, bty
= "n")
title("Independent")
```



```
#dev.off()


###Common intercept (Common Ki)
com.inter <- glm(formula = cbind(germinated, sown-germinated) ~
Treatment:period , family = binomial(link = "probit"),  data = des)
summary(com.inter)

##
## Call:
## glm(formula = cbind(germinated, sown - germinated) ~ Treatment:period,
##     family = binomial(link = "probit"), data = des)
##
## Coefficients:
##                                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)                       3.981964   0.193851   20.54   <2e-16 ***
## TreatmentDesorption 130:period -0.030063   0.001709  -17.59   <2e-16 ***
## TreatmentDesorption 150:period -0.089767   0.004793  -18.73   <2e-16 ***
## TreatmentDesorption 170:period -0.262164   0.013179  -19.89   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1079.71  on 13  degrees of freedom
## Residual deviance:   40.39  on 10  degrees of freedom
## AIC: 90.015
##
## Number of Fisher Scoring iterations: 6

# generating coefficient and confidence intervals for plotting
coefficients.for.plotting2<- cbind(summary(com.inter)$coef[,c(1)],
confint(com.inter, level = 0.95)) # level can be modified. Because few data
points, intervals are large. Could use eg 75.

## Waiting for profiling to be done...

# plot
plot(des$period, des$germinated/des$sown, xlab="Time (days)",
ylab="Porportion germinated", xlim=c(0,200), ylim=c(0,1), mgp=c(2,.5,0),
pch=19, cex=1.2,
col=c("#4477AA","#228833","#EE6677")[unclass(des$Treatment)])

curve(pnorm(coefficients.for.plotting2[1] + coefficients.for.plotting2[2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=1,lwd=1, col = "#4477AA")
curve(pnorm(coefficients.for.plotting2[1]  +
coefficients.for.plotting2[3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=1,lwd=1, col = "#228833")
curve(pnorm(coefficients.for.plotting2[1]  +
coefficients.for.plotting2[4]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=1,lwd=1, col = "#EE6677")

### If confidence intervals are to be shown see below code ###

curve(pnorm(coefficients.for.plotting2[1,2] +
coefficients.for.plotting2[2,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=2,lwd=1, col = "#4477AA")
curve(pnorm(coefficients.for.plotting2[1,3] +
coefficients.for.plotting2[2,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=2,lwd=1, col = "#4477AA")
```

```
curve(pnorm(coefficients.for.plotting2[1,2] +
coefficients.for.plotting2[3,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
      add=TRUE, lty=2,lwd=1, col = "#228833")
curve(pnorm(coefficients.for.plotting2[1,3] +
coefficients.for.plotting2[3,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=2,lwd=1, col = "#228833")

curve(pnorm(coefficients.for.plotting2[1,2] +
coefficients.for.plotting2[4,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=2,lwd=1, col = "#EE6677")
curve(pnorm(coefficients.for.plotting2[1,3] +
coefficients.for.plotting2[4,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=2,lwd=1, col = "#EE6677")

legend(175, 1, title = "RH (%)",
rev(unique(des$chamber.RH)),col=c("#4477AA","#228833","#EE6677"), pch=19, bty
= "n")
title("Common intercept")
```



```
#dev.off()


#  Table of coefficients for common intercept



###Common slope (common -sigma^-1)
com.slope <- glm(formula = cbind(germinated, sown-germinated) ~ Treatment +
period -1, family = binomial(link = "probit"),  data = des)
summary(com.slope)
```

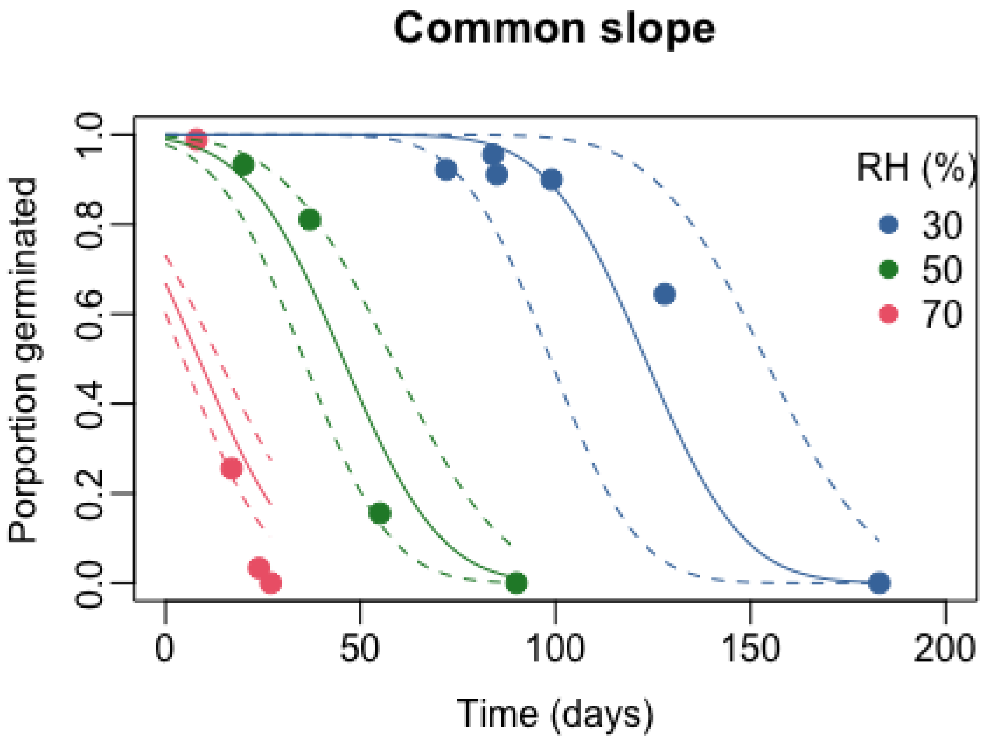
```
##
## Call:
## glm(formula = cbind(germinated, sown - germinated) ~ Treatment +
##     period - 1, family = binomial(link = "probit"), data = des)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## TreatmentDesorption 130  6.24593    0.35392  17.648  < 2e-16 ***
## TreatmentDesorption 150  2.31196    0.15725  14.702  < 2e-16 ***
## TreatmentDesorption 170  0.43695    0.09078   4.813 1.48e-06 ***
## period                  -0.05077    0.00312 -16.270  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1086.44  on 14  degrees of freedom
## Residual deviance:  255.08  on 10  degrees of freedom
## AIC: 304.71
##
## Number of Fisher Scoring iterations: 6
```

```
#generating coefficient and confidence intervals for plotting
coefficients.for.plotting3<- cbind(summary(com.slope)$coef[,c(1)],
confint(com.slope, level = 0.95)) # level can be modified. Because few data
points, intervals are large. Could use eg 75.
```

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

```
# plot
plot(des$period, des$germinated/des$sown, xlab="Time (days)",
ylab="Porportion germinated", xlim=c(0,200), ylim=c(0,1), mgp=c(2,.5,0),
pch=19, cex=1.2,
col=c("#4477AA","#228833","#EE6677")[unclass(des$Treatment)])

curve(pnorm(coefficients.for.plotting3[1] + coefficients.for.plotting3[4]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=1,lwd=1, col = "#4477AA")
```

```
curve(pnorm(coefficients.for.plotting3[2]  +
coefficients.for.plotting3[4]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=1,lwd=1, col = "#228833")
curve(pnorm(coefficients.for.plotting3[3]  +
coefficients.for.plotting3[4]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=1,lwd=1, col = "#EE6677")

### If confidence intervals are to be shown see below code ###

curve(pnorm(coefficients.for.plotting3[1,2] +
coefficients.for.plotting3[4,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=2,lwd=1, col = "#4477AA")
curve(pnorm(coefficients.for.plotting3[1,3] +
coefficients.for.plotting3[4,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 130")$period),
add=TRUE, lty=2,lwd=1, col = "#4477AA")

curve(pnorm(coefficients.for.plotting3[2,2] +
coefficients.for.plotting3[4,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
      add=TRUE, lty=2,lwd=1, col = "#228833")
curve(pnorm(coefficients.for.plotting3[2,3] +
coefficients.for.plotting3[4,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 150")$period),
add=TRUE, lty=2,lwd=1, col = "#228833")

curve(pnorm(coefficients.for.plotting3[3,2] +
coefficients.for.plotting3[4,2]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=2,lwd=1, col = "#EE6677")
curve(pnorm(coefficients.for.plotting3[3,3] +
coefficients.for.plotting3[4,3]*x),
      from = 0, to = max(subset(des, Treatment=="Desorption 170")$period),
add=TRUE, lty=2,lwd=1, col = "#EE6677")

legend(175, 1, title = "RH (%)",
rev(unique(des$chamber.RH)),col=c("#4477AA","#228833","#EE6677"), pch=19, bty
= "n")
title("Common slope")
```

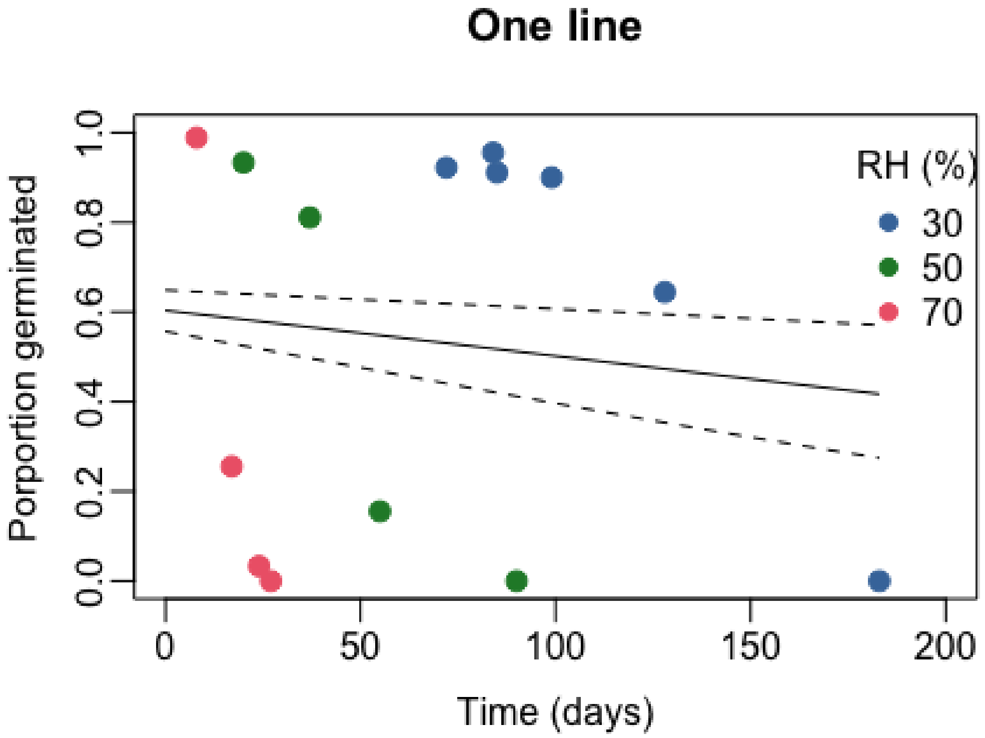


```
#dev.off()


## one line
one.line <- glm(formula = cbind(germinated, sown-germinated) ~ period ,
family = binomial(link = "probit"), data = des)
summary(one.line)

##
## Call:
## glm(formula = cbind(germinated, sown - germinated) ~ period,
##     family = binomial(link = "probit"), data = des)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.262001   0.060829   4.307 1.65e-05 ***
## period      -0.002573   0.000743  -3.464 0.000533 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1079.7  on 13  degrees of freedom
## Residual deviance: 1067.8  on 12  degrees of freedom
## AIC: 1113.4
##
## Number of Fisher Scoring iterations: 5
```

```r
#generating coefficient and confidence intervals for plotting
coefficients.for.plotting4<- cbind(summary(one.line)$coef[,c(1)],
confint(one.line, level = 0.95)) # level can be modified. Because few data
points, intervals are large. Could use eg 75.
```

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

```r
# plot
plot(des$period, des$germinated/des$sown, xlab="Time (days)",
ylab="Porportion germinated", xlim=c(0,200), ylim=c(0,1), mgp=c(2,.5,0),
pch=19, cex=1.2,
col=c("#4477AA","#228833","#EE6677")[unclass(des$Treatment)])

curve(pnorm(coefficients.for.plotting4[1] + coefficients.for.plotting4[2]*x),
      from = 0, to = max(des$period), add=TRUE, lty=1,lwd=1)

### If confidence intervals are to be shown see below code ###
curve(pnorm(coefficients.for.plotting4[1,2] +
coefficients.for.plotting4[2,2]*x),
      from = 0, to = max(des$period), add=TRUE, lty=2,lwd=1)
curve(pnorm(coefficients.for.plotting4[1,3] +
coefficients.for.plotting4[2,3]*x),
      from = 0, to = max(des$period), add=TRUE, lty=2,lwd=1)

legend(175, 1, title = "RH (%)",
rev(unique(des$chamber.RH)),col=c("#4477AA","#228833","#EE6677"), pch=19, bty
= "n")
title("One line")
```



```
#dev.off()

# Table of coefficients for one line model
table.oneline<-
signif(as.data.frame(summary(one.line)$coefficients[,c(1,2,4)]), 4)
table.oneline[2,1]<- signif(-1/table.oneline[2,1], 4)

# dose.p
table.oneline[3,1]<- signif(dose.p(one.line, cf = 1:2, p = 0.5), 4)
table.oneline[3,2]<- signif(unname(attributes(dose.p(one.line, cf = 1:2, p =
0.5))$SE[, 1]), 4)
table.oneline[4,1]<- signif(dose.p(one.line, cf = 1:2, p = 0.85), 4)
table.oneline[4,2]<- signif(unname(attributes(dose.p(one.line, cf = 1:2, p =
0.85))$SE[, 1]), 4)

row.names(table.oneline)<-c("Ki", "sigma", "p50", "p85")
table.oneline$`Std. Error` <- round(table.oneline$`Std. Error`, 4)

table.oneline[3,3] <- "-"
table.oneline[4,3] <- "-"
table.oneline$AIC<- "-"
table.oneline$AIC[1]<- round(summary(one.line)$aic, 4)
```

```
# Call the table
knitr::kable(table.oneline)
```

	Estimate	Std. Error	Pr(>|z|)	AIC
Ki	0.262	0.0608	1.653e-05	1113.4349
sigma	388.700	0.0007	0.000533	-
p50	101.800	17.1400	-	-
p85	-301.000	107.0000	-	-

```
### Compare models ###

# Create deviance table
dev.table<-data.frame(
  Model = c("independent", "Common.intercept", "Common.slope", "One.line"),
  Deviance = c(independent$deviance, com.inter$deviance, com.slope$deviance,
one.line$deviance),
  df = c(independent$df.residual,
com.inter$df.residual,com.slope$df.residual, one.line$df.residual),
  AIC = c(independent$aic, com.inter$aic, com.slope$aic, one.line$aic)
)

# Call the table.
knitr::kable(dev.table, row.names = FALSE)
```

Model	Deviance	df	AIC
independent	36.41096	8	90.03587
Common.intercept	40.39037	10	90.01528
Common.slope	255.08134	10	304.70624
One.line	1067.81000	12	1113.43490

```
# Here we demonstrate pairwise comparisons of common slope and common
intercept with  independent and one line.
# However, in practice this would only be done with the models that have the
lowest and closest in their AIC
# (e.g. independent and common intercept in this data presented).

# Common intercept vs Independent
df.change1<-com.inter$df.residual - independent$df.residual
df.change1

## [1] 2

F1<-((com.inter$deviance-
independent$deviance)/df.change1)/(independent$deviance/independent$df.residu
al)
F1

## [1] 0.437166
```

```
F1prob<-pf(F1, df.change1, independent$df.residual, lower.tail = FALSE) #
note the lower.tail = False is not default
F1prob<-format(signif(F1prob, 4), nsmall = 4)
F1prob

## [1] "0.6604"

F1sum<-c(df.change1, F1, F1prob)
F1sum

## [1] "2"                  "0.437166049341884" "0.6604"

# Common slope vs Independent
df.change2<-com.slope$df.residual - independent$df.residual
df.change2

## [1] 2

F2<-((com.slope$deviance-
independent$deviance)/df.change2)/(independent$deviance/independent$df.residu
al)
F2

## [1] 24.02248

F2prob<-pf(F2, df.change2, independent$df.residual, lower.tail = FALSE) #
note the lower.tail = False is not default
F2prob<-format(signif(F2prob, 4), nsmall = 4)
F2prob

## [1] "0.0004152"

F2sum<-c(df.change2, F2, F2prob)
F2sum

## [1] "2"                 "24.0224765318435" "0.0004152"

# Common intercept vs One line
df.change3<-one.line$df.residual - com.inter$df.residual
df.change3

## [1] 2

F3<-((one.line$deviance-
com.inter$deviance)/df.change3)/(com.inter$deviance/com.inter$df.residual)
F3

## [1] 127.1862

F3prob<-pf(F3, df.change3, one.line$df.residual, lower.tail = FALSE) # note
the lower.tail = False is not default
F3prob<-format(signif(F3prob, 4), nsmall = 4)
F3prob
```

```
## [1] "8.359e-09"

F3sum<-c(df.change3, F3, F3prob)
F3sum

## [1] "2"               "127.18620508823" "8.359e-09"

# Common slope vs One line
df.change4<-one.line$df.residual - com.slope$df.residual
df.change4

## [1] 2

F4<-((one.line$deviance-
com.slope$deviance)/df.change4)/(com.slope$deviance/com.slope$df.residual)
F4

## [1] 15.93077

F4prob<-pf(F4, df.change4, com.slope$df.residual, lower.tail = FALSE) # note
the lower.tail = False is not default
F4prob<-format(signif(F4prob, 4), nsmall = 4)
F4prob

## [1] "0.0007779"

F4sum<-c(df.change4, F4, F4prob)
F4sum

## [1] "2"                "15.9307746494971" "0.0007779"

# Combine into one summary table. Report in appendices
# Most important value is F probability
# If F probability > alpha, you can accept the model
# In this case there's no significant difference between common intercept vs
independent
F.table1<-data.frame(Model.comparison = c("Common intercept vs Independent",
                                          "Common slope vs Independent",
                                          "Common intercept vs One line",
                                          "Common slope vs One line "),
                     "DF change" = c(df.change1, df.change2, df.change3,
df.change4),
                     "F statistic" = c(F1, F2, F3, F4),
                     "F probability" = c(F1prob, F2prob, F3prob, F4prob))
# call the table
knitr::kable(F.table1)
```

Model.comparison	DF.change	F.statistic	F.probability
Common intercept vs Independent	2	0.437166	0.6604
Common slope vs Independent	2	24.022476	0.0004152
Common intercept vs One line	2	127.186205	8.359e-09

Model.comparison	DF.change	F.statistic	F.probability
Common slope vs One line	2	15.930775	0.0007779

```
rm(df.change1, df.change2, df.change3, df.change4, F1, F2, F3, F4, F1prob,
F2prob, F3prob, F4prob, F1sum, F2sum, F3sum, F4sum)
# N.B. Common line  = one line
# N.B. Independent

# Note: A quick way to view the deviance between two models is with function
anova()
# adding, test = test="Chisq", will output a p-value.
anova(independent, com.inter,  test="Chisq")

## Analysis of Deviance Table
##
## Model 1: cbind(germinated, sown - germinated) ~ Treatment +
Treatment:period -
##     1
## Model 2: cbind(germinated, sown - germinated) ~ Treatment:period
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         8     36.411
## 2        10     40.390 -2  -3.9794   0.1367

###  Table of coefficients
### Presented for only the selected model. In this case the independent
model.

table.independent<-
round(as.data.frame(summary(independent)$coefficients[,c(1,2,4)]), 3)
table.independent[c(4:6),1]<- signif(-1/table.independent[c(4:6),1], 3)
table.independent[c(4:6),2] <- table.independent[
c(4:6),2]*table.independent[ c(4:6),1]

# dose.p
table.independent[7,1]<- signif(dose.p(independent, cf = c(1,4), p = 0.5), 3)
table.independent[7,2]<- signif(unname(attributes(dose.p(independent, cf =
c(1,4), p = 0.5))$SE[, 1]), 3)
table.independent[8,1]<- signif(dose.p(independent, cf = c(2,5), p = 0.5), 3)
table.independent[8,2]<- signif(unname(attributes(dose.p(independent, cf =
c(2,5), p = 0.5))$SE[, 1]), 3)
table.independent[9,1]<- signif(dose.p(independent, cf = c(3,6), p = 0.5), 3)
table.independent[9,2]<- signif(unname(attributes(dose.p(independent, cf =
c(3,6), p = 0.5))$SE[, 1]), 3)

row.names(table.independent)<-c( "Ki-Desorption 130", "Ki-Desorption
150","Ki-Desorption 170","sigma-Desorption 130", "sigma-Desorption
150","sigma-Desorption 170", "p50-Desorption 130", "p50-Desorption 150","p50-
Desorption 170")
table.independent$`Std. Error` <- round(table.independent$`Std. Error`, 3)
```

```r
table.independent[c(7:9),3] <- "-"
table.independent$AIC<- "-"
table.independent$AIC[1]<- round(summary(independent)$aic, 3)
names(table.independent)<- c("Estimate", "SE", "P", "AIC")
table.independent$P <- ifelse(table.independent$P=="0", "<0.001",
table.independent$P)

# Call the table.
knitr::kable(table.independent)
```

	Estimate	SE	P	AIC
Ki-Desorption 130	4.316	0.281	<0.001	90.036
Ki-Desorption 150	3.434	0.344	<0.001	-
Ki-Desorption 170	3.978	0.428	<0.001	-
sigma-Desorption 130	30.300	0.061	<0.001	-
sigma-Desorption 150	12.800	0.102	<0.001	-
sigma-Desorption 170	3.820	0.099	<0.001	-
p50-Desorption 130	131.000	2.730	-	-
p50-Desorption 150	44.200	1.250	-	-
p50-Desorption 170	15.200	0.449	-	-