

Cumulative Weed Emergence

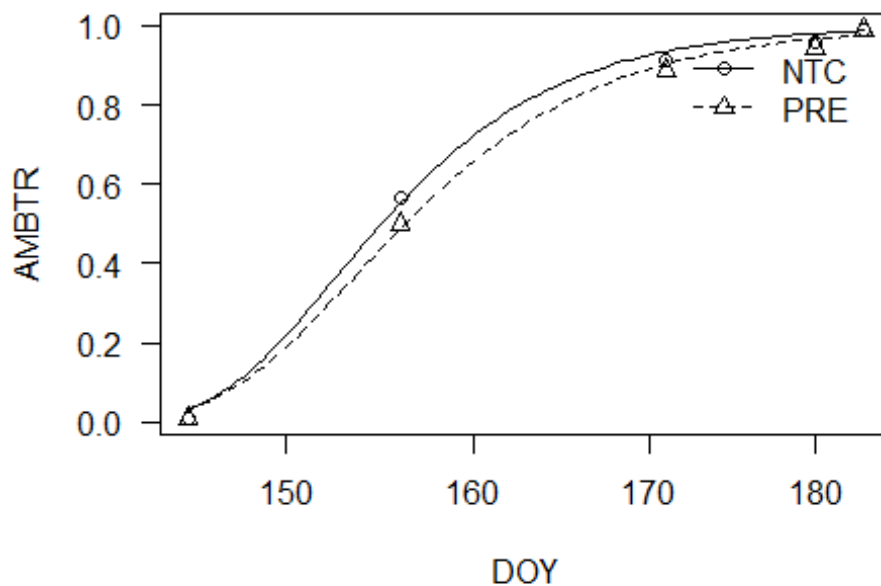
SS

3/9/2020

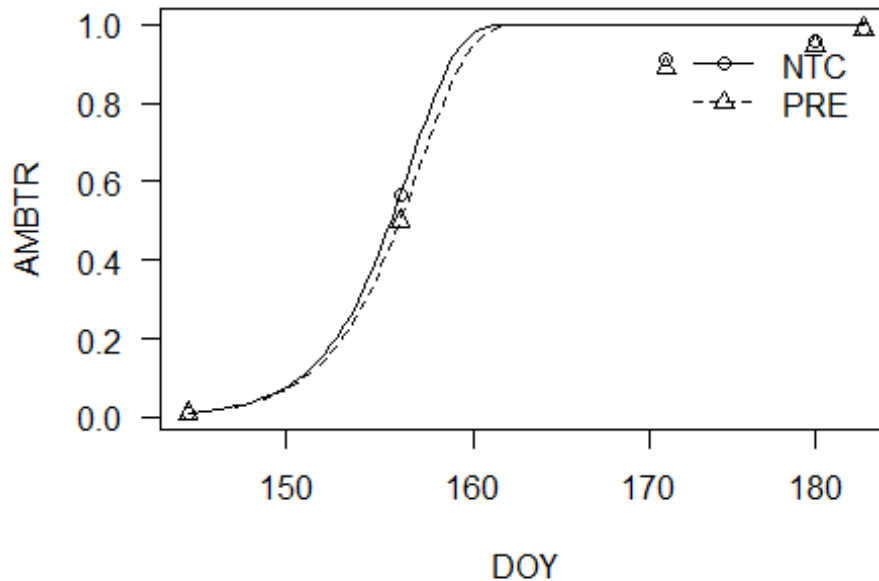
```
#NLR model Janesville 2018 - giant ragweed emergence
model = drm(AMBTR ~ DOY, Trt, fct = 14(), data=data1)
mselect(model, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",
"Res var", "Lack of fit", "no"), icfct = AIC)

##          logLik          IC Lack of fit          Res var
## 14      32.87758 -47.75517             NA 0.0004081173
## 14      32.87758 -47.75517             NA 0.0004081173
## W1.4    32.63351 -47.26703             NA 0.0004285335
## W1.3    27.93987 -41.87973             NA 0.0005478223
## W2.3    21.39903 -28.79807             NA 0.0020266052
## W2.4    21.39861 -24.79723             NA 0.0040535513

model2.2 = drm(AMBTR ~ DOY, Trt, fct = W1.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data1)
model2.3 = drm(AMBTR ~ DOY, Trt, fct = W2.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data1)
#summary(model2.2)
plot(model2.2) #this one is better (W1.3)
```



```
plot(model2.3)
```



```
#ED(model2.2, c(0.5,0.9), type="absolute", interval = "delta")
#EDcomp(model2.2, c(0.5,0.5), type="absolute")
#EDcomp(model2.2, c(0.9,0.9), type="absolute")

t.test(mAMBTR ~ Trt, data=data1.2)

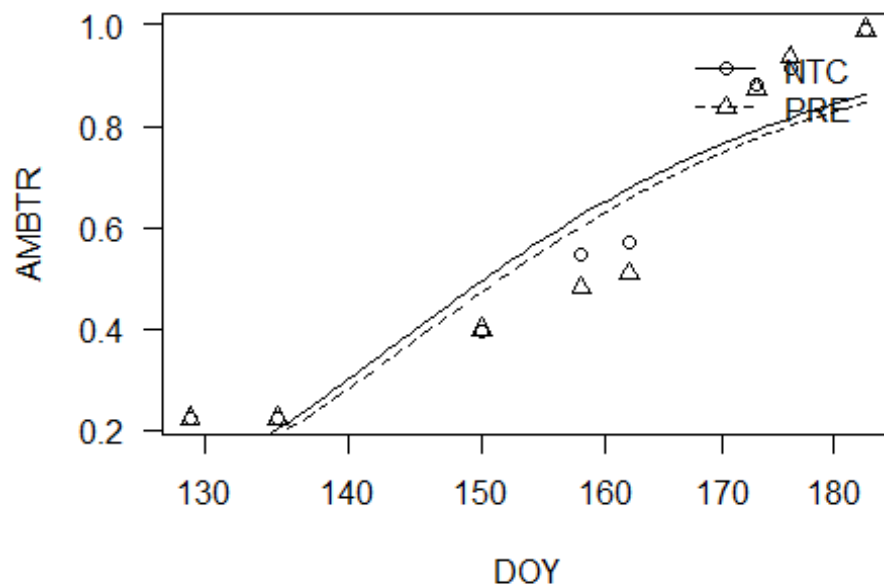
##
##  Welch Two Sample t-test
##
## data:  mAMBTR by Trt
## t = 1.5037, df = 3.1679, p-value = 0.225
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -29.83973  86.43973
## sample estimates:
## mean in group NTC mean in group PRE
##           49.8           21.5

#NLR model - Janesville 2019 giant ragweed emergence
model3 = drm(AMBTR ~ DOY, Trt, fct = 14(), data=data2)
mselect(model3, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",
"Res var", "Lack of fit", "no"), icfct = AIC)

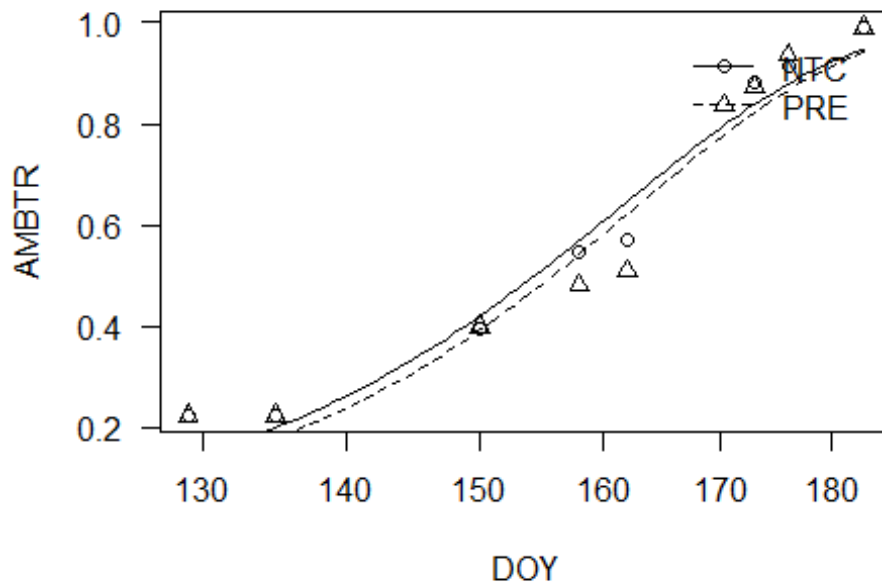
##           logLik           IC Lack of fit           Res var
## W2.4 35.84423 -53.68846           NA 0.001326437
```

```
## l4 33.71104 -49.42207 NA 0.001731773
## l4 33.71104 -49.42207 NA 0.001731773
## W1.4 31.60129 -45.20257 NA 0.002254356
## W2.3 27.57019 -41.14039 NA 0.002985023
## W1.3 25.89972 -37.79944 NA 0.003678175

model4.2 = drm(AMBTR ~ DOY, Trt, fct = W1.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data2)
model4.3 = drm(AMBTR ~ DOY, Trt, fct = W2.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data2)
#summary(model4.2)
plot(model4.2)
```



```
plot(model4.3) #this one is better (W2.3)
```



```
#ED(model4.2, c(0.5,0.9), type="absolute", interval = "delta")
#EDcomp(model4.2, c(0.5,0.5), type="absolute")
#EDcomp(model4.2, c(0.9,0.9), type="absolute")

t.test(mAMBTR ~ Trt, data=data2.2)

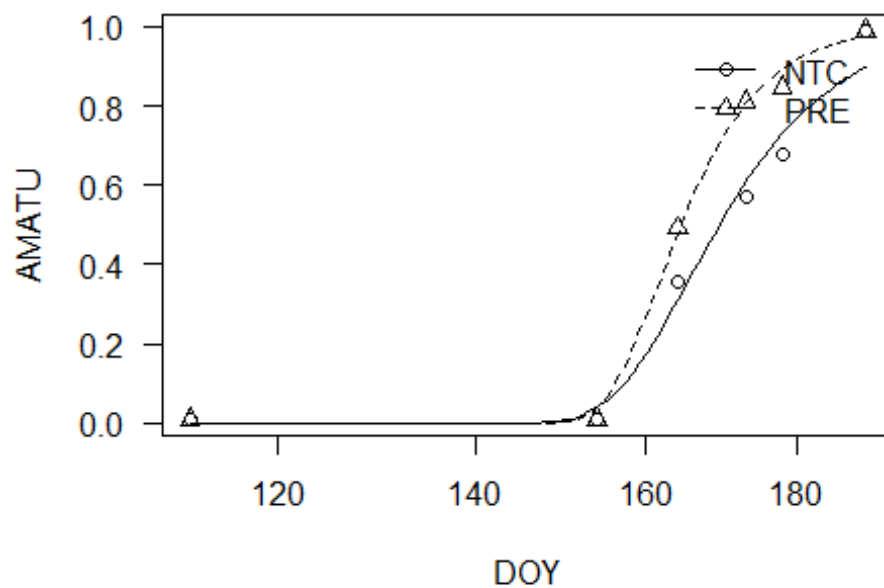
##
## Welch Two Sample t-test
##
## data: mAMBTR by Trt
## t = 1.1914, df = 5.8535, p-value = 0.2796
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -60.22139 173.17139
## sample estimates:
## mean in group NTC mean in group PRE
## 250.250 193.775

#NLR model - Brooklyn 2019 waterhemp emergence
model5 = drm(AMATU ~ DOY, Trt, fct = 14(), data=data3)
mselect(model5, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",
"Res var", "Lack of fit", "no"), icfct = AIC)

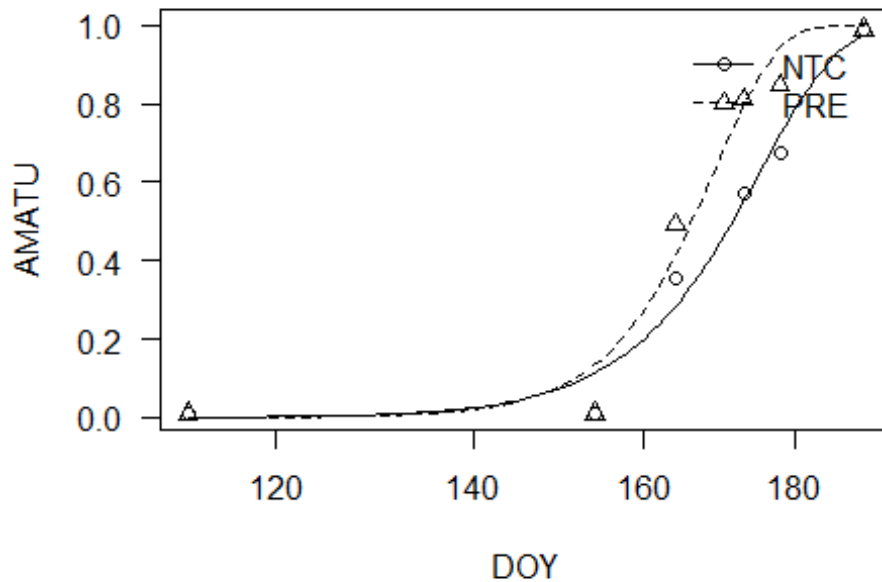
## logLik IC Lack of fit Res var
## W1.3 24.19331 -34.38662 NA 0.002076756
## W1.4 24.31815 -30.63631 NA 0.003050986
## 14 20.06456 -22.12913 NA 0.006199054
```

```
## 14    20.06456 -22.12913          NA 0.006199054
## W2.3 17.75750 -21.51501          NA 0.006070502
## W2.4 17.91197 -17.82394          NA 0.008874323

model6 = drm(AMATU ~ DOY, Trt, fct = W1.3(fixed=c(NA, 1, NA), names = c("b",
"c", "d")), data=data3)
model6.2 = drm(AMATU ~ DOY, Trt, fct = W2.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data3)
#summary(model6)
plot(model6) #this one is better(W1.3)
```



```
plot(model6.2)
```



```
#ED(model6, c(0.5,0.9), type="absolute", interval = "delta")
```

```
#EDcomp(model6, c(0.5,0.5), type="absolute")
```

```
#EDcomp(model6, c(0.9,0.9), type="absolute")
```

```
t.test(mAMATU ~ Trt, data=data3.2)
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: mAMATU by Trt
```

```
## t = 11.449, df = 3.2895, p-value = 0.0009208
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## 1699.845 2923.205
```

```
## sample estimates:
```

```
## mean in group NTC mean in group PRE
```

```
## 2497.225 185.700
```

```
#NLR model - Arlington 2018 common ragweed emergence
```

```
model7 = drm(AMBEL ~ DOY, fct = 14(), data=data4)
```

```
mselect(model7, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",  
"Res var", "Lack of fit", "no"), icfct = AIC)
```

```
## logLik IC Lack of fit Res var
```

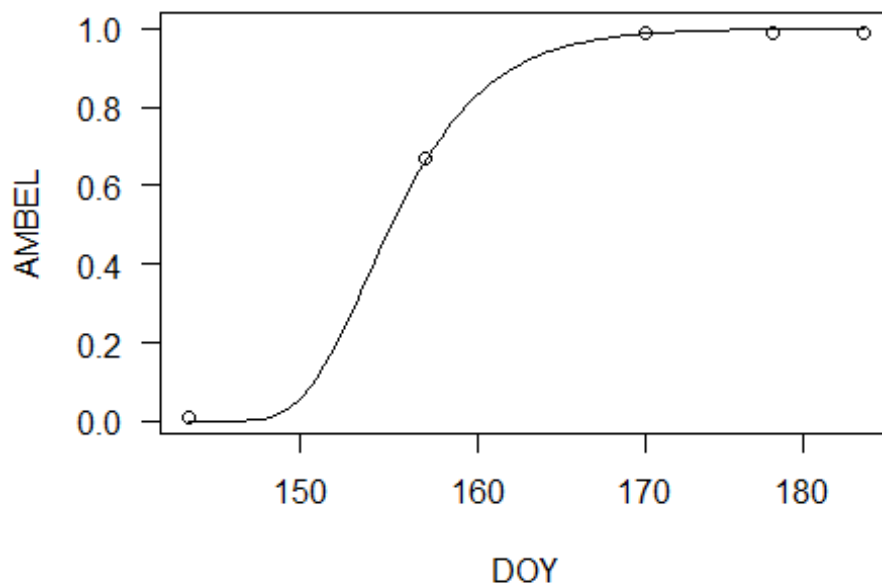
```
## W2.3 89.04501 -170.09001 4.687315e-58 1.541973e-09
```

```
## W2.4 84.12944 -158.25888 1.362702e-59 4.808219e-09
```

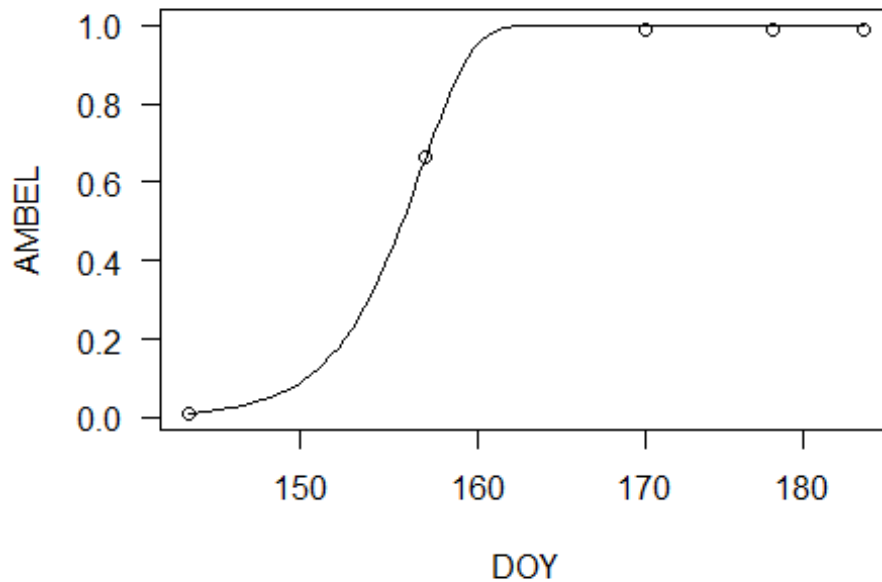
```
## 14 57.12182 -104.24364 1.861104e-65 1.066194e-06
```

```
## l4    57.12182 -104.24364 1.861104e-65 1.066194e-06
## W1.4  50.01406  -90.02812 5.325258e-67 4.417823e-06
## W1.3  39.19857  -70.39714 7.029229e-69 3.293694e-05

model8 = drm(AMBEL ~ DOY, fct = W1.3(fixed=c(NA, 1, NA), names = c("b", "c",
"d")), data=data4)
model8.2 = drm(AMBEL ~ DOY, fct = W2.3(fixed=c(NA, 1, NA), names = c("b",
"c", "d")), data=data4)
#summary(model8)
plot(model8)
```



```
plot(model8.2) #this one is better (W2.3)
```



```
#ED(model8, c(0.5,0.9), type="absolute", interval = "delta")
```

```
t.test(mAMBEL ~ Trt, data=data4.2)
```

```
##
## Welch Two Sample t-test
##
## data: mAMBEL by Trt
## t = 1.7818, df = 3.7865, p-value = 0.1534
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -7.967443 34.817443
## sample estimates:
## mean in group NTC mean in group PRE
##          20.175          6.750
```

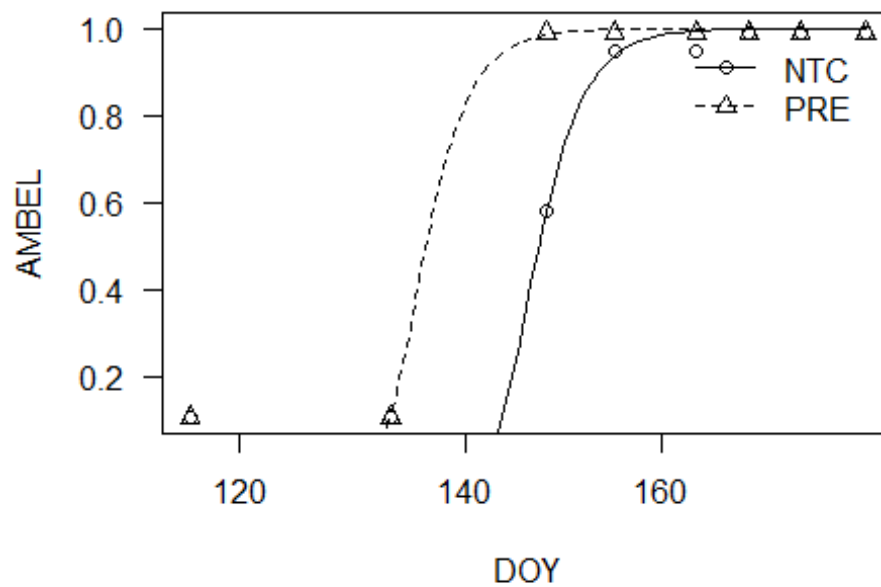
```
#NLR model - Arlington 2019 common ragweed emergence
```

```
model9 = drm(AMBEL ~ DOY, Trt, fct = 14(), data=data5)
mselect(model9, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",
"Res var", "Lack of fit", "no"), icfct = AIC)
```

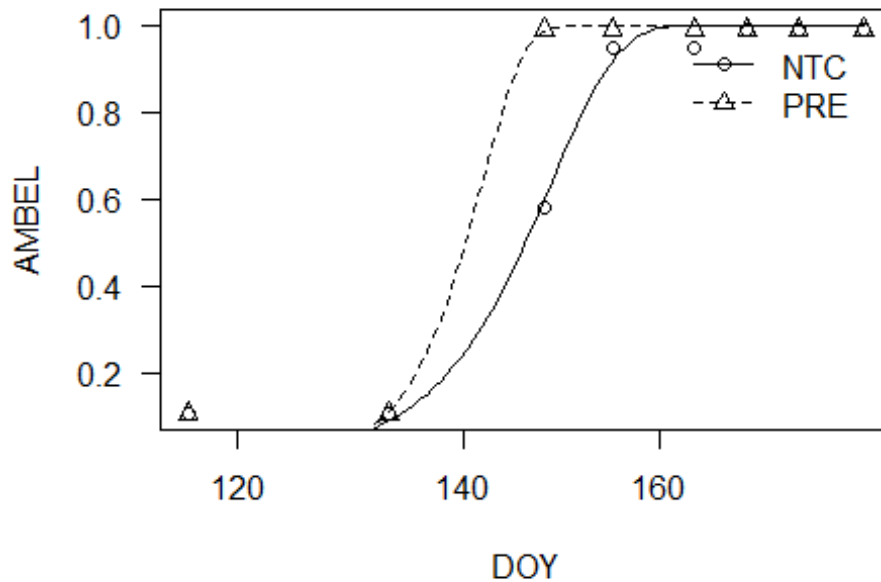
	logLik	IC	Lack of fit	Res var
## W1.4	52.67501	-87.35003	NA	0.0001618070
## 14	52.55764	-87.11527	NA	0.0001641985
## 14	52.55764	-87.11527	NA	0.0001641985
## W2.4	50.80963	-83.61926	NA	0.0002042975


```
## W2.3 29.07087 -44.14175      NA 0.0024744608
## W1.3 26.39999 -38.79997      NA 0.0034552110

model10.2 = drm(AMBEL ~ DOY, Trt, fct = W1.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data5)
model10.3 = drm(AMBEL ~ DOY, Trt, fct = W2.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data5)
#summary(model10.2)
plot(model10.2)
```



```
plot(model10.3) #this one is better (W2.3)
```



```
#ED(model10.2, c(0.5,0.9), type="absolute", interval = "delta")
#EDcomp(model10.2, c(0.5,0.5), type="absolute")
#EDcomp(model10.2, c(0.9,0.9), type="absolute")

t.test(mAMBEL ~ Trt, data=data5.2)

##
##  Welch Two Sample t-test
##
## data:  mAMBEL by Trt
## t = 2.8957, df = 3, p-value = 0.06272
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.396126 50.796126
## sample estimates:
## mean in group NTC mean in group PRE
##                29.6                5.4

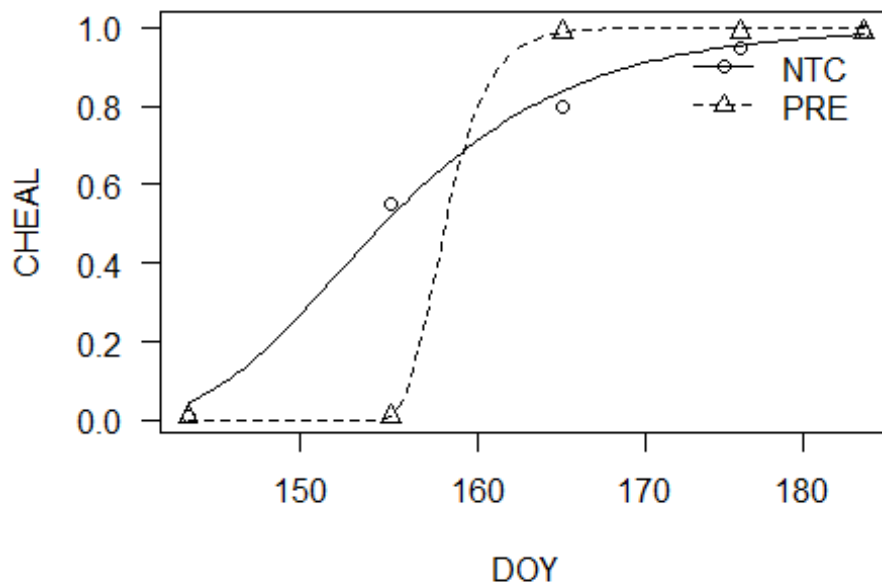
#NLR model - Lancaster 2018 common LQ emergence
model11 = drm(CHEAL ~ DOY, Trt, fct = 14(), data=data6)
mselect(model11, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",
"Res var", "Lack of fit", "no"), icfct = AIC)

## Warning in sqrt(diag(varMat)): NaNs produced

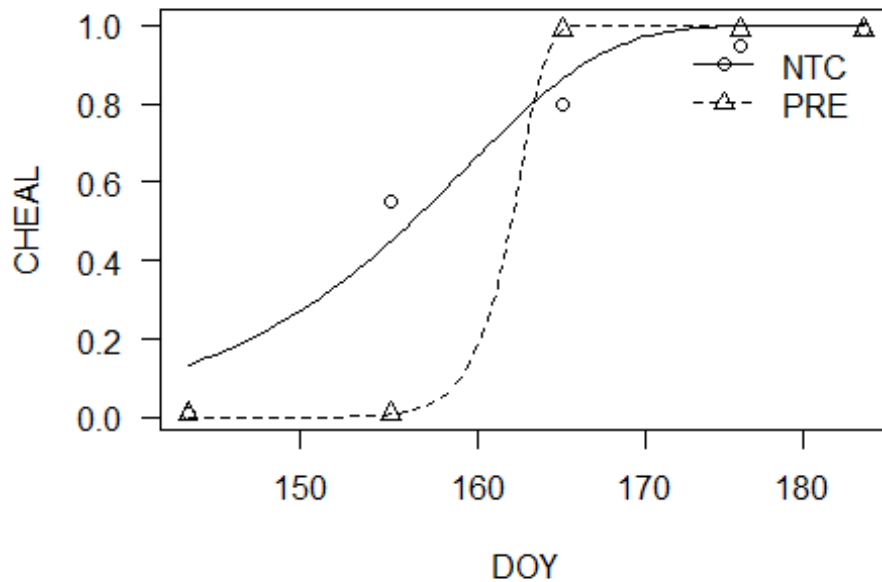
##      logLik      IC Lack of fit      Res var
## 14  33.59482 -49.18963          NA 0.0003535795
```

```
## l4    33.59482 -49.18963      NA 0.0003535795
## W1.4  29.34242 -40.68485      NA 0.0008276471
## W1.3  25.32555 -36.65109      NA 0.0009240952
## W2.3  16.83994 -19.67987      NA 0.0050439109
## W2.4  16.86654 -15.73308      NA 0.0100342922

model12.2 = drm(CHEAL ~ DOY, Trt, fct = W1.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data6)
model12.3 = drm(CHEAL ~ DOY, Trt, fct = W2.3(fixed=c(NA, 1, NA), names =
c("b", "c", "d")), data=data6)
#summary(model12.2)
plot(model12.2) #this one is better (W1.3)
```



```
plot(model12.3)
```



```
#ED(model12.2, c(0.5,0.9), type="absolute", interval = "delta")
#EDcomp(model12.2, c(0.5,0.5), type="absolute")
#EDcomp(model12.2, c(0.9,0.9), type="absolute")

t.test(mCHEAL ~ Trt, data=data6.2)

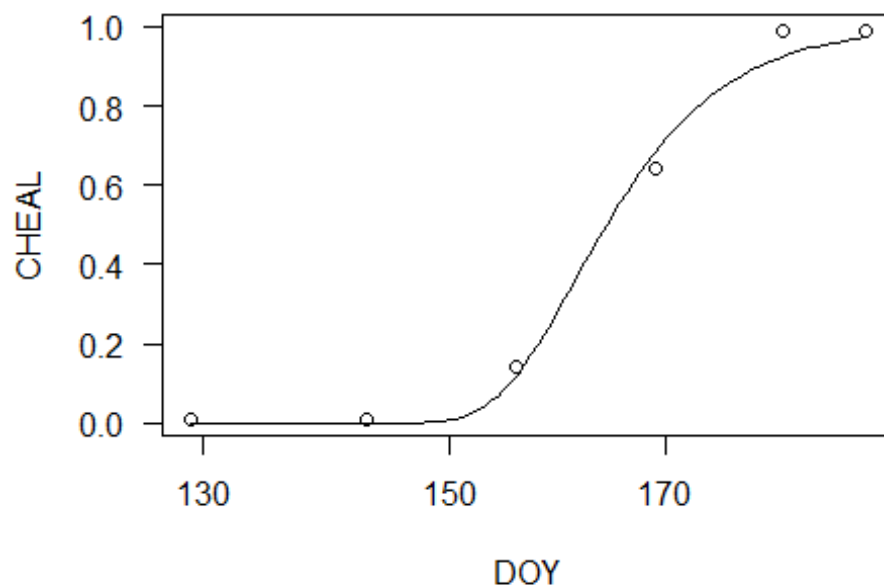
##
##  Welch Two Sample t-test
##
## data:  mCHEAL by Trt
## t = 3.0727, df = 3.0641, p-value = 0.05295
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.9509183 81.6509183
## sample estimates:
## mean in group NTC mean in group PRE
##           41.70           1.35

#NLR model - Lancaster 2019 common LQ emergence
model13 = drm(CHEAL ~ DOY, fct = 14(), data=data7)
mselect(model13, list(14(), W2.3(), W1.3(), W1.4(), W2.4()), sorted=c("IC",
"Res var", "Lack of fit", "no"), icfct = AIC)

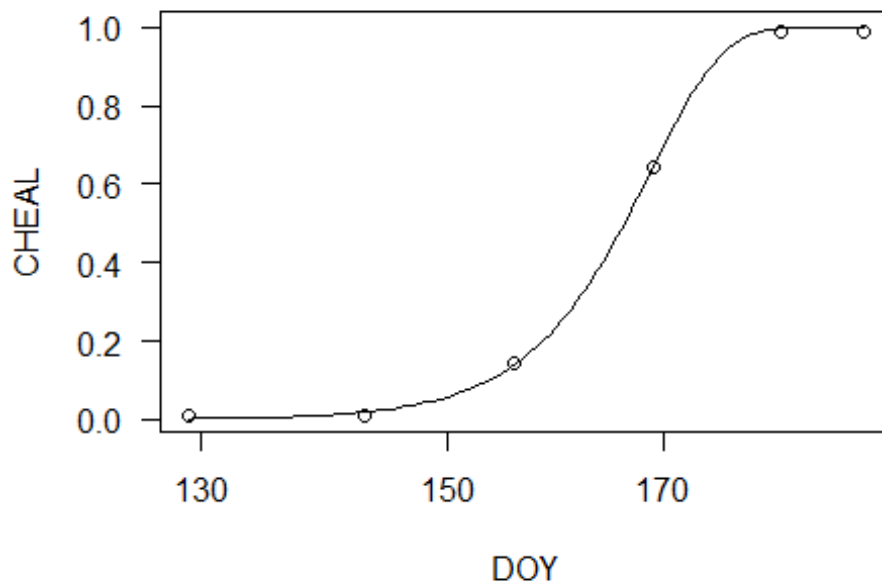
##           logLik           IC Lack of fit           Res var
## W2.3 23.24639 -38.49278           NA 5.050057e-05
## W2.4 23.23651 -36.47302           NA 7.600073e-05
## 14    17.33911 -24.67822           NA 5.426923e-04
```

```
## l4    17.33911 -24.67822      NA 5.426923e-04
## W1.3  13.97931 -19.95862      NA 1.108774e-03
## W1.4  14.25161 -18.50321      NA 1.518852e-03

model14 = drm(CHEAL ~ DOY, fct = W1.3(fixed=c(NA, 1, NA), names = c("b", "c",
"d")), data=data7)
model14.2 = drm(CHEAL ~ DOY, fct = W2.3(fixed=c(NA, 1, NA), names = c("b",
"c", "d")), data=data7)
#summary(model14)
plot(model14)
```



```
plot(model14.2) #this one is better (W2.3)
```



```
#ED(model14, c(0.5,0.9), type="absolute", interval = "delta")
```

```
t.test(mCHEAL ~ Trt, data=data7.2)
```

```
##
##  Welch Two Sample t-test
##
## data:  mCHEAL by Trt
## t = 1.9939, df = 3, p-value = 0.1401
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -11.23562  48.93562
## sample estimates:
## mean in group NTC mean in group PRE
##           18.85           0.00
```