LTDE Michaelis Menten Experiment

Mario E. Muscarella, Jay T. Lennon

09 March, 2016

Overview

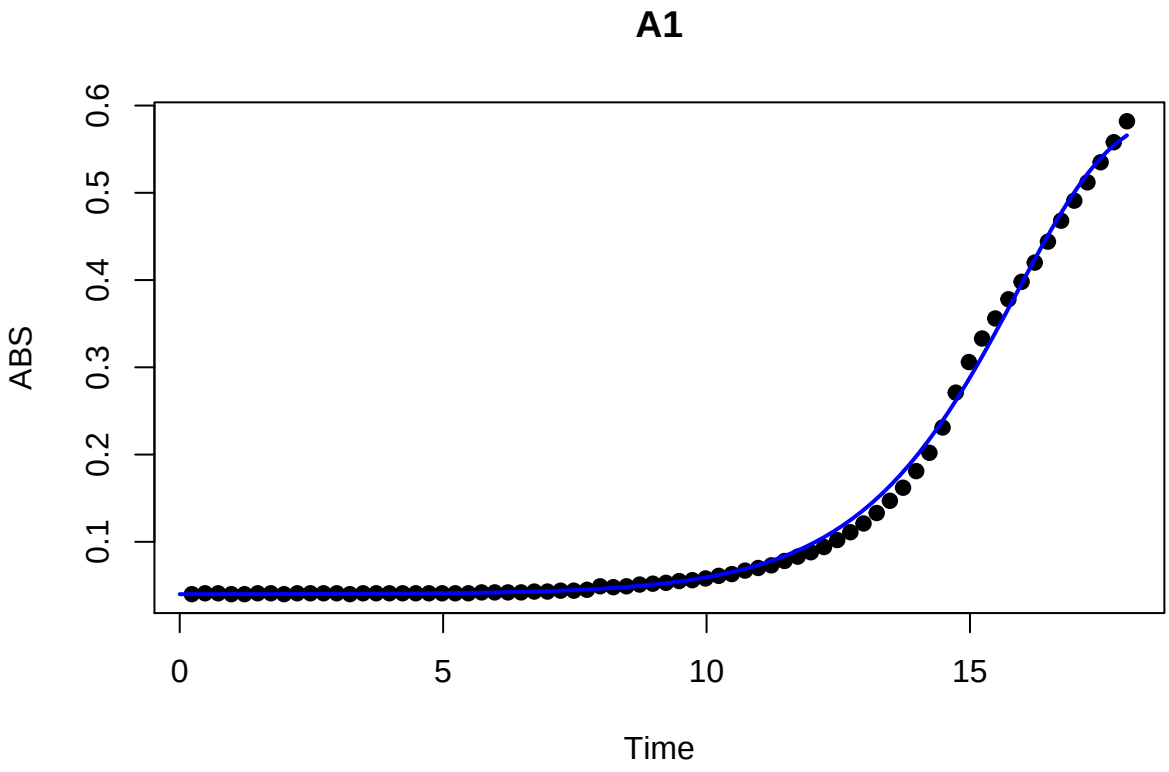
Experiment 1: Plate Reader Growth Curvse

Data Import

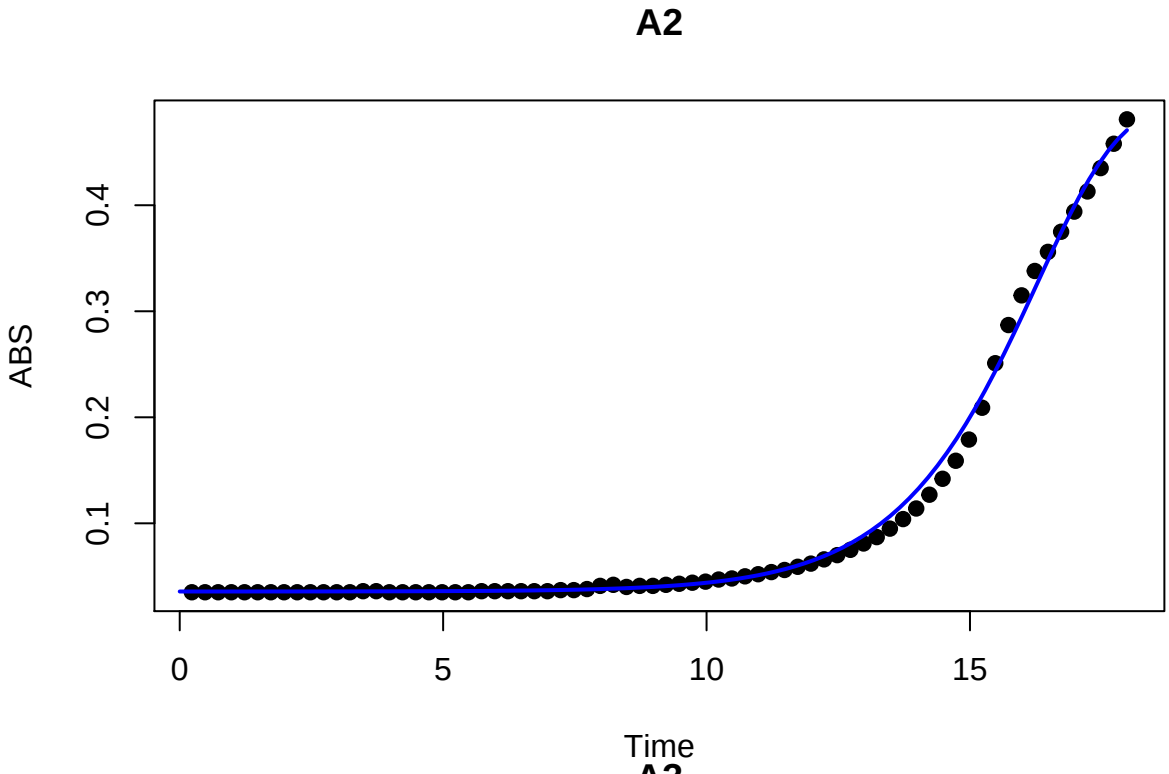
```
# Run Growth Curve Analysis
input <- "../data/MichaelisMenten/MMdynamicsGrowthCurve_18hrs_160226_182404.txt"
# Create Directory For Output
dir.create("../output", showWarnings = FALSE)
growth.modGomp(input, "KBS0802", skip=65, delta = 0.02)
```

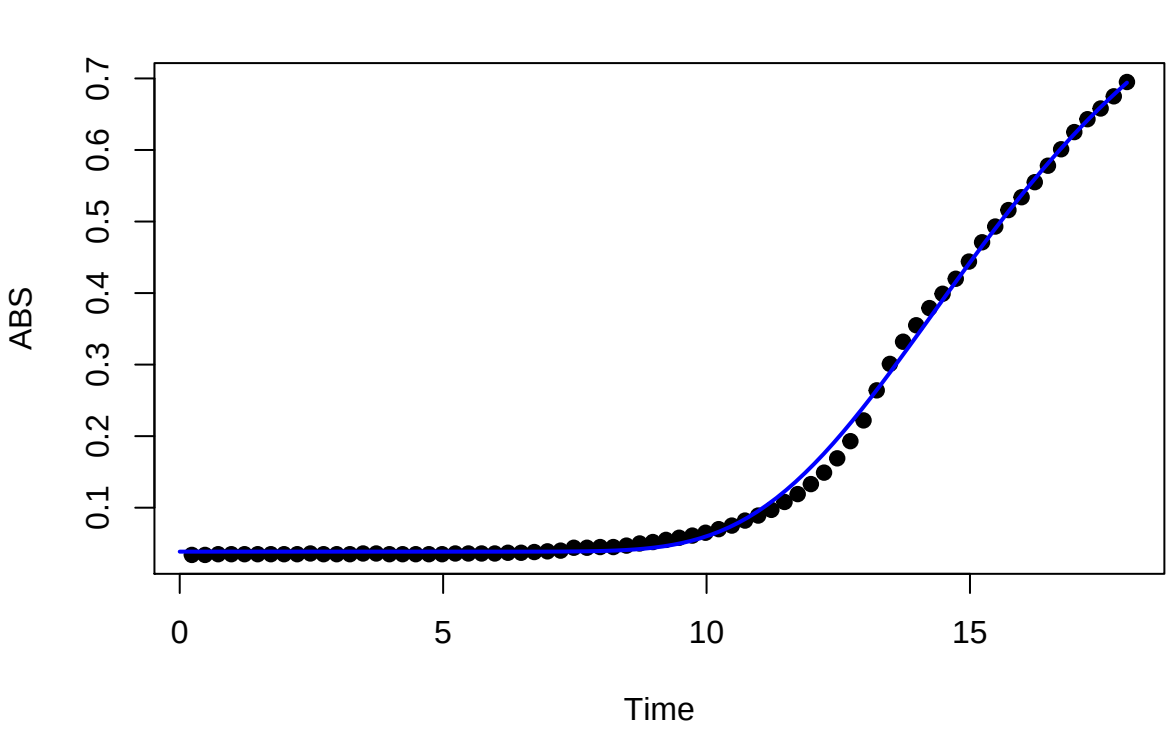
```
## Loading required package: bbmle
```

```
## Loading required package: stats4
```




```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (A): reverting from spline to linear approximation
```






```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
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```
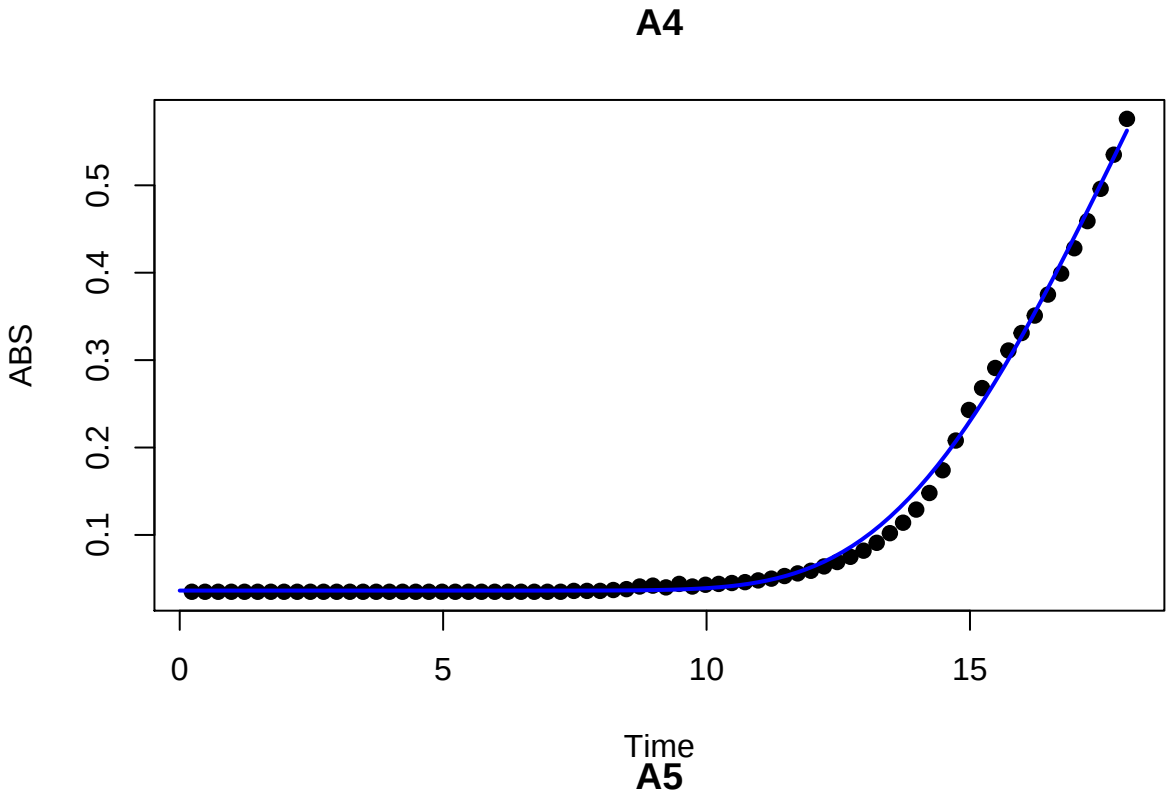
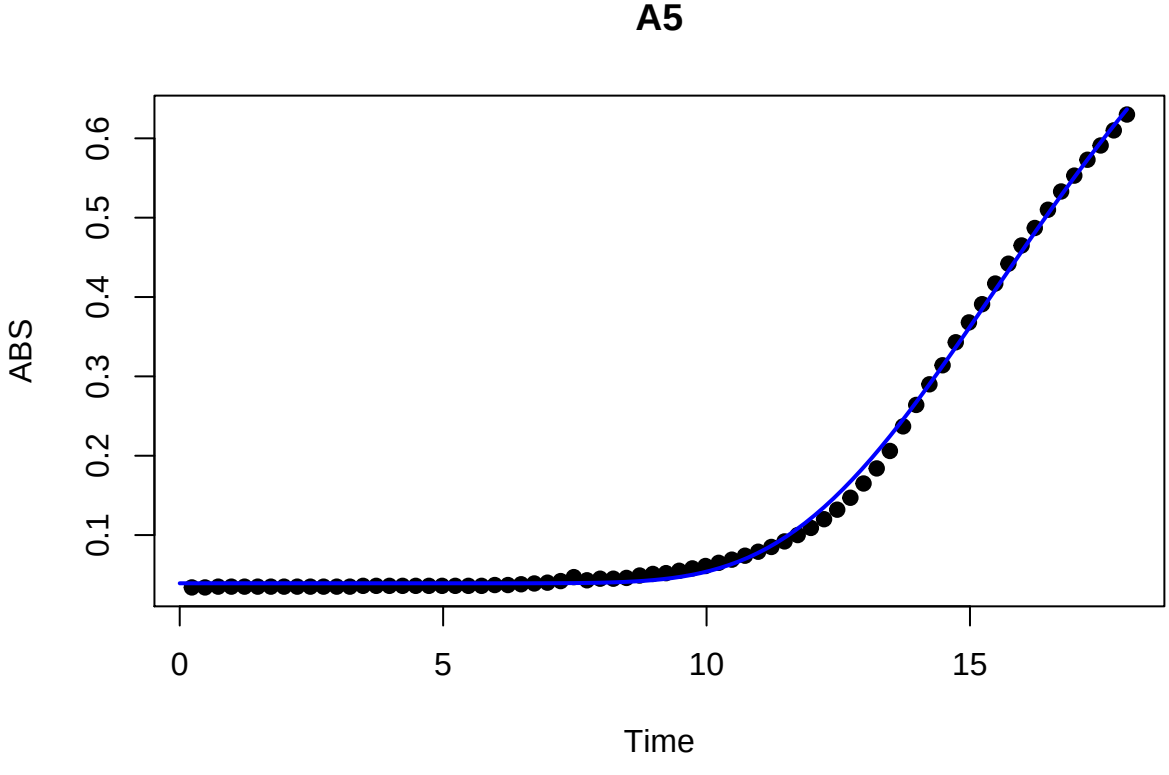
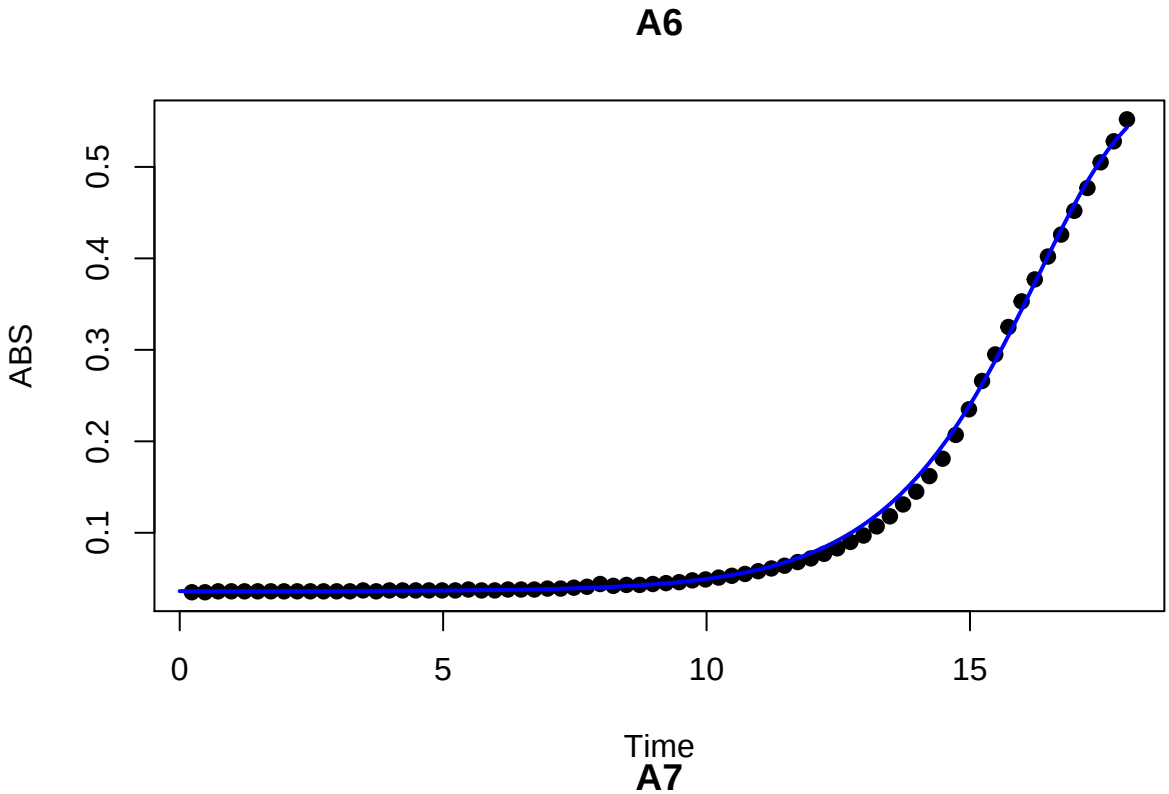

```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (umax): reverting from spline to linear approximation
```

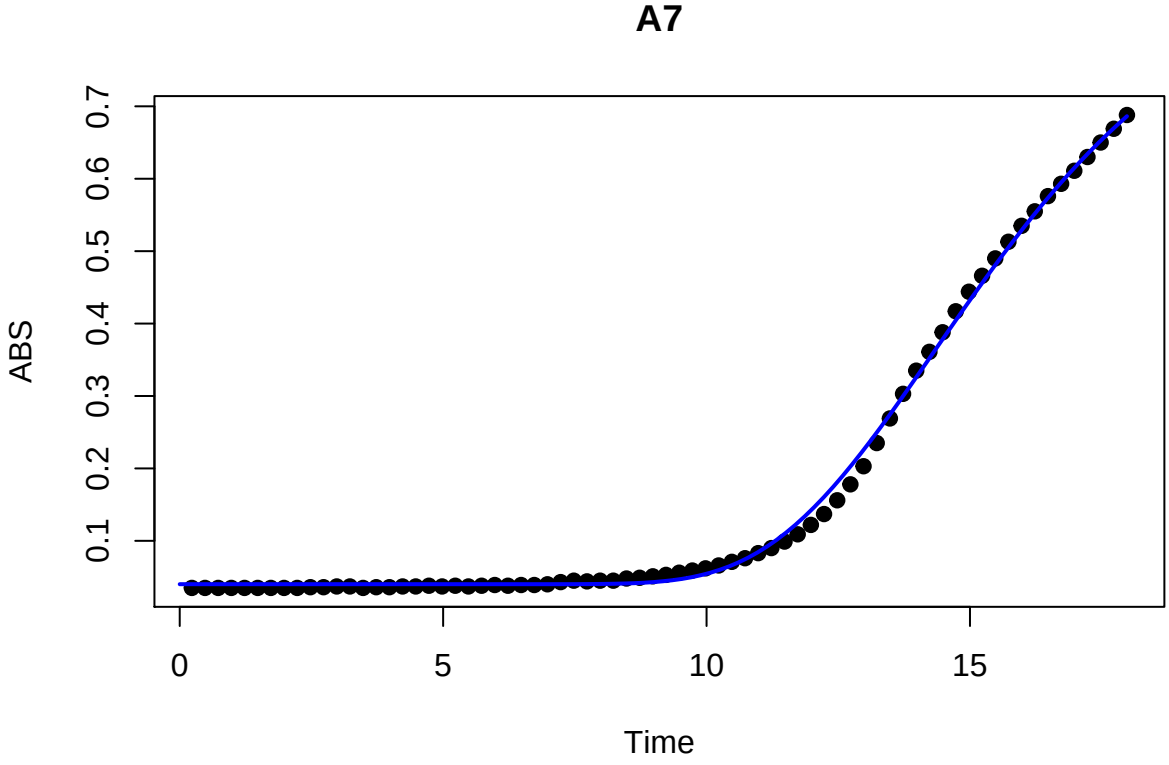
```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (L): reverting from spline to linear approximation
```






```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (A): reverting from spline to linear approximation
```

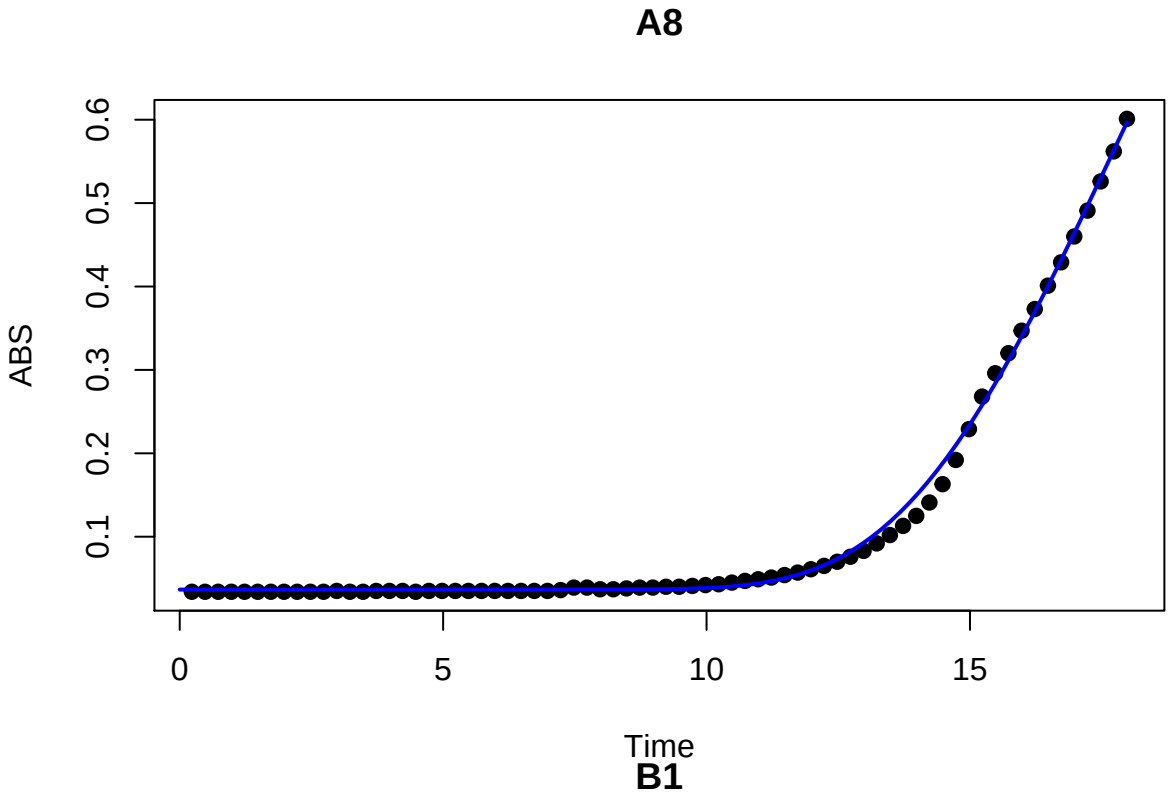


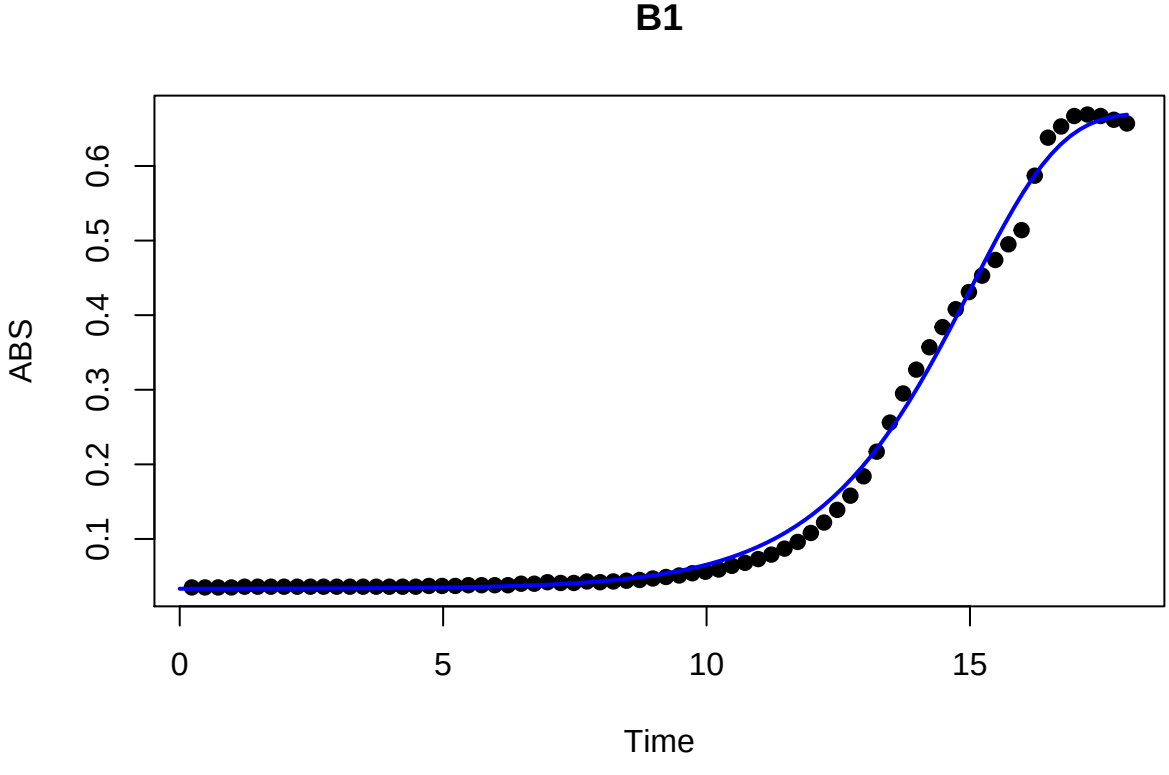


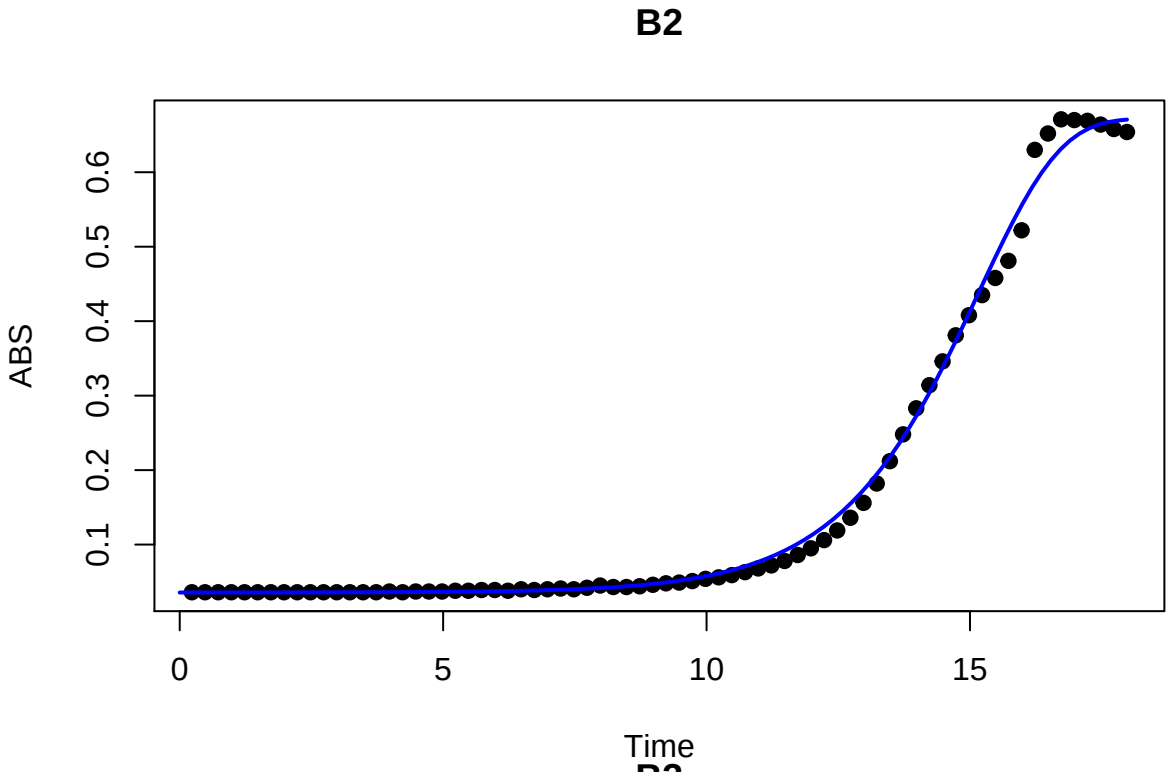

```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (A): reverting from spline to linear approximation
```

```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (umax): reverting from spline to linear approximation
```

```
## Warning in .local(object, parm, level, ...): non-monotonic spline fit to
## profile (L): reverting from spline to linear approximation
```






B2
ABS
0.1
0.2
0.3
0.4
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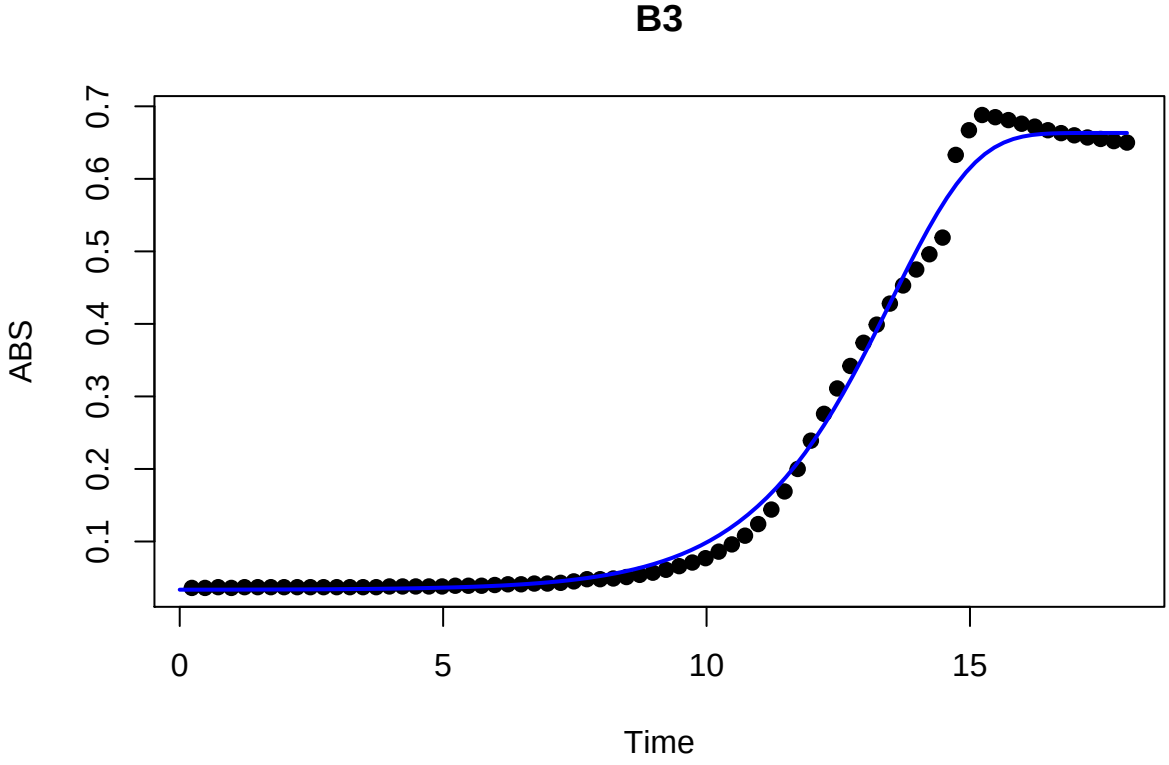
5
10
15
Time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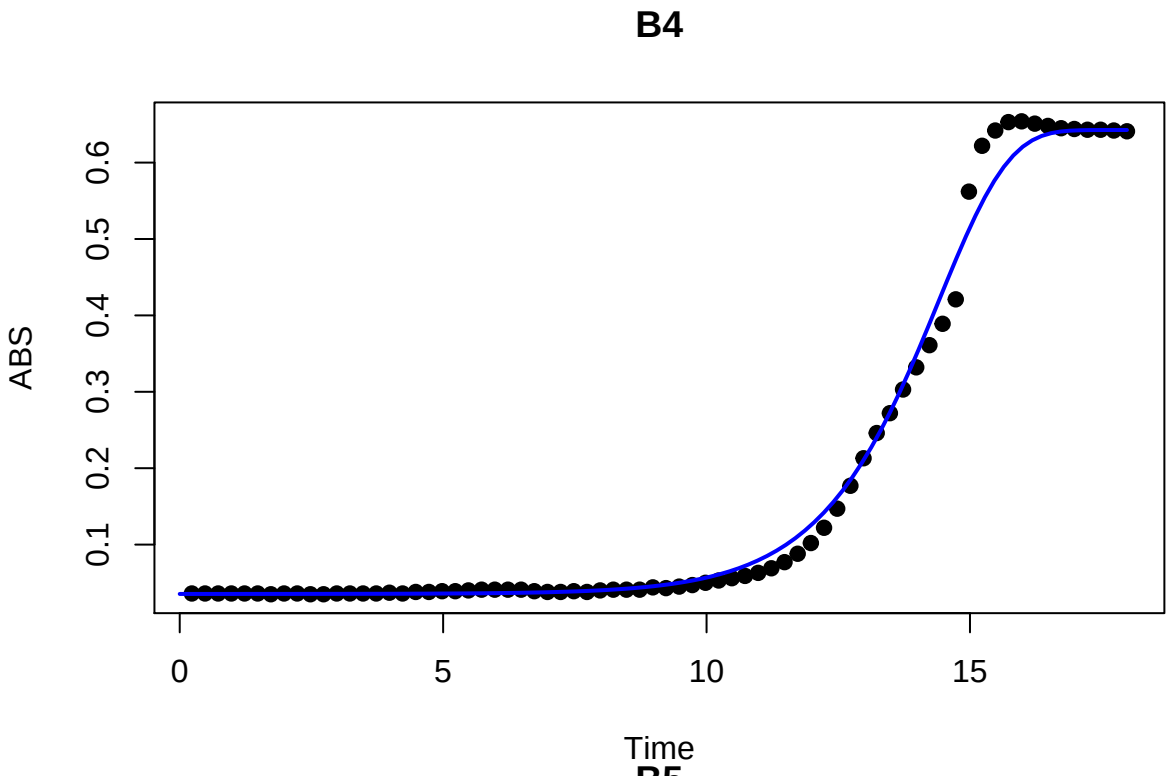
Time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ABS
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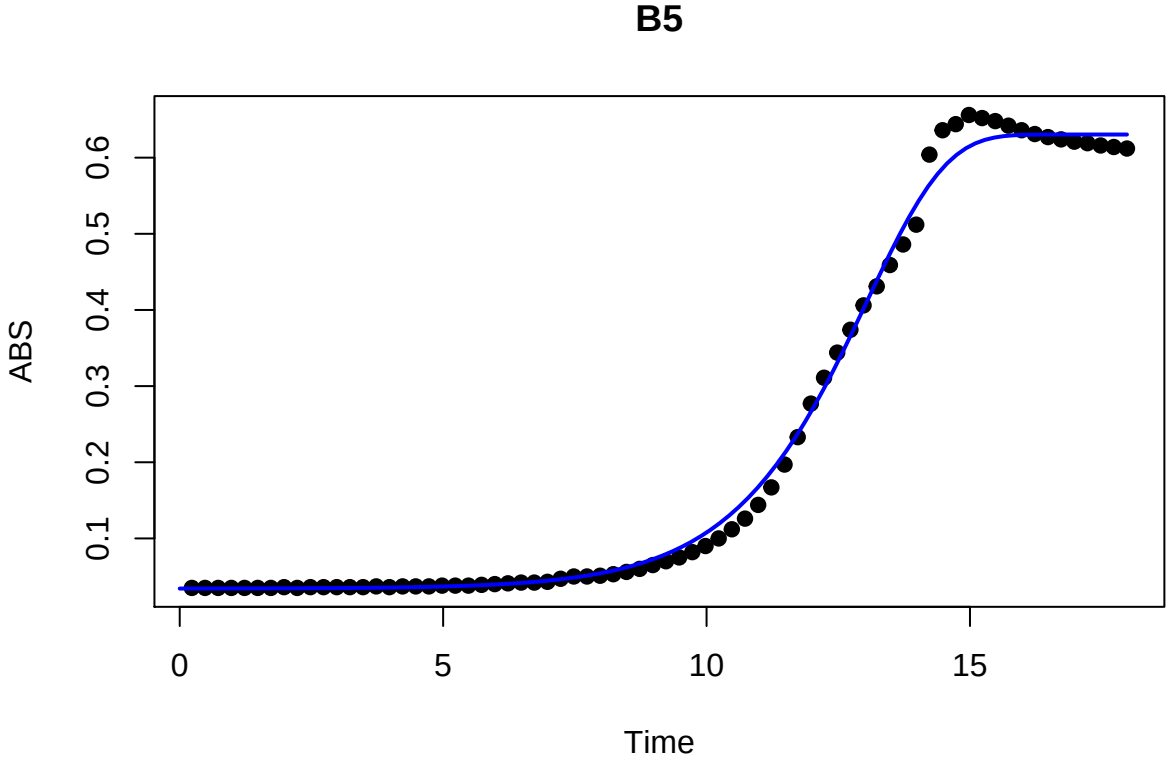
Time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ABS
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0.6
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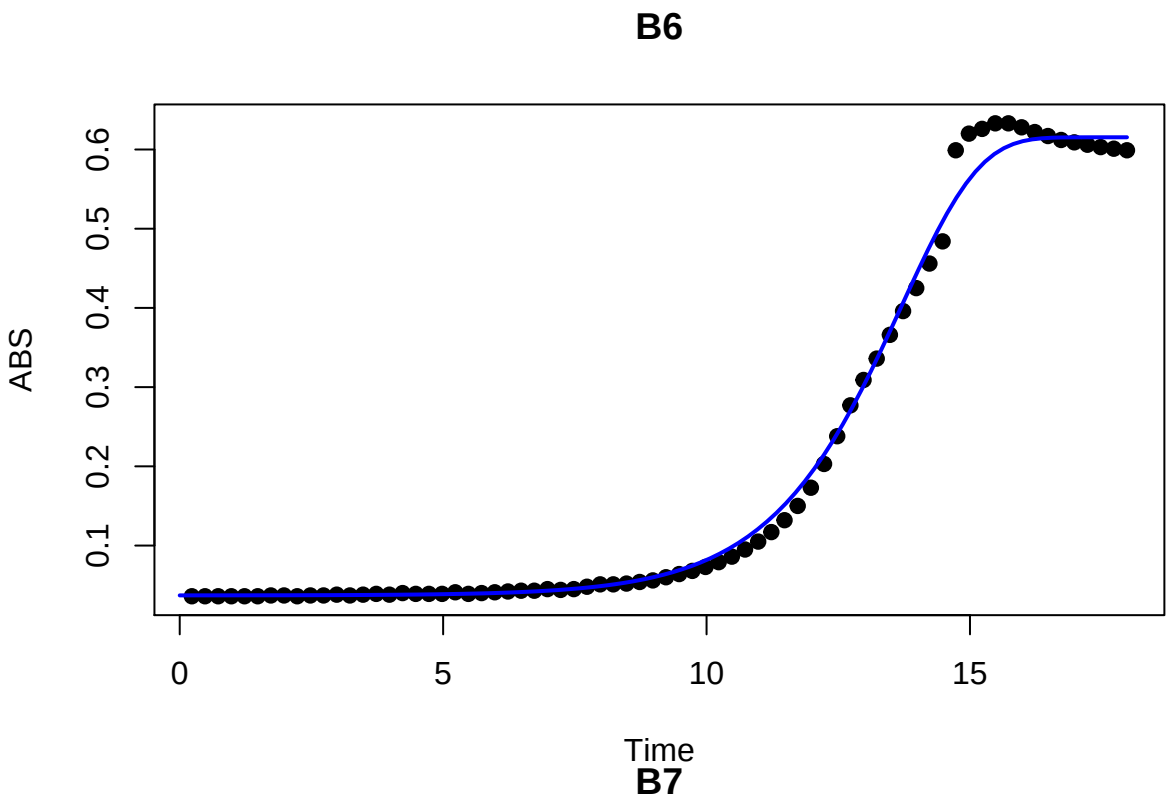
15
Time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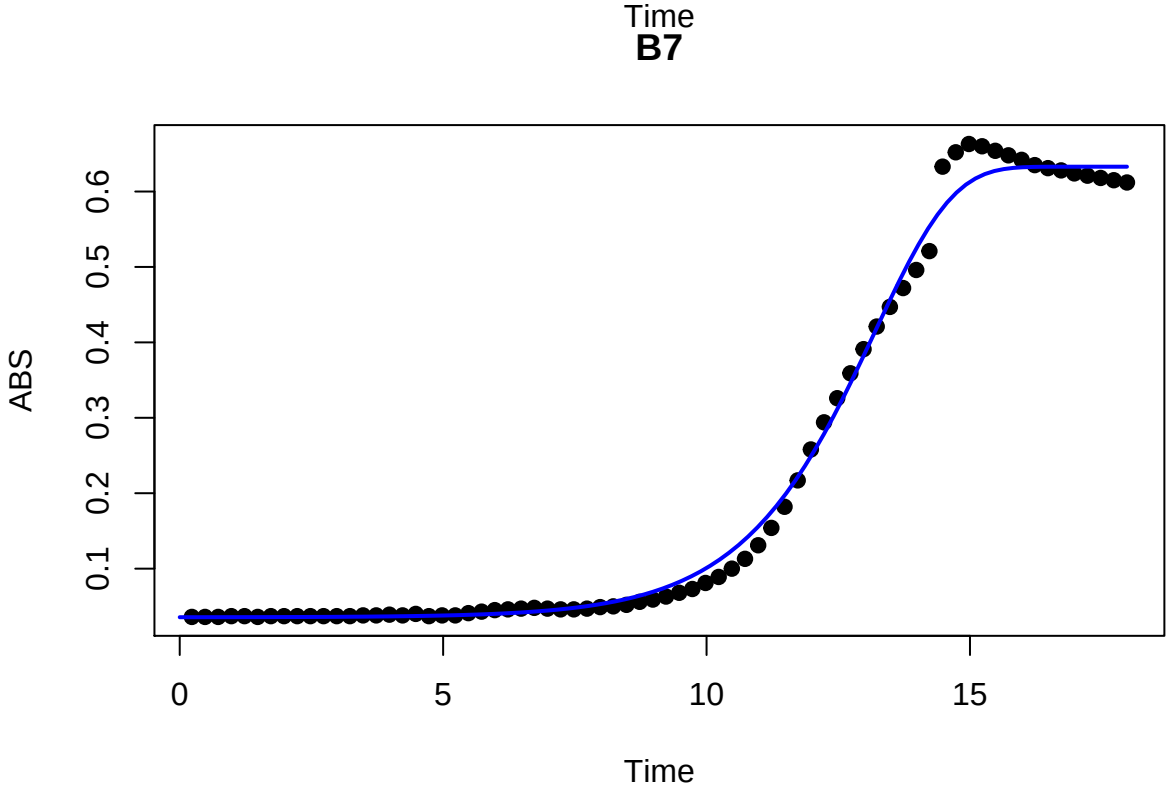
Time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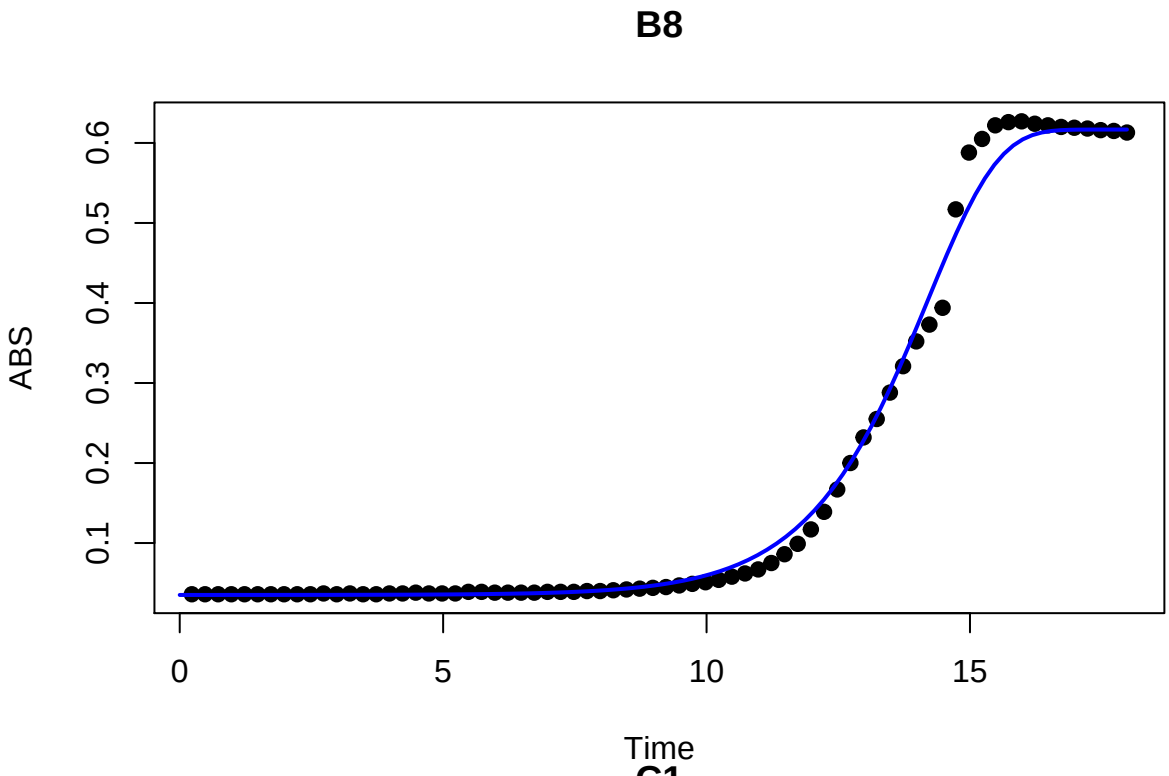
Time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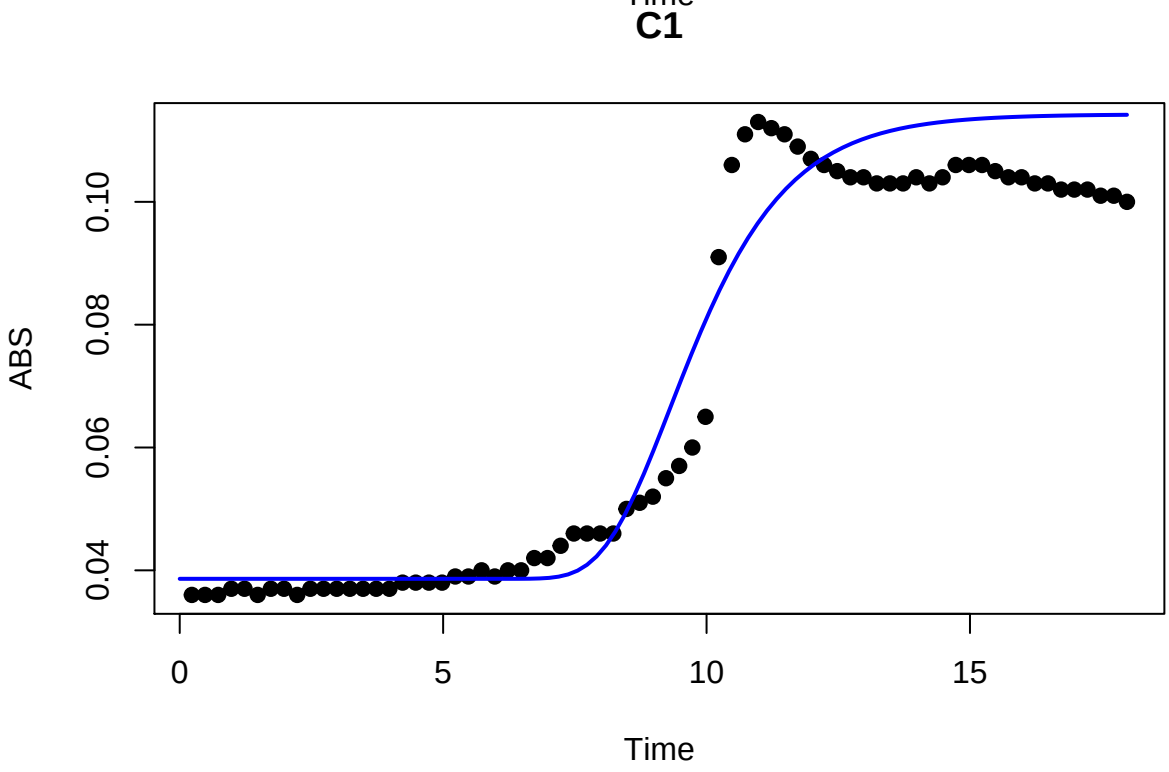
Time


C1
ABS
0.04
0.06
0.08
0.10
0
5
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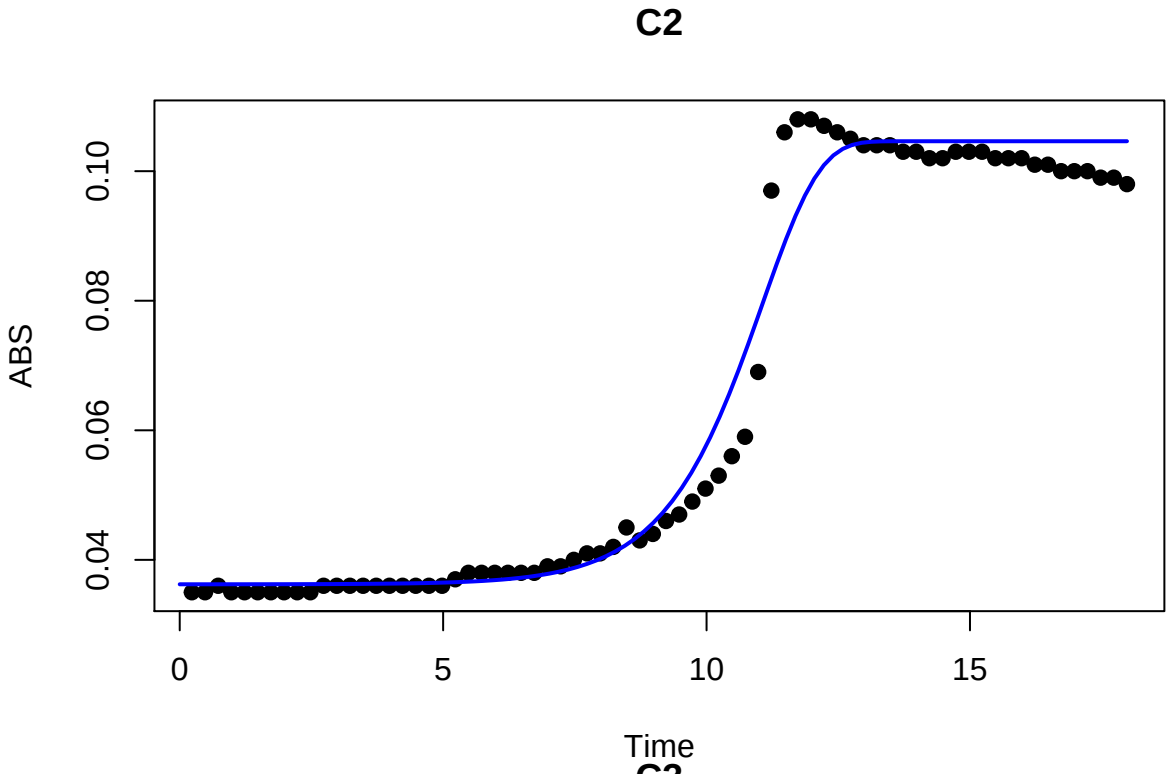
Time


C2
ABS
0.04
0.06
0.08
0.10
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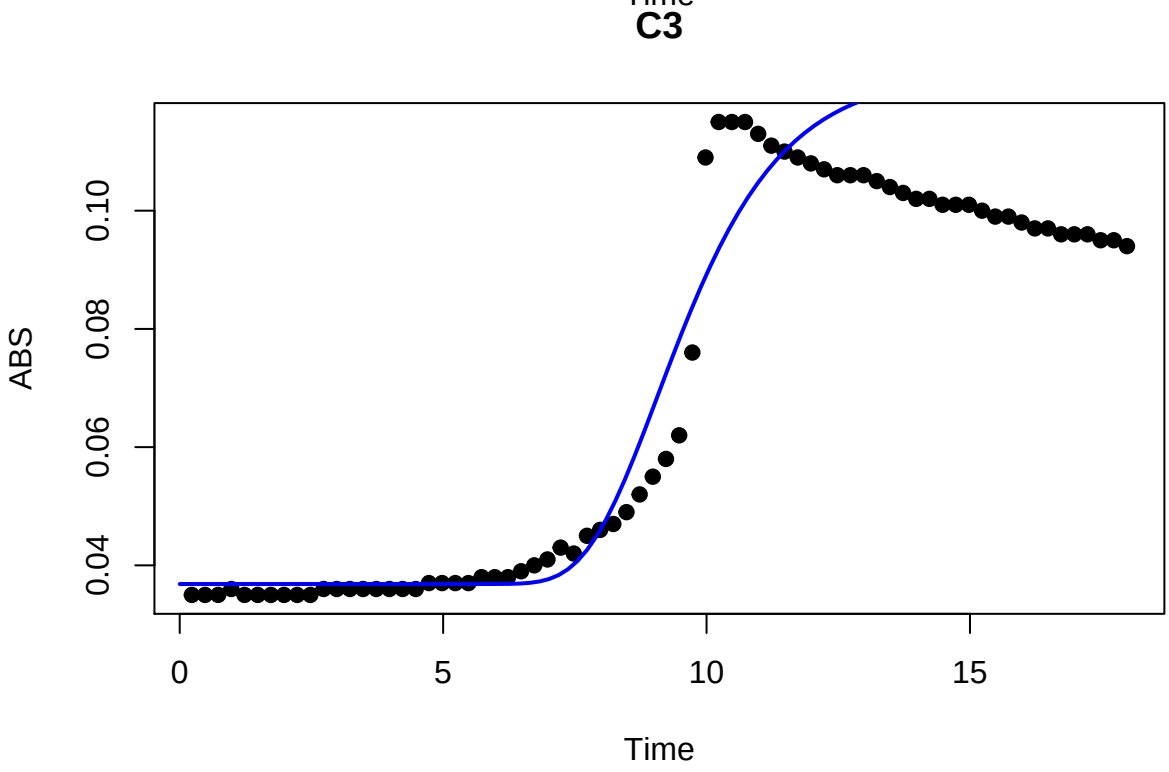
Time


C3
ABS
0.04
0.06
0.08
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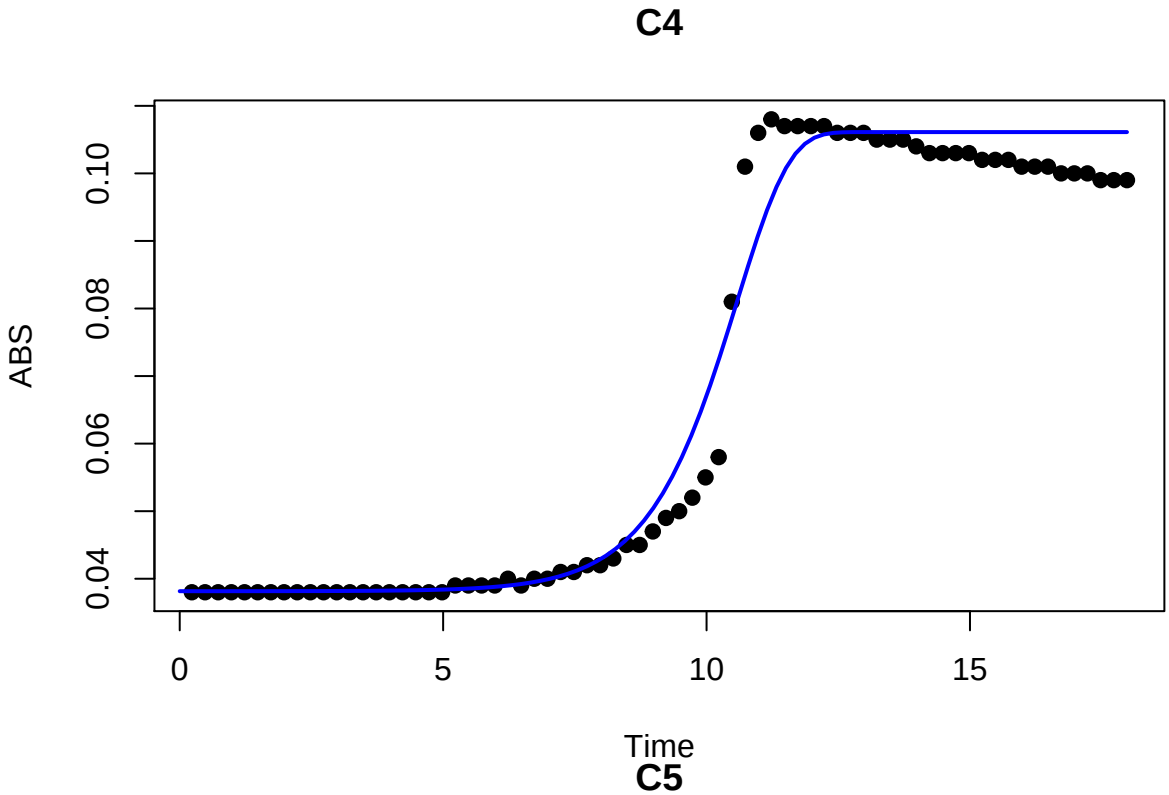
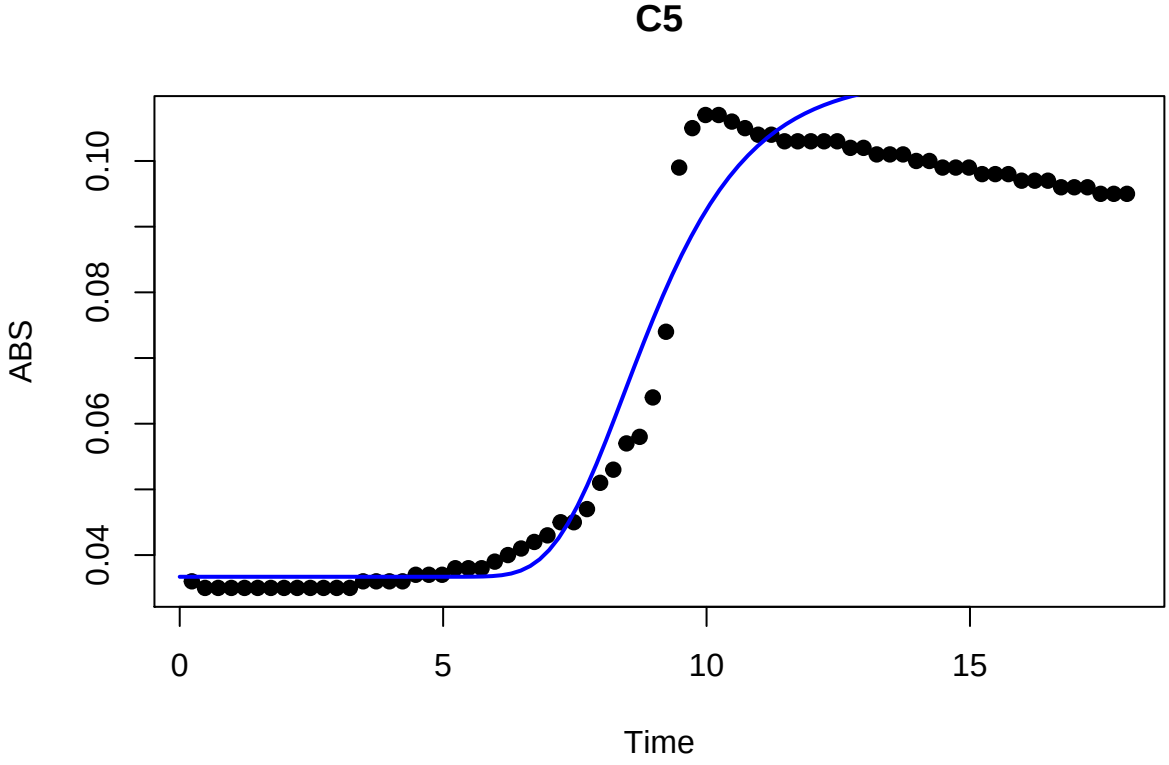
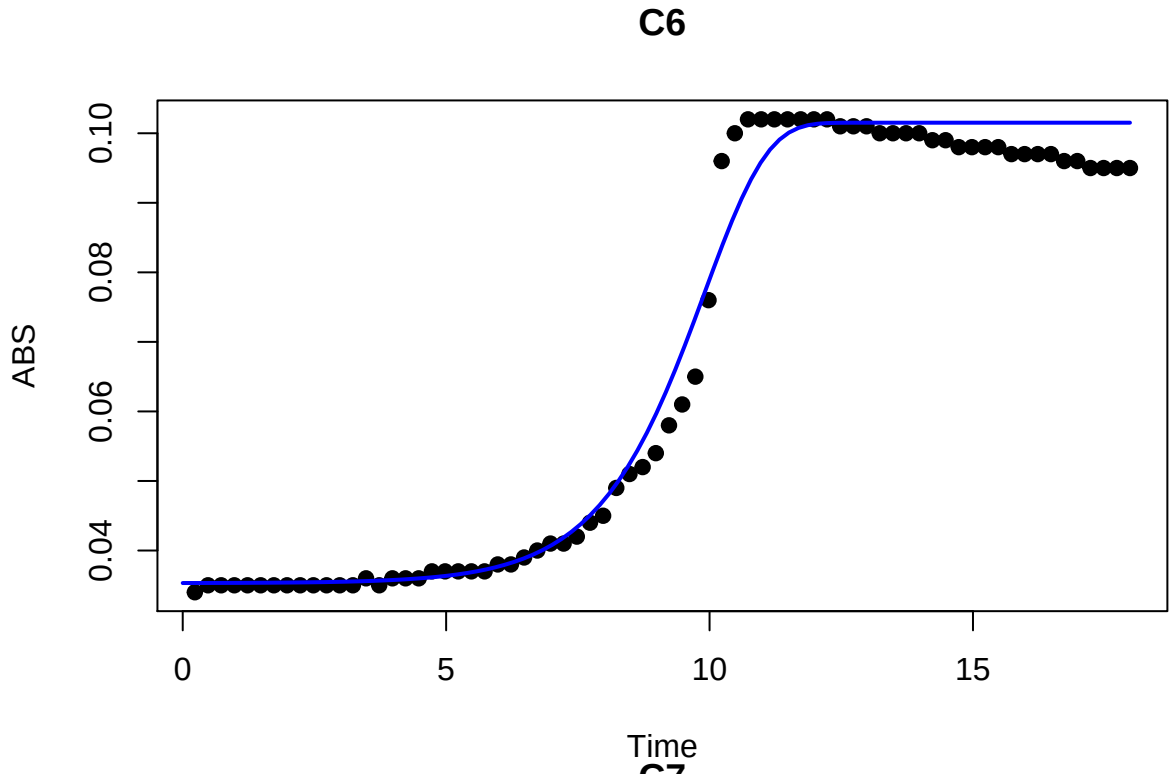
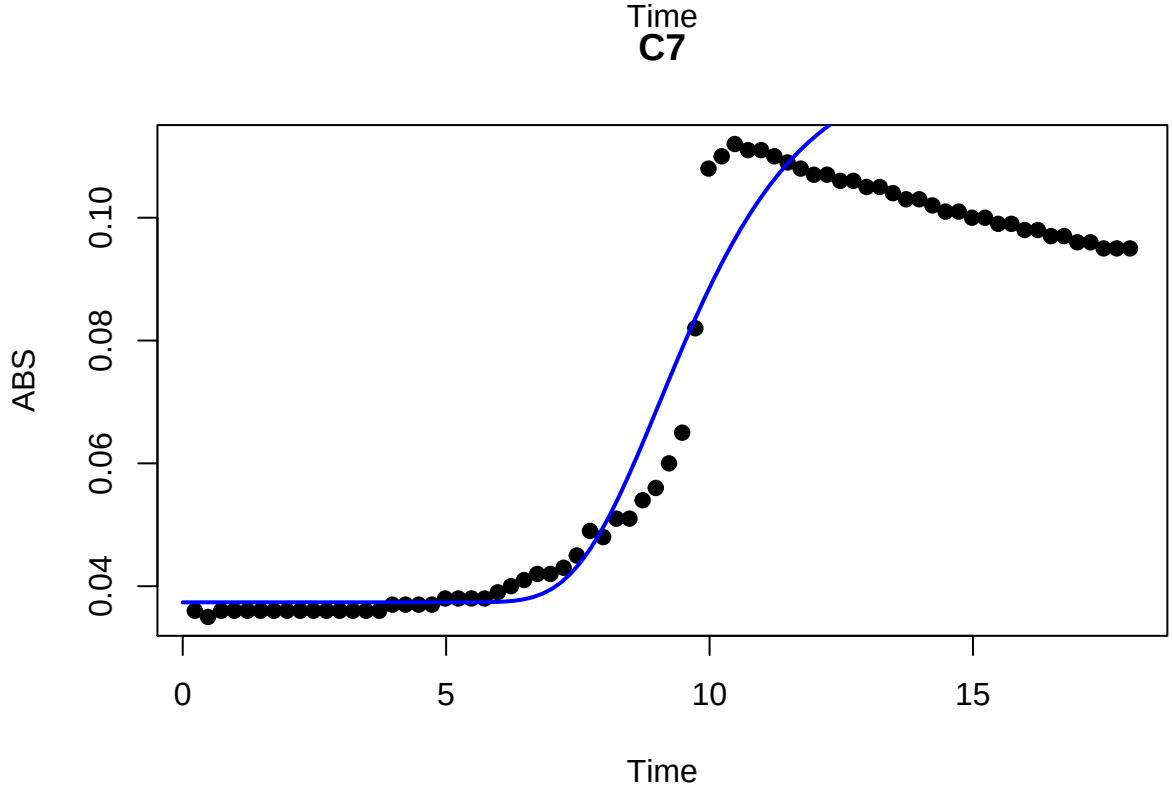
Time

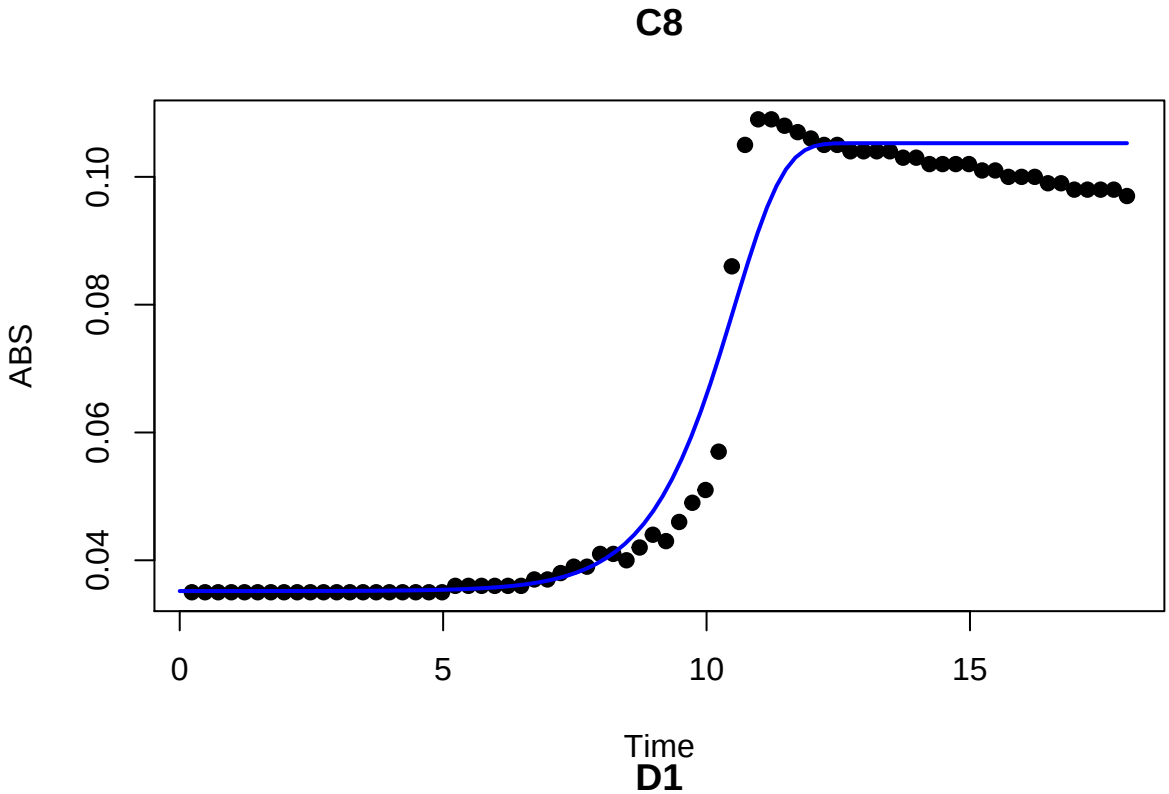


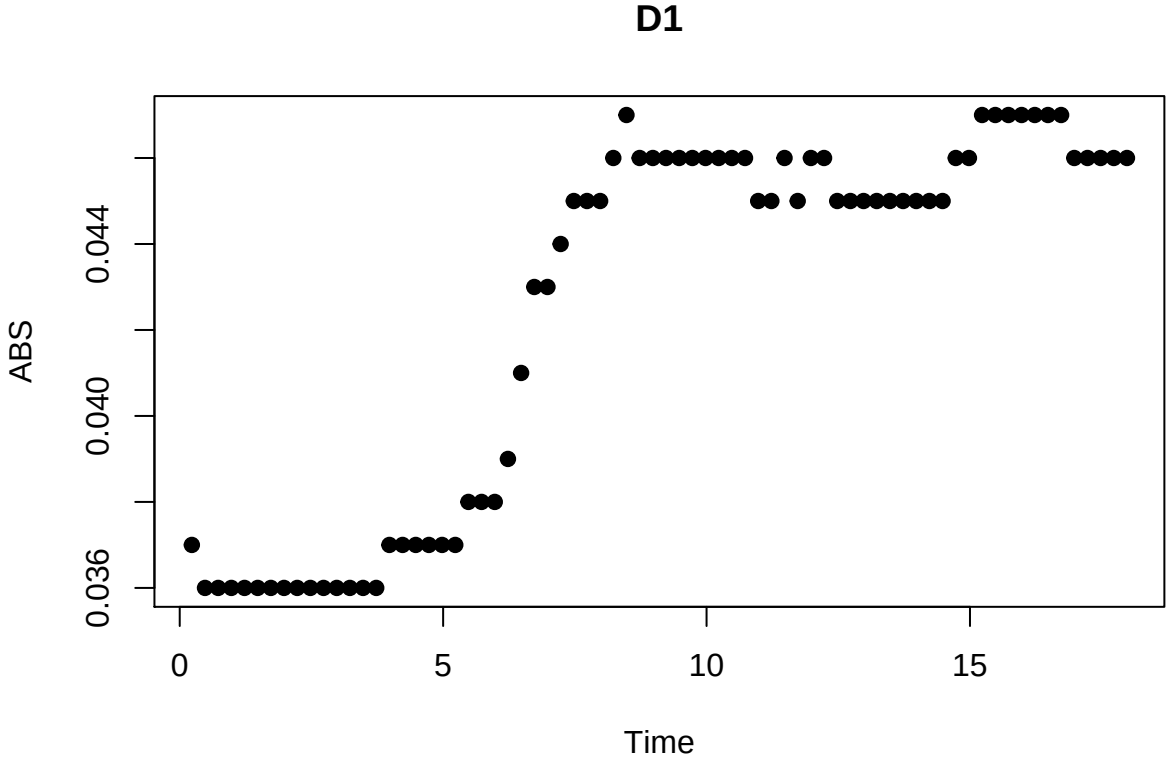


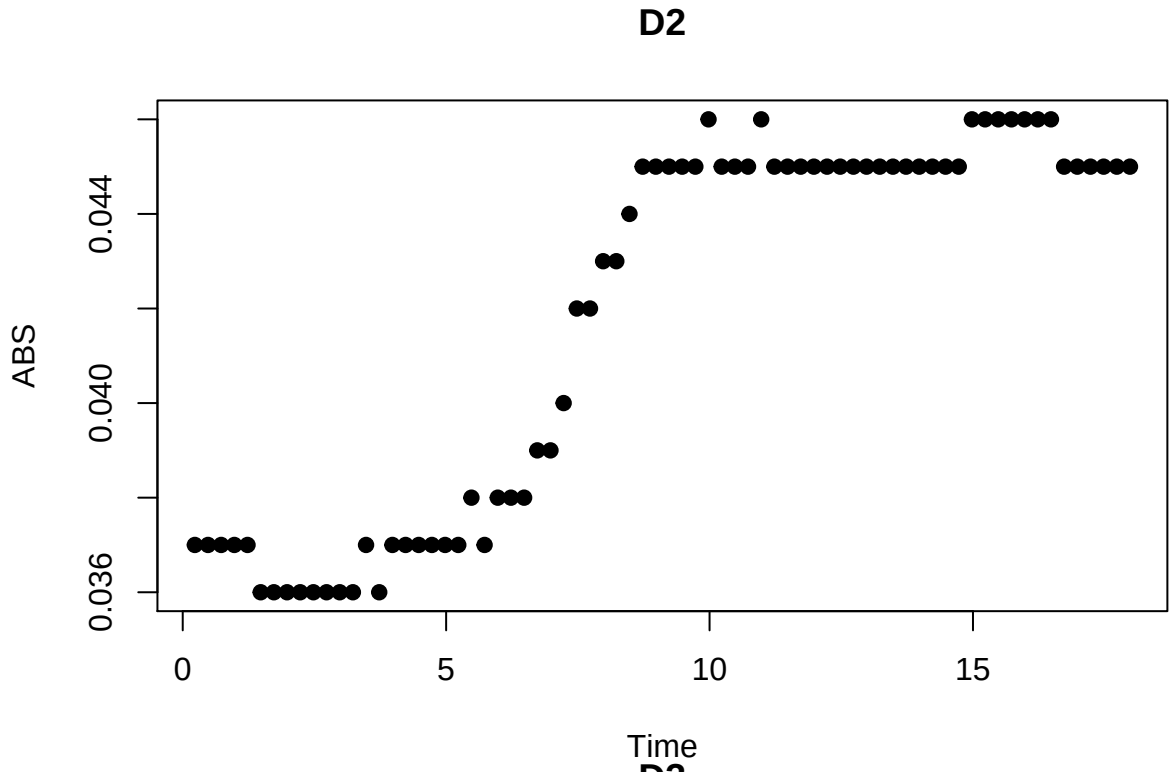

```
## Profiling has found a better solution,so original fit had not converged:

## (new deviance=-627.2, old deviance=-627, diff=-0.1614)

## Returning better fit ...
```

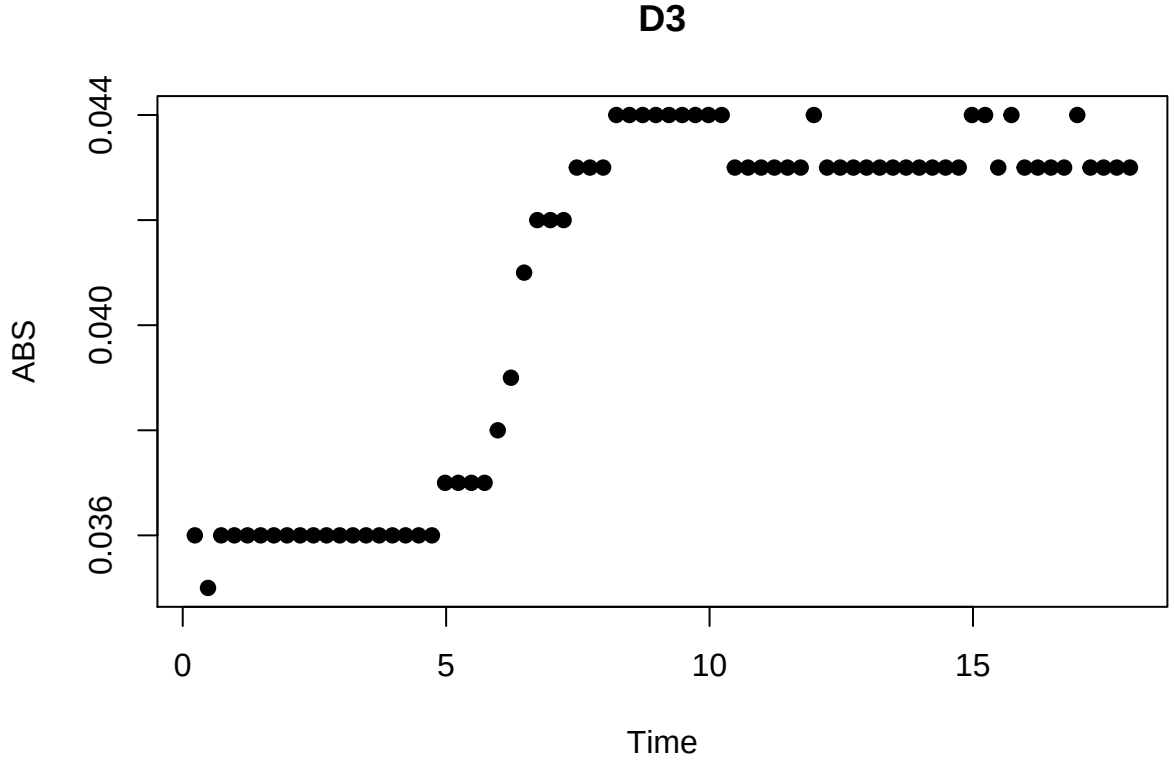

C6
ABS
0.04
0.06
0.08
0.10
0
5
10
15
Time

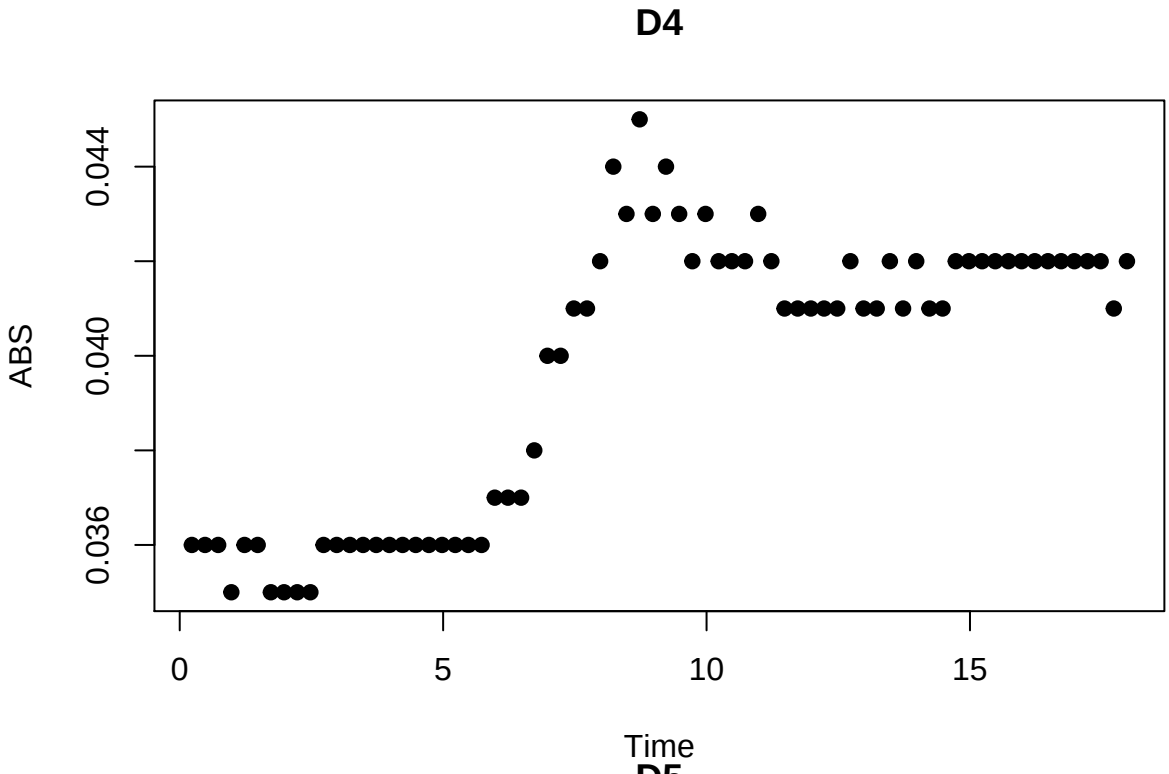

C7
ABS
0.04
0.06
0.08
0.10
0
5
10
15
Time


C8
ABS
0.04
0.06
0.08
0.10
0
5
10
15
Time


D1
ABS
0.036
0.040
0.044
0
5
10
15
Time


D2
ABS
0.036
0.040
0.044
0
5
10
15
Time


D3
ABS
0.036
0.040
0.044
0
5
10
15
Time


D4
ABS
0.036
0.040
0.044
0
5
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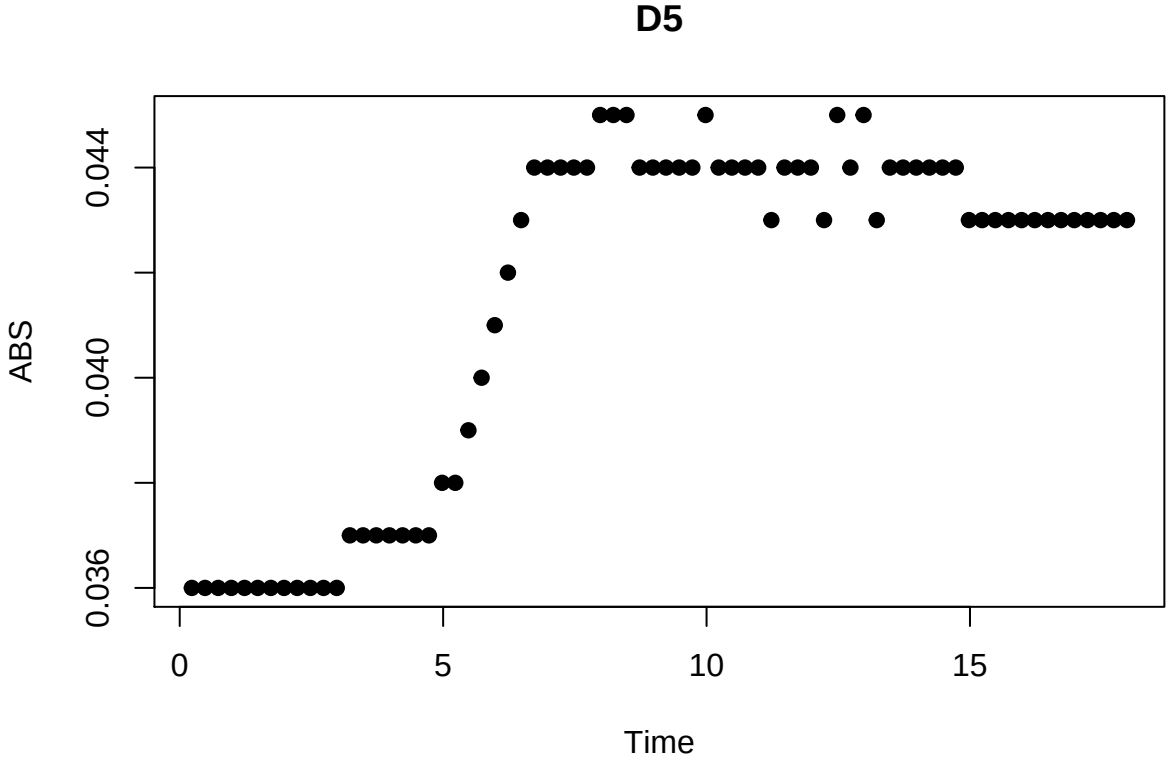
15
Time


D5
ABS
0.036
0.040
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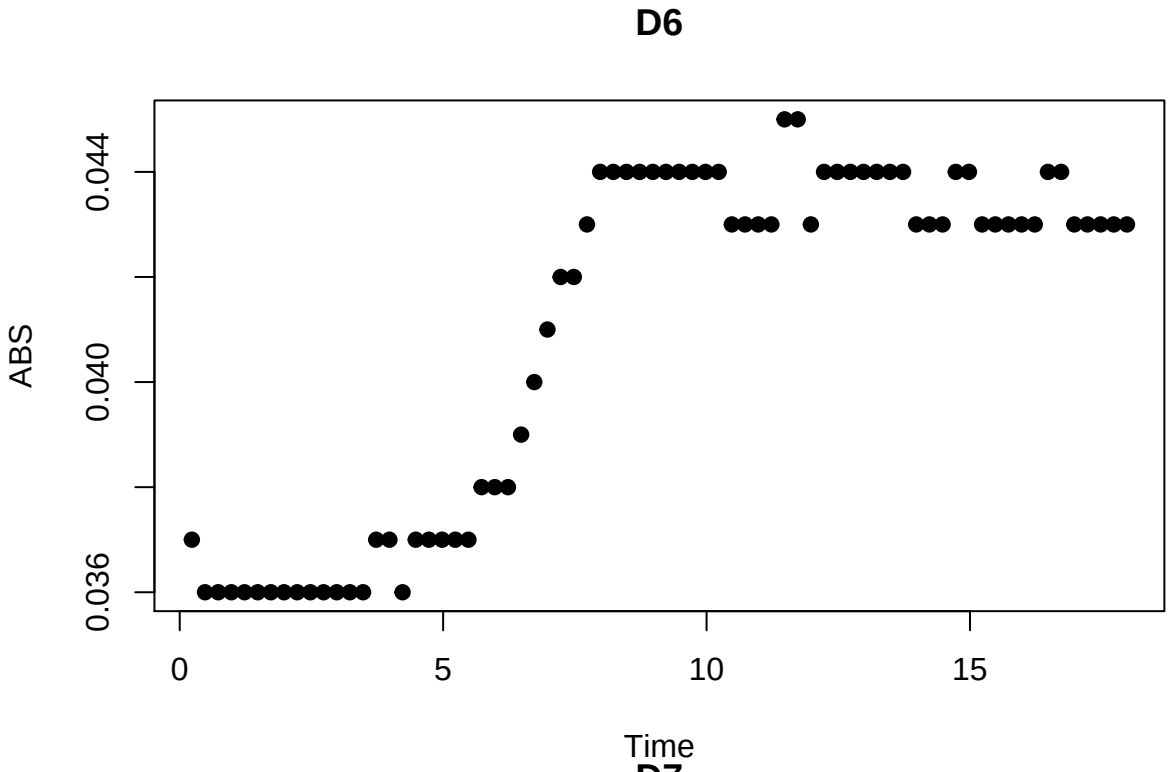
Time


D6
ABS
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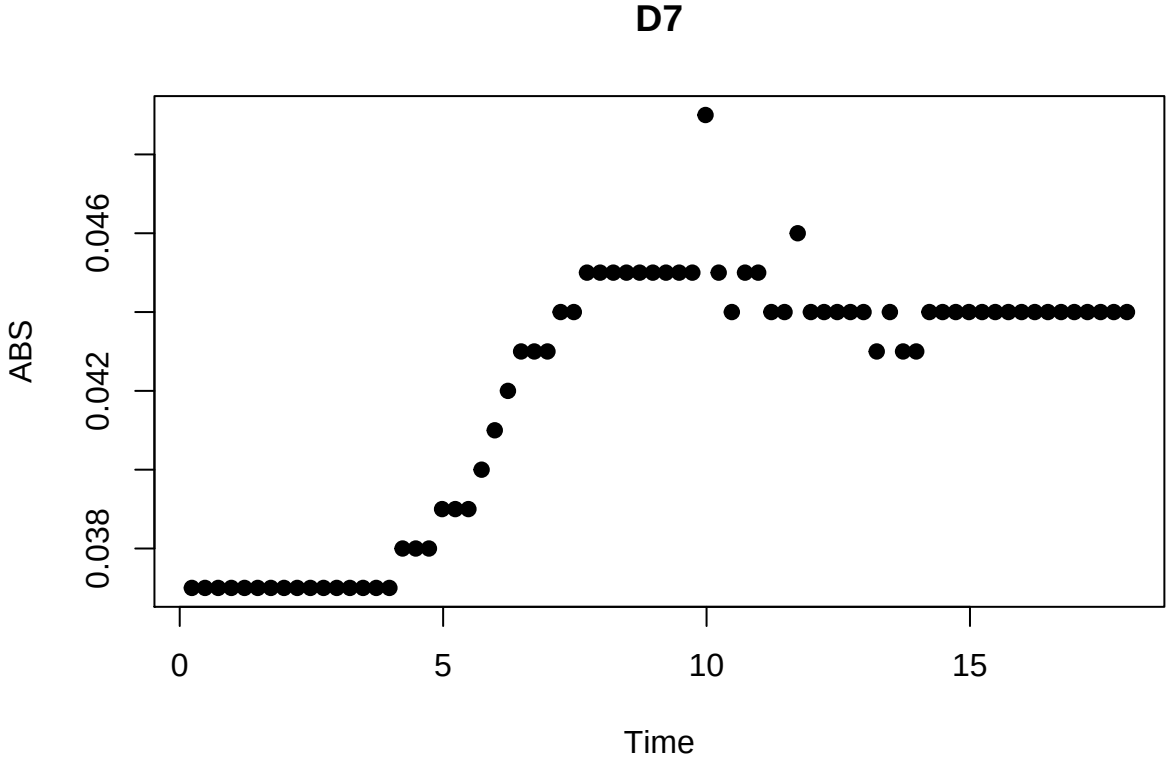
Time


D7
ABS
0.038
0.042
0.046
0
5
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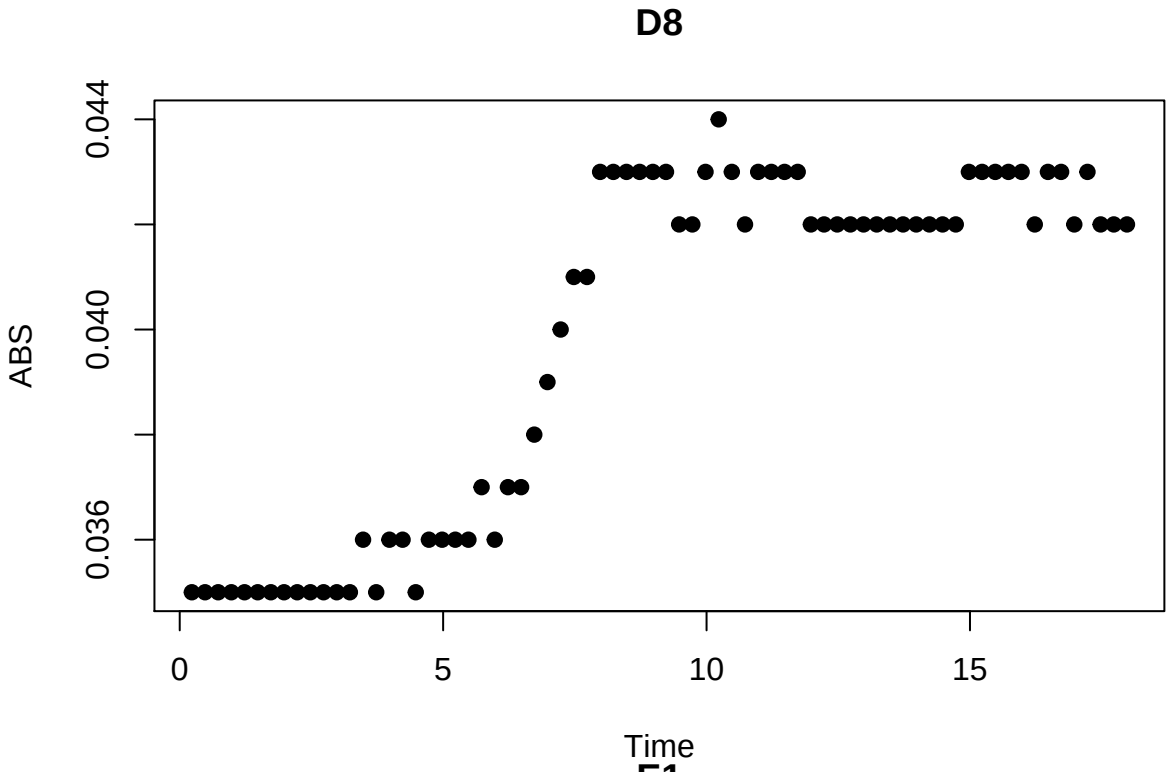
15
Time


D8
ABS
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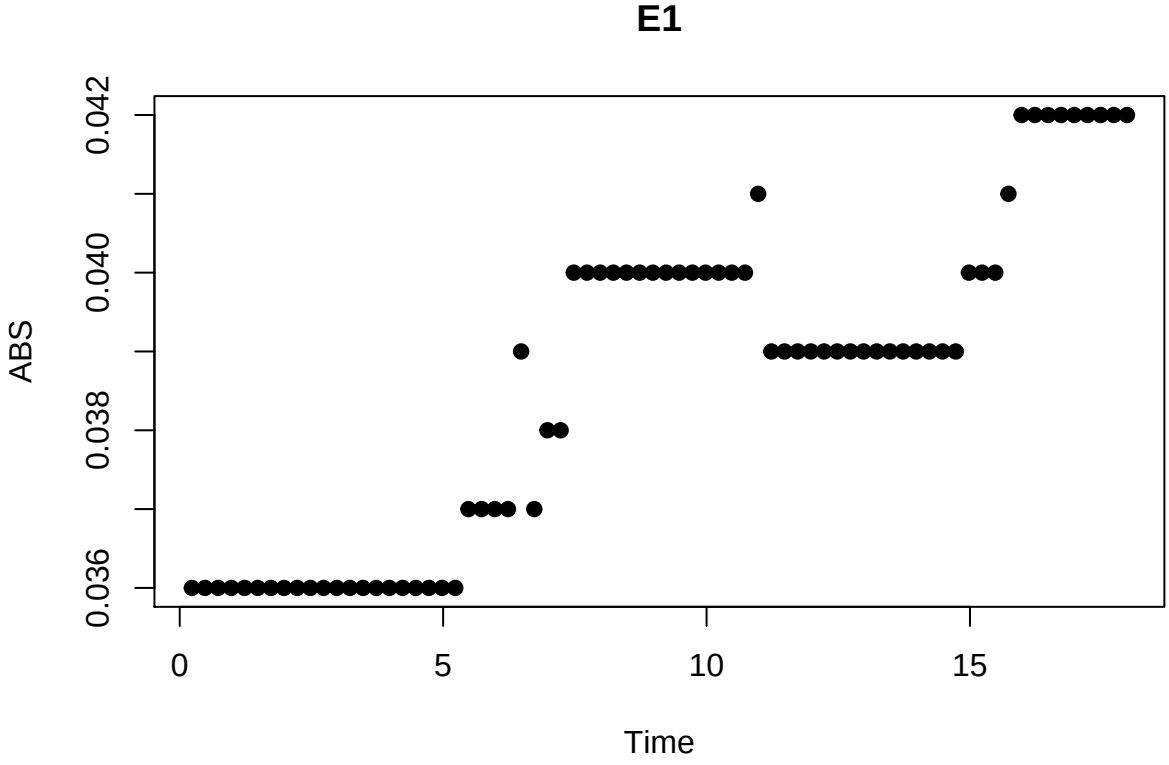
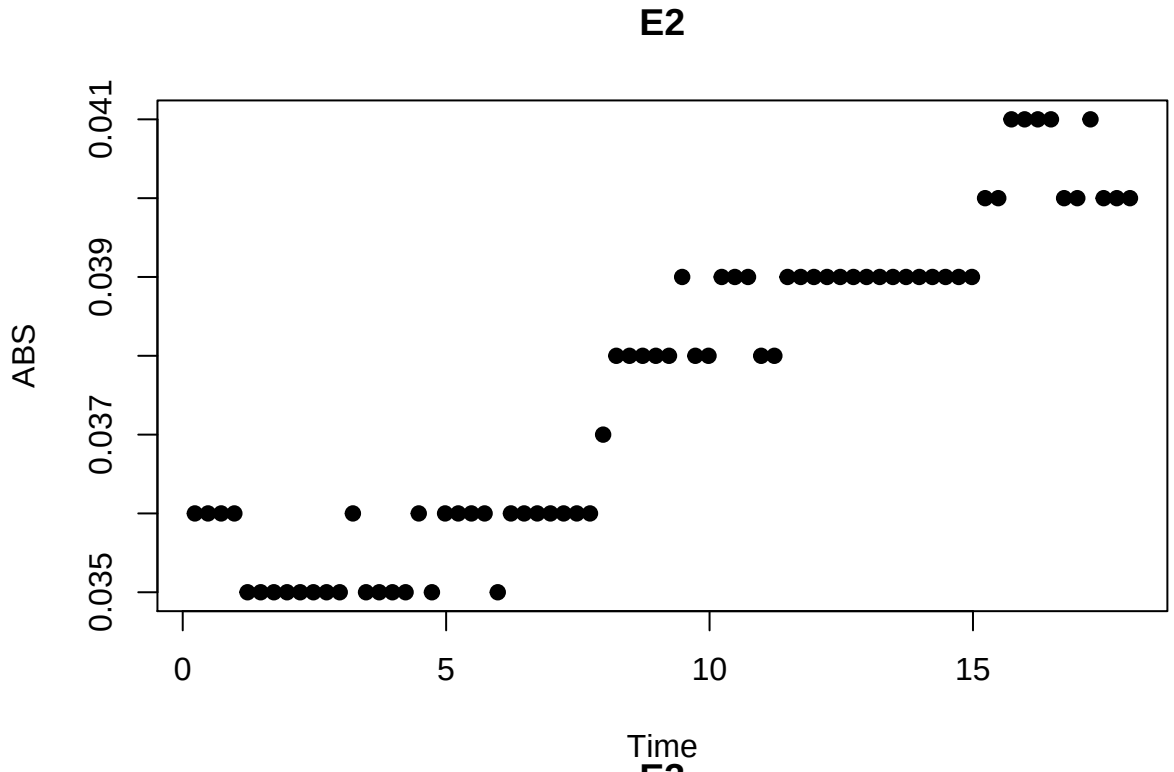
Time


E1
ABS
0.036
0.038
0.040
0.042
0
5
10
15
Time


E2
ABS
0.035
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0.039
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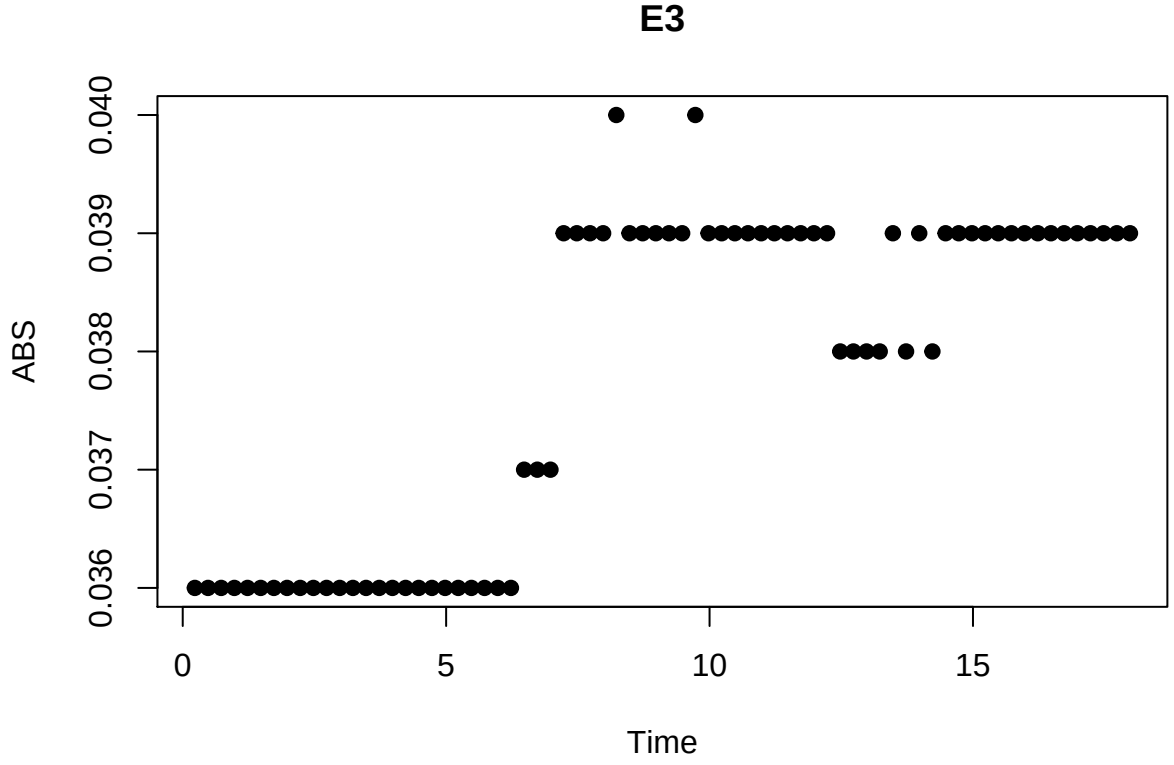
Time


E3
ABS
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0.037
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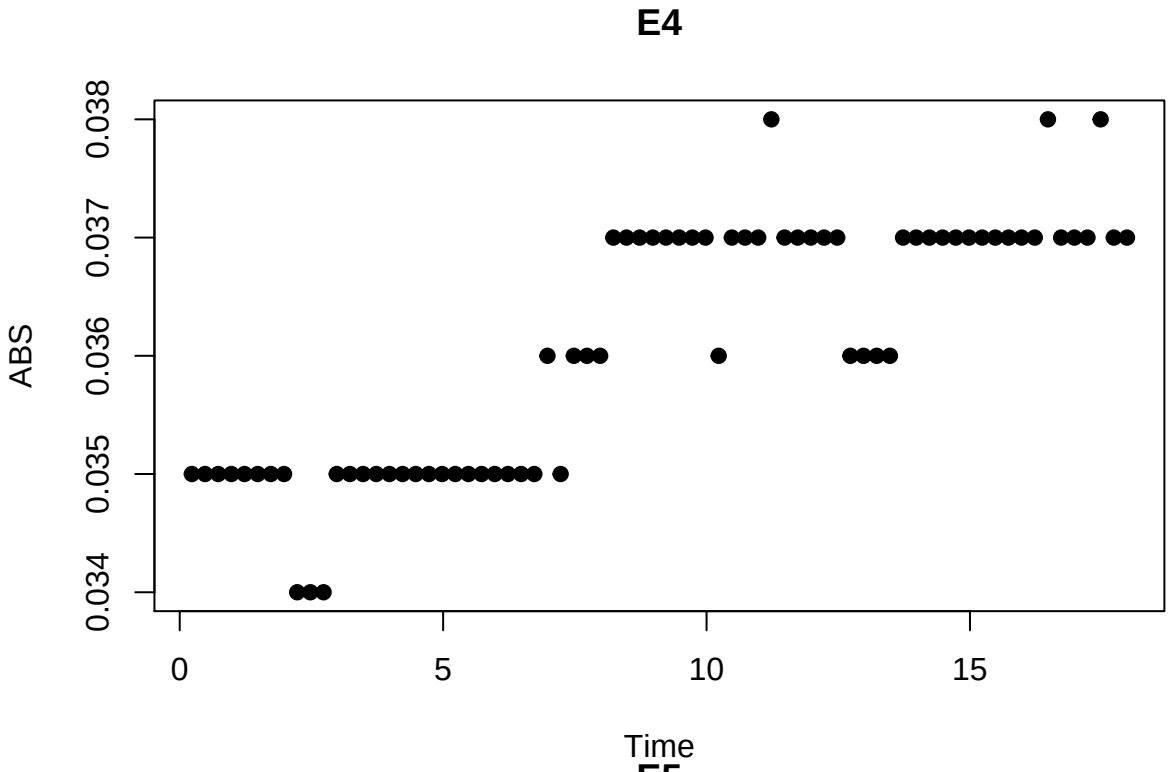
0
5
10
15
Time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ABS
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0
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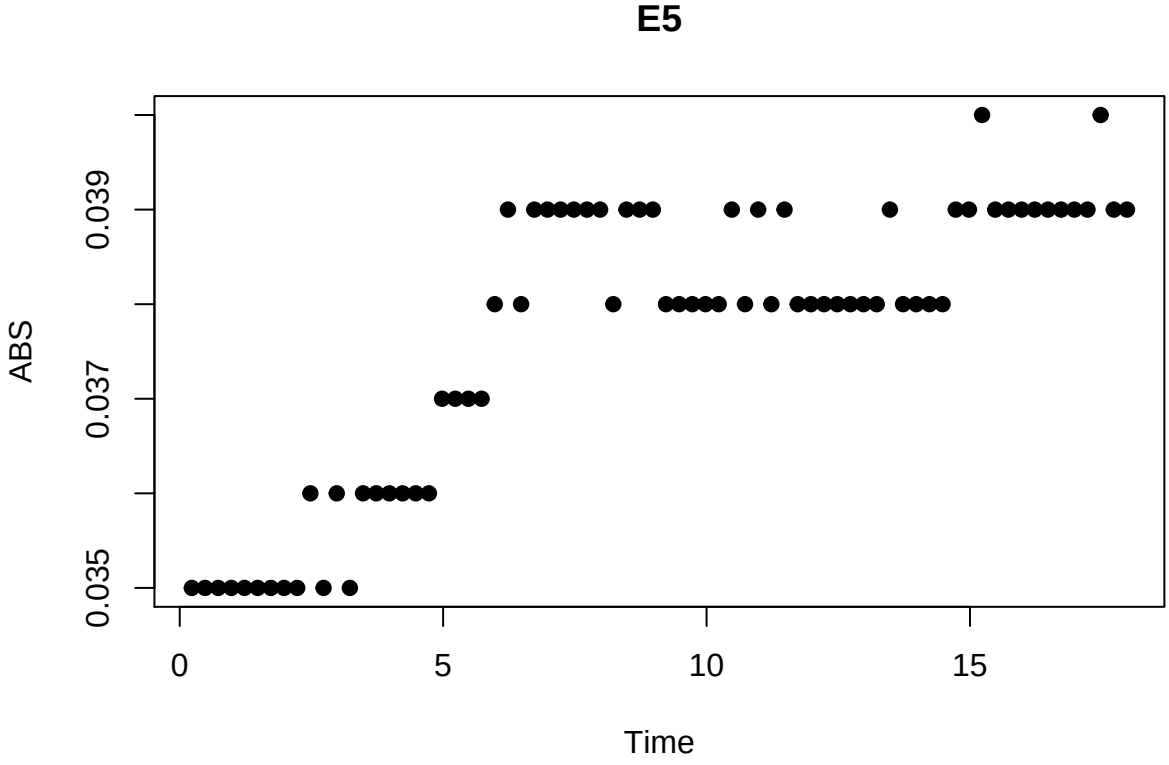
10
15
Time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ABS
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0.037
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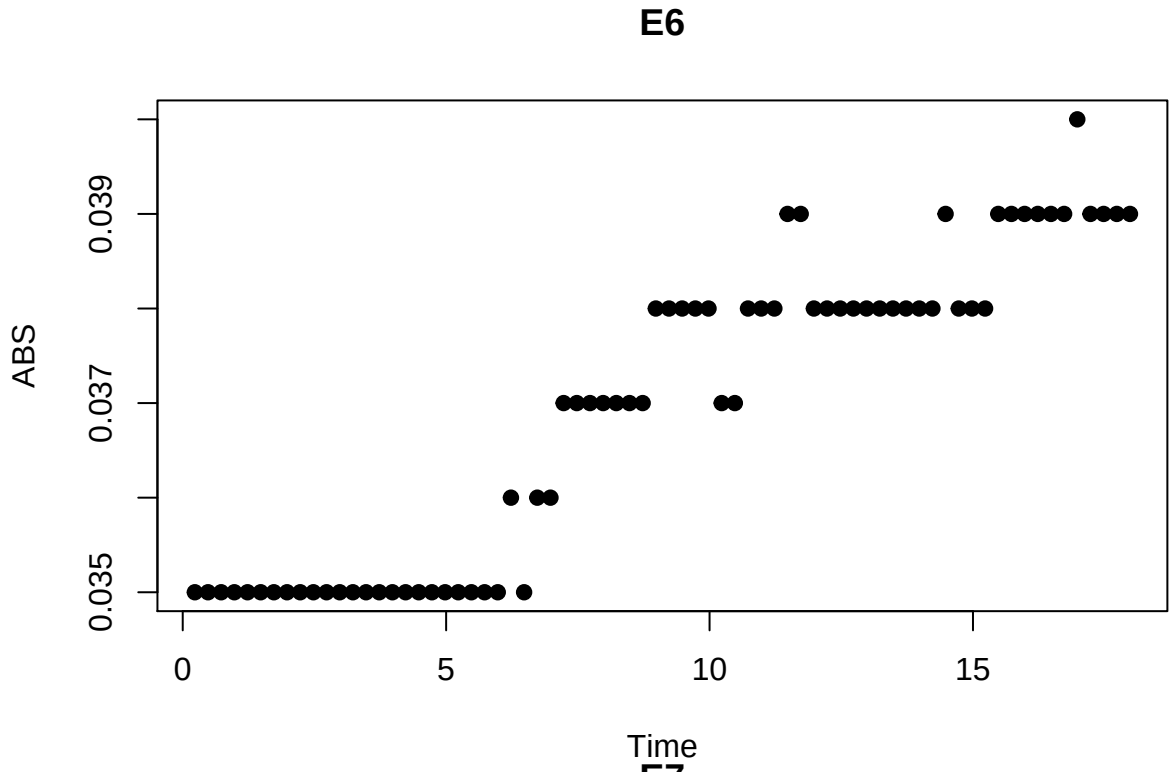
5
10
15
Time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ABS
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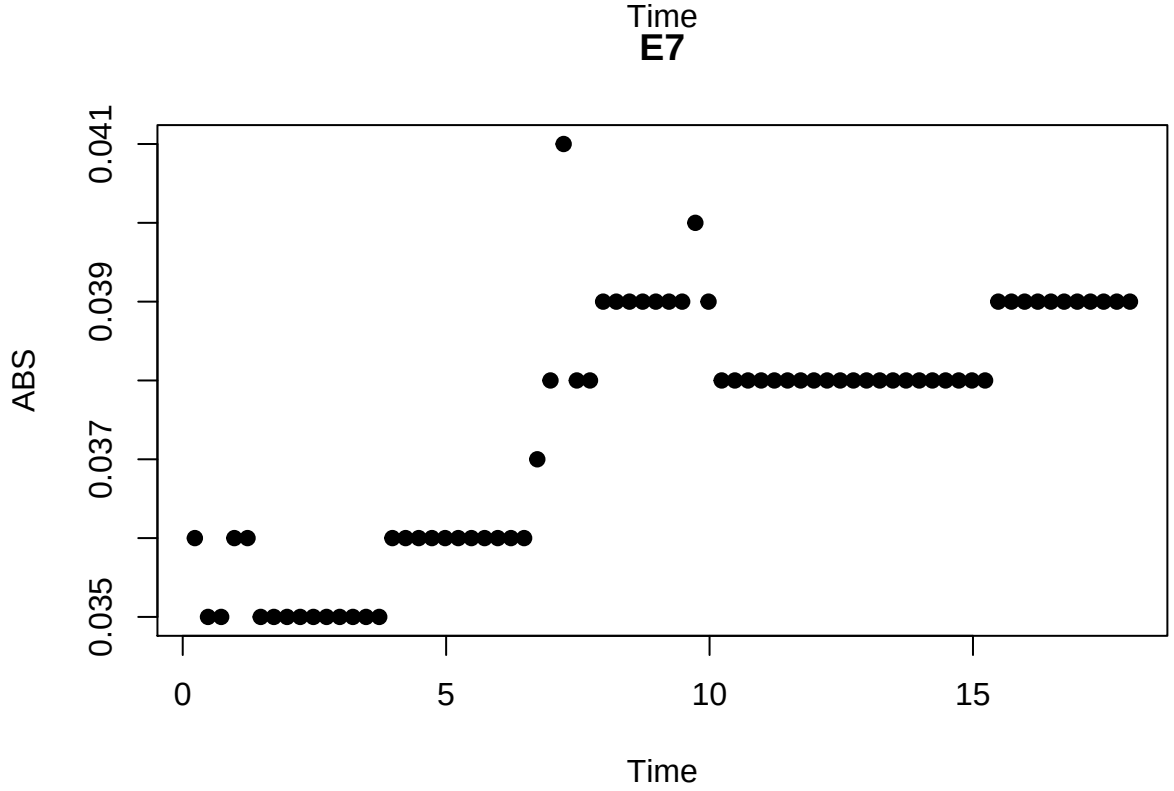
Time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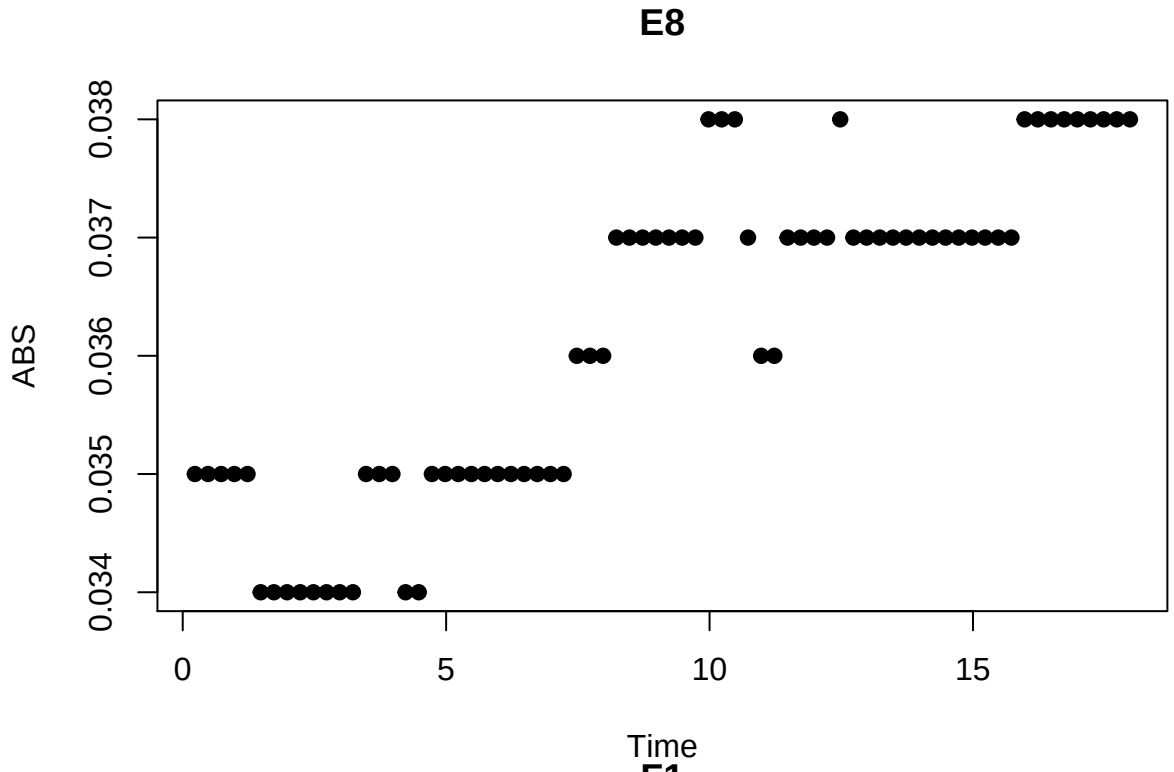
Time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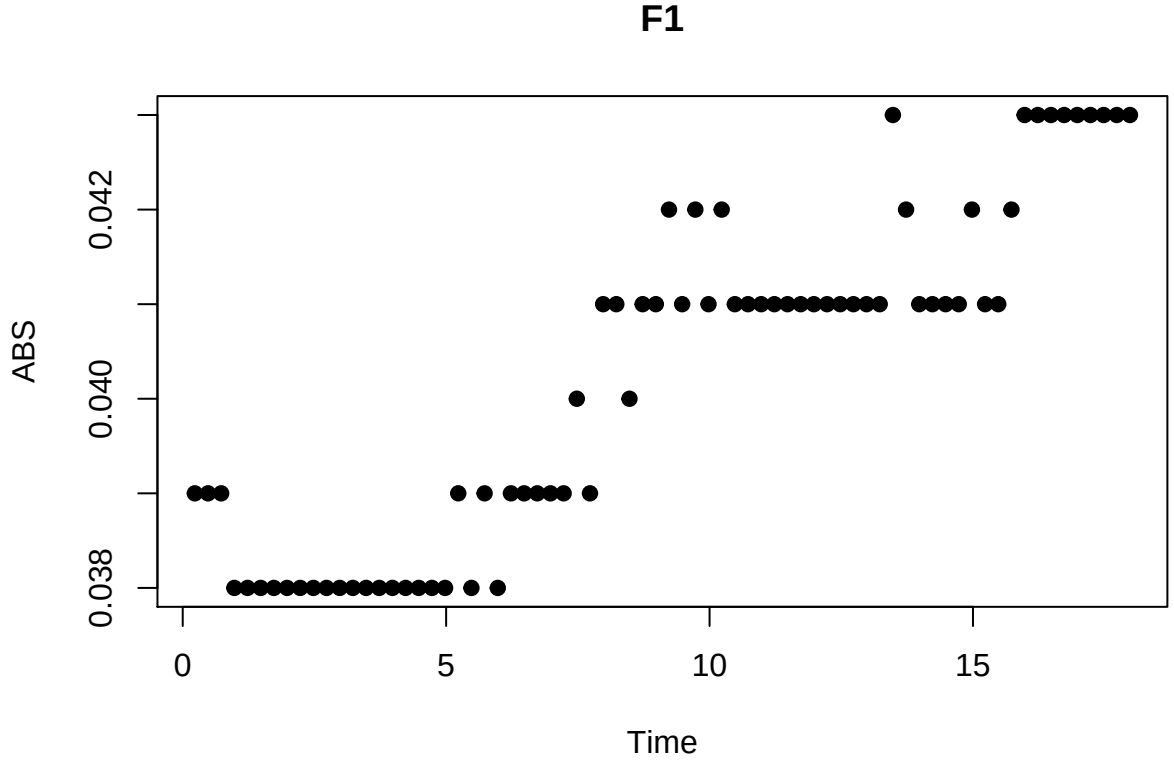
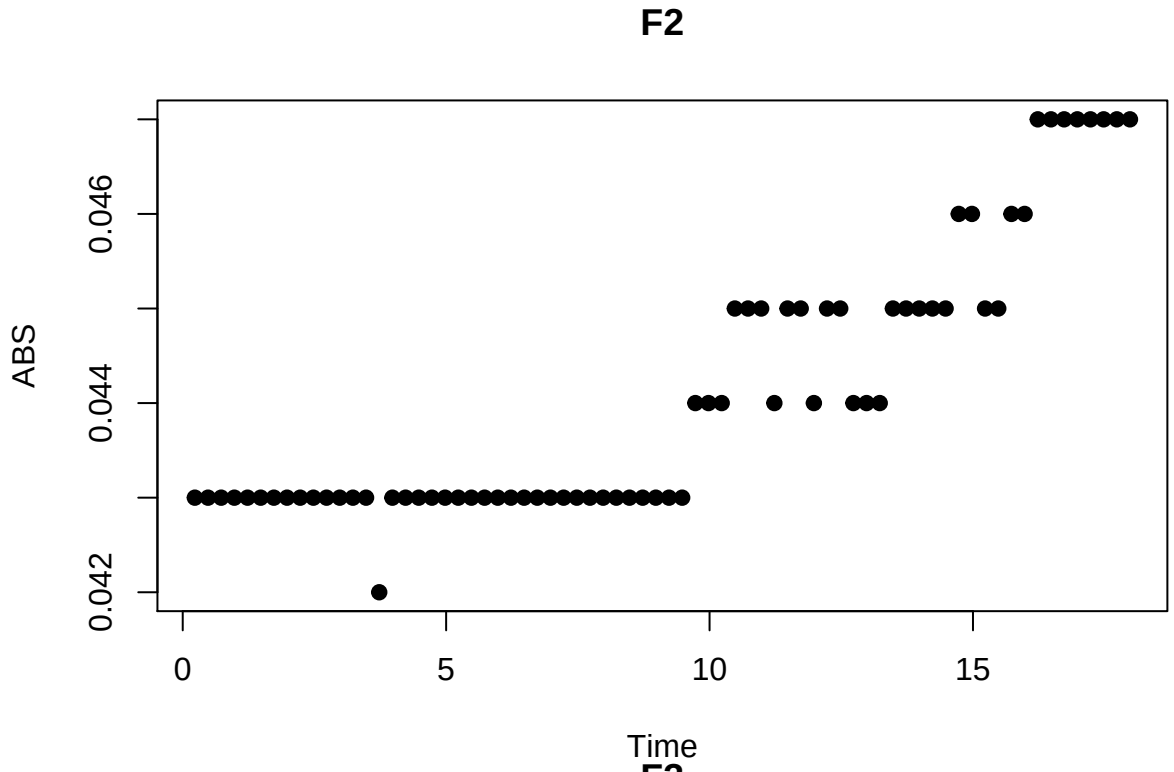
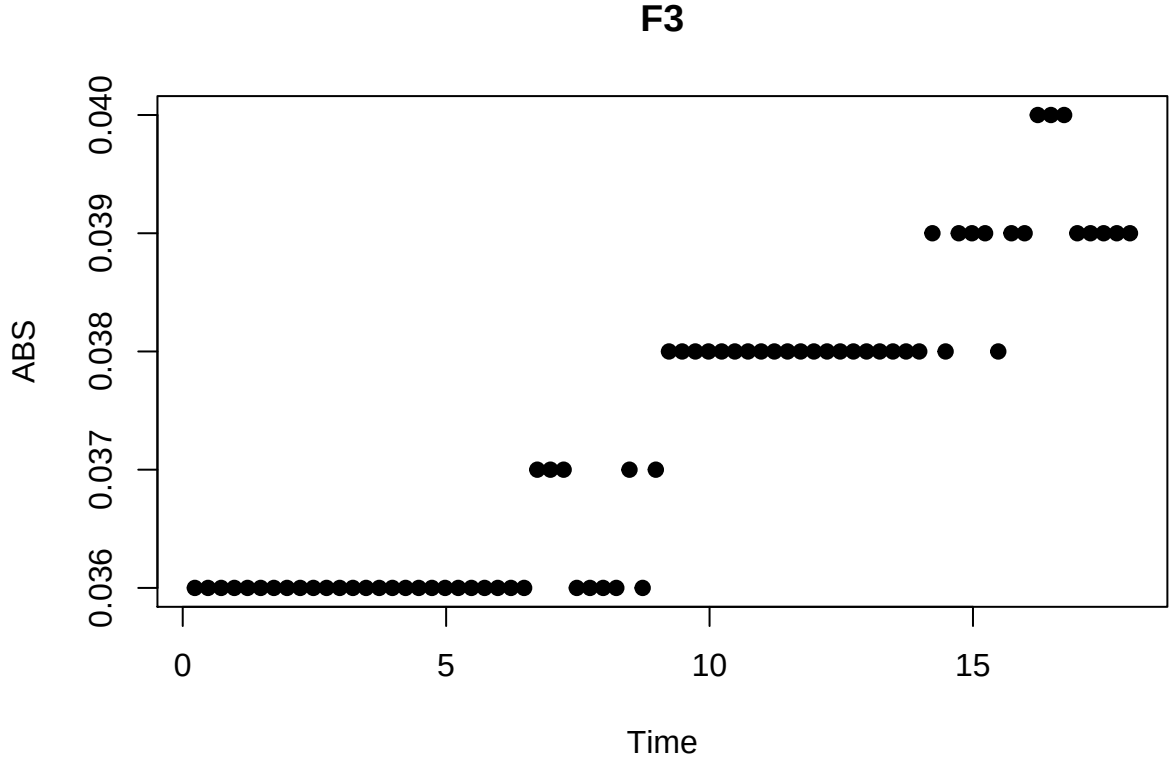
Time


F1
ABS
0.038
0.040
0.042
0
5
10
15
Time


F2
ABS
0.042
0.044
0.046
0
5
10
15
Time


F3
ABS
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0.037
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0.039
0.040
0
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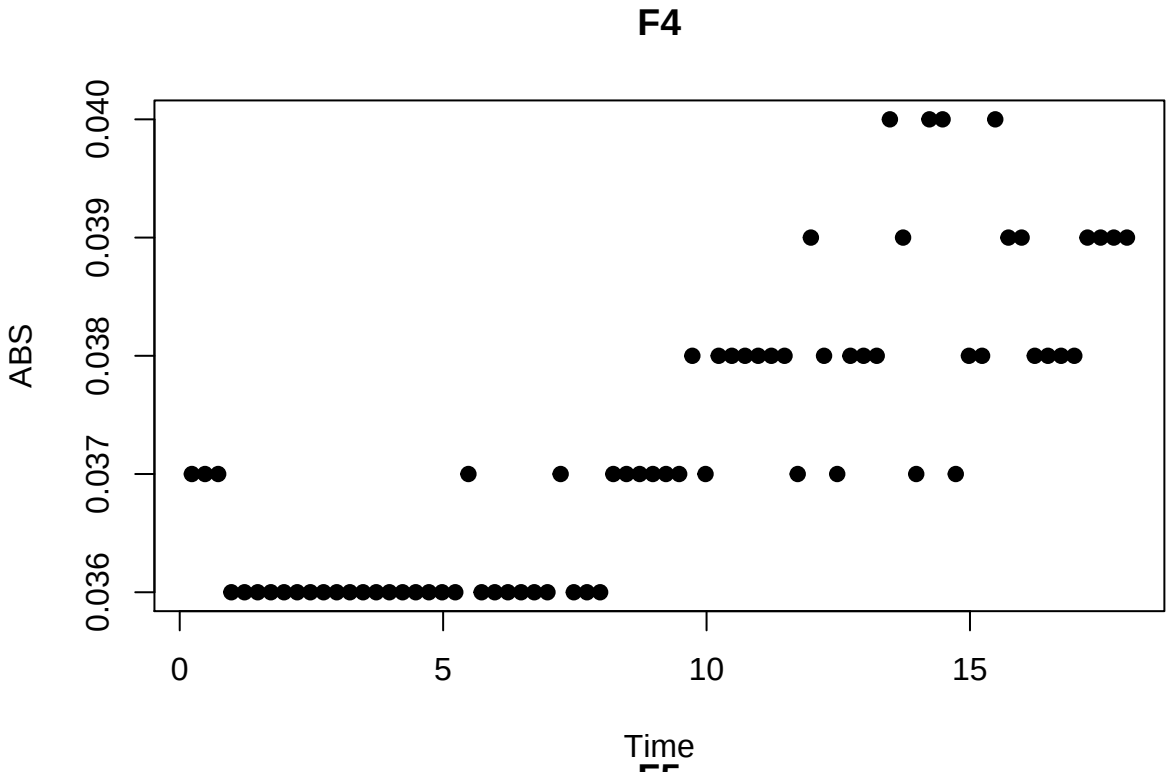
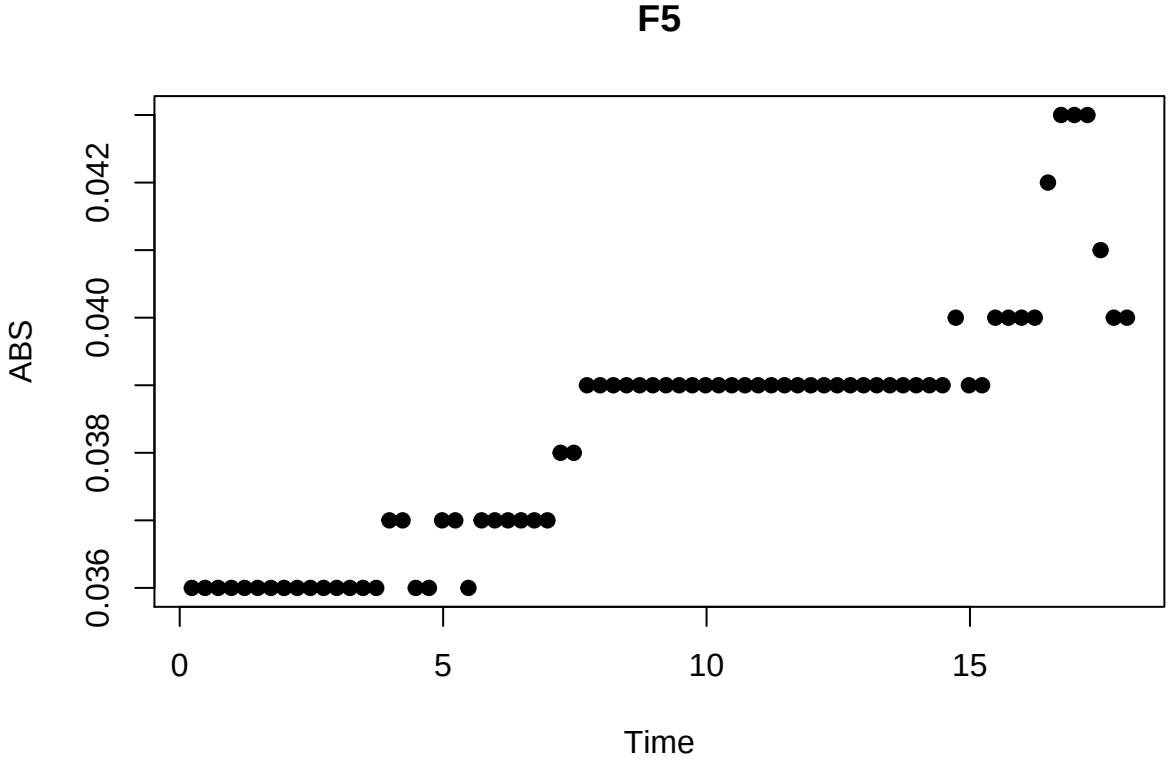
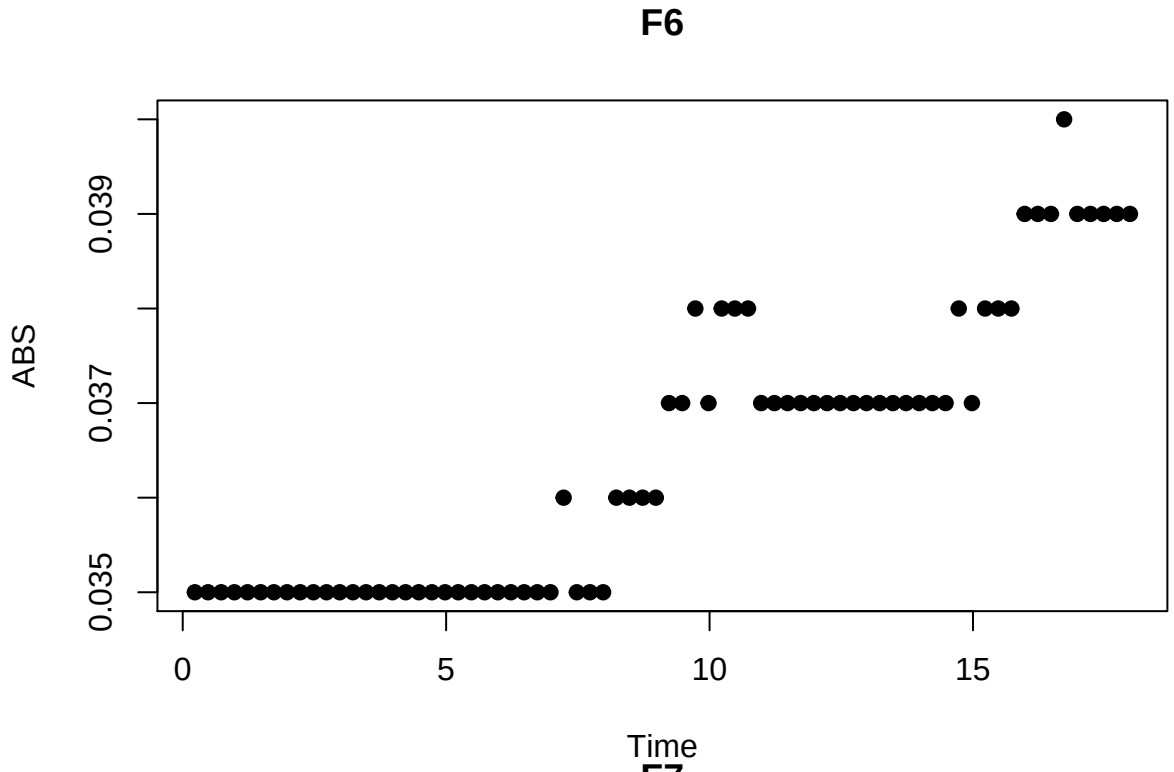
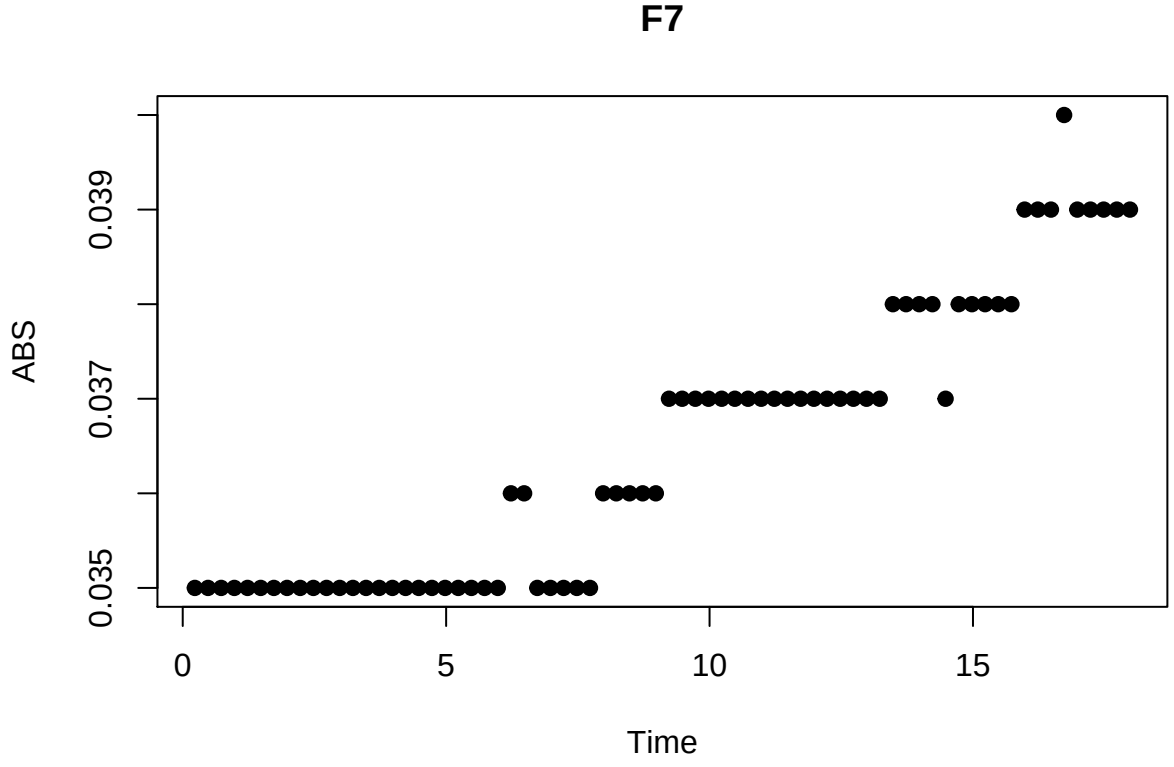
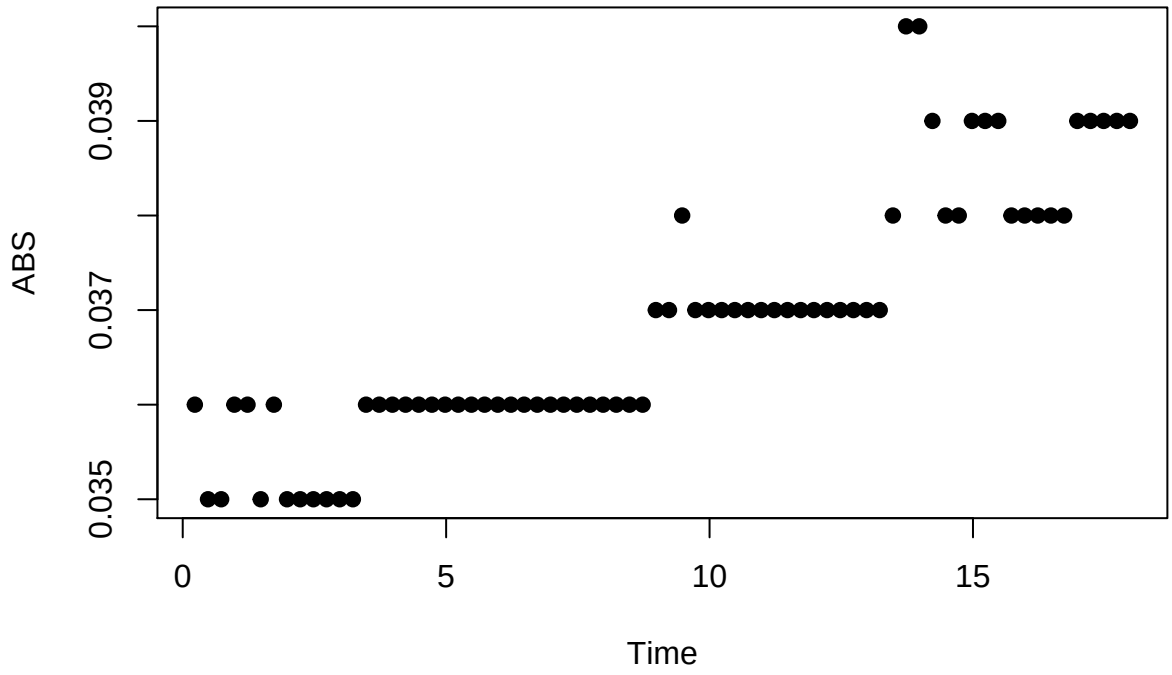
10
15
Time


F4
ABS
0.036
0.037
0.038
0.039
0.040
0
5
10
15
Time


F5
ABS
0.036
0.038
0.040
0.042
0
5
10
15
Time


F6
ABS
0.035
0.037
0.039
0
5
10
15
Time


F7
ABS
0.035
0.037
0.039
0
5
10
15
Time

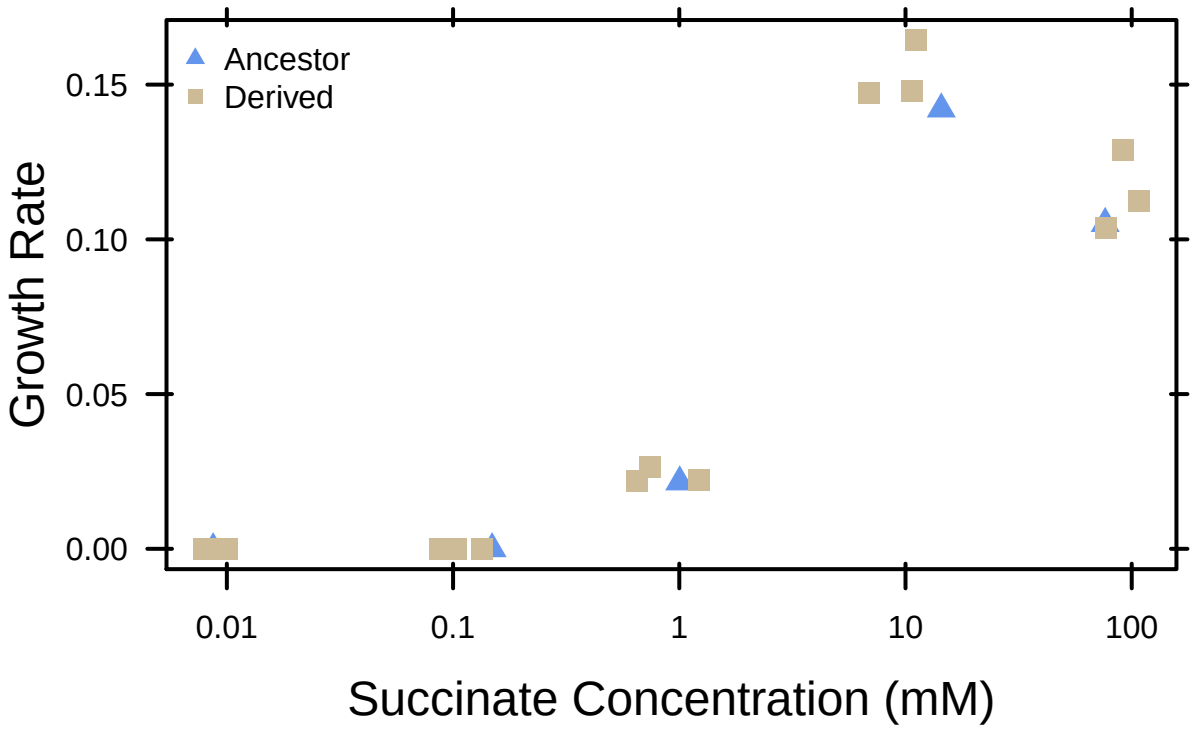



```
KBS0802_MM <- read.csv("../output/KBS0802.txt", header = T)
KBS0802_key <- read.csv("../data/MichaelisMenten/KBS0802_key.txt", header = T)

KBS0802_rate <- merge(KBS0802_key, KBS0802_MM[,c(1,4)], by = "Curve", all.x = T)
for (i in 1:dim(KBS0802_rate)[1]){
  if (is.na(KBS0802_rate$umax[i]) == TRUE){
    KBS0802_rate$umax[i] <- 0
  }
}
KBS0802_rate$Concentration <- as.character(KBS0802_rate$Concentration)

rate.l <- melt(as.data.frame(KBS0802_rate))
```

```
## Using Curve, Strain, Concentration as id variables
```

```
rate.MM <- cast(rate.l, Strain + Concentration ~ variable, mean)
rate.MM$Concentration <- as.numeric(rate.MM$Concentration)

syms <- rep(NA, length(rate.MM$Strain))
for (i in 1:length(syms)){
if (grepl("Anc", rate.MM$Strain[i]) == TRUE){
  syms[i] <- 17
} else {
  syms[i] <- 15
}}

cols <- rep(NA, length(rate.MM$Strain))
for (i in 1:length(cols)){
if (grepl("Anc", rate.MM$Strain[i]) == TRUE){
```

```
  cols[i] <- "cornflowerblue"
} else {
  cols[i] <- "wheat3"
}}

# Define Plot Parameters
par(mar = c(5, 5, 3, 1) + 0.1)

plot(rate.MM$umax ~ jitter(log10(rate.MM$Concentration)),
     xlab = "", ylab = "",
     xaxt = "n", yaxt = "n",
     pch = syms, col = cols, cex = 1.5)

legend("topleft", legend = c("Ancestor", "Derived"),
       bty = 'n', pch = c(17, 15), col = c("cornflowerblue", "wheat3"))

labs <- levels(as.factor(rate.MM$Concentration))
poss <- log10(as.numeric(levels(as.factor(rate.MM$Concentration))))

# Add Axes
axis(side = 1, labels = labs, lwd.ticks = 2, cex.axis = 1, las = 1, at = poss)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02, at = poss)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 1, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01, at = poss)
axis(side = 2, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01, at = poss)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)

# Add Axis Labels
mtext("Succinate Concentration (mM)", side = 1, line = 3, cex = 1.5)
mtext("Growth Rate", side = 2, line = 3, cex = 1.5)

# Add Box
box(lwd = 2)
```




```
# concentration <- c(1,2,3,5,10,15,20,25,30,35);
# rate <- c(2.8,4.2,3.5,6.3,15.7,21.3,23.7,25.1,25.8,25.9)
# plot(concentration, rate, las=1, pch=16)
# mmModel <- nls(rate~Vm*concentration/(K+concentration), start=list(Vm=30, K=25))
#
# summary(mmModel)
# coef(mmModel)
#
# library(drc) # for fitting Michaelis Menten model
# model.drm <- drm (v ~ S, data = mm, fct = MM.2())
#
# mml <- data.frame(S = seq(0, max(mm$S), length.out = 100))
# mml$v <- predict(model.drm, newdata = mml)
#
#
# model.nls <- nls(v ~ Vm * S/(K+S), data = mm,
#                  start = list(K = max(mm$v)/2, Vm = max(mm$v)))
# summary(model.drm)
# summary(model.nls)
```