LTDE Death Rate Experiment

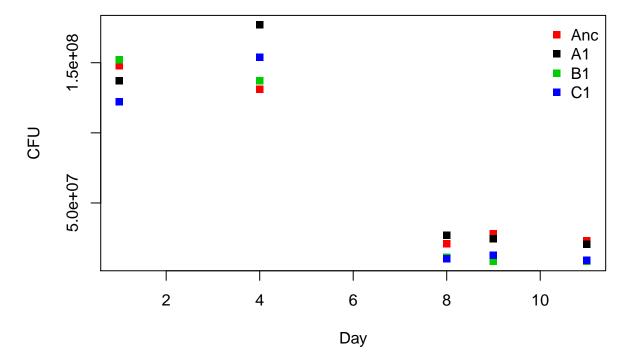
Mollie Carrison, Mario E. Muscarella, Jay T. Lennon 25 February, 2016

Import Data

```
KBS0802 <- read.delim("../data/DeathCurves/KBS0802.txt", header = T, row.names = NULL)
levels(KBS0802$Organism) <- c("Anc", "A1", "B1", "C1")</pre>
```

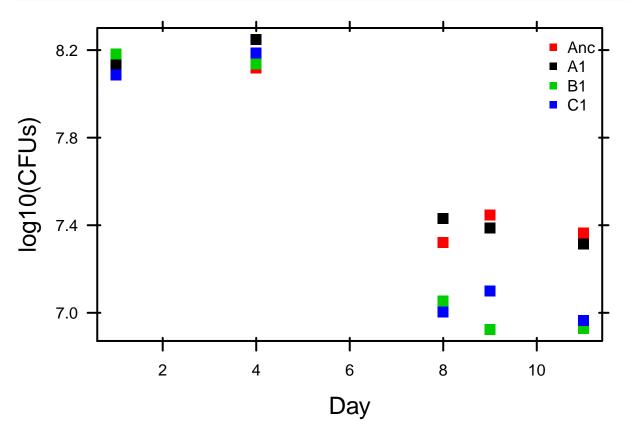
Plot Raw Data

```
plot(CFU ~ Day, data = KBS0802, col = order(levels(KBS0802$Organism)), pch = 15)
legend("topright", legend = levels(KBS0802$Organism),
    bty = 'n', pch = 15, col = order(levels(KBS0802$Organism)))
```



Plot Log Data

```
legend("topright", legend = levels(KBS0802$Organism),
       bty = 'n', pch = 15, col = order(levels(KBS0802$Organism)))
# Add Axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1,
     at = c(7, 7.4, 7.8, 8.2))
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02,
     at = c(7, 7.4, 7.8, 8.2))
axis(side = 1, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 2, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01,
     at = c(7, 7.4, 7.8, 8.2))
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01,
     at = c(7, 7.4, 7.8, 8.2))
# Add Axis Labels
mtext("Day", side = 1, line = 3, cex = 1.5)
mtext("log10(CFUs)", side = 2, line = 3, cex = 1.5)
# Add Box
box(lwd = 2)
```

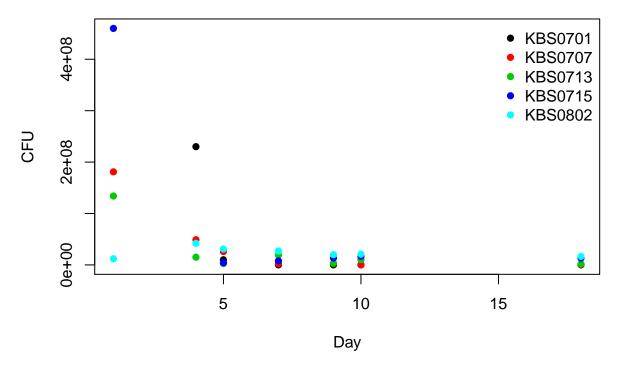


Ancestor Plots

```
ancestors <- read.delim("../data/DeathCurves/AncestorDeathCurves.txt",header=T, row.names = NULL)</pre>
```

Basic Ancestor Plot

```
plot(CFU ~ Day, data = ancestors, col = order(levels(ancestors$Organism)), pch = 16)
legend("topright", legend = levels(ancestors$Organism),
    bty = 'n', pch = 16, col = order(levels(ancestors$Organism)))
```

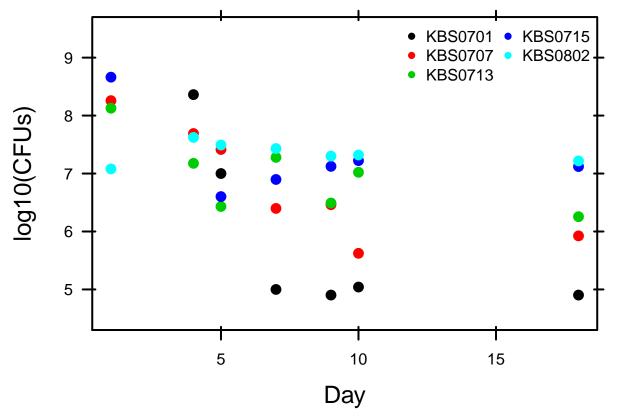


Log Ancestor Plot

```
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
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)
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)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)

# Add Axis Labels
mtext("Day", side = 1, line = 3, cex = 1.5)
mtext("log10(CFUs)", side = 2, line = 3, cex = 1.5)

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



710 and 724 Ancestors

```
KBS0710 <- read.delim("../data/DeathCurves/KBS0710.txt", header=T, row.names=NULL)
KBS0710$CFU <- KBS0710$Colonies / KBS0710$Dilution * 10

# Define Plot Parameters
par(mar = c(5, 5, 3, 1) + 0.1)
library(RColorBrewer)
(palette(gray(seq(0,.9,len = 10))))

## [1] "black" "red" "green3" "blue" "cyan" "magenta" "yellow"</pre>
```

[8] "gray"

```
syms <- rep(NA, length(KBS0710$Organism))</pre>
for (i in 1:length(syms)){
if (grepl("A", KBS0710$Organism[i]) == TRUE){
  syms[i] <- 17
} else {
  syms[i] <- 19
}}
cols <- rep(NA, length(KBS0710$Organism))</pre>
for (i in 1:length(cols)){
if (grepl("A", KBS0710$Organism[i]) == TRUE){
  cols[i] <- "cornflowerblue"</pre>
} else {
  cols[i] <- "wheat3"</pre>
}}
# Initialize Plot
plot(log10(CFU) ~ Day, data = KBS0710, col = cols,
     pch = syms, las = 1, cex = 1.5, xaxt = 'n', yaxt = 'n', xlab = '', ylab = '',
     ylim = c(6, 8.5))
legend("topright", legend = c("Ancestor", "Derived"), ncol = 2,
       bty = 'n', pch = c(17, 19), col = c("cornflowerblue", "wheat3"))
# Add Axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
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)
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)
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)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
# Add Axis Labels
mtext("Day", side = 1, line = 3, cex = 1.5)
mtext("log10(CFUs)", side = 2, line = 3, cex = 1.5)
mtext("Starvation: KBS0710", side = 3, line = 1, cex = 1.5)
# Add Box
box(lwd = 2)
```

Starvation: KBS0710 8.5 7.5 7.0 6.5 Day

```
KBS0724 <- read.delim("../data/DeathCurves/KBS0724.txt", header=T, row.names=NULL)
KBS0724$CFU <- KBS0724$Colonies / KBS0724$Dilution * 10
# Define Plot Parameters
par(mar = c(5, 5, 3, 1) + 0.1)
syms <- rep(NA, length(KBS0724$Organism))</pre>
for (i in 1:length(syms)){
if (grep1("A", KBS0724$Organism[i]) == TRUE){
  syms[i] <- 17
} else {
  syms[i] <- 19
}}
cols <- rep(NA, length(KBS0724$Organism))</pre>
for (i in 1:length(cols)){
if (grepl("A", KBS0724$Organism[i]) == TRUE){
  cols[i] <- "cornflowerblue"</pre>
} else {
  cols[i] <- "wheat3"</pre>
}}
# Initialize Plot
plot(log10(CFU) ~ Day, data = KBS0724, col = cols,
     pch = syms, las = 1, cex = 1.5, xaxt = 'n', yaxt = 'n', xlab = '', ylab = '',
     ylim = c(5.5, 7.5))
legend("topright", legend = c("Ancestor", "Derived"), ncol = 2,
```

```
bty = 'n', pch = c(17, 19), col = c("cornflowerblue", "wheat3"))
# Add Axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
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)
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)
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)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
# Add Axis Labels
mtext("Day", side = 1, line = 3, cex = 1.5)
mtext("log10(CFUs)", side = 2, line = 3, cex = 1.5)
mtext("Starvation: KBS0724", side = 3, line = 1, cex = 1.5)
# Add Box
box(lwd = 2)
```

