

Assessing community microbial community activity with flow cytometry

M.L. Larsen, W. Shoemaker, K. Locey, and J.T. Lennon

17 October, 2015

Project Overview

The microbes within communities have wide ranging metabolic activities that are influenced by resource availability. We can classify their metabolic activity with DNA and RNA content. Here, we seek to enumerate the fractions of the active (greater RNA than DNA), dormant (less RNA to DNA), and dead populations of cultured strains and environmental communities.

Initial setup

All analyses were completed with R version 3.2.2 (2015-08-14).

FIGURE 1: CONCEPTUAL OPVERVIEW

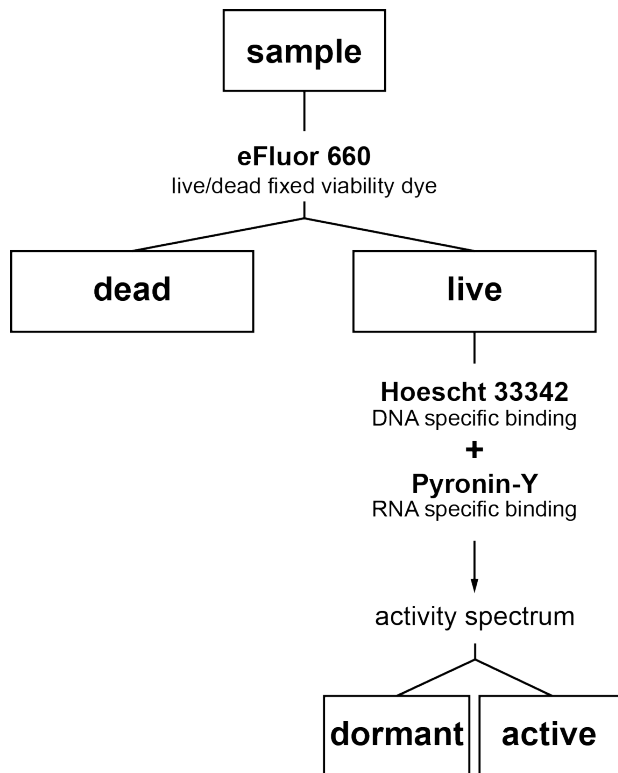


FIGURE 2: TIMECOURSE ACTIVITY IN LAB CULTURED S-TRAINS

Data for this figure was generated from `flowDataScript.R`.

FIGURE 3: ACTIVITY OF ENVIRONMENTAL STRAINS

```
# Other pond files can be found in the following path
#path <- "../Dimensions/Aim3/DATA/FlowCytometryData/output/data/"
```

```
pop.dat <- read.csv("../data/061815_BCSP_015.fcs.csv", header = TRUE)
```

```
head(pop.dat)
```

```
##   X Pacific.Blue.A  PI..B..A PI..B..A.1
## 1 1      0.6093657 0.7751588 1.2720747
## 2 2      1.5582841 1.5294933 0.9815240
## 3 3      1.0151689 1.4739659 1.4519415
## 4 4      0.5640575 0.5419037 0.9607241
## 5 5      1.2972847 1.0150521 0.7824436
## 6 6      1.5875543 0.4443456 0.2798932
```

```
pop.dat <- pop.dat[,-1]
```

```
colnames(pop.dat) <- c("DNA", "RNA", "RDratio")
```

```
#
```

```
png(filename = "../figures/figure3.png", width = 1800, height = 1000, res = 96*2)
```

```
par(mfrow = c(1,2))
```

```
plot(pop.dat$DNA, pop.dat$RNA,
```

```
      xlab = "DNA(Pacific Blue-A)", ylab = "RNA(Pyronin Y)",
```

```
      xlim = c(0,4), ylim = c(0,3.5),
```

```
      las = 1)
```

```
  #points(RDratio, col = "red")
```

```
abline(0, 1, col = "red", lwd = 2)
```

```
d <- density(pop.dat$RDratio,
```

```
            adjust = 10, kernel = "gaussian",
```

```
            from = -1, to = 10, n = 512)
```

```
plot(d, las = 1, main = NA)
```

```
abline(v = mean(pop.dat$RDratio), col = "red", lwd = 2)
```

```
abline(v = median(pop.dat$RDratio), col = "blue", lwd = 2)
```

```
legend("topright", c("RNA/DNA mean", "RNA/DNA median"), col = c("red", "blue"), lwd = 2, bty = 'n')
```

```
dev.off()
```

```
## pdf
```

```
## 2
```

```
graphics.off()
```