# Modeling Microbial Mutualisms

*Jay T. Lennon*

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## Overview

Simulation model that explores interactions between Esherichia coli and Rhodopseudomonas palustris. Under anaerobic conditions, glucose is consumed by E. coli and converts some of this to fermentation byproducts, which serve as a carbon and energy source for R. palustris. In turn, R. palustris fixes atmospheric nitrogen, which is converted into ammonia and serves as E. coli's sole source of nitrogen. Following attempts to captures these baisc features using a set of coupled differential equations.

## Set working directory

```
rm(list=ls()) # clears your working directory
getwd() # tells you your current working directory
```

```
## [1] "/Users/lennonj/GitHub/Task3"
```

```
setwd("~/GitHub/Task3") # sets your working directory
```

## Install packages

```
# install.packages("deSolve") # run this first time
require("deSolve") # installs any dependencies
```

```
## Loading required package: deSolve
```

## Mutualism function

```
mutfun <- function(t, y, parms) {
  with(as.list(c(y, parms)), {
    dgdt <- (D * Gin) - (uE * (G/(Kg + G))) - (D * G) # Glucose
    dndt <- (D * Nin) - (uR * (N/(Kn + N))) - (D * N) # N2
    dcdt <- (E * (uE * (G/(Kg + G))) * a) - (D * C) # Fermentation Product
    dadt <- (R * (uR * (C/(Kc + C))) * z) - (D * A) # NH4
    dedt <- uE * (G/(Kg + G)) * (A/(Ka + A)) - (D * E) # E. coli
    drdt <- uR * (N/(Kn + N)) * (C/(Kc + C)) - (D * R) # R. palustris
    return(list(c(dgdt, dcdt, dndt, dadt, dedt, drdt)))
  })
}
```

## Parameters and initial conditions

```
# Parameters
parms <- c(uE = 0.347, # E. coli max growth rate (h^-1)
           uR = 0.063, # R. palustrix max growth rate (h^-1)

           D = 1/48, # Dilution rate (h^1)

           Kg = 0.020, # half saturation constant for glucose (mM)
           Kc = 0.011, # half saturation constatnt for fermentation product (mM)
           Kn = 0.100, # half saturation constant for N2 (mM)
           Ka = 0.010, # half saturation constant for ammonia (mM)

           a = 1.625*10^-7, # conversion for G -> ferment prod per E. coli
           z = 1.625*10^-9, # conversion for N2 -> NH3 per R. palustris

           Gin <- 25,
           Nin <- 100)

# Initial conditions
init <- c(G = 25,# Glucose (mM)
          N = 100,    # N2 (mM)
          C = 0.0001, # Fermentation product (mM)
          A = 0.0001, # NH4 (mM)
          E = 1,      # E. coli (biomass? units?)
          R = 1)     # R. palustris (biomass?, units?)

# Time range and time step
Tmax = 1000
TimeStep = 0.1
Time = seq(0, Tmax, by = TimeStep)
```

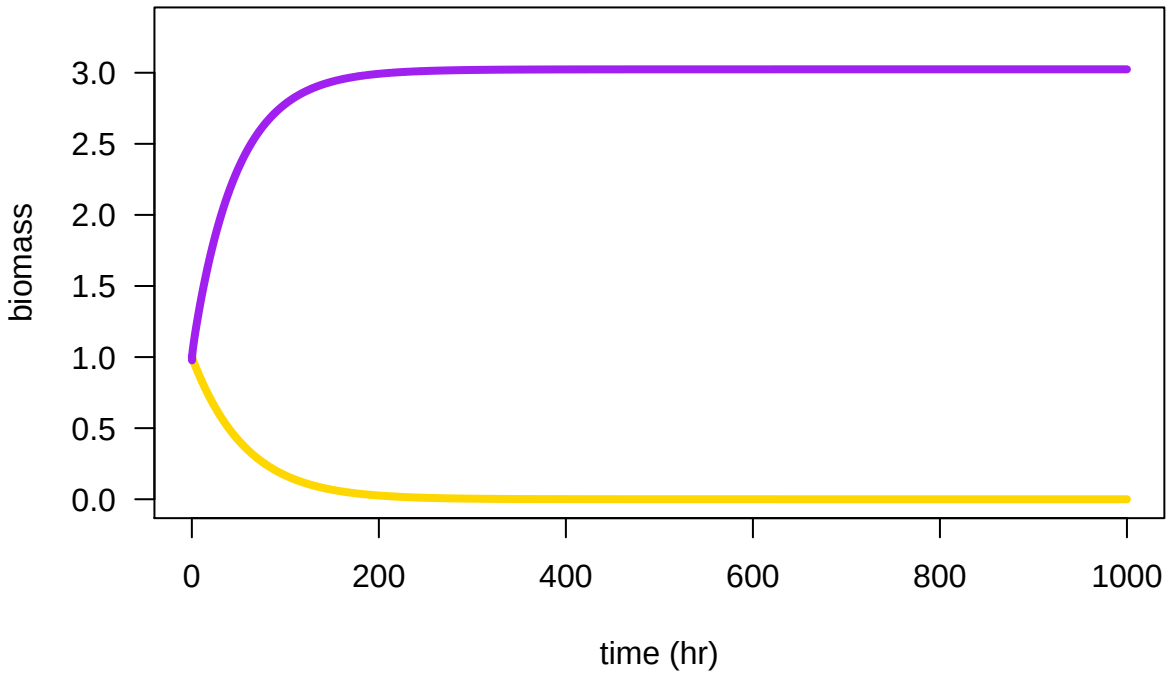
## Output

```
out <- ode(y = init, times = Time, func = mutfun, parms = parms, method = "rk4")
```

## Plotting

```
plot(out[,1], out[,6], xlab = "time (hr)", ylab = "biomass", type = "l", las = 1,
     col = "gold", lwd = 4, ylim = c(0, 1.1*max(out[,7]))) # plot E. coli biomass

points(out[,1], out[,7], type = "l", col = "purple", lwd = 4)
```


biomass
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
200
400
600
800
1000
time (hr)