

Threshold Task Performance Exploration

This document will be solidly based off of a simulation originally created in the early 2000's by Myerscough and Oldroyd in a paper titled "Simulation models of the role of genetic variability in social insect task allocation"

Let's start by creating a population:

```
nSubFam <- 3
nIndiv <- 100
Threshs <- rep(sample(0:100,nSubFam))
population <- data.frame(SubFam = rep(1:nSubFam,each=nIndiv),
                          Thresh = rep(Threshs,each=nIndiv),
                          Status = rep(0,nSubFam*nIndiv))
head(population)
```

```
##   SubFam Thresh Status
## 1      1     62      0
## 2      1     62      0
## 3      1     62      0
## 4      1     62      0
## 5      1     62      0
## 6      1     62      0
```

Now, let's run these individuals through a time-series random generator.

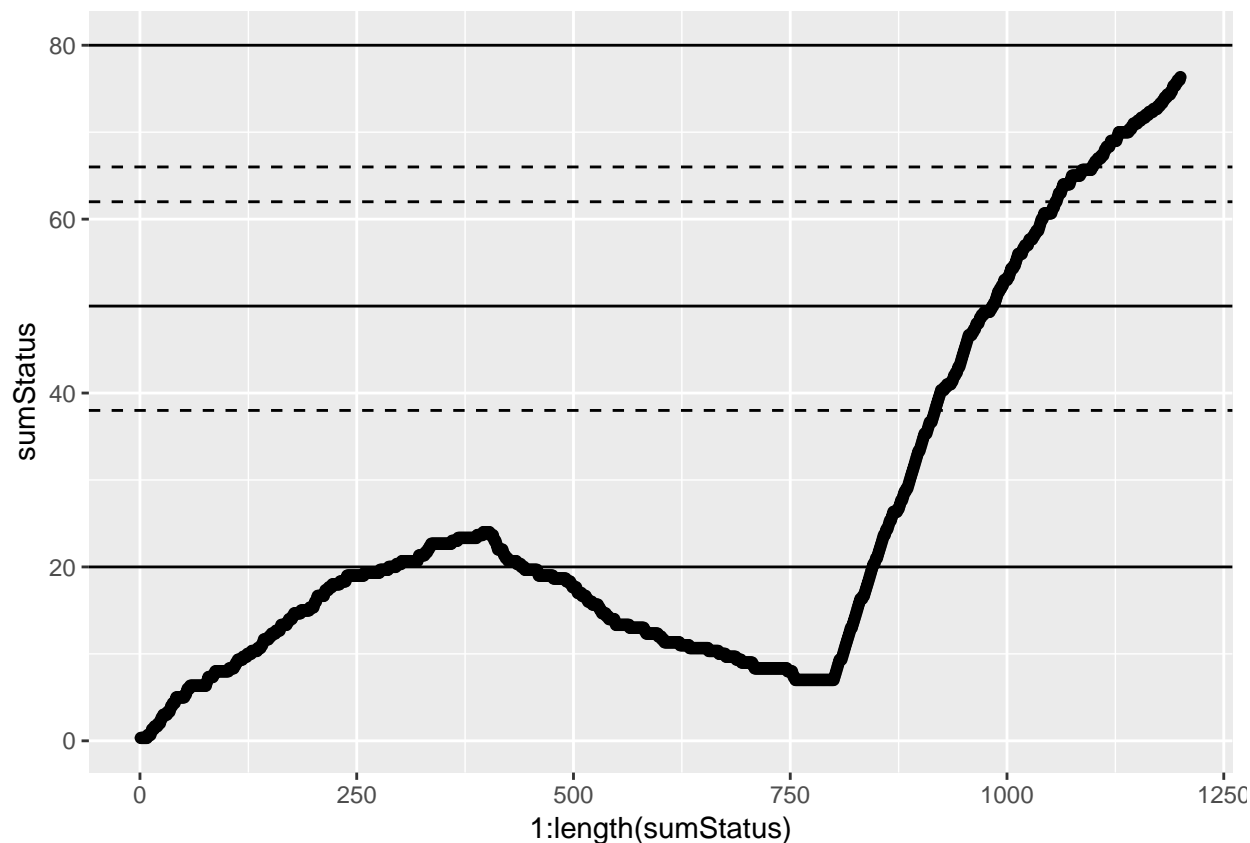
```
nGen <- 1200
nEachGen <- 1
Thresh <- c(50,20,80)
sumStatus <- 1

for(genNum in 1:nGen)
{
  temprows <- sample(1:nrow(population),nEachGen)
  population$Status[temprows] <-
    ifelse(population$Thresh[temprows]
            < Thresh[ceiling(genNum/(nGen/length(Thresh)))],1,0)
  sumStatus[genNum] <- sum(population$Status)/(nIndiv*nSubFam)*100
}

head(population)
```

```
##   SubFam Thresh Status
## 1      1     62      0
## 2      1     62      1
## 3      1     62      1
## 4      1     62      1
## 5      1     62      1
## 6      1     62      0
```

```
ggplot(data=data.frame(sumStatus=sumStatus)) +
  geom_point(mapping=aes(x=1:length(sumStatus),y=sumStatus)) +
  geom_hline(yintercept=Thresh) +
  geom_hline(yintercept=Threshs,linetype="dashed")
```



This was a pretty simple simulation paper.

Myerscough, M. R., and B. P. Oldroyd. "Simulation models of the role of genetic variability in social insect task allocation." *Insectes Sociaux* 51.2 (2004): 146-152.

There are several apparent limitations of this study. First and foremost, their method of selecting an individual each time step was not realistic. That is, they selected a single individual at random, not at all based on how task allocation occurs in nature. Given that task allocation in nature generally takes place by exposure to some stimulus say, a pheromone, I propose a more realistic individual selection type. Each time step, every individual is assigned a randomly distributed number based on a distribution representative of their chance of exposure to the stimulus that may provoke task performance. Certain values on this distribution will represent a "yes" to exposure, in which case the threshold of the associated subfamily will be compared against the given stimulus strength.

```
population$Status <- rep(0,nSubFam*nIndiv)

nGen <- 1200
Thresh <- c(50,20,80)
sumStatus <- 1

for(genNum in 1:nGen)
{
  temprows <- ifelse(rnorm(nrow(population),0,1)>2.5,1,0)

  population$Status <-
    ifelse(temprows==1 &
      population$Thresh<Thresh[ceiling(genNum/(nGen/length(Thresh)))],1,population$Status)
  population$Status <-
```

```

    ifelse(temprows==1 &
      population$Thresh>Thresh[ceiling(genNum/(nGen/length(Thresh)))],0,population$Status)

    sumStatus[genNum] <- sum(population$Status)/(nIndiv*nSubFam)*100
  }

```

```
head(population)
```

```
##   SubFam Thresh Status
## 1      1     62      1
## 2      1     62      1
## 3      1     62      1
## 4      1     62      1
## 5      1     62      1
## 6      1     62      1

```

```

ggplot(data=data.frame(sumStatus=sumStatus)) +
  geom_point(mapping=aes(x=1:length(sumStatus),y=sumStatus)) +
  geom_hline(yintercept=Thresh) +
  geom_hline(yintercept=Threshs,linetype="dashed")

```

