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"

```
library(tidyverse)
                                                     ----- tidyverse 1.2.1 --
## -- Attaching packages -----
## v ggplot2 3.0.0
                     v purrr
                                 0.2.5
## v tibble 1.4.2
                                 0.7.6
                       v dplyr
## v tidyr
           0.8.1
                       v stringr 1.3.1
## v readr
             1.1.1
                     v forcats 0.3.0
## -- Conflicts -----
                                                ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                     masks stats::lag()
library(dplyr)
Let's start by creating a population:
nSubFam <- 2
nIndiv <- 100
population <- data.frame(SubFam = rep(1:nSubFam,each=nIndiv),</pre>
                         Thresh = rep(rep(sample(0:100, nSubFam)), each=nIndiv),
                         Status = rep(0,nSubFam*nIndiv))
head(population)
     SubFam Thresh Status
##
## 1
         1
                81
## 2
                81
                        0
          1
## 3
         1
                81
                        0
## 4
         1
                81
                        0
## 5
                81
         1
## 6
          1
                81
                        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)</pre>
  population$Status[temprows] <-</pre>
    ifelse(population$Thresh[temprows]>Thresh[ceiling(genNum/(nGen/3))],1,0)
  sumStatus[genNum] <- sum(population$Status)</pre>
}
head(population)
     SubFam Thresh Status
```

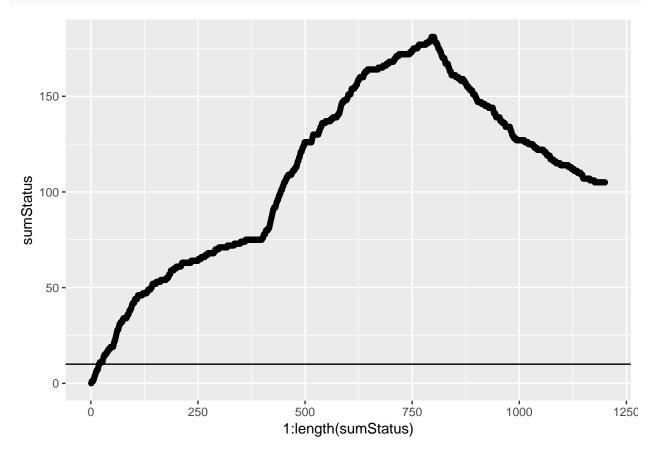
1

1

81

```
## 2
            1
                   81
                            1
## 3
            1
                   81
                            1
                   81
## 4
            1
                            1
## 5
            1
                   81
                            1
                   81
            1
                            1
```

```
ggplot(data=data.frame(sumStatus=sumStatus)) +
  geom_point(mapping=aes(x=1:length(sumStatus),y=sumStatus)) +
  geom_hline(mapping=aes(yintercept=10))
```



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.