EM1 Behavior Analysis - No Change from Baseline

Kyle Emerson

12/14/2022

## R Markdown

This RMarkdown will contain start to finish analysis of Behavioral Assay information compiled from the Emerson 1 Microbial Experiment (Aim 2). This is raw behavioral analysis at baseline and in response to the addition of sensory cues. It is updated to be more streamlined and easier to knit the output and be placed into my data notebook. Note: This is updated for Manuscript Writing and all analysis was done in RStudio

**Baseline Behavior**

library(readr)

## Warning: package 'readr' was built under R version 4.1.3

library(tidyr)

## Warning: package 'tidyr' was built under R version 4.1.3

library(dplyr)

## Warning: package 'dplyr' was built under R version 4.1.3

##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':  
##   
## filter, lag

## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

library(stringr)  
library(ggbiplot)

## Loading required package: ggplot2

## Warning: package 'ggplot2' was built under R version 4.1.3

## Loading required package: plyr

## Warning: package 'plyr' was built under R version 4.1.3

## ------------------------------------------------------------------------------

## You have loaded plyr after dplyr - this is likely to cause problems.  
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:  
## library(plyr); library(dplyr)

## ------------------------------------------------------------------------------

##   
## Attaching package: 'plyr'

## The following objects are masked from 'package:dplyr':  
##   
## arrange, count, desc, failwith, id, mutate, rename, summarise,  
## summarize

## Loading required package: scales

## Warning: package 'scales' was built under R version 4.1.3

##   
## Attaching package: 'scales'

## The following object is masked from 'package:readr':  
##   
## col\_factor

## Loading required package: grid

library(moments)

## Warning: package 'moments' was built under R version 4.1.3

library(psych)

## Warning: package 'psych' was built under R version 4.1.3

##   
## Attaching package: 'psych'

## The following objects are masked from 'package:scales':  
##   
## alpha, rescale

## The following objects are masked from 'package:ggplot2':  
##   
## %+%, alpha

library(pastecs)

##   
## Attaching package: 'pastecs'

## The following objects are masked from 'package:dplyr':  
##   
## first, last

## The following object is masked from 'package:tidyr':  
##   
## extract

library(ggplot2)  
library(car)

## Warning: package 'car' was built under R version 4.1.3

## Loading required package: carData

## Warning: package 'carData' was built under R version 4.1.3

##   
## Attaching package: 'car'

## The following object is masked from 'package:psych':  
##   
## logit

## The following object is masked from 'package:dplyr':  
##   
## recode

library(lme4)

## Warning: package 'lme4' was built under R version 4.1.3

## Loading required package: Matrix

## Warning: package 'Matrix' was built under R version 4.1.3

##   
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':  
##   
## expand, pack, unpack

file.choose()

## [1] "C:\\R\\Emerson-Microbial-1\\EM1 Behavior.docx"

baseline <- read\_csv("C:\\Users\\kjeme\\OneDrive\\Desktop\\Woodley Lab\\Aim 2 - Emerson Microbial 1\\Emersion Microbial Experiment 1 (2021)\\Data Project\\Emerson Microbial Exp1\_baseline.csv")

## Rows: 22 Columns: 24

## -- Column specification --------------------------------------------------------  
## Delimiter: ","  
## chr (1): ID  
## dbl (18): MicroTrtmt, Av. Speed (mm/s), Mob. Av. Speed (mm/s), Av. Accel (m...  
## time (5): Visible Time (m:s), Invisible Time (m:s), Tot. Time Frozen (m:s),...  
##   
## i Use `spec()` to retrieve the full column specification for this data.  
## i Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

for (i in 2:ncol(baseline)) {  
 if (str\_detect(baseline[1,i],"%")) {  
 baseline[,i] <-as.numeric(strsplit(c(baseline[[i]]), "%"))  
 }  
}

Ways to turn percentages, units, etc into numeric columns for data analysis.

base.df <- baseline %>%  
 select(`Av. Speed (mm/s)`, `Total Distance (mm)`, `Av. Accel (mm/s^2)`, `Mobility Rate (%)`, `Exploration Rate (%)`, `Total Distance (mm)`, `Time In Center (m:s)`, `Tot. Time Frozen (m:s)`, `Exploration Rate (%)` )  
  
base.df$`Time In Center (m:s)`<- (as.numeric(base.df$`Time In Center (m:s)`))/3600  
  
base.df$`Tot. Time Frozen (m:s)`<- (as.numeric(base.df$`Tot. Time Frozen (m:s)`))/3600

Consolodate down to the DVs we want to analyze in our PCA and get some columns into minutes for easier analysis.

KMO(base.df)

## Kaiser-Meyer-Olkin factor adequacy  
## Call: KMO(r = base.df)  
## Overall MSA = 0.64  
## MSA for each item =   
## Av. Speed (mm/s) Total Distance (mm) Av. Accel (mm/s^2)   
## 0.63 0.62 0.78   
## Mobility Rate (%) Exploration Rate (%) Time In Center (m:s)   
## 0.68 0.20 0.76   
## Tot. Time Frozen (m:s)   
## 0.64

Pass KMO assumptions.

cortest.bartlett(base.df)

## R was not square, finding R from data

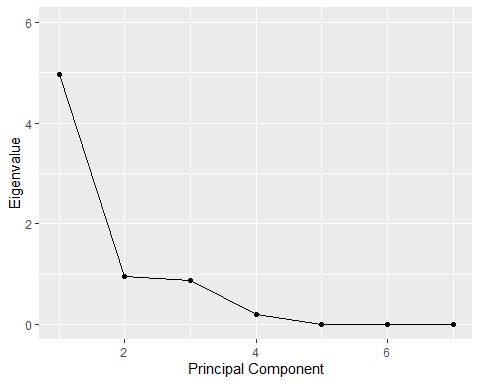
## $chisq  
## [1] 391.9574  
##   
## $p.value  
## [1] 4.272099e-70  
##   
## $df  
## [1] 21

Pass again. Now can do PCA.

pca1 <- principal(base.df, nfactors = 3, rotate = "varimax")  
summary(pca1)

##   
## Factor analysis with Call: principal(r = base.df, nfactors = 3, rotate = "varimax")  
##   
## Test of the hypothesis that 3 factors are sufficient.  
## The degrees of freedom for the model is 3 and the objective function was 10.35   
## The number of observations was 22 with Chi Square = 163.95 with prob < 2.6e-35   
##   
## The root mean square of the residuals (RMSA) is 0.03

qplot(c(1:7), pca1$values) +  
 geom\_line() +  
 xlab("Principal Component") +  
 ylab("Eigenvalue") +  
 ylim(0,6)



3 PC’s is sufficient.

Factor <- pca1$scores  
df <- cbind(base.df, Factor)  
ID <- baseline$ID  
MicroTrtmt <- baseline$MicroTrtmt  
df <- cbind(df, ID)  
df <- cbind(df, MicroTrtmt)  
df$MicroTrtmt = factor(df$MicroTrtmt)

Now, have our final working data frame that includes our variables of interest, our PC values, our Tadpole ID’s and their microbial treatments (1 = Natural, 2 = Autoclaved). Now, we can use GLMMs to evaluate treatment effect on baseline behavior.

pca1$loadings

##   
## Loadings:  
## RC1 RC2 RC3   
## Av. Speed (mm/s) 0.981 -0.134  
## Total Distance (mm) 0.980 -0.136  
## Av. Accel (mm/s^2) 0.966 -0.138  
## Mobility Rate (%) 0.946 0.214   
## Exploration Rate (%) 0.149 0.986   
## Time In Center (m:s) -0.167 0.986  
## Tot. Time Frozen (m:s) -0.940 -0.189 0.116  
##   
## RC1 RC2 RC3  
## SS loadings 4.684 1.066 1.049  
## Proportion Var 0.669 0.152 0.150  
## Cumulative Var 0.669 0.821 0.971

PCA1 = Speed, Distance, Accel, Mobility rate and total time frozen

PCA2 = Exploration Rate

PCA3 = Time in Center Cumulative 97% of variance explained

PC1.aov <- aov(RC1~MicroTrtmt, data = df)  
summary(PC1.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0.032 0.0317 0.03 0.864  
## Residuals 20 20.968 1.0484

PC2.aov <- aov(RC2~MicroTrtmt, data = df)  
summary(PC2.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0.339 0.339 0.328 0.573  
## Residuals 20 20.661 1.033

PC3.aov <- aov(RC3~MicroTrtmt, data = df)  
summary(PC3.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0.391 0.3911 0.38 0.545  
## Residuals 20 20.609 1.0304

None significant. Figures for all DVs can be found in Baseline Behavior.R script, but for now we are going to continue on. NOTE: For Visual Empty, Visual Food, and Olfactory, some of the future data frames are going to be named similarly to ones used in Baseline Behavior. It is imperative you clear your environment now when running this code!

*Clear Environment*

**Visual Empty Behavior**

file.choose()

## [1] "C:\\R\\Emerson-Microbial-1\\EM1 Behavior.docx"

visualempty <- read\_csv("C:\\Users\\kjeme\\OneDrive\\Desktop\\Woodley Lab\\Aim 2 - Emerson Microbial 1\\Emersion Microbial Experiment 1 (2021)\\Data Project\\Emerson Microbial Exp1\_visualempty.csv")

## Rows: 22 Columns: 25  
## -- Column specification --------------------------------------------------------  
## Delimiter: ","  
## chr (5): ID, Mobility Rate (%), Visibility Rate (%), Invisibility Rate (%)...  
## dbl (14): MicroTrtmt, Av. Speed (mm/s), Mob. Av. Speed (mm/s), Av. Accel (m...  
## time (6): Visible Time (m:s), Invisible Time (m:s), Tot. Time Frozen (m:s),...  
##   
## i Use `spec()` to retrieve the full column specification for this data.  
## i Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

for (i in 2:ncol(visualempty)) {  
 if (str\_detect(visualempty[1,i],"%")) {  
 visualempty[,i] <-as.numeric(strsplit(c(visualempty[[i]]), "%"))  
 }  
}  
  
visempty.df <- visualempty %>%  
 select(`Av. Speed (mm/s)`, `Total Distance (mm)`, `Av. Accel (mm/s^2)`, `Mobility Rate (%)`, `Exploration Rate (%)`, `Total Distance (mm)`, `Time in Center (m:s)`, `Tot. Time Frozen (m:s)`, `Exploration Rate (%)`, 'Time near object (m:s)')  
  
visempty.df$`Time in Center (m:s)`<- (as.numeric(visempty.df$`Time in Center (m:s)`))/3600  
visempty.df$`Tot. Time Frozen (m:s)`<- (as.numeric(visempty.df$`Tot. Time Frozen (m:s)`))/3600  
visempty.df$`Time near object (m:s)`<- (as.numeric(visempty.df$`Time near object (m:s)`))/3600  
  
KMO(visempty.df)

## Kaiser-Meyer-Olkin factor adequacy  
## Call: KMO(r = visempty.df)  
## Overall MSA = 0.65  
## MSA for each item =   
## Av. Speed (mm/s) Total Distance (mm) Av. Accel (mm/s^2)   
## 0.65 0.64 0.69   
## Mobility Rate (%) Exploration Rate (%) Time in Center (m:s)   
## 0.68 0.54 0.75   
## Tot. Time Frozen (m:s) Time near object (m:s)   
## 0.66 0.39

Pass.

cortest.bartlett(visempty.df)

## R was not square, finding R from data

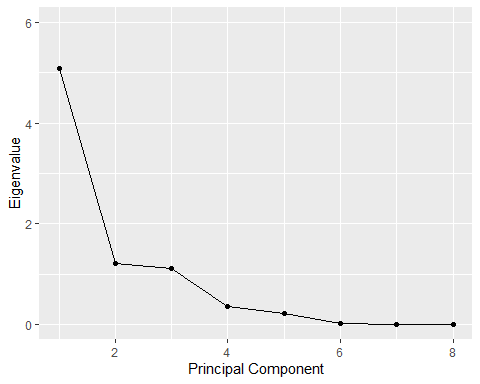
## $chisq  
## [1] 368.8857  
##   
## $p.value  
## [1] 3.899142e-61  
##   
## $df  
## [1] 28

Pass.

pca2 <- principal(visempty.df, nfactors = 3, rotate = "varimax")  
summary(pca2)

##   
## Factor analysis with Call: principal(r = visempty.df, nfactors = 3, rotate = "varimax")  
##   
## Test of the hypothesis that 3 factors are sufficient.  
## The degrees of freedom for the model is 7 and the objective function was 10.23   
## The number of observations was 22 with Chi Square = 158.49 with prob < 6.7e-31   
##   
## The root mean square of the residuals (RMSA) is 0.05

qplot(c(1:8), pca2$values) +  
 geom\_line() +  
 xlab("Principal Component") +  
 ylab("Eigenvalue") +  
 ylim(0,6)



3 fit.

Factor <- pca2$scores  
df <- cbind(visempty.df, Factor)  
ID <- visualempty$ID  
MicroTrtmt <- visualempty$MicroTrtmt  
df <- cbind(df, ID)  
df <- cbind(df, MicroTrtmt)  
df$MicroTrtmt = factor(df$MicroTrtmt)  
  
pca2$loadings

##   
## Loadings:  
## RC1 RC2 RC3   
## Av. Speed (mm/s) 0.983 0.100   
## Total Distance (mm) 0.983 0.102   
## Av. Accel (mm/s^2) 0.962 0.120   
## Mobility Rate (%) 0.933 0.213   
## Exploration Rate (%) 0.844 0.412  
## Time in Center (m:s) -0.323 -0.789 0.361  
## Tot. Time Frozen (m:s) -0.939 -0.215   
## Time near object (m:s) -0.153 -0.939  
##   
## RC1 RC2 RC3  
## SS loadings 4.745 1.464 1.210  
## Proportion Var 0.593 0.183 0.151  
## Cumulative Var 0.593 0.776 0.927

PCA1 = Speed, Distance, Accel, Mobility rate and total time frozen

PCA2 = Exploration Rate and Time in Center

PCA3 = Time Near Object Cumulative 93% of variance explained

PC1.aov <- aov(RC1~MicroTrtmt, data = df)  
summary(PC1.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 1.862 1.8618 1.946 0.178  
## Residuals 20 19.138 0.9569

PC2.aov <- aov(RC2~MicroTrtmt, data = df)  
summary(PC2.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## MicroTrtmt 1 2.81 2.8098 3.089 0.0941 .  
## Residuals 20 18.19 0.9095   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

PC3.aov <- aov(RC3~MicroTrtmt, data = df)  
summary(PC3.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0 0.0005 0 0.984  
## Residuals 20 21 1.0500

Nothing of significance. All figures can be found in Visual Empty Behavior.R script.

*Clear Environment*

**Visual Food Behavior**

file.choose()

## [1] "C:\\R\\Emerson-Microbial-1\\EM1 Behavior.docx"

visualfood <- read\_csv("C:\\Users\\kjeme\\OneDrive\\Desktop\\Woodley Lab\\Aim 2 - Emerson Microbial 1\\Emersion Microbial Experiment 1 (2021)\\Data Project\\Emerson Microbial Exp1\_visualfood.csv")

## Rows: 22 Columns: 25  
## -- Column specification --------------------------------------------------------  
## Delimiter: ","  
## chr (5): ID, Mobility Rate (%), Visibility Rate (%), Invisibility Rate (%)...  
## dbl (14): MicroTrtmt, Av. Speed (mm/s), Mob. Av. Speed (mm/s), Av. Accel (m...  
## time (6): Visible Time (m:s), Invisible Time (m:s), Tot. Time Frozen (m:s),...  
##   
## i Use `spec()` to retrieve the full column specification for this data.  
## i Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

for (i in 2:ncol(visualfood)) {  
 if (str\_detect(visualfood[1,i],"%")) {  
 visualfood[,i] <-as.numeric(strsplit(c(visualfood[[i]]), "%"))  
 }  
}  
  
visfood.df <- visualfood %>%  
 select(`Av. Speed (mm/s)`, `Total Distance (mm)`, `Av. Accel (mm/s^2)`, `Mobility Rate (%)`, `Exploration Rate (%)`, `Total Distance (mm)`, `Time in Center (m:s)`, `Tot. Time Frozen (m:s)`, `Exploration Rate (%)`, 'Time near object (m:s)')  
  
visfood.df$`Time in Center (m:s)`<- (as.numeric(visfood.df$`Time in Center (m:s)`))/3600  
visfood.df$`Tot. Time Frozen (m:s)`<- (as.numeric(visfood.df$`Tot. Time Frozen (m:s)`))/3600  
visfood.df$`Time near object (m:s)`<- (as.numeric(visfood.df$`Time near object (m:s)`))/3600  
  
KMO(visfood.df)

## Kaiser-Meyer-Olkin factor adequacy  
## Call: KMO(r = visfood.df)  
## Overall MSA = 0.7  
## MSA for each item =   
## Av. Speed (mm/s) Total Distance (mm) Av. Accel (mm/s^2)   
## 0.69 0.68 0.72   
## Mobility Rate (%) Exploration Rate (%) Time in Center (m:s)   
## 0.77 0.27 0.58   
## Tot. Time Frozen (m:s) Time near object (m:s)   
## 0.72 0.37

Pass.

cortest.bartlett(visfood.df)

## R was not square, finding R from data

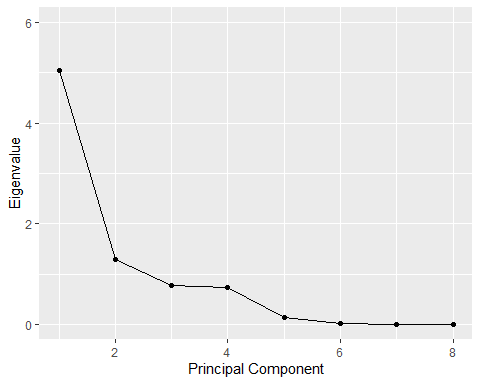
## $chisq  
## [1] 356.4438  
##   
## $p.value  
## [1] 1.259231e-58  
##   
## $df  
## [1] 28

Pass.

pca3 <- principal(visfood.df, nfactors = 2, rotate = "varimax")  
summary(pca3)

##   
## Factor analysis with Call: principal(r = visfood.df, nfactors = 2, rotate = "varimax")  
##   
## Test of the hypothesis that 2 factors are sufficient.  
## The degrees of freedom for the model is 13 and the objective function was 9.09   
## The number of observations was 22 with Chi Square = 147.02 with prob < 8.2e-25   
##   
## The root mean square of the residuals (RMSA) is 0.09

qplot(c(1:8), pca3$values) +  
 geom\_line() +  
 xlab("Principal Component") +  
 ylab("Eigenvalue") +  
 ylim(0,6)



2 PCs will be used.

Factor <- pca3$scores  
df <- cbind(visfood.df, Factor)  
ID <- visualfood$ID  
MicroTrtmt <- visualfood$MicroTrtmt  
df <- cbind(df, ID)  
df <- cbind(df, MicroTrtmt)  
df$MicroTrtmt = factor(df$MicroTrtmt)  
  
pca3$loadings

##   
## Loadings:  
## RC1 RC2   
## Av. Speed (mm/s) 0.986   
## Total Distance (mm) 0.987   
## Av. Accel (mm/s^2) 0.975   
## Mobility Rate (%) 0.963   
## Exploration Rate (%) 0.122 0.784  
## Time in Center (m:s) -0.518 -0.191  
## Tot. Time Frozen (m:s) -0.958   
## Time near object (m:s) -0.123 0.788  
##   
## RC1 RC2  
## SS loadings 5.042 1.287  
## Proportion Var 0.630 0.161  
## Cumulative Var 0.630 0.791

PCA1 = Speed, Distance, Accel, Mobility rate and total time frozen

PCA2 = Exploration Rate and Time near object

Cumulative 79% of variance explained

PC1.aov <- aov(RC1~MicroTrtmt, data = df)  
summary(PC1.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## MicroTrtmt 1 3.051 3.0514 3.4 0.0801 .  
## Residuals 20 17.949 0.8974   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

PC2.aov <- aov(RC2~MicroTrtmt, data = df)  
summary(PC2.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0.006 0.0062 0.006 0.94  
## Residuals 20 20.994 1.0497

Nothing of significance. All figures can be found in Visual Food Behavior.R script.

*Clear environment*

**Olfactory Behavior**

file.choose()

## [1] "C:\\R\\Emerson-Microbial-1\\EM1 Behavior.docx"

olfactory <- read\_csv("C:\\Users\\kjeme\\OneDrive\\Desktop\\Woodley Lab\\Aim 2 - Emerson Microbial 1\\Emersion Microbial Experiment 1 (2021)\\Data Project\\Emerson Microbial Exp1\_olfactory.csv")

## Rows: 22 Columns: 25  
## -- Column specification --------------------------------------------------------  
## Delimiter: ","  
## chr (5): ID, Mobility Rate (%), Visibility Rate (%), Invisibility Rate (%)...  
## dbl (14): MicroTrtmt, Av. Speed (mm/s), Mob. Av. Speed (mm/s), Av. Accel (m...  
## time (6): Visible Time (m:s), Invisible Time (m:s), Tot. Time Frozen (m:s),...  
##   
## i Use `spec()` to retrieve the full column specification for this data.  
## i Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

for (i in 2:ncol(olfactory)) {  
 if (str\_detect(olfactory[1,i],"%")) {  
 olfactory[,i] <-as.numeric(strsplit(c(olfactory[[i]]), "%"))  
 }  
}  
  
olfactory.df <- olfactory %>%  
 select(`Av. Speed (mm/s)`, `Total Distance (mm)`, `Av. Accel (mm/s^2)`, `Mobility Rate (%)`, `Exploration Rate (%)`, `Total Distance (mm)`, `Time in Center (m:s)`, `Tot. Time Frozen (m:s)`, `Exploration Rate (%)`, 'Time near cue (m:s)')  
  
olfactory.df$`Time in Center (m:s)`<- (as.numeric(olfactory.df$`Time in Center (m:s)`))/3600  
olfactory.df$`Tot. Time Frozen (m:s)`<- (as.numeric(olfactory.df$`Tot. Time Frozen (m:s)`))/3600  
olfactory.df$`Time near cue (m:s)`<- (as.numeric(olfactory.df$`Time near cue (m:s)`))/3600  
  
KMO(olfactory.df)

## Kaiser-Meyer-Olkin factor adequacy  
## Call: KMO(r = olfactory.df)  
## Overall MSA = 0.73  
## MSA for each item =   
## Av. Speed (mm/s) Total Distance (mm) Av. Accel (mm/s^2)   
## 0.73 0.71 0.78   
## Mobility Rate (%) Exploration Rate (%) Time in Center (m:s)   
## 0.79 0.87 0.51   
## Tot. Time Frozen (m:s) Time near cue (m:s)   
## 0.76 0.06

Pass.

cortest.bartlett(olfactory.df)

## R was not square, finding R from data

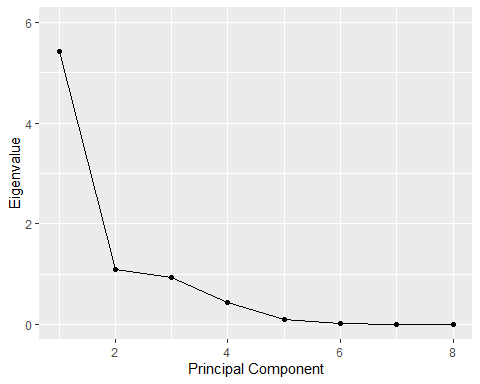
## $chisq  
## [1] 386.6084  
##   
## $p.value  
## [1] 1.013826e-64  
##   
## $df  
## [1] 28

Pass.

pca4 <- principal(olfactory.df, nfactors = 3, rotate = "varimax")  
summary(pca4)

##   
## Factor analysis with Call: principal(r = olfactory.df, nfactors = 3, rotate = "varimax")  
##   
## Test of the hypothesis that 3 factors are sufficient.  
## The degrees of freedom for the model is 7 and the objective function was 8.8   
## The number of observations was 22 with Chi Square = 136.42 with prob < 2.9e-26   
##   
## The root mean square of the residuals (RMSA) is 0.05

qplot(c(1:8), pca4$values) +  
 geom\_line() +  
 xlab("Principal Component") +  
 ylab("Eigenvalue") +  
 ylim(0,6)



3 fit.

Factor <- pca4$scores  
df <- cbind(olfactory.df, Factor)  
ID <- olfactory$ID  
MicroTrtmt <- olfactory$MicroTrtmt  
df <- cbind(df, ID)  
df <- cbind(df, MicroTrtmt)  
df$MicroTrtmt = factor(df$MicroTrtmt)  
  
pca4$loadings

##   
## Loadings:  
## RC1 RC3 RC2   
## Av. Speed (mm/s) 0.964 -0.219   
## Total Distance (mm) 0.964 -0.222   
## Av. Accel (mm/s^2) 0.950 -0.240   
## Mobility Rate (%) 0.967 -0.150   
## Exploration Rate (%) 0.708 0.312 0.386  
## Time in Center (m:s) -0.263 0.916   
## Tot. Time Frozen (m:s) -0.973 0.141   
## Time near cue (m:s) 0.966  
##   
## RC1 RC3 RC2  
## SS loadings 5.220 1.140 1.096  
## Proportion Var 0.652 0.142 0.137  
## Cumulative Var 0.652 0.795 0.932

PCA1 = Speed, Distance, Accel, Mobility rate, Exploaration Rate and total time frozen

PCA2 = Time in Center

PCA3 = Time Near Cue

Cumulative 93% of variance explained

PC1.aov <- aov(RC1~MicroTrtmt, data = df)  
summary(PC1.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 1.203 1.2033 1.216 0.283  
## Residuals 20 19.797 0.9898

PC2.aov <- aov(RC2~MicroTrtmt, data = df)  
summary(PC2.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0.038 0.0378 0.036 0.851  
## Residuals 20 20.962 1.0481

PC3.aov <- aov(RC3~MicroTrtmt, data = df)  
summary(PC3.aov)

## Df Sum Sq Mean Sq F value Pr(>F)  
## MicroTrtmt 1 0.782 0.7816 0.773 0.39  
## Residuals 20 20.218 1.0109

Nothing of significane. Overall, independent behavioral responses were not significantly effected by our treatments. Our next analysis will be to evaluate if/how tadpole behavioral responses to sensory stimuli differ from behavioral responses at baseline, again using PCA.