

Visualization of EEG Signals in MEDA

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Below is a set of visualizations using the MEDA library from NeuroData. Our data is a set of various observations (about 200,000) from a 128-channel EEG test.

```
subject_file <- "C:/Users/Ronak Mehta/Desktop/NeuroData/NDARAA075AMK_RestingState_data.csv"
first_obs_no <- 1
last_obs_no <- 100001
sep <- 50
```

Setting Variables and Ingesting Data

The following selects the columns to take from the ingested CSV. In this case, we take the first 100000 samples, and use every 50th data point to make these visualizations.

```
library(data.table, quietly = TRUE)
library(meda, quietly = TRUE)

## 
## -----
## Welcome to dendextend version 1.5.2
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## Or contact: <tal.galili@gmail.com>
##
## To suppress this message use: suppressPackageStartupMessages(library(dendextend))
## ----- 

## 
## Attaching package: 'dendextend'

## The following object is masked from 'package:data.table':
##   set

## The following object is masked from 'package:stats':
##   cutree

## 
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##   lowess

## Package 'mclust' version 5.3

## Type 'citation("mclust")' for citing this R package in publications.
```

```

## randomForest 4.6-12
## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:gridExtra':
##
##     combine

## The following object is masked from 'package:ggplot2':
##
##     margin

# Set the columns (observations) we want to take.
columns <- seq(first_obs_no, last_obs_no, sep)

# Set column names to the electrodes.
col_names <- rep("E", 128)
for (i in 1:length(col_names)) { col_names[i] <- paste(col_names[i], as.character(i), sep = "") }

# Ingest CSV of subject's data.
dat <- transpose(fread(input = subject_file,
                        sep = ",",
                        nrows = 128,
                        header = FALSE,
                        showProgress = TRUE,
                        select = columns,
                        data.table = FALSE))

##
Read 0.0% of 128 rows
Read 128 rows and 2001 (of 182086) columns from 0.158 GB file in 00:00:09
colnames(dat) <- col_names

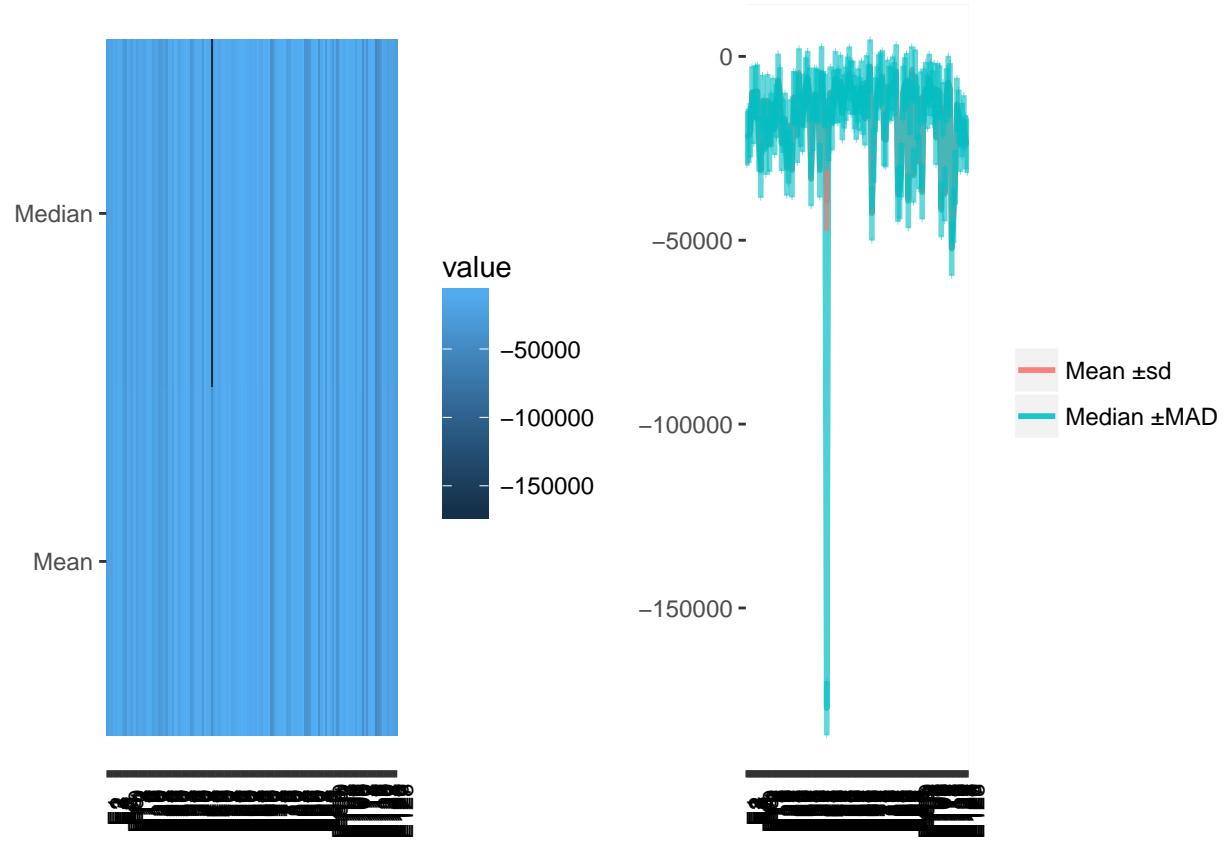
```

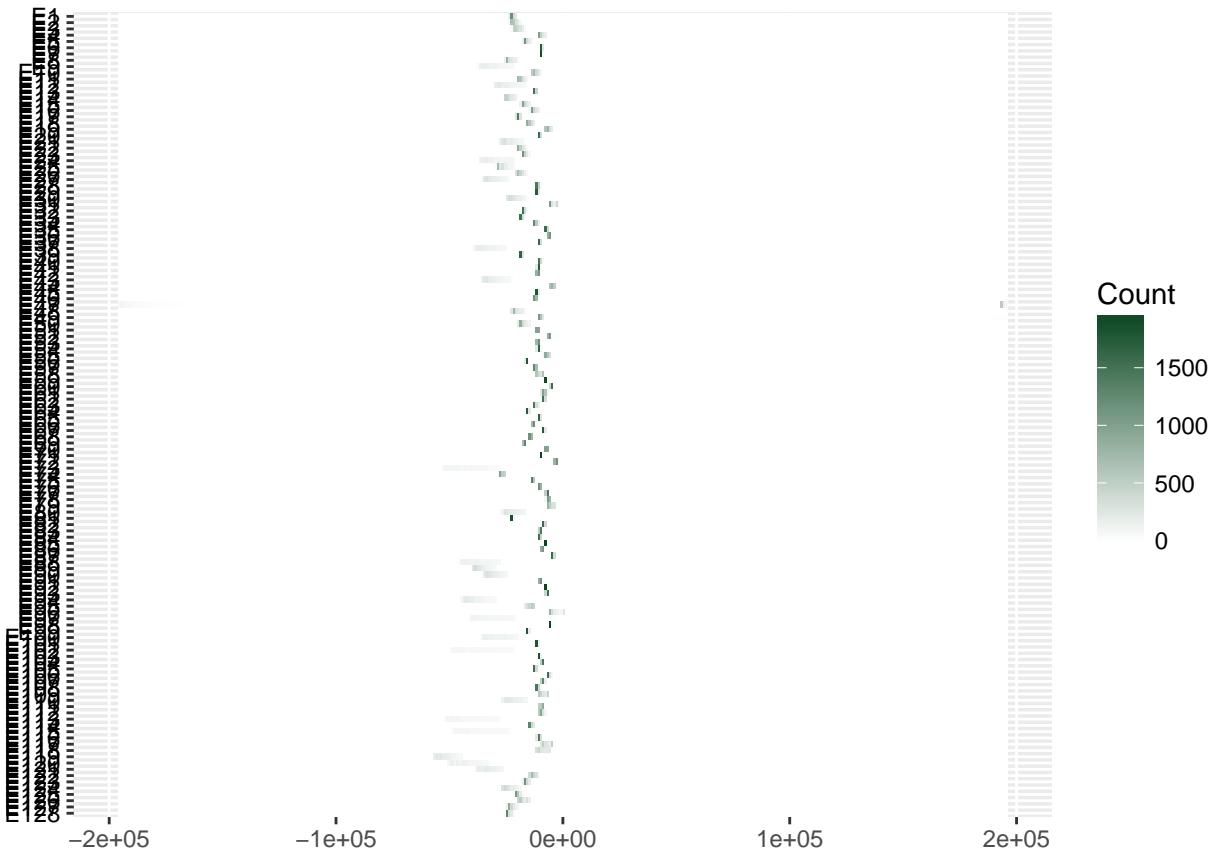
Plot Exploratory Analyses

Each plot is shown below.

Location Plots

```
plot(mlocation(dat))
```

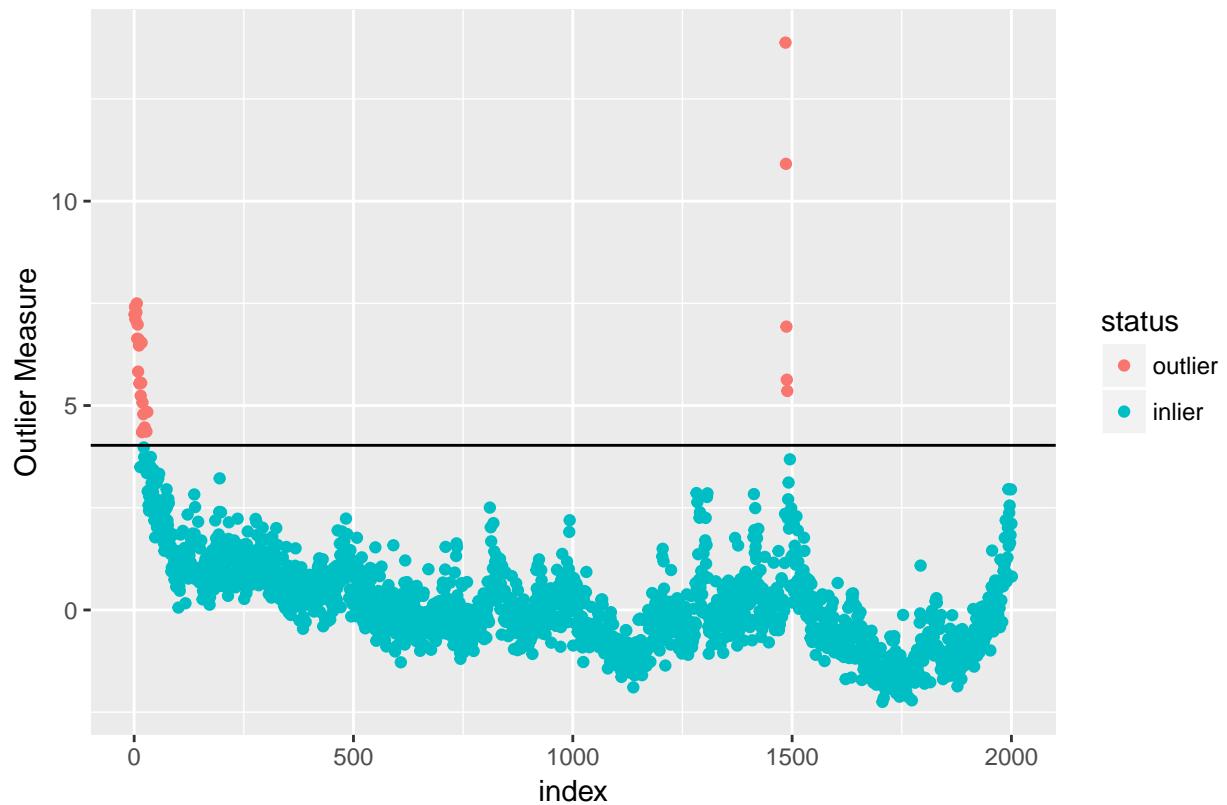




Outlier Plot

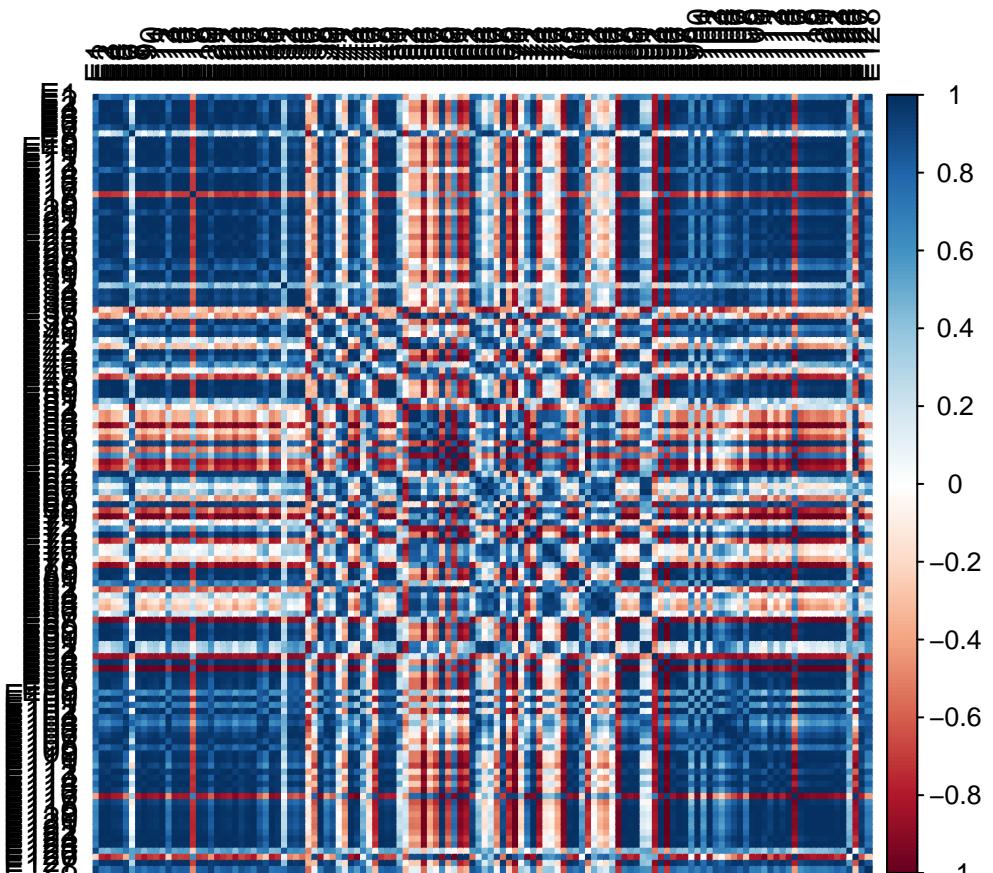
```
print(plot(outliers(dat)))
```

Outliers 3^*sd from mean



Correlation Matrix

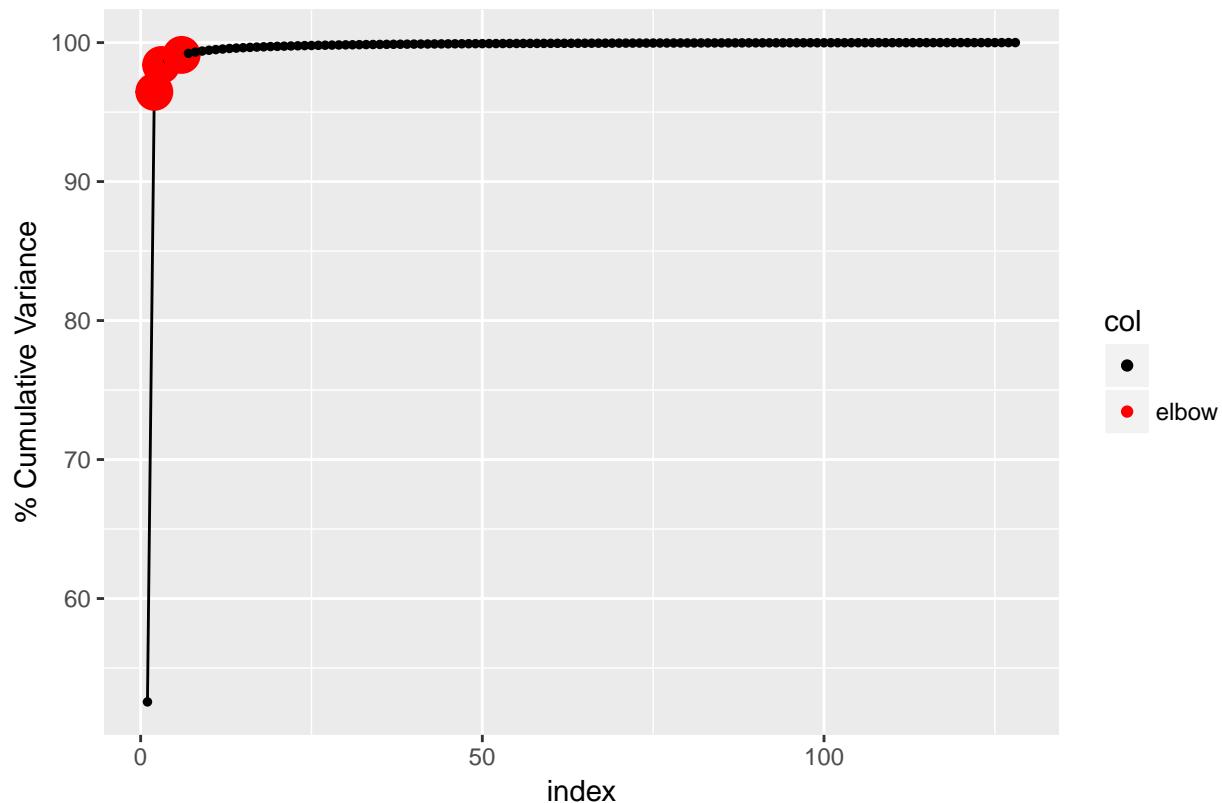
```
plot(medacor(dat))
```



Cumulative Variance Plot

```
print(plot(cumvar(dat)))
```

Cumulative Sum of variance in PC's

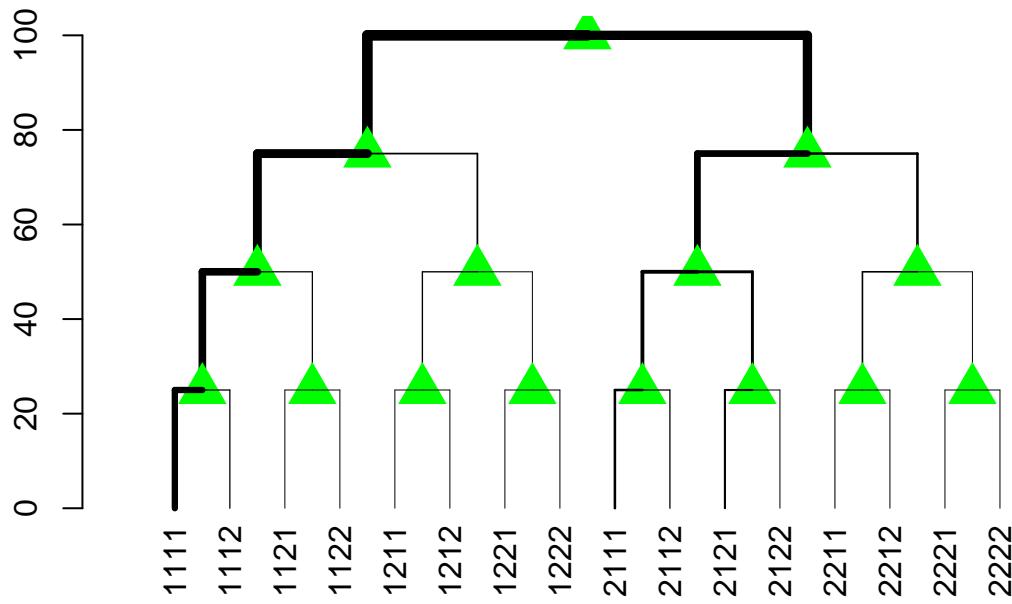


Fit Clusters with GMM

```
h <- hmc(dat)
```

Dendrogram

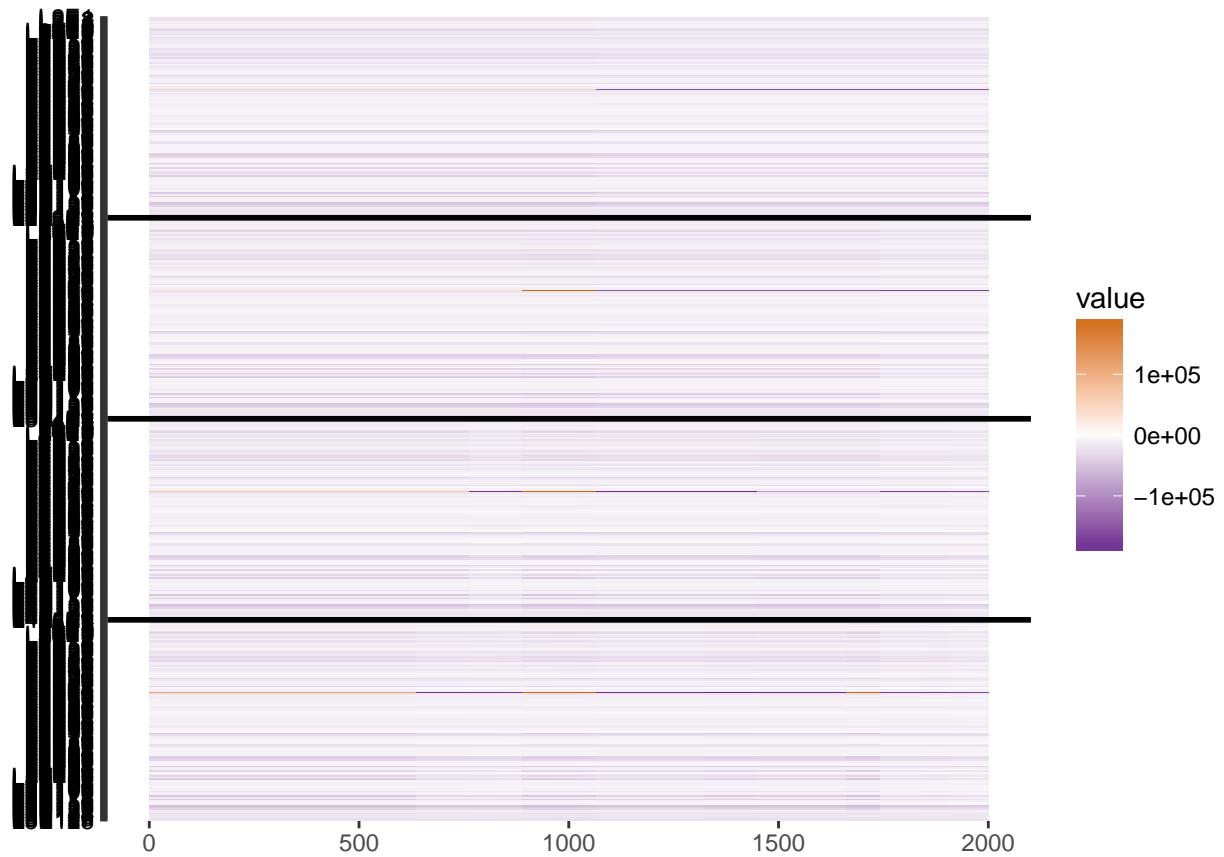
```
plotDend(h)
```



```
##   1111   1112   1121   1122   1211   1212   1221   1222   2111   2112
## 0.3173 0.0640 0.0335 0.0295 0.0390 0.0285 0.0120 0.0090 0.1279 0.0640
##   2121   2122   2211   2212   2221   2222
## 0.1059 0.0405 0.0535 0.0285 0.0275 0.0195
```

Stacked Cluster Means Plot

```
print(stackM(h, centered = TRUE))
```



Cluster Means

```
clusterMeans(h)
```

