Analysis of EEG Time Series

Ronak Mehta

October 9, 2017

The following runs Principal Component Analysis (PCA) on the time series of Subject 0's EEG signals from the Healthy Brain network.\

Required packages below, along with path to subject's CSV file.

```
require(stats)
require(data.table)
```

```
## Loading required package: data.table
```

```
subject_file <- "C:/Users/Ronak Mehta/Desktop/NeuroData/NDARAA075AMK_RestingState_data.csv"
knitr::opts_chunk$set(fig.width=8, fig.height=6)
```

Select Downsampling parameters

Input the first observation index, last observation index, and the separation between observations.

```
first_obs_no <- 1
last_obs_no <- 180001
sep <- 50
```

Ingest Data

The data ingests as a data frame with rows representing observations, and columns representing electrodes.

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

# Injest 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 3601 (of 182086) columns from 0.158 GB file in 00:00:09
```

```
# 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 = "") }
colnames(dat) <- col_names
```
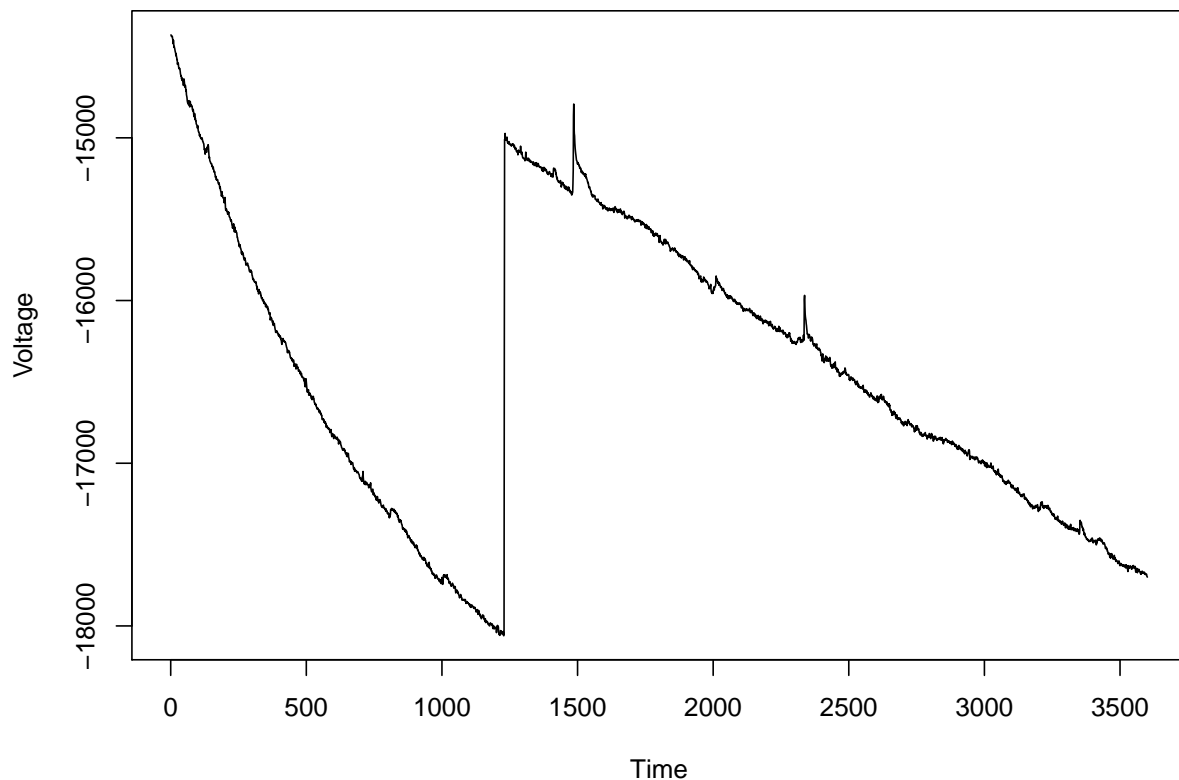
Plot Average Times Series

We take the average of each of the channels, and plot that time series. It hikes up aggressively at around observation $1250 \cdot 50 = 62500$.

```
avg.ts <- rowMeans(dat)

# Plot time series.
ts.plot(avg.ts, gpars = list(col = c("black")), ylab = "Voltage")
```
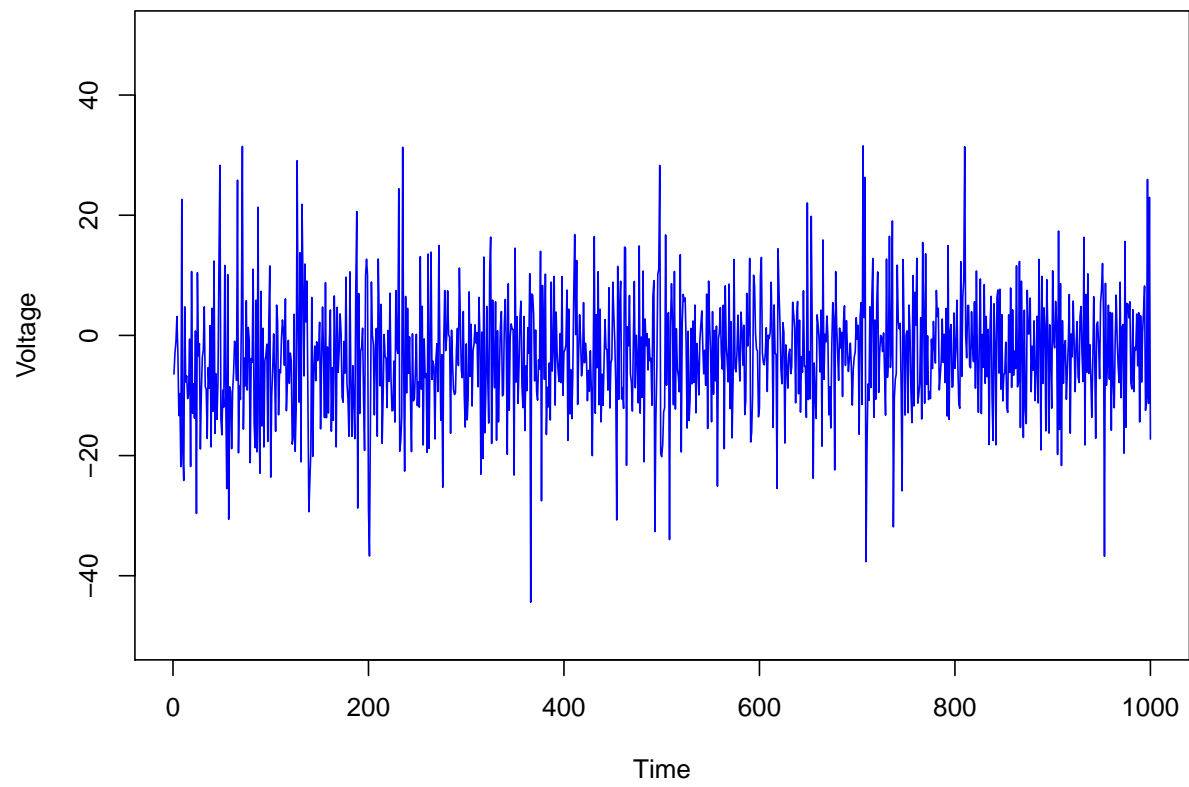

Analysis

We split the series into two pieces for analysis - the first 1000 observations above and the last 2000. We will also difference them both once. The second half of the EEG signal appears to follow an ARIMA(0, 1, 2) model.
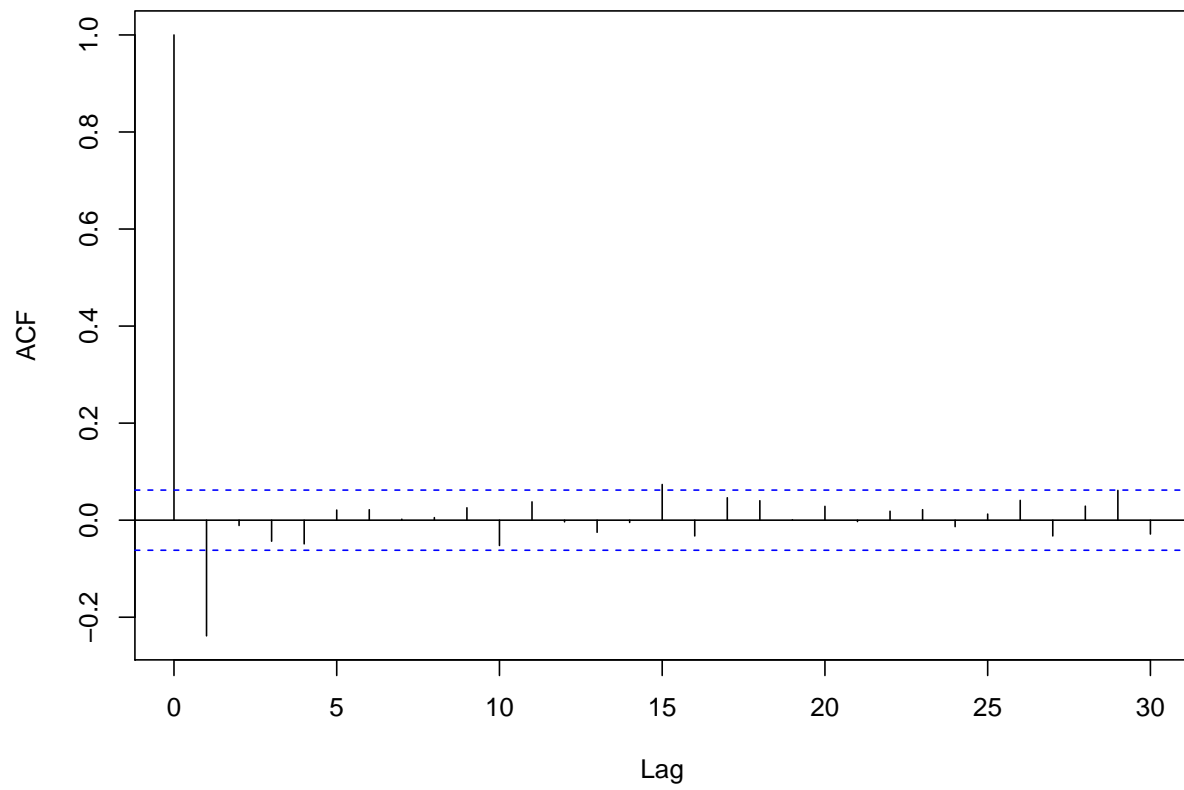
```
series1 <- avg.ts[2:1001] - avg.ts[1:1000]
series2 <- avg.ts[1502:3501] - avg.ts[1501:3500]

# First half
ts.plot(series1, gpars = list(col = c("blue")), ylab = "Voltage", ylim = c(-50, 50))
```
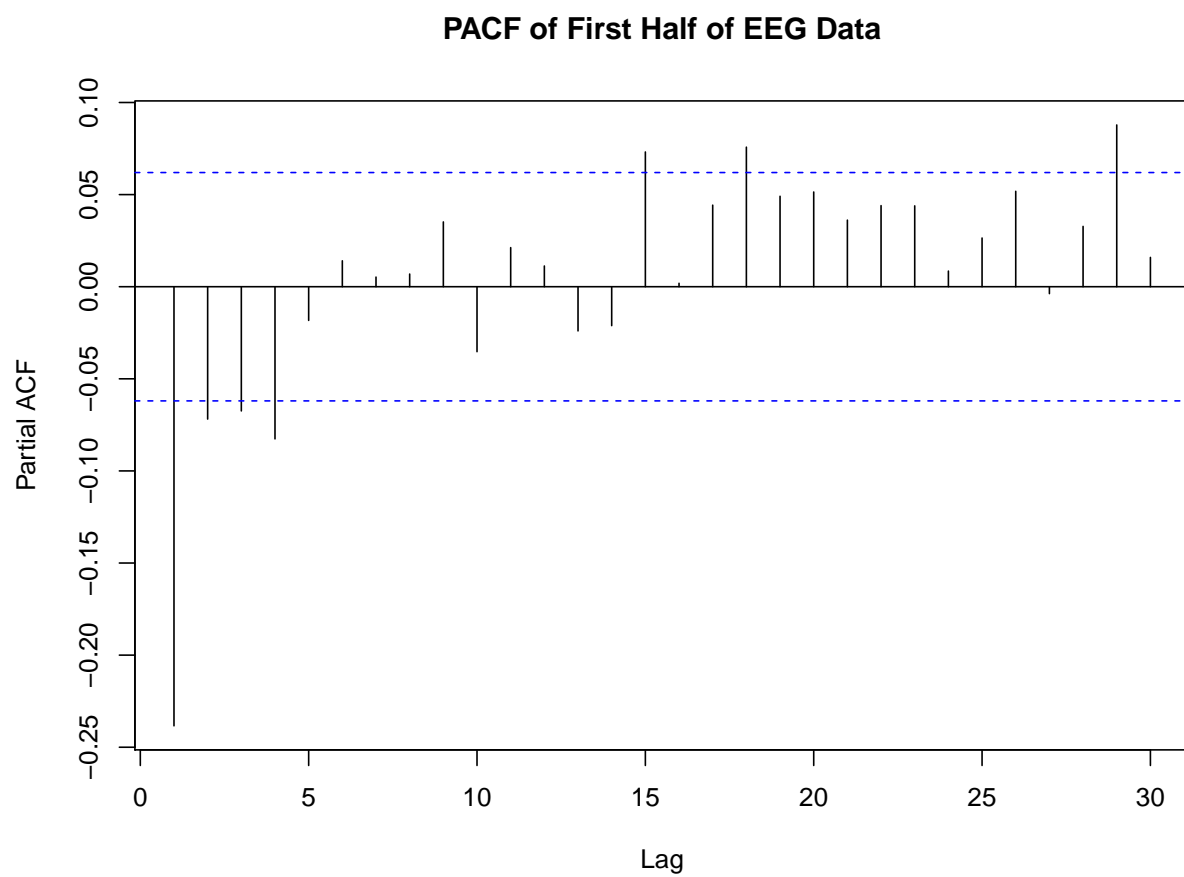
```
acf(series1, main = "ACF of First Half of EEG Data")
```
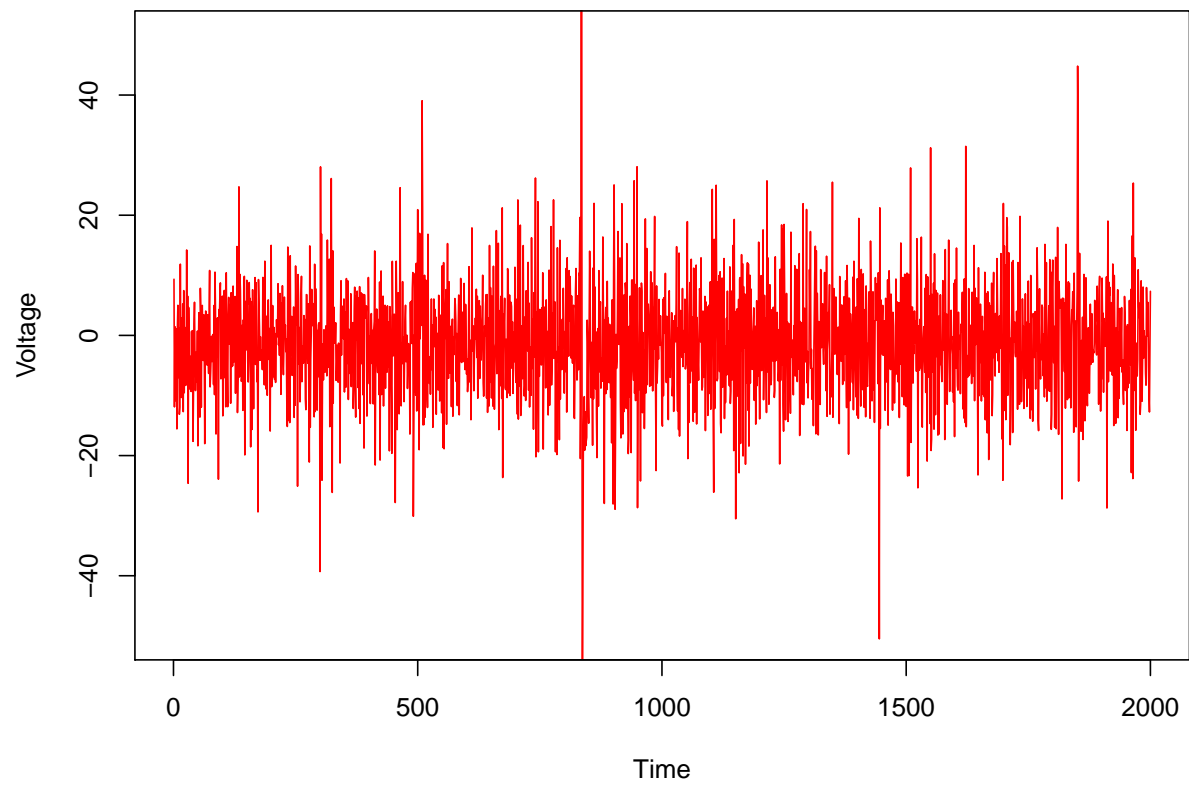
ACF of First Half of EEG Data


```r
pacf(series1, main = "PACF of First Half of EEG Data")
```
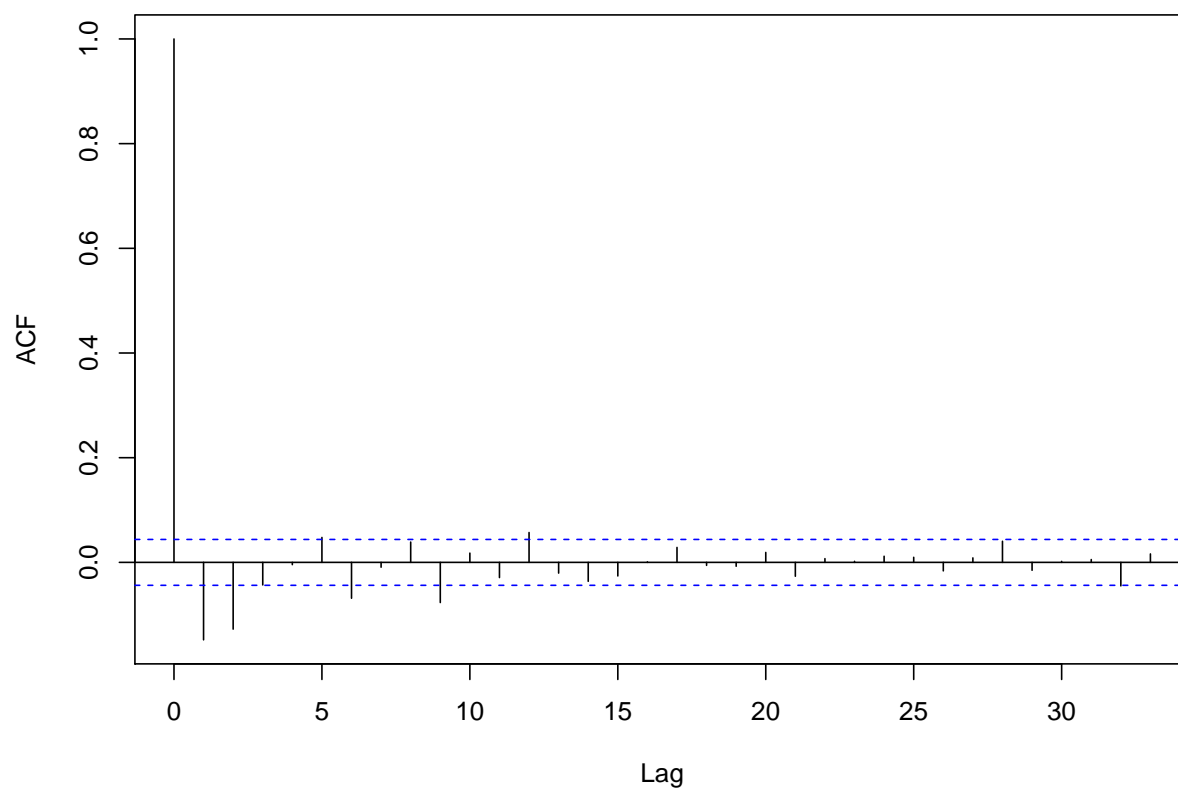
PACF of First Half of EEG Data


```r
# Second half
ts.plot(series2, gpars = list(col = c("red")), ylab = "Voltage", ylim = c(-50, 50))
```

```r
acf(series2, main = "ACF of Second Half of EEG Data")
```

ACF of Second Half of EEG Data


```
pacf(series2, main = "ACF of Second Half of EEG Data")
```

ACF of Second Half of EEG Data