

EM ALGORITHM

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2023-04-03

#PRACTICING EM ALGORITHM WITH FAMUSS DATASET

```
library(haplo.stats)
```

```
#READING IN FAMUSS DATA
```

```
fm <- read.delim("http://www.biostat.umn.edu/~cavanr/FMS_data.txt",header = T,  
                sep = "\t")
```

```
#Attach famuss datase
```

```
attach(fm)
```

```
head(fm)
```

```
Geno <- cbind(substr(actn3_r577x,1,1),substr(actn3_r577x,2,2),substr(actn3_1671064,1,1),substr(actn3_1671064,2,2))
```

```
head(Geno)
```

```
Geno_1 <- cbind(substr(actn3_r577x,1,1),substr(actn3_r577x,2,2),substr(actn3_1671064,1,1),substr(actn3_1671064,2,2))  
head(Geno_1)
```

```
SNPnames <- c("actn3_r577x","actn3_1671064","actn3_rs1815739","actn3_rs540874")
```

```
SNPname <- c("actn3_r577x","actn3_1671064")
```

```
##Subset African American and Caucasian and apply the haplo.emfunction to each group
```

```
Geno.C <- Geno[Race=="Caucasian" & !is.na(Race),]
```

```
dim(Geno.C)
```

```
Geno.D <- Geno_1[Race=="AfricanAm" & !is.na(Race),]
```

```
dim(Geno.D)
```

```
Geno.F <- Geno_1[Race=="Caucasian" & !is.na(Race),]
```

```
dim(Geno.F)
```

```
HaploEM <- haplo.em(Geno.C,locus.label = SNPnames,control = haplo.em.control(min.posterior = 1e-4))  
HaploEM
```

```
HPEM <- haplo.em(Geno.F,locus.label = SNPname,control = haplo.em.control(min.posterior = 1e-3))  
HPEM
```

```
str(HPEM)
```

```
str(HaploEM)
```

