Compare equilibrium solution with Berkeley Madonna output

Note, BM output is produced using 164 age categories and 5 heterogeneity categories. Same values and breaks are used here for equilibrium solution.

Title

```
Words
## Loading malariaModelFit
Text
# define treatment levels corresponding to BM output files
ft <- c("0.0", "0.2", "0.4")
# read in BM output as list
BM list <- list()
for (i in 1:length(ft)) {
 name <- paste0("BM_output/BM_ft",ft[i],".csv")</pre>
 BM_list[[i]] <- read.csv(malariaModelFit_file(name))</pre>
# get EIR range
EIR <- BM_list[[1]]$EIRY_eq</pre>
# load parameters
age <- default_age()</pre>
h <- gq_normal(5)
p <- load_parameters("parameters_Griffin2014.txt")</pre>
# save solution to list
eqList <- list()
for (i in 1:length(ft)) {
  eqList[[i]] <- list()
 for (j in 1:length(EIR)) {
      eqList[[i]][[j]] <- human_equilibrium_fast(EIR[j], as.numeric(ft[i]), p, age, h$nodes, h$weights)
}
# save state proportions in array
stateNames <- c("S", "T", "D", "A", "U", "P")
m <- array(0, dim=c(length(ft), length(EIR), length(stateNames)))</pre>
for (i in 1:length(eqList)) {
 for (j in 1:length(eqList[[i]])) {
    m[i,j,] <- colSums(subset(eqList[[i]][[j]]$states, select=stateNames))</pre>
}
```

Produce plots









