

This is a note for Golden Gate Association analysis

Producing an html table

```
output <-  
  matrix(paste("Content", LETTERS[1:16]),  
         ncol=4, byrow = TRUE)  
  
library(htmlTable)  
  
htmlTable(output,  
  header = paste(c("1st", "2nd",  
                   "3rd", "4th"), "header"),  
  rnames = paste(c("1st", "2nd",  
                   "3rd", "4th"), "row"),  
  rgroup = c("Group A",  
             "Group B"),  
  n.rgroup = c(2,2),  
  cgroup = c("Cgroup 1", "Cgroup 2&dagger;"),  
  n.cgroup = c(2,2),  
  caption="Basic table with both column spanners (groups) and row groups",  
  tfoot="&dagger; A table footer comment")
```

Basic table with both column spanners (groups) and row groups

Cgroup 1

Cgroup 2†

1st header

2nd header

3rd header

4th header

Group A

1st row

Content A

Content B

Content C

Content D

2nd row

Content E

Content F

Content G

Content H

Group B

3rd row

Content I

Content J

Content K

Content L

4th row

Content M

Content N

Content O

Content P

† A table footer comment

,

Table 1: Genotype case I

Disease-level	AA	AB	BB
Severe	SNPCnt	SNPCnt	SNPCnt
Mile	SNPCnt	SNPCnt	SNPCnt

Table 2: Genotype case II

Disease-level	AA	AB/BB
Severe	SNPCnt	SNPCnt
Mile	SNPCnt	SNPCnt

Table 3: Genotype case III

Disease-level	AA/AB	BB
Severe	SNPCnt	SNPCnt
Mile	SNPCnt	SNPCnt