

# R Notebook

```
library(dplyr)
library(tidyr)
library(zoo)
library(ggplot2)
library(ggpubr)
library(ggfortify)
library(SNFtool)
library(data.table)
library(RColorBrewer)
library(plyr)
library(vcd)
library(UpSetR)
library(MASS)
library(alluvial)
library(ggalluvial)
alluv_path<-"C:/Users/yangmu/Desktop/rosmap/SNF sample analysis/alluv_df"
```

```
rosmap_path<-'C:/Users/yangmu/Desktop/rosmap/'
dm <- read.csv(file.path(alluv_path,paste0('DM_limitby_DM','".csv"))', header = TRUE)
rd <- read.csv(file.path(alluv_path,paste0('RD_limitby_RD','".csv"))',header = TRUE)
regression <- read.csv("C:/Users/yangmu/Desktop/rosmap/SNF sample analysis/regression.csv",header = TRUE)
data_clinical <- read.csv(file.path(rosmap_path,'ROSMAP_clinical.csv'), header = TRUE)
id_map <- data_clinical %>%
  dplyr::select(projid,individualID)
```

```
rd2 <- rd %>%
  dplyr::select(individualID,clustnum4) %>%
  dplyr::rename(RD = clustnum4)
```

```
dm2 <- dm %>%
  dplyr::select(individualID,clustnum2) %>%
  dplyr::rename(DM = clustnum2)
```

```
#full <- inner_join(rd2,dm2,by='individualID')
regression <- inner_join(id_map,regression,by='projid')
full_rd <- inner_join(rd2,regression,by='individualID')
full_dm <- inner_join(dm2,regression,by='individualID')
```

```
table_rd <- full_rd %>%
  mutate(RD = as.factor(RD)) %>%
  dplyr::select(RD,cogn_global,cogn_ep,cogn_wo,cogn_se,cogn_ps,cogn_po,cogdx)

aggregate(table_rd[, 2:7], list(table_rd$RD), mean, na.rm = TRUE)
```

```
##   Group.1 cogn_global   cogn_ep   cogn_wo   cogn_se   cogn_ps   cogn_po
```

```
## 1      1 -1.1601446 -1.1231215 -0.8468974 -0.8956362 -1.1861746 -0.7575679
## 2      2 -0.5653810 -0.5245242 -0.4367454 -0.4139008 -0.7764982 -0.4971315
## 3      3 -0.6164584 -0.5182140 -0.4728472 -0.6135798 -0.8584988 -0.5789927
## 4      4 -0.5309078 -0.5055035 -0.3373664 -0.4436722 -0.6862958 -0.4043583
```

```
aggregate(table_rd[, 2:7], list(table_rd$RD), sd, na.rm = TRUE)
```

```
##   Group.1 cogn_global cogn_ep cogn_wo cogn_se cogn_ps cogn_po
## 1      1    1.1532693 1.279393 1.0553515 1.4464804 1.1170757 1.1494216
## 2      2    0.8849197 1.088210 0.9243917 0.9617066 1.0007020 0.8419403
## 3      3    1.0363878 1.246016 1.0993471 1.2357863 1.0265671 0.9928260
## 4      4    0.9326423 1.199131 0.8912385 0.9559748 0.8846688 0.9201179
```

```
#aggregate(table_rd[, 2:7], list(table_rd$RD), min, na.rm = TRUE)
prop.table(table(table_rd$RD, table_rd$cogdx), 1)
```

```
##
##           1           2           4
## 1 0.2321429 0.2232143 0.5446429
## 2 0.4000000 0.2750000 0.3250000
## 3 0.4045802 0.2290076 0.3664122
## 4 0.4000000 0.2916667 0.3083333
```

```
table_dm <- full_dm %>%
  mutate(DM = as.factor(DM)) %>%
  dplyr::select(DM, cogn_global, cogn_ep, cogn_wo, cogn_se, cogn_ps, cogn_po, cogdx)

aggregate(table_dm[, 2:7], list(table_dm$DM), mean, na.rm = TRUE)
```

```
##   Group.1 cogn_global cogn_ep cogn_wo cogn_se cogn_ps cogn_po
## 1      1 -0.4090796 -0.2662669 -0.3172296 -0.3041693 -0.7146063 -0.3893350
## 2      2 -1.1140947 -1.0358374 -0.8144658 -0.9508668 -0.9691761 -0.5846182
```

```
aggregate(table_dm[, 2:7], list(table_dm$DM), sd, na.rm = TRUE)
```

```
##   Group.1 cogn_global cogn_ep cogn_wo cogn_se cogn_ps cogn_po
## 1      1    0.8832735 1.143572 0.9513729 1.011504 0.9007242 0.9720903
## 2      2    1.2012151 1.215444 1.1328013 1.456797 1.1422293 1.1221704
```

```
#aggregate(table_rd[, 2:7], list(table_rd$RD), min, na.rm = TRUE)
prop.table(table(table_dm$DM, table_dm$cogdx), 1)
```

```
##
##           1           2           4
## 1 0.4000000 0.3040000 0.2960000
## 2 0.2564103 0.2393162 0.5042735
```

```
ad_rd <- full_rd %>%
  mutate(RD = as.factor(RD)) %>%
  dplyr::select(RD, amyloid_sqrt, plaq_d_sqrt, plaq_n_sqrt, tangles_sqrt, nft_sqrt, braaksc, ceradsc, ad_reagan)

aggregate(ad_rd[, 2:7], list(ad_rd$RD), mean, na.rm = TRUE)
```

```
##   Group.1 amyloid_sqrt plaq_d_sqrt plaq_n_sqrt tangles_sqrt nft_sqrt braaksc
## 1      1      2.105597  0.7674826  0.9040979    2.468629 0.7973091 3.830357
## 2      2      1.335488  0.6304238  0.6001180    1.984572 0.5952868 3.306250
## 3      3      1.342024  0.6287060  0.6252259    1.828202 0.5784934 3.213740
## 4      4      1.462643  0.7336623  0.6773674    2.171536 0.6479689 3.358333
```

```
aggregate(ad_rd[, 2:7], list(ad_rd$RD), sd, na.rm = TRUE)
```

```
##   Group.1 amyloid_sqrt plaq_d_sqrt plaq_n_sqrt tangles_sqrt nft_sqrt braaksc
## 1      1      1.069601  0.4681437  0.5439947    1.451831 0.4903970 1.192230
## 2      2      1.042706  0.5579470  0.5047969    1.215088 0.3609063 1.192201
## 3      3      1.027477  0.4928229  0.5230193    1.123906 0.3432236 1.196197
## 4      4      1.108642  0.5873949  0.5362538    1.489085 0.4184228 1.389007
```

```
prop.table(table(ad_rd$RD,ad_rd$ceradsc),1)
```

```
##
##           0           1
## 1 0.2321429 0.7678571
## 2 0.4312500 0.5687500
## 3 0.4122137 0.5877863
## 4 0.3916667 0.6083333
```

```
prop.table(table(ad_rd$RD,ad_rd$ad_reagan),1)
```

```
##
##           0           1
## 1 0.2410714 0.7589286
## 2 0.4437500 0.5562500
## 3 0.4503817 0.5496183
## 4 0.4416667 0.5583333
```

```
ad_dm <- full_dm %>%
  mutate(DM = as.factor(DM)) %>%
  dplyr::select(DM,amyloid_sqrt,plaq_d_sqrt,plaq_n_sqrt,tangles_sqrt,nft_sqrt,braaksc,ceradsc,ad_reagan)
aggregate(ad_dm[, 2:7], list(ad_dm$DM), mean, na.rm = TRUE)
```

```
##   Group.1 amyloid_sqrt plaq_d_sqrt plaq_n_sqrt tangles_sqrt nft_sqrt braaksc
## 1      1      1.438742  0.5837738  0.6018679    1.769848 0.5489566 3.168000
## 2      2      1.989873  0.7079551  0.8558030    2.612881 0.7896737 3.880342
```

```
aggregate(ad_dm[, 2:7], list(ad_dm$DM), sd, na.rm = TRUE)
```

```
##   Group.1 amyloid_sqrt plaq_d_sqrt plaq_n_sqrt tangles_sqrt nft_sqrt braaksc
## 1      1      1.167597  0.5018294  0.5191329    1.088652 0.3360359 1.318210
## 2      2      1.131080  0.4847638  0.5386746    1.499651 0.4653690 1.051783
```

```
prop.table(table(ad_dm$DM,ad_dm$apoe4),1)
```

```
##  
##           0           1  
##  1 0.8160000 0.1840000  
##  2 0.7008547 0.2991453
```

```
prop.table(table(ad_dm$DM,ad_dm$ad_reagan),1)
```

```
##  
##           0           1  
##  1 0.4880000 0.5120000  
##  2 0.2564103 0.7435897
```