NDMG Comparison

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```
library(ggplot2)
library(grid)
library(gridExtra)
library(reshape2)
library(data.table)
require(igraph)
require(scales)
```

Loading

```
ndmg.dwi.adj = as.matrix(read.csv('./ndmgd.csv', sep=",", header=FALSE))
derek.dwi.adj = as.matrix(read.csv('./natd.csv', sep=",", header=FALSE))
ndmg.func.adj = as.matrix(read.csv('./ndmgf.csv', sep=",", header=FALSE))
fmriprep.func.adj = as.matrix(read.csv('./fmriprep.csv', sep=",", header=FALSE))
colnames(ndmg.dwi.adj) <- as.character(seq(1, dim(ndmg.dwi.adj)[1]))
colnames(derek.dwi.adj) <- as.character(seq(1, dim(derek.dwi.adj)[1]))
colnames(ndmg.func.adj) <- as.character(seq(1, dim(ndmg.func.adj)[1]))
colnames(fmriprep.func.adj) <- as.character(seq(1, dim(fmriprep.func.adj)[1]))
diag(ndmg.dwi.adj) <- 0

ptr <- function(x) {
  nz <- x[x != 0]
  r <- rank(nz)*2/(length(nz) + 1)
  x[x != 0] <- r
  x <- (x - min(x))/(max(x) - min(x))
  return(x)
}

ndmg.dwi.adj <- ptr(ndmg.dwi.adj)
derek.dwi.adj <- ptr(derek.dwi.adj)
#ndmg.dwi.adj <- (ndmg.dwi.adj - min(ndmg.dwi.adj))/(max(ndmg.dwi.adj) - min(ndmg.dwi.adj))
#fmriprep.func.adj <- (fmriprep.func.adj - min(fmriprep.func.adj))/(max(fmriprep.func.adj) - min(fmripr
```

```
ndmg.dwi.dat <- melt(ndmg.dwi.adj)
derek.dwi.dat <- melt(derek.dwi.adj)
ndmg.func.dat <- melt(ndmg.func.adj)
fmriprep.func.dat <- melt(fmriprep.func.adj)
```

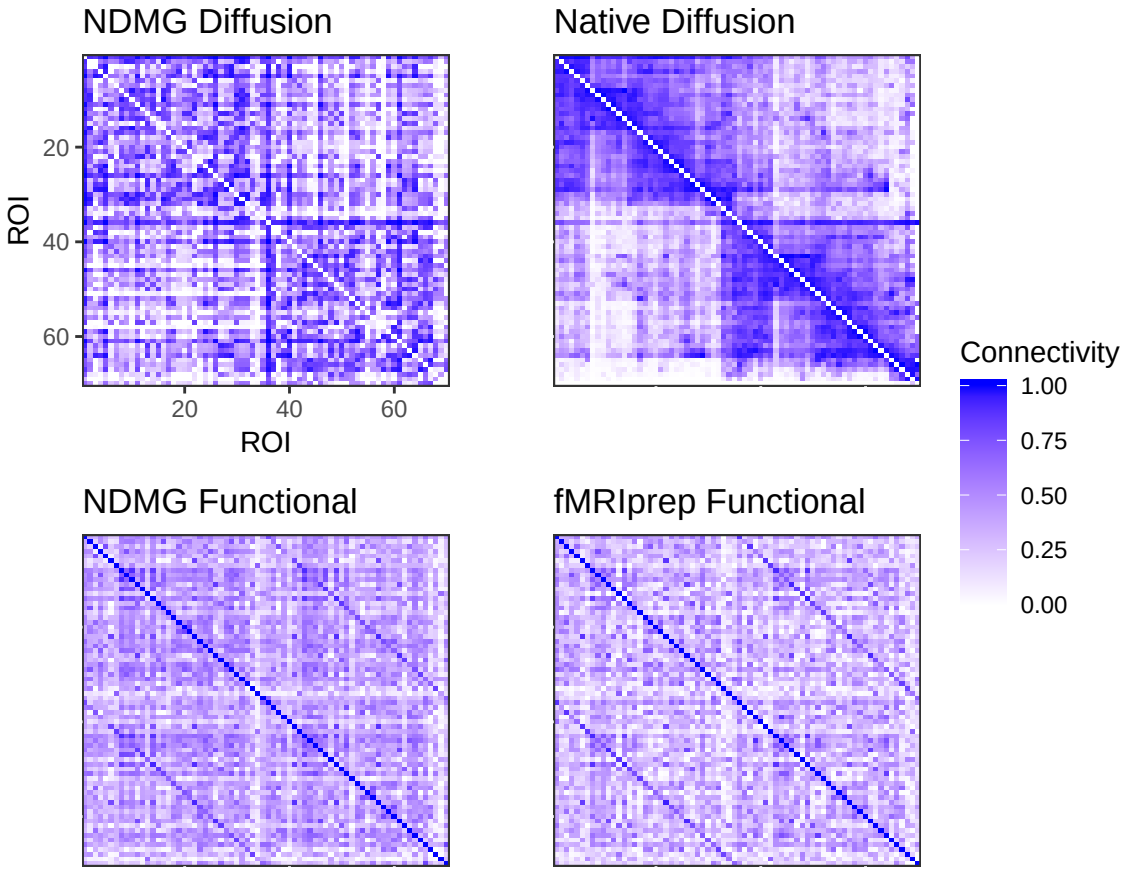
Plotting

```
titles=list("NDMG Diffusion", "Native Diffusion", "NDMG Functional", "fMRIprep Functional")
mtxs = list(ndmg.dwi.dat, derek.dwi.dat, ndmg.func.dat, fmriprep.func.dat)
```

```
plots = lapply(1:length(mtxs), function(i) {
  mtx = mtxs[[i]]
  ggplot(mtx, aes(x=Var1, y=Var2, fill=value)) +
    geom_tile() +
    scale_y_reverse(expand=c(0, 0)) +
    xlab("ROI") +
    ylab("ROI") +
    ggtitle(titles[[i]]) +
    scale_fill_gradient(name="Connectivity", low="white", high="blue") +
    theme_bw() +
    scale_x_continuous(expand=c(0, 0))
})
```

```
sim_leg <- g_legend(plots[[1]])
plots <- lapply(1:length(plots), function(i) {
  if (i != 1) {
    plots[[i]] <- plots[[i]] + theme(legend.position=NaN,
        axis.text.y=element_text(colour = 'white'),
        axis.ticks.y=element_line(colour = 'white'),
        axis.title.x=element_text(colour = 'white'),
        axis.title.y=element_text(colour = 'white'),
        axis.text.x=element_text(colour = 'white'),
        axis.ticks.x=element_line(colour = 'white'))
  }
  plots[[i]] <- plots[[i]] + guides(fill=FALSE)
})

grid.arrange(arrangeGrob(grobs=plots, nrow=2), sim_leg, ncol=2, widths=c(0.9, 0.2))
```


NDMG Diffusion
Native Diffusion
NDMG Functional
fMRIprep Functional
ROI
20
40
60
ROI
20
40
60
Connectivity
1.00
0.75
0.50
0.25
0.00