

MGC on PFactor

Vidur Kailash

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Created 2 random 5x5 matrices to test MGC to make sure it was working properly.

```
require(mgc)

## Loading required package: mgc
## Loading required package: SDMTools

X <- matrix(abs(runif(25)), ncol=5)
X <- upper.tri(X)*X; X <- X + t(X)
X

##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 0.0000000 0.91958045 0.82766779 0.46801736 0.9513645
## [2,] 0.9195805 0.00000000 0.39243113 0.01631873 0.9276307
## [3,] 0.8276678 0.39243113 0.00000000 0.01863992 0.8695778
## [4,] 0.4680174 0.01631873 0.01863992 0.00000000 0.8520979
## [5,] 0.9513645 0.92763072 0.86957777 0.85209787 0.0000000

Y <- matrix(abs(runif(25)), ncol=5)
Y <- upper.tri(Y)*Y; Y <- Y + t(Y)
Y

##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 0.0000000 0.6485027 0.6416070 0.4714865 0.4764098
## [2,] 0.6485027 0.0000000 0.7917895 0.6632409 0.5978392
## [3,] 0.6416070 0.7917895 0.0000000 0.3137999 0.3285329
## [4,] 0.4714865 0.6632409 0.3137999 0.0000000 0.9927310
## [5,] 0.4764098 0.5978392 0.3285329 0.9927310 0.0000000

res <- mgc.test(X,Y)
print(res$statMGC)

## [1] 0.4250802
```

Since MGC requires 2 nxn distance matrices to inputted, I did the following caluculations on the pfactor data and the connectome data to get the input data in usaable form.

I found 5 patients with realtively high p factor vlaues. I found the pairwise distacnes of each and created a 5x5 matrix with the results and called that matrix 'x'.

I then got the corresponding connectomes from ndmg output (using the connectomes from the desikan poarcellation). I converted the connectomes into numpy matrices (shown in

jupyter notebook) and found the frobenius norm of the distance matrices. This became the second 5x5 distance matrix.

I then ran MGC on the 2 nxn matrices and got a statMGC value of -0.2202395.

```
require(mgc)
require(ggplot2)

## Loading required package: ggplot2

require(latex2exp)

## Loading required package: latex2exp

x = matrix( c(0, 0.0134725, 0.33970251, 0.647503, 0.0656137, 0.0134725, 0, 0.
353175, 0.6609755, 0.0790862, 0.33970251, 0.353175, 0, 0.3078005, 0.27408879,
0.647503, 0.6609755, 0.3078005, 0, 0.58188927, 0.0656137, 0.0790862, 0.274088
79, 0.58188927, 0), nrow=5, ncol=5)
x

##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 0.0000000 0.0134725 0.3397025 0.6475030 0.0656137
## [2,] 0.0134725 0.0000000 0.3531750 0.6609755 0.0790862
## [3,] 0.3397025 0.3531750 0.0000000 0.3078005 0.2740888
## [4,] 0.6475030 0.6609755 0.3078005 0.0000000 0.5818893
## [5,] 0.0656137 0.0790862 0.2740888 0.5818893 0.0000000

y = matrix( c(0, 21.0134223, 16.49268088, 23.9195127, 19.01896152, 21.0134223
, 0, 11.0393952, 12.62081885, 10.5266986, 16.49268088, 11.0393952, 0, 14.5288
314, 10.7402878, 23.9195127, 12.62081885, 14.5288314, 0, 12.42300484, 19.0189
6152, 10.5266986, 10.7402878, 12.42300484, 0), nrow=5, ncol=5)
y

##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 0.00000 21.01342 16.49268 23.91951 19.01896
## [2,] 21.01342 0.00000 11.03940 12.62082 10.52670
## [3,] 16.49268 11.03940 0.00000 14.52883 10.74029
## [4,] 23.91951 12.62082 14.52883 0.00000 12.42300
## [5,] 19.01896 10.52670 10.74029 12.42300 0.00000

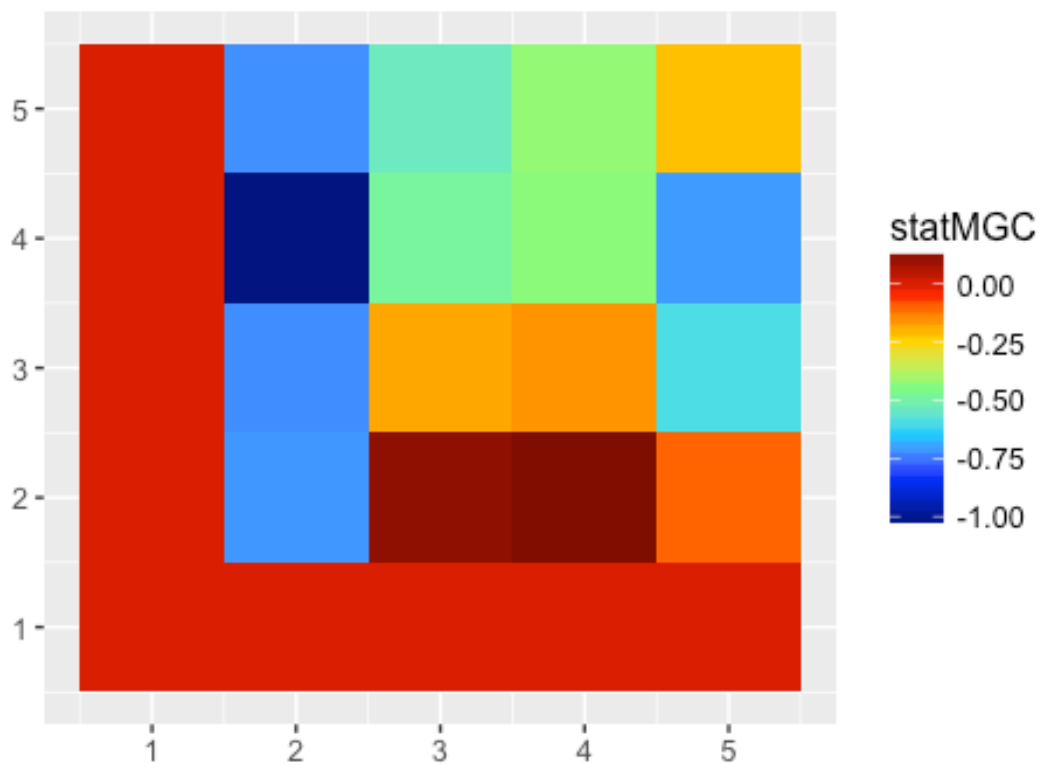
mgc.test(x, y)

## $pMGC
## [1] 0.706
##
## $statMGC
## [1] -0.2202395
##
## $pLocalCorr
##           [,1] [,2] [,3] [,4] [,5]
## [1,]      1 1.000 1.000 1.000 1.000
## [2,]      1 1.000 0.982 1.000 0.942
```

```
## [3,] 1 0.627 0.855 1.000 0.822
## [4,] 1 0.549 0.767 0.991 0.745
## [5,] 1 0.535 0.971 1.000 0.706
##
## $localCorr
##      [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 0 0.0000000 0.0000000 0.0000000 0.0000000
## [2,] 0 -0.7115987 -0.7233131 -1.0242553 -0.7189781
## [3,] 0 0.1118481 -0.1849661 -0.4852445 -0.5364851
## [4,] 0 0.1380807 -0.1593607 -0.4320417 -0.4226489
## [5,] 0 -0.1023249 -0.5943204 -0.7069746 -0.2202395
##
## $optimalScale
## [1] 25

res <- mgc.test(x,y)
mgc.plot.plot_matrix(res$localCorr, title = TeX("MGC Corr Map, Pfactor and Co
nnectomes"), legend.name=TeX("statMGC"))
```

MGC Corr Map, Pfactor and Connectomes



```
print(res$optimalScale)
```

```
## [1] 25
```

```
print(res$statMGC)
```

```
## [1] -0.2202395
```