

brain network

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1. Importing the Dataset

The dataset depend on the right brain and left brain. The problem is to evaluate the dependency between the cortical region.

```
knitr::opts_chunk$set(echo = TRUE)

#####Importing the Data#####

data=load("~/Sapienza Learning Materials/SDS 1 Homework/sdshw2/hw2_data.RData")
data=mts
D=ncol(data)
n=nrow(data)
```

2. Application of simultaneous bootstrapped confidence intervals for a generic association measure row

```
knitr::opts_chunk$set(echo = TRUE)

#####simultaneous bootstrapped confidence intervals for a generic association measure row#####

#Correlation matrix

R_cap=cor(data)

# Dimension of the correlation matrix
dim(cor(data))

## [1] 81 81

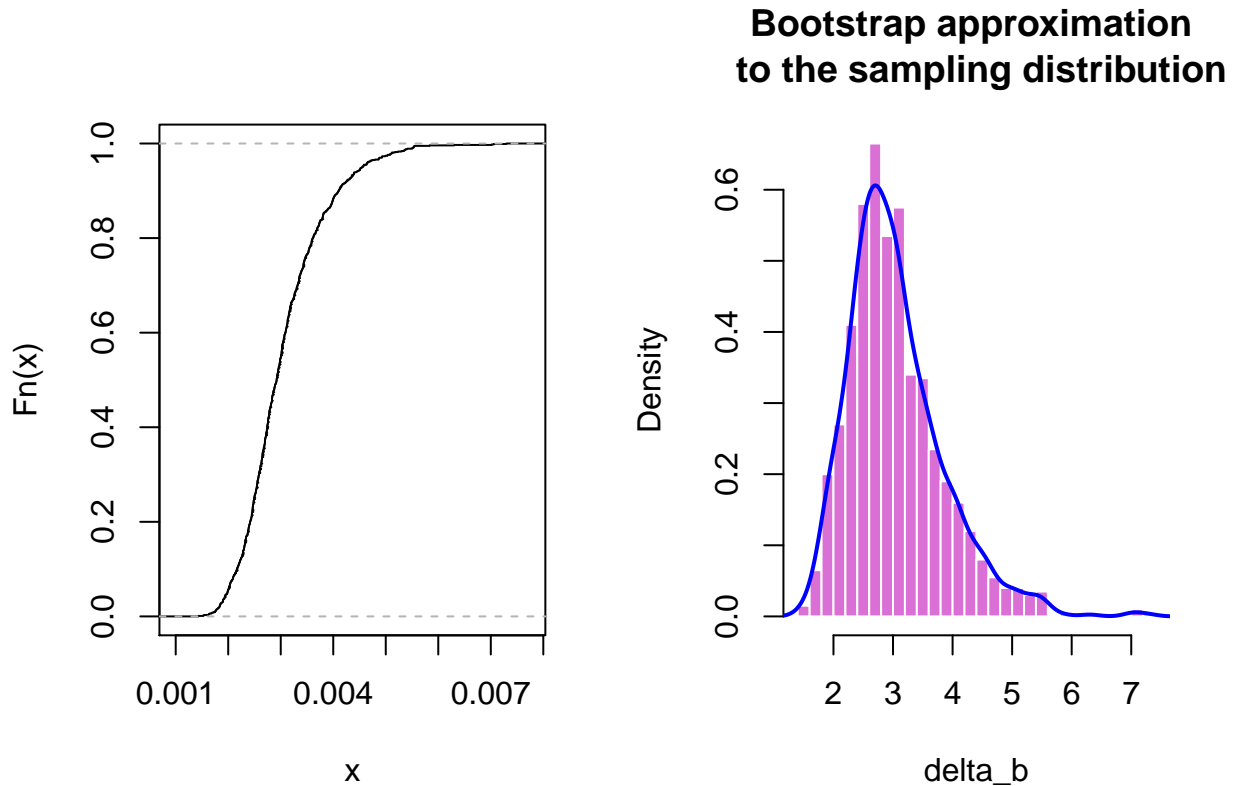
# Number of bootstraps
B = 1000
delta_b = rep(NA, B)

for (b in 1:B){
  idx = sample(1:n, replace = T)
  bsamp = data[idx,]          # bootstrap sample
  R_star = cor(bsamp)         # save
  delta_b[b] = sqrt(n)*(max(abs(R_star-R_cap)))
}

# Bootstrap ECDF > G*(t)

Gstar = ecdf((1/B)*(delta_b))
par(mfrow=c(1,2))
plot(Gstar, main = "")
```

```
hist(delta_b,prob=TRUE, breaks = 25, col = "orchid", border = "white",
      main = "Bootstrap approximation \n to the sampling distribution")
lines(density(delta_b), col="blue", lwd=2) # add a density estimate with defaults
```



```
knitr::opts_chunk$set(echo = TRUE)

# Bootstrap standard error
se_boot <- sqrt(var(delta_b))
se_boot

## [1] 0.7994819

# Bootstrap / CI / 95%
alpha=0.05
t_alpha <- quantile(delta_b, 1-alpha)
t_alpha

##          95%
## 4.544401

lb=R_cap-(t_alpha/sqrt(n))
ub=R_cap+(t_alpha/sqrt(n))

# Write the function
R_mat=function(epsilon){
```

```

Pmatrix = (lb>epsilon)+(ub< -(epsilon))
Pmatrix
sig_values=which(Pmatrix==1, arr.in= TRUE)
# code to get the desired rowname and colname
data1 <- data.frame(matrix(ncol = 3))
x <- c('from','to' , "Correlation")

i<-1
#data1=data.frame(p1=character(),p2=character(),p3)
while (i <= nrow(sig_values)){
  data1<-rbind(data1,c(rownames(R_cap)[sig_values[i,1]],colnames(R_cap)[sig_values[i,2]],
    R_cap[sig_values[i,1],sig_values[i,2]]))
  i<-i+1
}

colnames(data1) <- x

data1<-data1[-1,]
data1$Correlation <- as.numeric(as.character(data1$Correlation))
return(data1)
}
table=R_mat(0.69)
head(table)

##   from to Correlation
## 2   1R 1R   1.0000000
## 3   2R 2R   1.0000000
## 4   3R 2R   0.9894943
## 5   6R 2R   0.9839382
## 6   8R 2R   0.9865838
## 7  24R 2R   0.9921027

knitr::opts_chunk$set(echo = TRUE)

```

3. Graph Analysis

The below graph shows the connectivity between different portions of our brain. Here, the value of epsilon=0.69 and the connectivity between the hemisphere is clear and specific.

```

knitr::opts_chunk$set(echo = TRUE)

##### Plot the data #####
library(ggraph)
library(igraph)

only_sig <- table[abs(table$Correlation) !=1, ]
new_g <- graph_from_data_frame(only_sig, F)

correlation = cut_number((only_sig$ "Correlation"), 4)
col = c("#E1AF00", "#EBCC2A", "#78B7C5", "#3B9AB2")
names(col) = levels(correlation)
ggraph(new_g, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col=correlation))+
  geom_node_point() +

```

```
geom_node_text(aes(label = name), repel=TRUE)+
geom_
```

```
## Error in eval(expr, envir, enclos): object 'geom_' not found
```

```
knitr::opts_chunk$set(echo = TRUE)
```

3.1 Graph analysis at $\epsilon=0.40$ and $\epsilon=0.55$

As the value of epsilon decreases the connectivity of between and within hemisphere increases.

```
knitr::opts_chunk$set(echo = TRUE)
```

```
table=R_mat(0.40)
head(table)
```

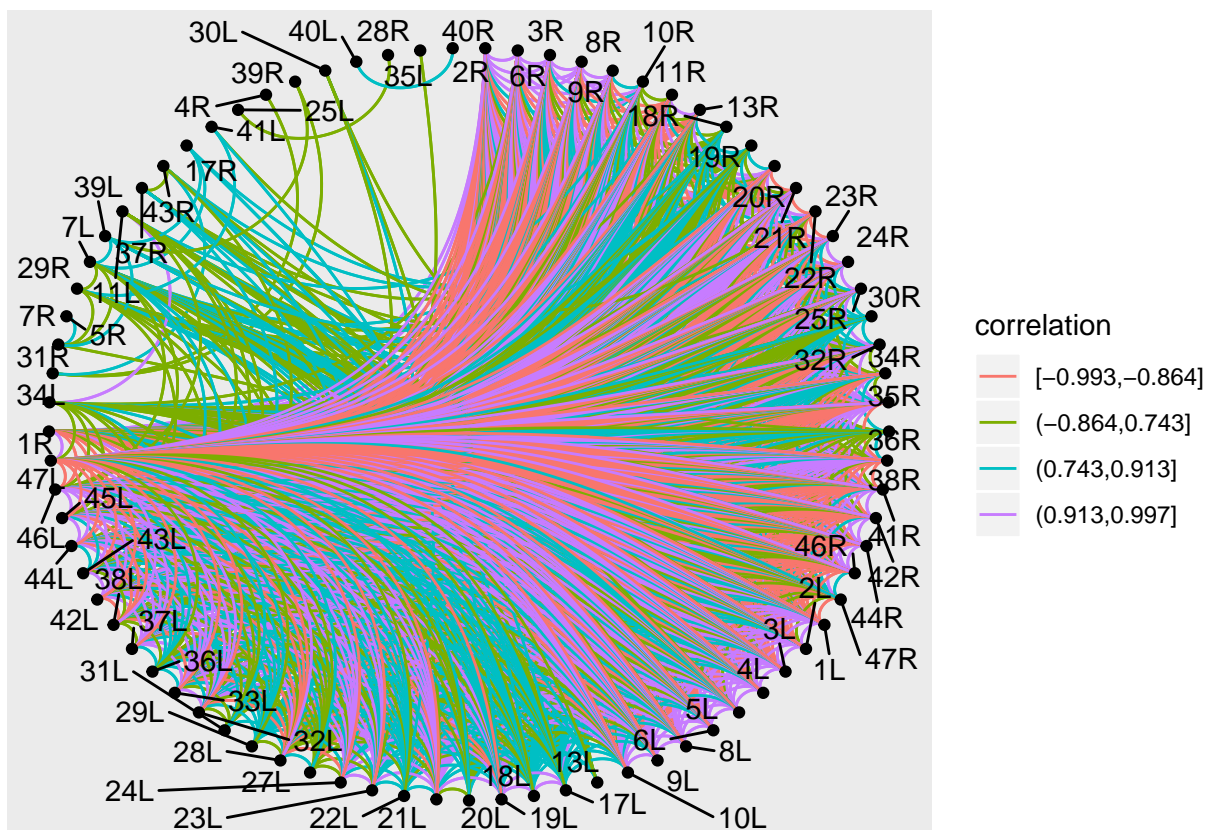
```
##   from to Correlation
## 2   1R 1R   1.0000000
## 3   2R 1R   0.9787156
## 4   3R 1R   0.9686066
## 5   6R 1R   0.9637880
## 6   8R 1R   0.9602842
## 7   9R 1R   0.9465585
```

```
##### Plot the data #####
```

```
only_sig <- table[abs(table$Correlation) !=1, ]
new_g <- graph_from_data_frame(only_sig, F)
```

```
correlation = cut_number((only_sig$ "Correlation"), 4)
col = c("#E1AF00", "#EBCC2A", "#78B7C5", "#3B9AB2")
names(col) = levels(correlation)
```

```
ggraph(new_g, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col=correlation))+
  geom_node_point() +
  geom_node_text(aes(label = name), repel=TRUE)
```



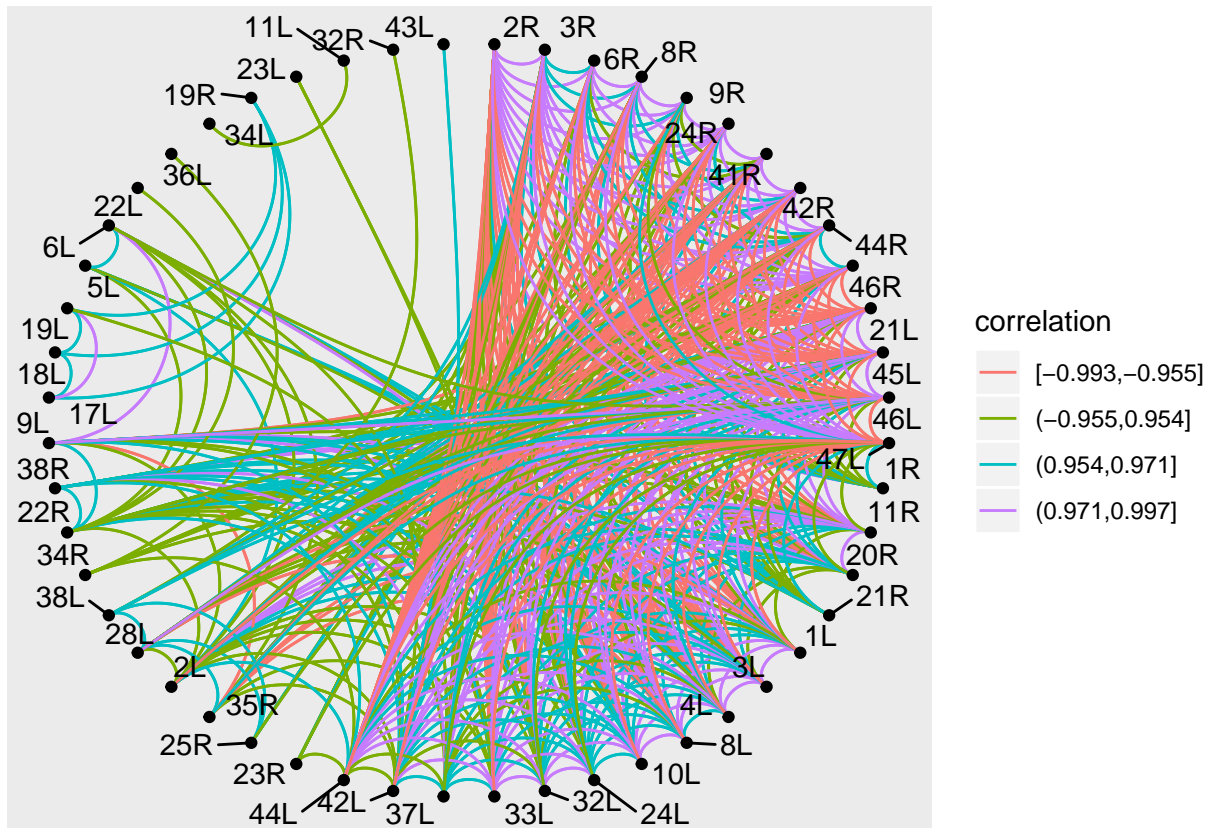
```
table=R_mat(0.65)
head(table)

##   from to Correlation
## 2   1R 1R   1.0000000
## 3   2R 1R   0.9787156
## 4   3R 1R   0.9686066
## 5   6R 1R   0.9637880
## 6   8R 1R   0.9602842
## 7   9R 1R   0.9465585

##### Plot the data #####

only_sig <- table[abs(table$Correlation) !=1, ]
new_g <- graph_from_data_frame(only_sig, F)

correlation = cut_number((only_sig$ "Correlation"), 4)
col = c("#E1AF00", "#EBCC2A", "#78B7C5", "#3B9AB2")
names(col) = levels(correlation)
ggraph(new_g, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col=correlation))+
  geom_node_point() +
  geom_node_text(aes(label = name), repel=TRUE)
```



```
knitr::opts_chunk$set(echo = TRUE)
```

Remarks

In this case we've used the pearson correlation method. The connectivity amongst the hemisphere and the value of the epsilon are inversely related. As the value of epsilon increases the connectivity between the hemisphere decreases and with the small value of epsilon the connectivity between the hemisphere is more. Moreover, if the value of the epsilon is really high, there exists no connectivity between and within the hemisphere.

4. Consider the partial correlation: Performing the same task using SIN package

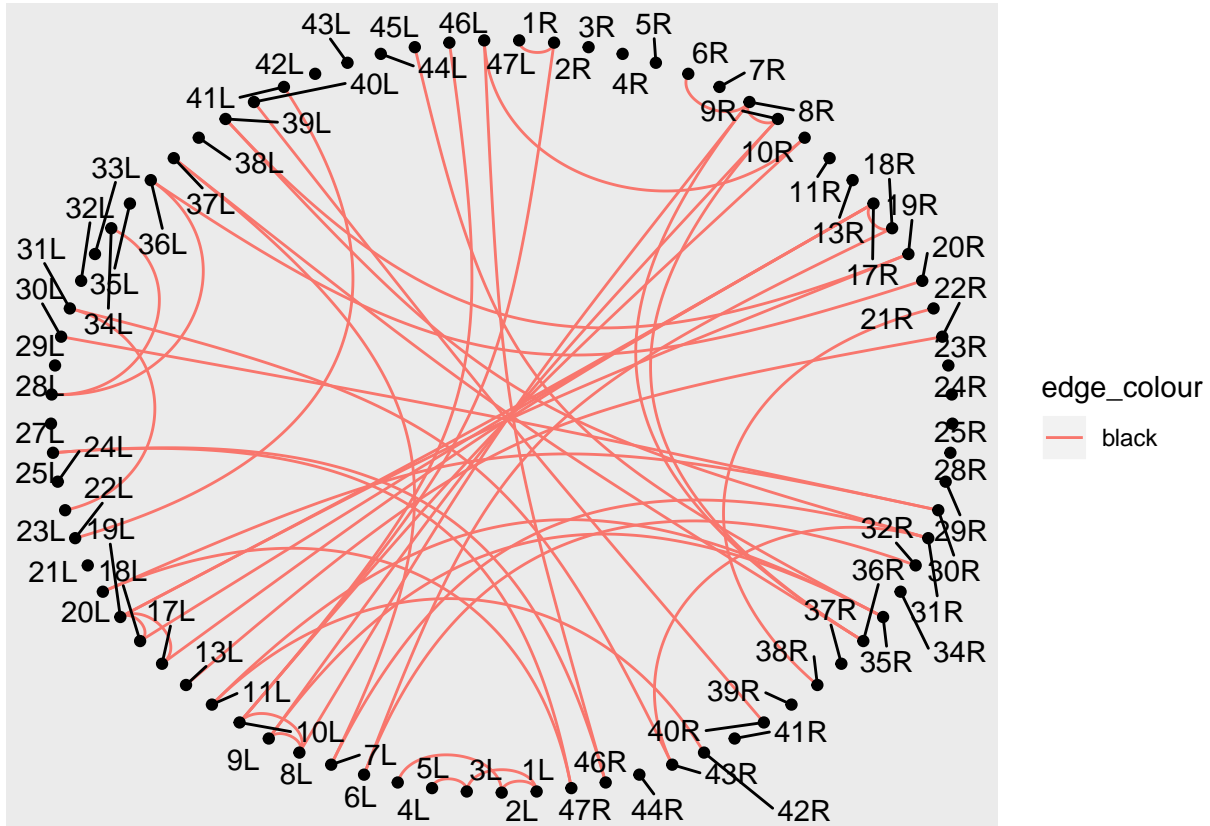
```
knitr::opts_chunk$set(echo = TRUE)

##### Partial Correlation#####

library(SIN)
out=sinUG(R_cap,nrow(data))
par(mfrow = c(1,2))
alpha = 0.05
E.SIN = getgraph(out, alpha)

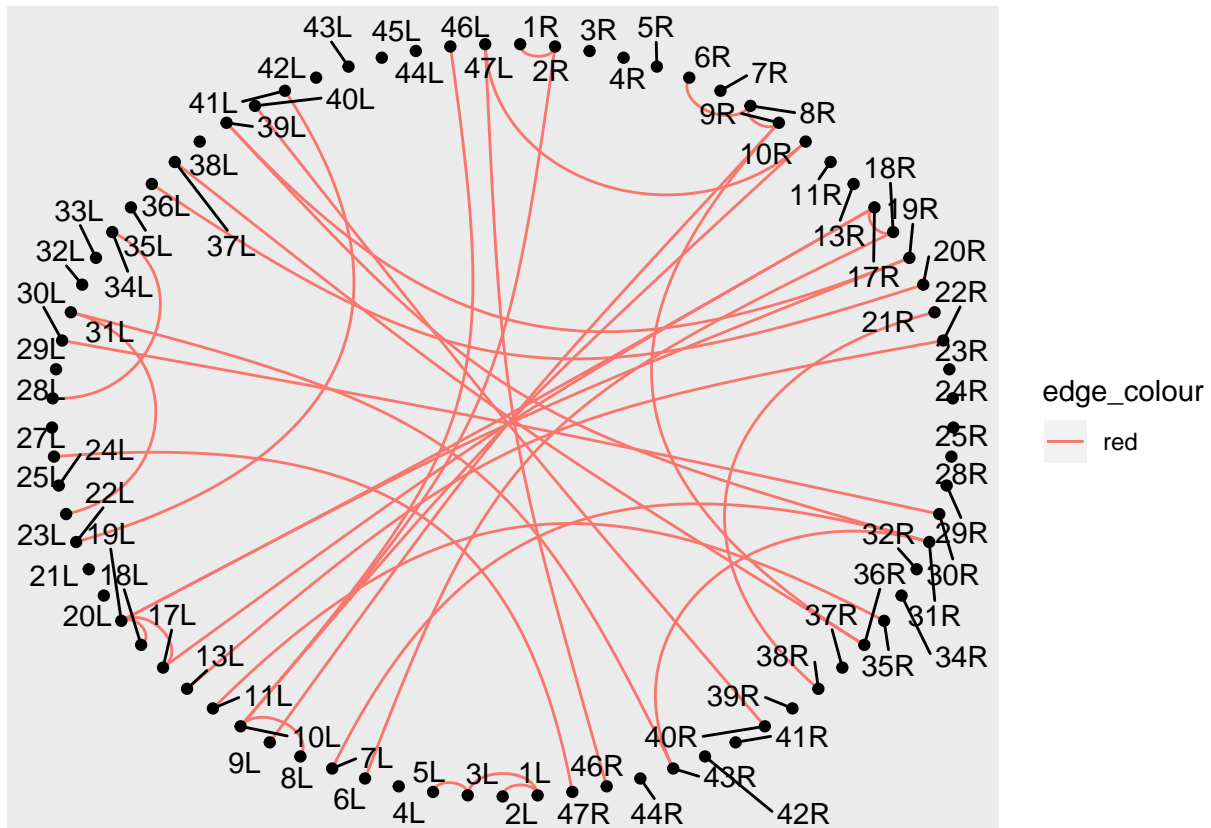
G.SIN = graph.adjacency(E.SIN, mode = "undirected")
```

```
ggraph(G.SIN, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col= 'black'))+
  geom_node_point() +
  geom_node_text(aes(label = name), repel=TRUE)
```



```
alpha = 0.01
E.SIN = getgraph(out, alpha)

G.SIN = graph.adjacency(E.SIN, mode = "undirected")
#correlation = cut_number((only_sig$ "correlation"), 4)
col = c("#E1AF00", "#EBCC2A", "#78B7C5", "#3B9AB2")
#names(col) = levels(correlation)
ggraph(G.SIN, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col='red'))+
  geom_node_point() +
  geom_node_text(aes(label = name), repel=TRUE)
```

Remarks:

Like, with the `ci` s we are chopping the lower correlation values but with the `sin` package we are chopping statically insignificant values.

```
knitr::opts_chunk$set(echo = TRUE)
```

5. Additional exploration

5.1 Exploring the Right brain

As mentioned and shown in the above graph the connectivity between the hemisphere is quite clear. But in order to get a more clear picture of within the hemisphere we consider the right brain separately. The `epsilon` value the same as 0.69 but the connectivity is more strong within the right hemisphere.

```
knitr::opts_chunk$set(echo = TRUE)
```

```
##### Exploration #####

### Exploring the right portion of our brain ###

Data_right=data[,1:39]
R_cap.right=cor(Data_right)

# Number of bootstraps
B = 1000
```



```

delta_b = rep(NA, B)

for (b in 1:B){
  idx = sample(1:n, replace = T)
  bsamp = Data_right[idx,] # bootstrap sample
  R_star = cor(bsamp) # save
  delta_b[b] = sqrt(n)*(max(abs(R_star-R_cap.right)))
}

# Bootstrap / CI / 95%
alpha=0.05
t_alpha <- quantile(delta_b, 1-alpha)
t_alpha

##      95%
## 3.971939

lb.right=R_cap.right-(t_alpha/sqrt(n))
ub.right=R_cap.right+(t_alpha/sqrt(n))

# Write the function

R_mat=function(epsilon){
  Pmatrix = (lb.right>epsilon)+(ub.right< -(epsilon))
  Pmatrix
  sig_values=which(Pmatrix==1, arr.in= TRUE)
  # code to get the desired rowname and colname
  data1 <- data.frame(matrix(ncol = 3))
  x <- c('from', 'to' , "Correlation")

  i<-1
  #data1=data.frame(p1=character(),p2=character(),p3)
  while (i <= nrow(sig_values)){
    data1<-rbind(data1,c(rownames(R_cap.right)[sig_values[i,1]],colnames(R_cap.right)[sig_values[i,2]],
      R_cap.right[sig_values[i,1],sig_values[i,2]]))
    i<-i+1
  }

  colnames(data1) <- x

  data1<-data1[-1,]
  data1$Correlation <- as.numeric(as.character(data1$Correlation))
  return(data1)
}
table.right=R_mat(0.69)

only_sig.right <- table.right[abs(table.right$Correlation) !=1, ]
new_g.right <- graph_from_data_frame(only_sig.right, F)

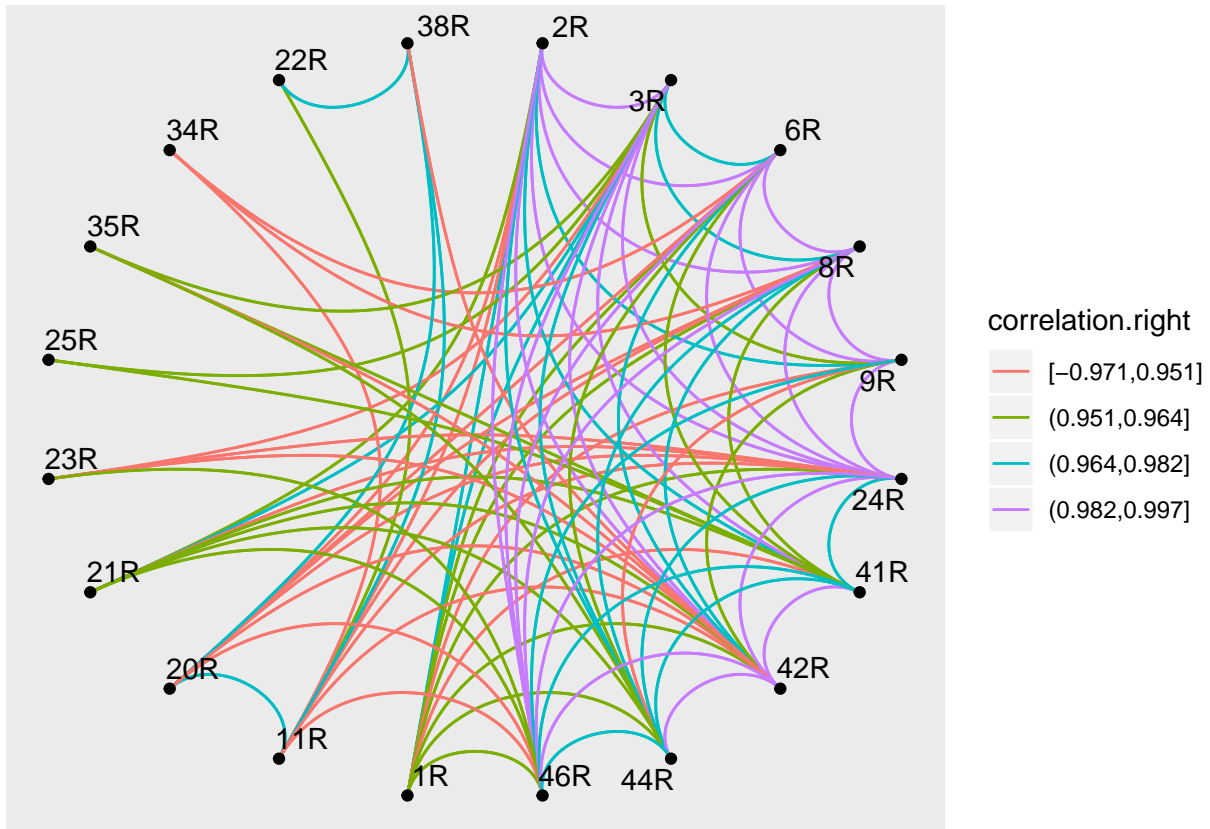
correlation.right = cut_number((only_sig.right$ "Correlation"), 4)
col = c("#E1AF00", "#EBCC2A", "#78B7C5", "#3B9AB2")
names(col) = levels(correlation.right)

```

```

par(mfrow=c(1,2))
ggraph(new_g.right, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col=correlation.right))+
  geom_node_point() +
  geom_node_text(aes(label = name), repel=TRUE)

```



5.2 Exploring the Left brain

Similarly, the connectivity within the left hemisphere is more strong and clearly visible, keeping the value of the epsilon same.

```

knitr::opts_chunk$set(echo = TRUE)

### Exploring the left portion of our brain ###

Data_left=data[,40:81]
R_cap.left=cor(Data_left)

# Number of bootstraps
B = 1000
delta_b = rep(NA, B)

for (b in 1:B){
  idx = sample(1:n, replace = T)
  bsamp = Data_left[idx,] # bootstrap sample
  R_star = cor(bsamp) # save
}

```

```

    delta_b[b] = sqrt(n)*(max(abs(R_star-R_cap.left)))
  }

# Bootstrap / CI / 95%
alpha=0.05
t_alpha <- quantile(delta_b, 1-alpha)
t_alpha

##      95%
## 4.16959

lb.left=R_cap.left-(t_alpha/sqrt(n))
ub.left=R_cap.left+(t_alpha/sqrt(n))

# Write the function

R_mat=function(epsilon){
  Pmatrix = (lb.left>epsilon)+(ub.left< -(epsilon))
  Pmatrix
  sig_values=which(Pmatrix==1, arr.in= TRUE)
  # code to get the desired rowname and colname
  data1 <- data.frame(matrix(ncol = 3))
  x <- c('from','to' , "Correlation")

  i<-1
  #data1=data.frame(p1=character(),p2=character(),p3)
  while (i <= nrow(sig_values)){
    data1<-rbind(data1,c(rownames(R_cap.left)[sig_values[i,1]],colnames(R_cap.left)[sig_values[i,2]],
                        R_cap.left[sig_values[i,1],sig_values[i,2]]))
    i<-i+1
  }

  colnames(data1) <- x

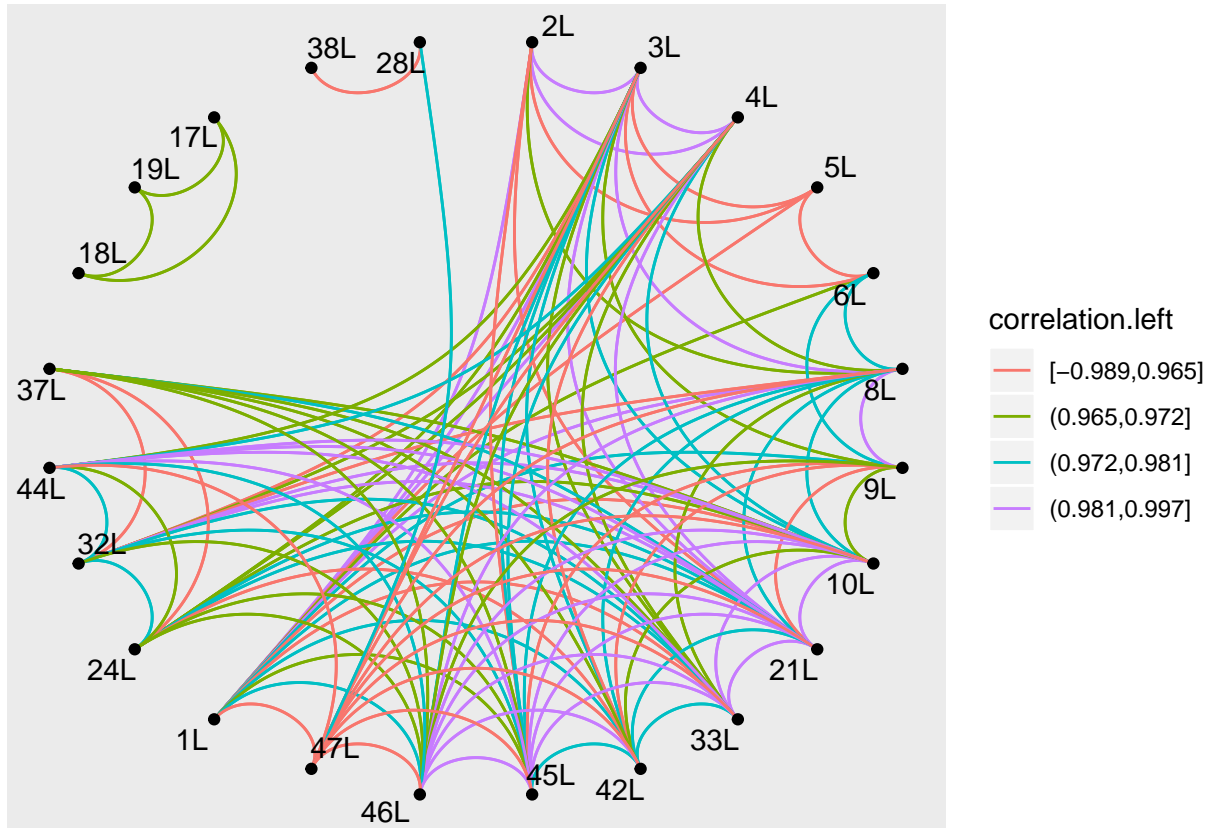
  data1<-data1[-1,]
  data1$Correlation <- as.numeric(as.character(data1$Correlation))
  return(data1)
}
table.left=R_mat(0.69)

only_sig.left <- table.left[abs(table.left$Correlation) !=1, ]
new_g.left <- graph_from_data_frame(only_sig.left, F)

correlation.left = cut_number((only_sig.left$ "Correlation"), 4)

col = c("#E1AF00", "#EBCC2A", "#78B7C5", "#3B9AB2")
names(col) = levels(correlation.left)
ggraph(new_g.left, layout = 'linear', circular = TRUE) +
  geom_edge_arc(aes(col=correlation.left))+
  geom_node_point() +
  geom_node_text(aes(label = name), repel=TRUE)

```



```
knitr::opts_chunk$set(echo = TRUE)

# Some numerical comparisons between the left and the right portions.

### Lenth:
length=c(length(only_sig.left$Correlation),length(only_sig.right$Correlation))

### Maximum and minimum
max=c(max(only_sig.left$Correlation),max(only_sig.right$Correlation))
min=c(min(only_sig.right$Correlation),min(only_sig.left$Correlation))

dataframe=data.frame(length,max,min)
rownames(dataframe)=c("Left_Part","Right_Part")
dataframe

##           length      max      min
## Left_Part    234 0.9973952 -0.9710428
## Right_Part   182 0.9968595 -0.9886874
```

Conclusion

We addressed the issue of dependency between the cortical region. By analysing the graph the dependency between the cortical region is established. The connections are significantly high toward the right hemisphere while exploring between and within the hemisphere. It can also be concluded from the graphs that the correlation within the hemisphere is higher than the correlation between the hemisphere. Moreover, we see that the maximum correlation between the nodes of the left part is higher than the right part. Again, the right part shows higher negative correlation than the left part.