main

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1 WGCNA

- @author = 'Apua Paquola'
- Edits by K.J. Benjamin
- Edits2 by Arthur S. Feltrin
  - New scale-free plots, export data to create network on cytoscape/igraph and format for jupyter notebook (05/2019)
  - Conversion from Rscript to jupyter notebook

Final edits by K.J. Benjamin for publication

[1]:
```
PARAM_NETWORK_TYPE = 'signed'
```

1.1 Prepare Data and Traits Table

[2]:
```
filter_outliers = function(expression, z_threshold = 2.5)
{
    # Input: an expression matrix
    # Output: an expression matrix with outliers removed
    # Remove samples with z normalized total distance from other samples >␣
 ↪z_threshold

    sample_distance = dist(expression)
    dist_z = scale(colSums(as.matrix(sample_distance)))
    stopifnot(all(rownames(dist_z) == rownames(expression)))

    keepSamples = dist_z < z_threshold

    new_expression = expression[keepSamples,]
    new_expression
}
```

[3]:
```
prepare_data=function()
{
  suppressMessages(library(dplyr))
  # Load sample data
```

```
sample_table = read.csv('/ceph/users/arthurfeltrin/phase3_new/0-annotation_data/Caudate_RiboZero_phenotype_SCHIZO-CAUC_AA-PRS_binary-table.csv')
#sample_table<-sample_table[-grep("BPNOS",sample_table$primarydx),]
sample_table = subset(sample_table, agedeath >= 17)
rownames(sample_table) = sample_table[,62]
sample_table = subset(sample_table, select = c(agedeath, sex, Race_CAUC, primarydx, RIN, antipsychotics))
colnames(sample_table)<-c("Age","Sex","Race_EA","Primarydx","RIN","Antipsychotics_False")

#get DRD2 junction expression
load("../../differential_expression/_m/junctions/voomSVA.RData")
drd2j = v$E %>% as.data.frame %>% tibble::rownames_to_column() %>%
  filter(rowname %in% c('chr11:113412884-113415420(-)',
                        'chr11:113414462-113415420(-)',
                        'chr11:113412884-113414374(-)')) %>%
  tibble::column_to_rownames("rowname")

# Load residualized expression
load("../../differential_expression/_m/genes/voomSVA.RData")
vsd0 <- v$E %>% as.data.frame %>% replace(is.na(.), "")
vsd = rbind(vsd0, drd2j)
rm(vsd0)
dim(vsd)

# Keep only the columns and rows that are present in
# both the sample table and vsd file
samples = intersect(colnames(vsd), rownames(sample_table))
vsd = vsd[,samples]
sample_table = sample_table[samples,]

# WGCNA data import
library(WGCNA)
options(stringsAsFactors = FALSE)
datExpr0 = t(vsd)

# Remove offending genes and samples from the data
gsg = goodSamplesGenes(datExpr0, verbose = 3);
if (!gsg$allOK)
{
  datExpr0 = datExpr0[gsg$goodSamples, gsg$goodGenes]
}
datExpr=datExpr0
# Remove outliers
datExpr = filter_outliers(datExpr0, z_threshold = 2.0)
rm(datExpr0)
```

```
  # Clean data
  samples = intersect(rownames(datExpr), rownames(sample_table))
  sample_table = sample_table[samples,]
  datExpr = datExpr[samples,]
  dim(datExpr)
  save(datExpr, sample_table, file = '00.RData')
}
```

1.2 Create Sample Dendogram Based on Distance (h)

[4]:
```
prepare_traits = function()
{
    lnames = load('00.RData')
    # Associate traits with samples
    traitRows = match(rownames(datExpr), rownames(sample_table))
    datTraits = sample_table[traitRows,]
    # Diagnostic plot: Sample dendrogram and trait heatmap
    pdf(file='sample_dendrogram_and_trait_heatmap.pdf',height=16,width = 22)
    sampleTree2 = hclust(dist(datExpr), method = "average")
    # Convert traits to a color representation: white means
    # low, red means high, grey means missing entry
    traitColors = numbers2colors(traitRows, signed=FALSE);
    # Plot the sample dendrogram and the colors underneath.
    plotDendroAndColors(sampleTree2, traitColors, groupLabels="Avg. Counts",
                        main = "Sample dendrogram and trait heatmap",
                        cex.dendroLabels=0.7)
    dev.off()
    # Print output
    plotDendroAndColors(sampleTree2, traitColors, groupLabels="Avg. Counts",
                        main = "Sample dendrogram and trait heatmap",
                        cex.dendroLabels=0.75)
    save(datExpr, sample_table, datTraits, file = "01.RData")
}
```

1.3 Calculate Scale-Free Topology

[5]:
```
plot_power_parameter=function(datExpr, plot_filename)
{
    # Choose a set of soft-thresholding powers
    powers = seq(from = 1, to=30, by=1)
    # Call the network topology analysis function
    sft = pickSoftThreshold(datExpr, networkType = PARAM_NETWORK_TYPE,
                            powerVector = powers, verbose = 5)
    # Plot the results:
    pdf(file=plot_filename)
    par(mfcol = c(2,2));
    par(mar = c(4.2, 4.5 , 2.2, 0.5),oma=c(0,0,2,0))
```

```
   cex1 = 0.7;
   # Scale-free topology fit index as a function of the
   # soft-thresholding power
   plot(sft$fitIndices[,1], -sign(sft$fitIndices[,3])*sft$fitIndices[,2],
        xlab="Soft Threshold (power)",
        ylab="Scale Free Topology Model Fit,signed R^2",type="n",
        main = paste("Scale independence"))
   text(sft$fitIndices[,1], -sign(sft$fitIndices[,3])*sft$fitIndices[,2],
        labels=powers,cex=cex1,col="blue");
   # this line corresponds to using an R^2 cut-off of h
   abline(h=0.80,col="red")
   # Mean connectivity as a function of the soft-thresholding power
   plot(sft$fitIndices[,1], sft$fitIndices[,5],
        xlab="Soft Threshold (power)", ylab="Mean Connectivity",
        type="n", main = paste("Mean connectivity"))
   text(sft$fitIndices[,1], sft$fitIndices[,5], labels=powers,␣
↪cex=cex1,col="blue")
   #####
   plot(sft$fitIndices[,1], sft$fitIndices[,6],
        xlab="Soft Threshold (power)", ylab="Median Connectivity",
        type="n", main = paste("Median connectivity"))
   text(sft$fitIndices[,1], sft$fitIndices[,6], labels=powers,␣
↪cex=cex1,col="blue")
   #####
   plot(sft$fitIndices[,1], sft$fitIndices[,7],
        xlab="Soft Threshold (power)", ylab="Max Connectivity",
        type="n", main = paste("Max connectivity"))
   text(sft$fitIndices[,1], sft$fitIndices[,7], labels=powers,␣
↪cex=cex1,col="blue")
   dev.off()
   ####plot on jupyter
   par(mfcol = c(2,2));
   par(mar = c(4.2, 4.5 , 2.2, 0.5),oma=c(0,0,2,0))
   cex1 = 0.7;
   # Scale-free topology fit index as a function of the
   # soft-thresholding power
   plot(sft$fitIndices[,1], -sign(sft$fitIndices[,3])*sft$fitIndices[,2],
        xlab="Soft Threshold (power)",
        ylab="Scale Free Topology Model Fit,signed R^2",type="n",
        main = paste("Scale independence"))
   text(sft$fitIndices[,1], -sign(sft$fitIndices[,3])*sft$fitIndices[,2],
        labels=powers,cex=cex1,col="blue");
   # this line corresponds to using an R^2 cut-off of h
   abline(h=0.80,col="red")
   # Mean connectivity as a function of the soft-thresholding power
   plot(sft$fitIndices[,1], sft$fitIndices[,5],
        xlab="Soft Threshold (power)", ylab="Mean Connectivity",
```

```
        type="n", main = paste("Mean connectivity"))
    text(sft$fitIndices[,1], sft$fitIndices[,5], labels=powers,␣
↪cex=cex1,col="blue")
    #####
    plot(sft$fitIndices[,1], sft$fitIndices[,6],
        xlab="Soft Threshold (power)", ylab="Median Connectivity",
        type="n", main = paste("Median connectivity"))
    text(sft$fitIndices[,1], sft$fitIndices[,6], labels=powers,␣
↪cex=cex1,col="blue")
    #####
    plot(sft$fitIndices[,1], sft$fitIndices[,7],
        xlab="Soft Threshold (power)",ylab="Max Connectivity", type="n",
        main = paste("Max connectivity"))
    text(sft$fitIndices[,1], sft$fitIndices[,7], labels=powers,␣
↪cex=cex1,col="blue")
}
```

[6]:
```
figure_out_power_parameter=function()
{
    library(WGCNA)
    options(stringsAsFactors = FALSE);
    enableWGCNAThreads(nThreads=16)
    lnames = load(file = '01.RData')
    plot_power_parameter(datExpr, 'power_parameter_selection.pdf')
}
```

1.4 Build the Network

[7]:
```
construct_network=function()
{
  library(WGCNA)
  options(stringsAsFactors = FALSE);
  enableWGCNAThreads(nThreads=16)
  lnames = load(file = "01.RData")

  # softPower value from previous plot power_parameter_selection.pdf
  softPower = 7; #check this value, it changes accordingly to your data! You␣
↪should
  # ALWAYS choose a value equal or above (better) 0.8
  cor <- WGCNA::cor
  net = blockwiseModules(datExpr,
                         power = softPower,
                         networkType = PARAM_NETWORK_TYPE,
                         TOMType = PARAM_NETWORK_TYPE,
                         numericLabels = TRUE,
                         corType = "bicor",
                         saveTOMs = TRUE, saveTOMFileBase = "TOM",
```

```
                          verbose = 3, maxBlockSize=30000)

  moduleLabels = net$colors
  moduleColors = labels2colors(net$colors)
  MEs = net$MEs;
  geneTree = net$dendrograms[[1]];
  save(net, MEs, moduleLabels, moduleColors, geneTree, softPower, file = "02.
 ↪RData")
}
#cyt = exportNetworkToCytoscape(modTOM,
```

1.5 Use Topology Overlap Matrix (TOM) to cluster the genes on the networks into different modules

[8]:
```
plot_cluster_dendrogram=function()
{
    library(WGCNA)
    options(stringsAsFactors = FALSE);
    enableWGCNAThreads(nThreads=16)
    load(file = "02.RData")
    pdf(file="cluster_dendrogram.pdf",height=16,width = 22)
    mergedColors = labels2colors(net$colors)
    plotDendroAndColors(net$dendrograms[[1]], mergedColors[net$blockGenes[[1]]],
                        "Module Colors", dendroLabels = FALSE, hang = 0.03,
                        addGuide = TRUE, guideHang = 0.05, cex.dendroLabels=0.3)
    dev.off()
    # Print output
    plotDendroAndColors(net$dendrograms[[1]], mergedColors[net$blockGenes[[1]]],
                        "Module Colors", dendroLabels = FALSE, hang = 0.03,
                        addGuide = TRUE, guideHang = 0.05, cex.dendroLabels=0.3)
}
```

1.6 Use Pearson Correlation to measure the correlation between each module eigenvalue (kME) and the various sample traits

[9]:
```
correlate_with_traits=function()
{
    library(WGCNA)
    options(stringsAsFactors = FALSE)
    enableWGCNAThreads(nThreads=16)
    lnames = load(file = "01.RData")
    lnames = load(file = "02.RData")
    # Define numbers of genes and samples
    nGenes = ncol(datExpr);
    nSamples = nrow(datExpr);
    # Recalculate MEs with color labels
    MEs0 = moduleEigengenes(datExpr, moduleColors)$eigengenes
```

```
    MEs = orderMEs(MEs0)
    moduleTraitCor = cor(MEs, datTraits, use = "p");
    moduleTraitPvalue = corPvalueStudent(moduleTraitCor, nSamples);
    # Plot
    pdf(file="module_trait_relationships.pdf", height=16,width = 22)
    # Will display correlations and their p-values
    textMatrix = paste(signif(moduleTraitCor, 2), "\n(",
                       signif(moduleTraitPvalue, 1), ")", sep = "");
    dim(textMatrix) = dim(moduleTraitCor)
    par(mar = c(6, 8.5, 3, 3));
    # Display the correlation values within a heatmap plot
    labeledHeatmap(Matrix = moduleTraitCor,
                   xLabels = names(datTraits),
                   yLabels = names(MEs),
                   ySymbols = names(MEs),
                   colorLabels = FALSE,
                   naColor = "grey",
                   colors = blueWhiteRed(50),
                   textMatrix = textMatrix,
                   setStdMargins = FALSE,
                   cex.text = 0.9,
                   zlim = c(-1,1),
                   main = paste("Module kME-Trait Correlation"))
    dev.off()
    # Print output
    textMatrix = paste(signif(moduleTraitCor, 2), "\n(",
                       signif(moduleTraitPvalue, 1), ")", sep = "");
    dim(textMatrix) = dim(moduleTraitCor)
    par(mar = c(12, 6.5, 3, 0.5));
    # Display the correlation values within a heatmap plot
    labeledHeatmap(Matrix = moduleTraitCor, xLabels = names(datTraits),
                   yLabels = names(MEs), ySymbols = names(MEs),
                   colorLabels = FALSE, naColor = "grey",
                   colors = blueWhiteRed(50), textMatrix = textMatrix,
                   setStdMargins = FALSE, cex.text = 0.55, zlim = c(-1,1),
                   main = paste("Module kME-Trait Correlation"))
}
```

1.7 Export the main results

[10]:
```
export_eigengene_tables = function()
{
    library(WGCNA)
    options(stringsAsFactors = FALSE)
    lnames = load(file = "01.RData")
    lnames = load(file = "02.RData")
    # Define numbers of genes and samples
```

```
    nGenes = ncol(datExpr)
    nSamples = nrow(datExpr)
    # Recalculate MEs with color labels
    MEs0 = moduleEigengenes(datExpr, moduleColors)$eigengenes
    rownames(MEs0) = rownames(datExpr)
    write.csv(MEs0, 'eigengenes.csv')
    # Write modules
    modules = data.frame(row.names=colnames(datExpr), module=moduleColors)
    write.csv(modules, 'modules.csv')
    save(datExpr,softPower,moduleColors, file = "cytoscapenetwork.Rdata")
}
```

1.8 Run the functions and plot the results

[11]:
```
prepare_data()
```

```
Loading required package: limma

Loading required package: dynamicTreeCut

Loading required package: fastcluster


Attaching package: ‘fastcluster’


The following object is masked from ‘package:stats’:

    hclust



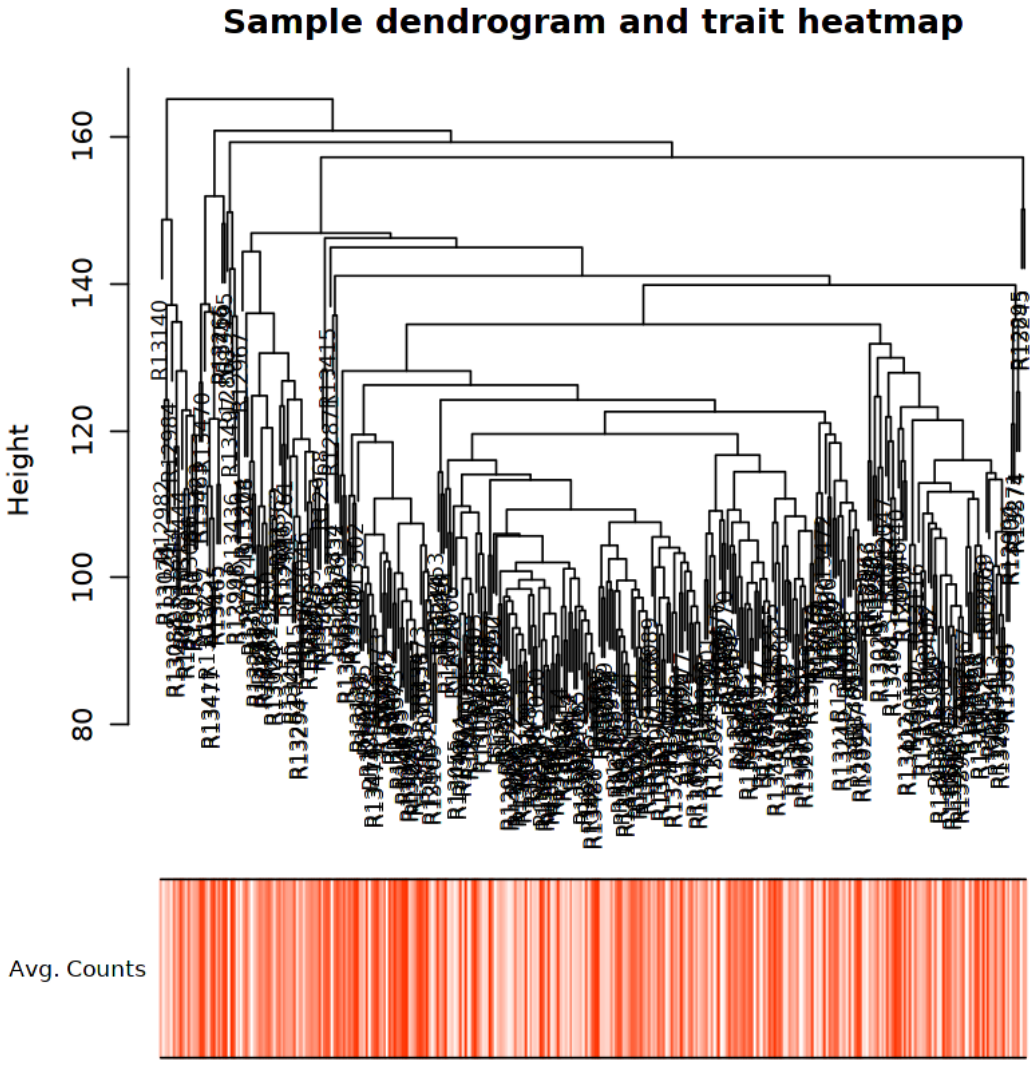

Attaching package: ‘WGCNA’


The following object is masked from ‘package:stats’:

    cor


 Flagging genes and samples with too many missing values…
  ..step 1
```

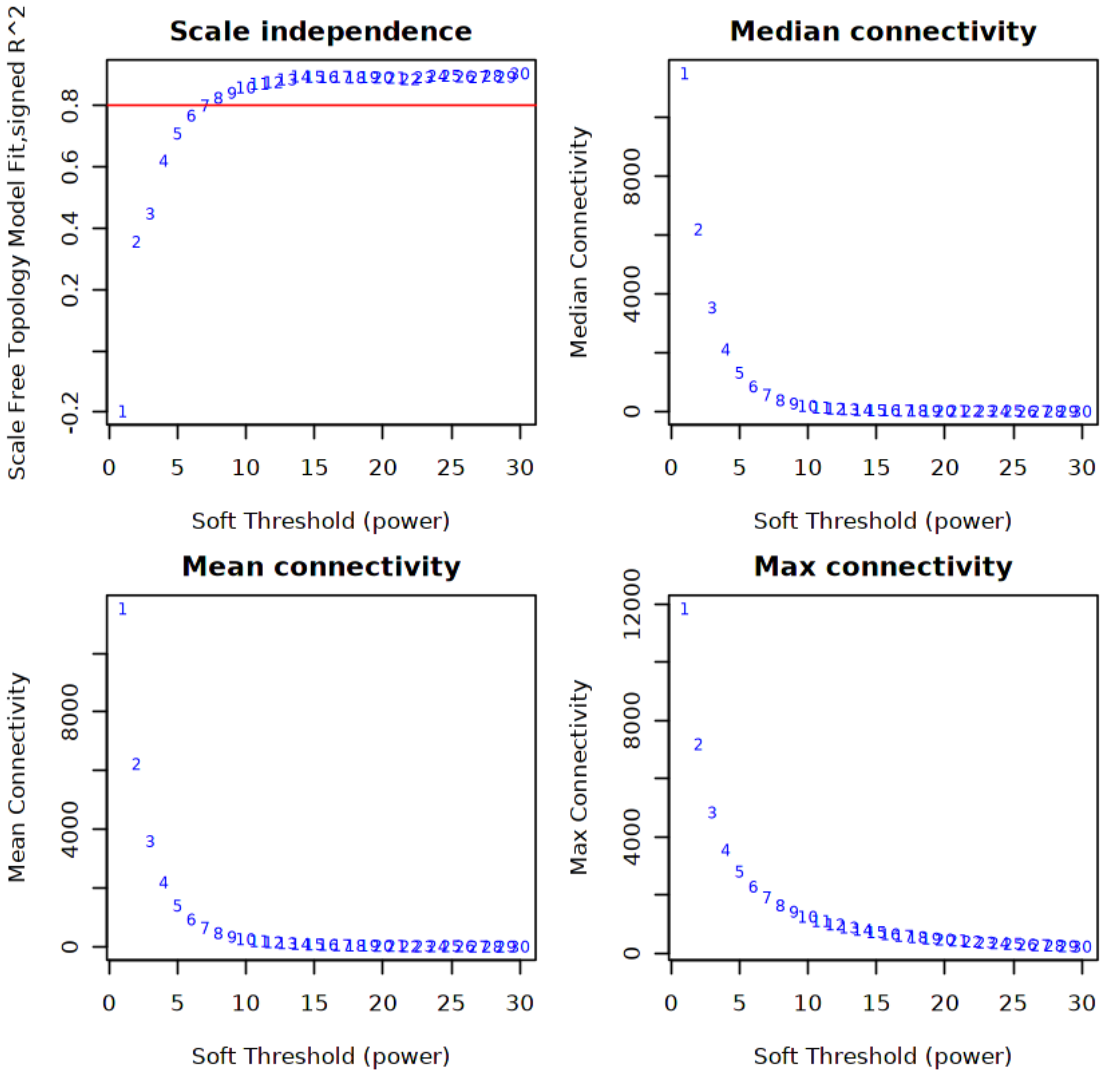
[12]:
```
# 1 - Sample dendrogram and trait heatmap
prepare_traits()
```



[13]:
```
# 2 - Scale Free Topology Model Fit
figure_out_power_parameter()
```

```
Allowing parallel execution with up to 16 working processes.
pickSoftThreshold: will use block size 1948.
 pickSoftThreshold: calculating connectivity for given powers…
   ..working on genes 1 through 1948 of 22961
   ..working on genes 1949 through 3896 of 22961
   ..working on genes 3897 through 5844 of 22961
   ..working on genes 5845 through 7792 of 22961
   ..working on genes 7793 through 9740 of 22961
   ..working on genes 9741 through 11688 of 22961
   ..working on genes 11689 through 13636 of 22961
```

```
   ..working on genes 13637 through 15584 of 22961
   ..working on genes 15585 through 17532 of 22961
   ..working on genes 17533 through 19480 of 22961
   ..working on genes 19481 through 21428 of 22961
   ..working on genes 21429 through 22961 of 22961
   Power SFT.R.sq  slope truncated.R.sq  mean.k. median.k. max.k.
1      1    0.196  56.00          0.951 11500.00  1.15e+04  11800
2      2    0.356 -10.60          0.933  6240.00  6.20e+03   7190
3      3    0.448  -3.90          0.864  3600.00  3.54e+03   4840
4      4    0.621  -2.50          0.924  2190.00  2.11e+03   3550
5      5    0.709  -2.21          0.941  1400.00  1.31e+03   2800
6      6    0.768  -1.98          0.957   935.00  8.40e+02   2290
7      7    0.801  -1.85          0.963   647.00  5.52e+02   1930
8      8    0.826  -1.77          0.966   462.00  3.71e+02   1650
9      9    0.842  -1.73          0.967   340.00  2.55e+02   1430
10    10    0.860  -1.69          0.970   256.00  1.78e+02   1250
11    11    0.872  -1.66          0.971   197.00  1.26e+02   1110
12    12    0.877  -1.66          0.968   155.00  9.03e+01    988
13    13    0.886  -1.65          0.970   123.00  6.55e+01    887
14    14    0.896  -1.64          0.972    99.60  4.77e+01    800
15    15    0.895  -1.64          0.966    81.50  3.52e+01    725
16    16    0.894  -1.64          0.964    67.50  2.62e+01    660
17    17    0.895  -1.63          0.963    56.40  1.96e+01    602
18    18    0.892  -1.63          0.960    47.60  1.49e+01    552
19    19    0.893  -1.61          0.959    40.40  1.13e+01    507
20    20    0.893  -1.61          0.957    34.60  8.62e+00    468
21    21    0.891  -1.60          0.955    29.80  6.64e+00    432
22    22    0.887  -1.60          0.951    25.80  5.15e+00    400
23    23    0.893  -1.59          0.954    22.50  3.99e+00    371
24    24    0.898  -1.58          0.957    19.70  3.12e+00    345
25    25    0.898  -1.57          0.957    17.30  2.45e+00    321
26    26    0.896  -1.56          0.955    15.30  1.93e+00    299
27    27    0.894  -1.56          0.954    13.60  1.52e+00    280
28    28    0.898  -1.55          0.957    12.10  1.21e+00    262
29    29    0.895  -1.55          0.954    10.80  9.61e-01    245
30    30    0.906  -1.53          0.961     9.65  7.63e-01    230
```



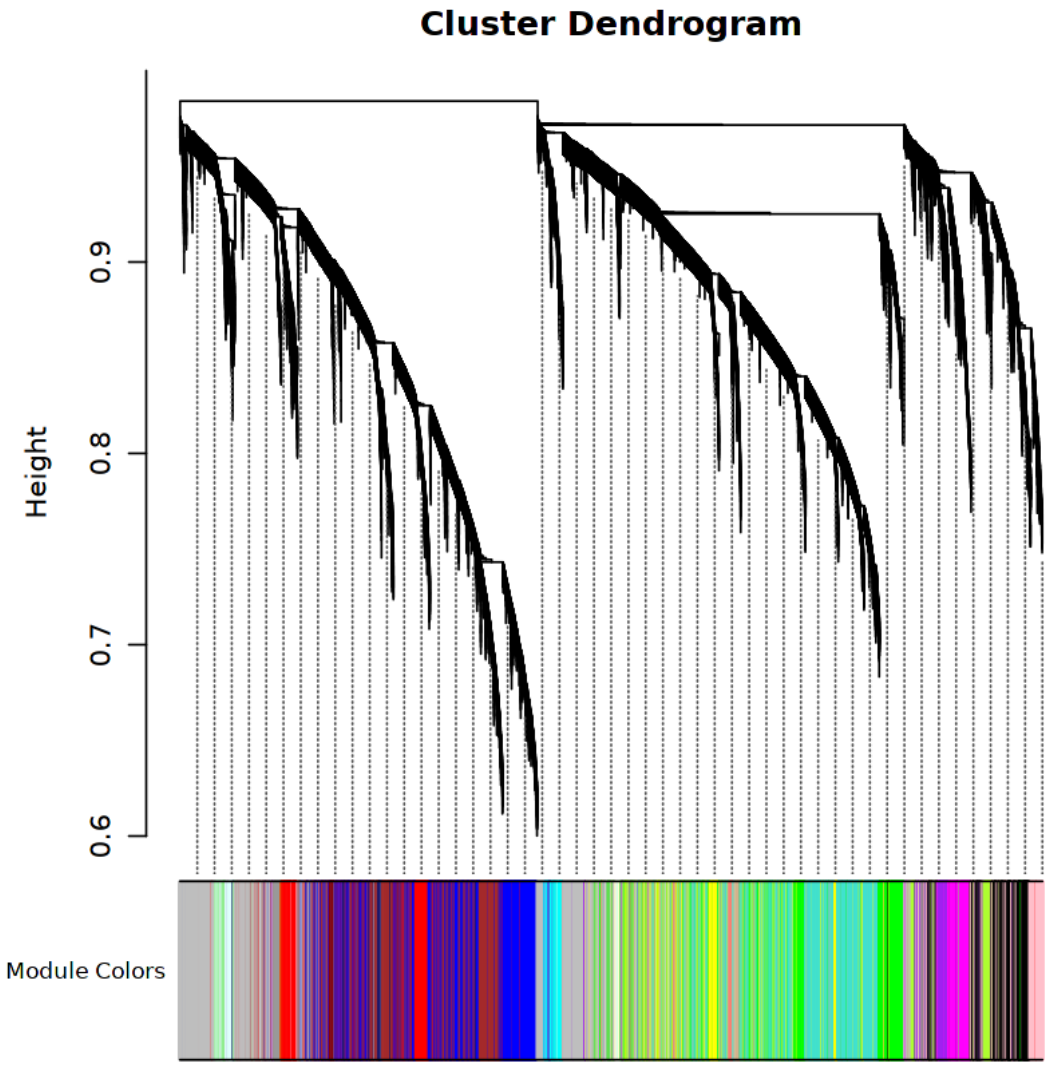
[14]:
```
construct_network()
```

```
Allowing parallel execution with up to 16 working processes.
 Calculating module eigengenes block-wise from all genes
   Flagging genes and samples with too many missing values…
    ..step 1
 ..Working on block 1 .
    TOM calculation: adjacency..
    ..will use 16 parallel threads.
     Fraction of slow calculations: 0.000000
    ..connectivity..
    ..matrix multiplication (system BLAS)..
    ..normalization..
```

```
   ..done.
  ..saving TOM for block 1 into file TOM-block.1.RData
…clustering..
…detecting modules..
…calculating module eigengenes..
…checking kME in modules..
    ..removing 798 genes from module 1 because their KME is too low.
    ..removing 1179 genes from module 2 because their KME is too low.
    ..removing 733 genes from module 3 because their KME is too low.
    ..removing 733 genes from module 4 because their KME is too low.
    ..removing 210 genes from module 5 because their KME is too low.
    ..removing 138 genes from module 6 because their KME is too low.
    ..removing 104 genes from module 7 because their KME is too low.
    ..removing 1 genes from module 8 because their KME is too low.
    ..removing 3 genes from module 10 because their KME is too low.
    ..removing 30 genes from module 11 because their KME is too low.
    ..removing 1 genes from module 18 because their KME is too low.
    ..removing 3 genes from module 19 because their KME is too low.
    ..removing 1 genes from module 20 because their KME is too low.
    ..removing 4 genes from module 22 because their KME is too low.
    ..removing 2 genes from module 23 because their KME is too low.
 ..reassigning 777 genes from module 1 to modules with higher KME.
 ..reassigning 670 genes from module 2 to modules with higher KME.
 ..reassigning 525 genes from module 3 to modules with higher KME.
 ..reassigning 500 genes from module 4 to modules with higher KME.
 ..reassigning 216 genes from module 5 to modules with higher KME.
 ..reassigning 179 genes from module 6 to modules with higher KME.
 ..reassigning 101 genes from module 7 to modules with higher KME.
 ..reassigning 55 genes from module 8 to modules with higher KME.
 ..reassigning 127 genes from module 9 to modules with higher KME.
 ..reassigning 67 genes from module 10 to modules with higher KME.
 ..reassigning 44 genes from module 11 to modules with higher KME.
 ..reassigning 75 genes from module 12 to modules with higher KME.
 ..reassigning 62 genes from module 13 to modules with higher KME.
 ..reassigning 74 genes from module 14 to modules with higher KME.
 ..reassigning 19 genes from module 15 to modules with higher KME.
 ..reassigning 10 genes from module 16 to modules with higher KME.
 ..reassigning 28 genes from module 17 to modules with higher KME.
 ..reassigning 23 genes from module 18 to modules with higher KME.
 ..reassigning 3 genes from module 20 to modules with higher KME.
 ..reassigning 7 genes from module 21 to modules with higher KME.
 ..reassigning 17 genes from module 22 to modules with higher KME.
 ..reassigning 7 genes from module 23 to modules with higher KME.
 ..reassigning 1 genes from module 24 to modules with higher KME.
 ..reassigning 1 genes from module 25 to modules with higher KME.
..merging modules that are too close..
    mergeCloseModules: Merging modules whose distance is less than 0.15
      Calculating new MEs…
```

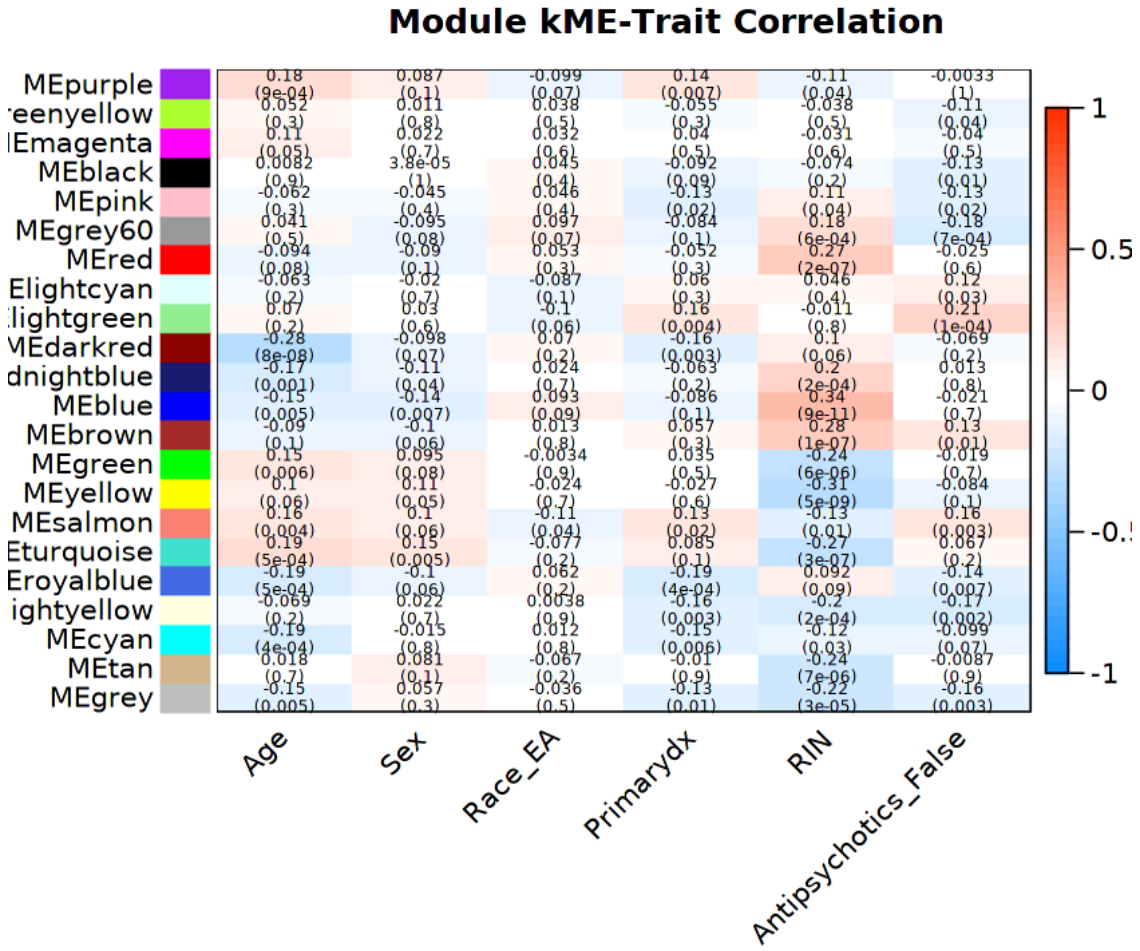
[15]:
```
#3 - TOM Dendogram
plot_cluster_dendrogram()
```

```
Allowing parallel execution with up to 16 working processes.
```



[16]:
```
#4 - Module Eigenvalue Correlation with sample's traits
correlate_with_traits()
```

```
Allowing parallel execution with up to 16 working processes.
```



[17]:
```
export_eigengene_tables()
```

1.9 Reproducibility Information

[18]:
```
Sys.time()
proc.time()
options(width = 120)
sessioninfo::session_info()
```

```
[1] "2021-08-07 10:06:47 EDT"
```

```
    user   system  elapsed
9066.619 3673.052  760.040
```

```
 Session info
setting  value
version  R version 4.0.3 (2020-10-10)
os       Arch Linux
system   x86_64, linux-gnu
ui       X11
language (EN)
collate  en_US.UTF-8
ctype    en_US.UTF-8
tz       America/New_York
date     2021-08-07

 Packages
package        * version  date       lib source
AnnotationDbi    1.52.0   2020-10-27 [1] Bioconductor
assertthat       0.2.1    2019-03-21 [1] CRAN (R 4.0.2)
backports        1.2.1    2020-12-09 [1] CRAN (R 4.0.2)
base64enc        0.1-3    2015-07-28 [1] CRAN (R 4.0.2)
Biobase          2.50.0   2020-10-27 [1] Bioconductor
BiocGenerics     0.36.1   2021-04-16 [1] Bioconductor
bit              4.0.4    2020-08-04 [1] CRAN (R 4.0.2)
bit64            4.0.5    2020-08-30 [1] CRAN (R 4.0.2)
blob             1.2.1    2020-01-20 [1] CRAN (R 4.0.2)
cachem           1.0.5    2021-05-15 [1] CRAN (R 4.0.3)
Cairo            1.5-12.2 2020-07-07 [1] CRAN (R 4.0.2)
checkmate        2.0.0    2020-02-06 [1] CRAN (R 4.0.2)
cli              3.0.0    2021-06-30 [1] CRAN (R 4.0.3)
cluster          2.1.0    2019-06-19 [2] CRAN (R 4.0.3)
codetools        0.2-16   2018-12-24 [2] CRAN (R 4.0.3)
colorspace       2.0-2    2021-06-24 [1] CRAN (R 4.0.3)
crayon           1.4.1    2021-02-08 [1] CRAN (R 4.0.3)
data.table       1.14.0   2021-02-21 [1] CRAN (R 4.0.3)
DBI              1.1.1    2021-01-15 [1] CRAN (R 4.0.2)
digest           0.6.27   2020-10-24 [1] CRAN (R 4.0.2)
doParallel       1.0.16   2020-10-16 [1] CRAN (R 4.0.3)
dplyr          * 1.0.7    2021-06-18 [1] CRAN (R 4.0.3)
dynamicTreeCut * 1.63-1   2016-03-11 [1] CRAN (R 4.0.3)
ellipsis         0.3.2    2021-04-29 [1] CRAN (R 4.0.3)
evaluate         0.14     2019-05-28 [1] CRAN (R 4.0.2)
fansi            0.5.0    2021-05-25 [1] CRAN (R 4.0.3)
fastcluster    * 1.2.3    2021-05-24 [1] CRAN (R 4.0.3)
fastmap          1.1.0    2021-01-25 [1] CRAN (R 4.0.2)
foreach          1.5.1    2020-10-15 [1] CRAN (R 4.0.2)
foreign          0.8-80   2020-05-24 [2] CRAN (R 4.0.3)
Formula          1.2-4    2020-10-16 [1] CRAN (R 4.0.2)
generics         0.1.0    2020-10-31 [1] CRAN (R 4.0.2)
ggplot2          3.3.5    2021-06-25 [1] CRAN (R 4.0.3)
glue             1.4.2    2020-08-27 [1] CRAN (R 4.0.2)
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GO.db            3.12.1   2021-04-08 [1] Bioconductor
gridExtra        2.3      2017-09-09 [1] CRAN (R 4.0.2)
gtable           0.3.0    2019-03-25 [1] CRAN (R 4.0.2)
Hmisc            4.5-0    2021-02-28 [1] CRAN (R 4.0.3)
htmlTable        2.2.1    2021-05-18 [1] CRAN (R 4.0.3)
htmltools        0.5.1.1  2021-01-22 [1] CRAN (R 4.0.2)
htmlwidgets      1.5.3    2020-12-10 [1] CRAN (R 4.0.2)
impute           1.64.0   2020-10-27 [1] Bioconductor
IRanges          2.24.1   2020-12-12 [1] Bioconductor
IRdisplay        1.0      2021-01-20 [1] CRAN (R 4.0.2)
IRkernel         1.2      2021-05-11 [1] CRAN (R 4.0.3)
iterators        1.0.13   2020-10-15 [1] CRAN (R 4.0.2)
jpeg             0.1-8.1  2019-10-24 [1] CRAN (R 4.0.2)
jsonlite         1.7.2    2020-12-09 [1] CRAN (R 4.0.2)
knitr            1.33     2021-04-24 [1] CRAN (R 4.0.3)
lattice          0.20-41  2020-04-02 [2] CRAN (R 4.0.3)
latticeExtra     0.6-29   2019-12-19 [1] CRAN (R 4.0.2)
lifecycle        1.0.0    2021-02-15 [1] CRAN (R 4.0.3)
limma          * 3.46.0   2020-10-27 [1] Bioconductor
magrittr         2.0.1    2020-11-17 [1] CRAN (R 4.0.2)
Matrix           1.3-4    2021-06-01 [1] CRAN (R 4.0.3)
matrixStats      0.59.0   2021-06-01 [1] CRAN (R 4.0.3)
memoise          2.0.0    2021-01-26 [1] CRAN (R 4.0.2)
munsell          0.5.0    2018-06-12 [1] CRAN (R 4.0.2)
nnet             7.3-14   2020-04-26 [2] CRAN (R 4.0.3)
pbdZMQ           0.3-5    2021-02-10 [1] CRAN (R 4.0.3)
pillar           1.6.1    2021-05-16 [1] CRAN (R 4.0.3)
pkgconfig        2.0.3    2019-09-22 [1] CRAN (R 4.0.2)
png              0.1-7    2013-12-03 [1] CRAN (R 4.0.2)
preprocessCore   1.52.1   2021-01-08 [1] Bioconductor
purrr            0.3.4    2020-04-17 [1] CRAN (R 4.0.2)
R6               2.5.0    2020-10-28 [1] CRAN (R 4.0.2)
RColorBrewer     1.1-2    2014-12-07 [1] CRAN (R 4.0.2)
Rcpp             1.0.7    2021-07-07 [1] CRAN (R 4.0.3)
repr             1.1.3    2021-01-21 [1] CRAN (R 4.0.2)
rlang            0.4.11   2021-04-30 [1] CRAN (R 4.0.3)
rpart            4.1-15   2019-04-12 [2] CRAN (R 4.0.3)
RSQLite          2.2.7    2021-04-22 [1] CRAN (R 4.0.3)
rstudioapi       0.13     2020-11-12 [1] CRAN (R 4.0.2)
S4Vectors        0.28.1   2020-12-09 [1] Bioconductor
scales           1.1.1    2020-05-11 [1] CRAN (R 4.0.2)
sessioninfo      1.1.1    2018-11-05 [1] CRAN (R 4.0.2)
stringi          1.7.3    2021-07-16 [1] CRAN (R 4.0.3)
stringr          1.4.0    2019-02-10 [1] CRAN (R 4.0.2)
survival         3.2-7    2020-09-28 [2] CRAN (R 4.0.3)
tibble           3.1.2    2021-05-16 [1] CRAN (R 4.0.3)
tidyselect       1.1.1    2021-04-30 [1] CRAN (R 4.0.3)
utf8             1.2.1    2021-03-12 [1] CRAN (R 4.0.3)
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 WGCNA          * 1.70-3   2021-02-28 [1] CRAN (R 4.0.3)
 withr            2.4.2    2021-04-18 [1] CRAN (R 4.0.3)
 xfun             0.24     2021-06-15 [1] CRAN (R 4.0.3)

[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0
[2] /usr/lib/R/library
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