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
  load("../../../differential_analysis/dlpfc/_m/genes/voomSVA.RData")
  sample_table = v$design %>% as.data.frame %>% select(-Intercept) %>%
```

```
    rename("Ancestry"="EA", "Sex"="Male")

  # Load residualized expression
  vsd <- data.table::fread(paste0("../../../differential_analysis/dlpfc/",
                                  "_m/genes/residualized_expression.tsv")) %>%
    replace(is.na(.), "") %>% tibble::column_to_rownames("V1")
  print(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
  suppressMessages(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 = 2.5)
  rm(datExpr0)
  # Clean data
  samples = intersect(rownames(datExpr), rownames(sample_table))
  sample_table = sample_table[samples,]
  datExpr = datExpr[samples,]
  print(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=22,width = 26)
```

```
    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 = 9; # Based on the hippocampus
  # 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")
}
```

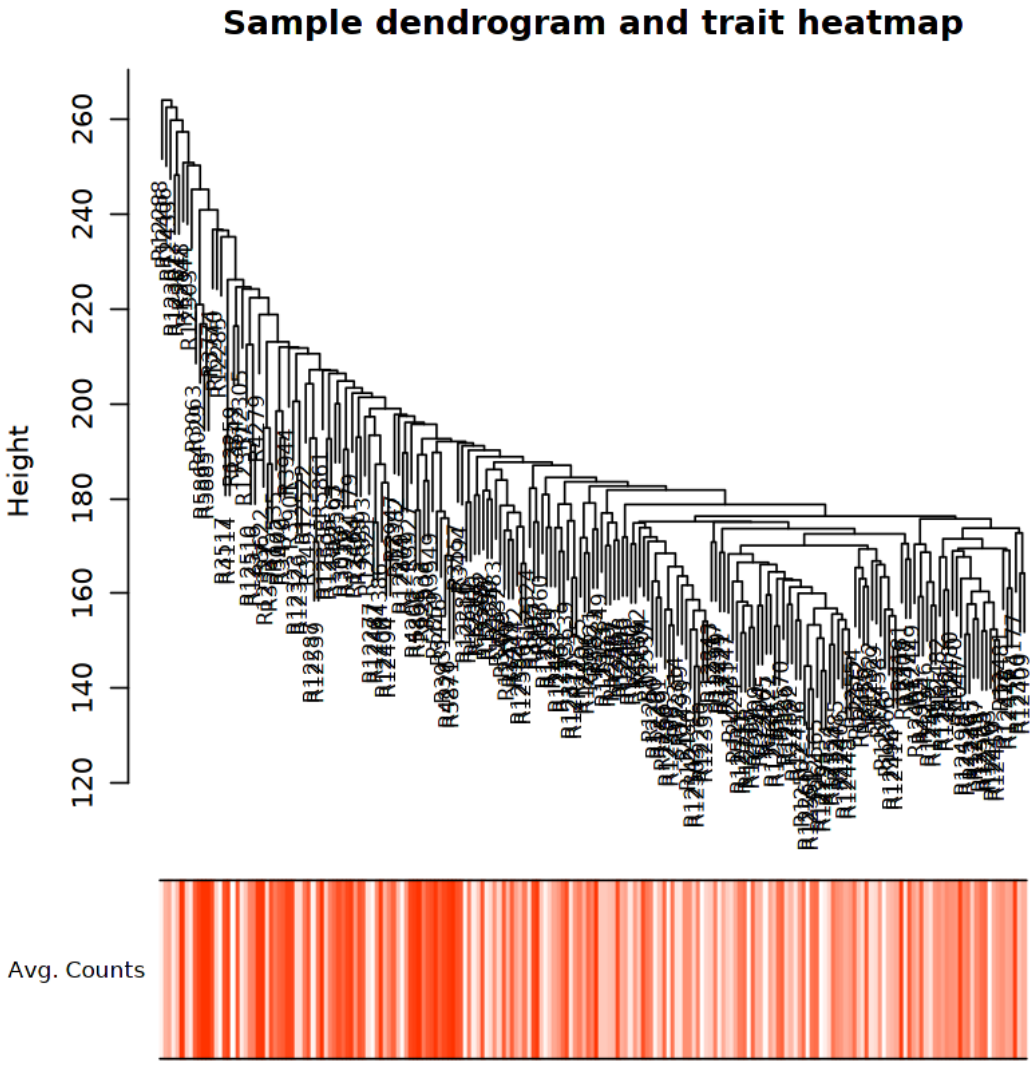
1.8 Run the functions and plot the results

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

```
Loading required package: limma
```

```
Warning message in
data.table::fread(paste0("../../../differential_analysis/dlpfc/", :
"Detected 211 column names but the data has 212 columns (i.e. invalid file).
Added 1 extra default column name for the first column which is guessed to be
row names or an index. Use setnames() afterwards if this guess is not correct,
or fix the file write command that created the file to create a valid file."
[1] 22398   211
 Flagging genes and samples with too many missing values…
  ..step 1
[1]   205 22398
```

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



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

```
pickSoftThreshold: will use block size 1997.
 pickSoftThreshold: calculating connectivity for given powers…
   ..working on genes 1 through 1997 of 22398
```

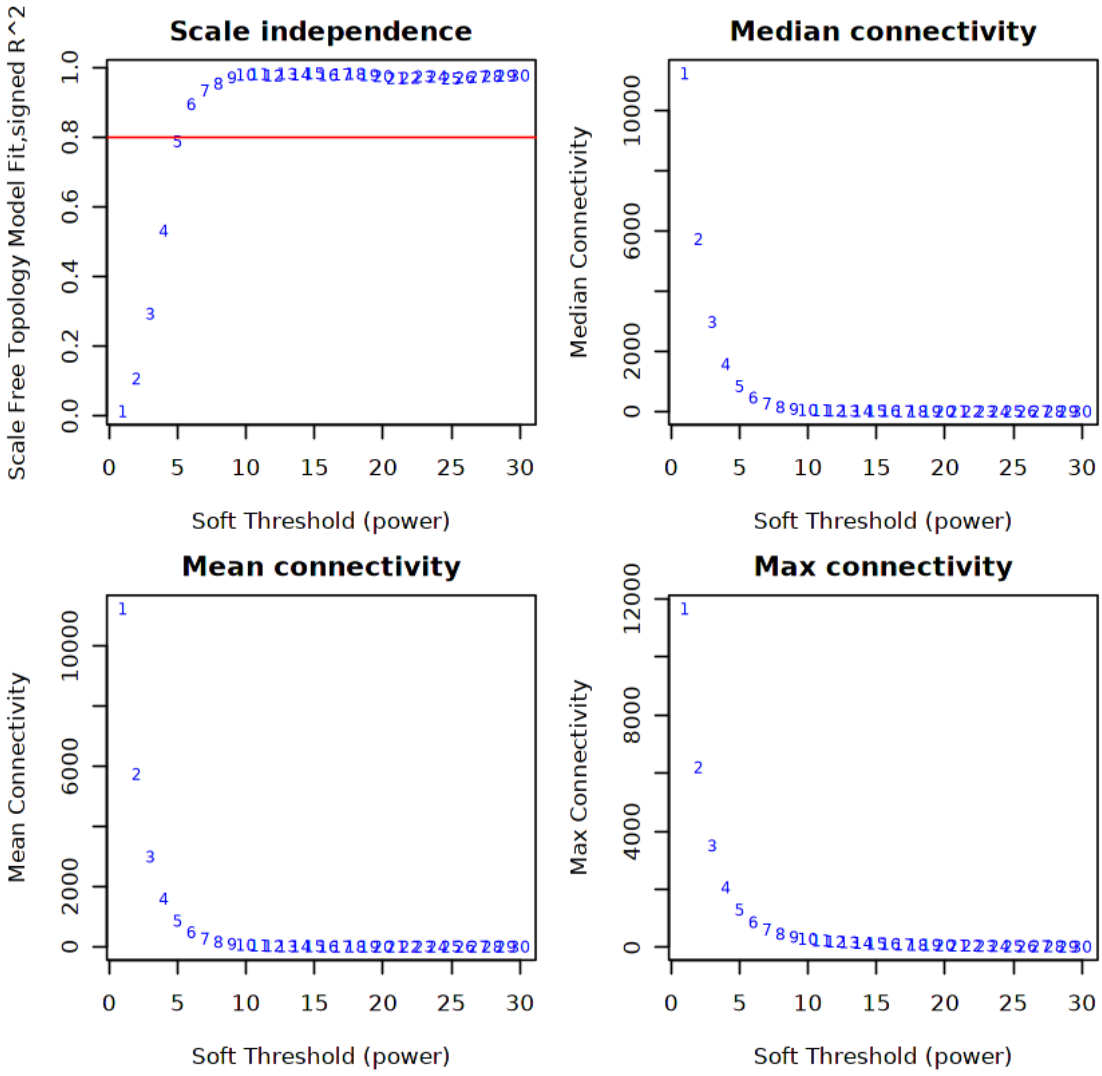
```
Warning message:
"executing %dopar% sequentially: no parallel backend registered"
```

```
   ..working on genes 1998 through 3994 of 22398
   ..working on genes 3995 through 5991 of 22398
   ..working on genes 5992 through 7988 of 22398
   ..working on genes 7989 through 9985 of 22398
   ..working on genes 9986 through 11982 of 22398
   ..working on genes 11983 through 13979 of 22398
   ..working on genes 13980 through 15976 of 22398
   ..working on genes 15977 through 17973 of 22398
   ..working on genes 17974 through 19970 of 22398
   ..working on genes 19971 through 21967 of 22398
   ..working on genes 21968 through 22398 of 22398
```

	Power	SFT.R.sq	slope	truncated.R.sq	mean.k.	median.k.	max.k.
1	1	0.0135	-14.70	0.917	1.12e+04	1.12e+04	11700.0
2	2	0.1070	-14.70	0.889	5.75e+03	5.73e+03	6210.0
3	3	0.2940	-12.60	0.859	3.00e+03	2.97e+03	3510.0
4	4	0.5310	-8.88	0.863	1.59e+03	1.56e+03	2080.0
5	5	0.7880	-7.10	0.938	8.60e+02	8.33e+02	1300.0
6	6	0.8940	-6.12	0.976	4.75e+02	4.51e+02	879.0
7	7	0.9340	-5.09	0.987	2.68e+02	2.47e+02	627.0
8	8	0.9540	-4.28	0.991	1.54e+02	1.38e+02	469.0
9	9	0.9710	-3.65	0.995	9.12e+01	7.77e+01	365.0
10	10	0.9780	-3.19	0.996	5.53e+01	4.44e+01	295.0
11	11	0.9800	-2.85	0.994	3.45e+01	2.57e+01	245.0
12	12	0.9760	-2.62	0.989	2.21e+01	1.51e+01	207.0
13	13	0.9810	-2.40	0.992	1.46e+01	8.95e+00	179.0
14	14	0.9800	-2.23	0.989	9.91e+00	5.37e+00	156.0
15	15	0.9820	-2.09	0.991	6.93e+00	3.26e+00	137.0
16	16	0.9780	-1.98	0.986	4.98e+00	2.01e+00	122.0
17	17	0.9790	-1.87	0.987	3.67e+00	1.25e+00	109.0
18	18	0.9810	-1.78	0.989	2.77e+00	7.86e-01	97.5
19	19	0.9770	-1.72	0.986	2.14e+00	4.99e-01	88.0
20	20	0.9750	-1.67	0.984	1.68e+00	3.20e-01	79.9
21	21	0.9690	-1.63	0.980	1.35e+00	2.07e-01	72.8
22	22	0.9690	-1.58	0.978	1.09e+00	1.36e-01	66.5
23	23	0.9730	-1.54	0.983	8.98e-01	8.96e-02	60.9
24	24	0.9740	-1.51	0.984	7.47e-01	5.95e-02	55.9
25	25	0.9680	-1.49	0.981	6.28e-01	3.95e-02	51.5
26	26	0.9700	-1.46	0.983	5.33e-01	2.65e-02	47.4

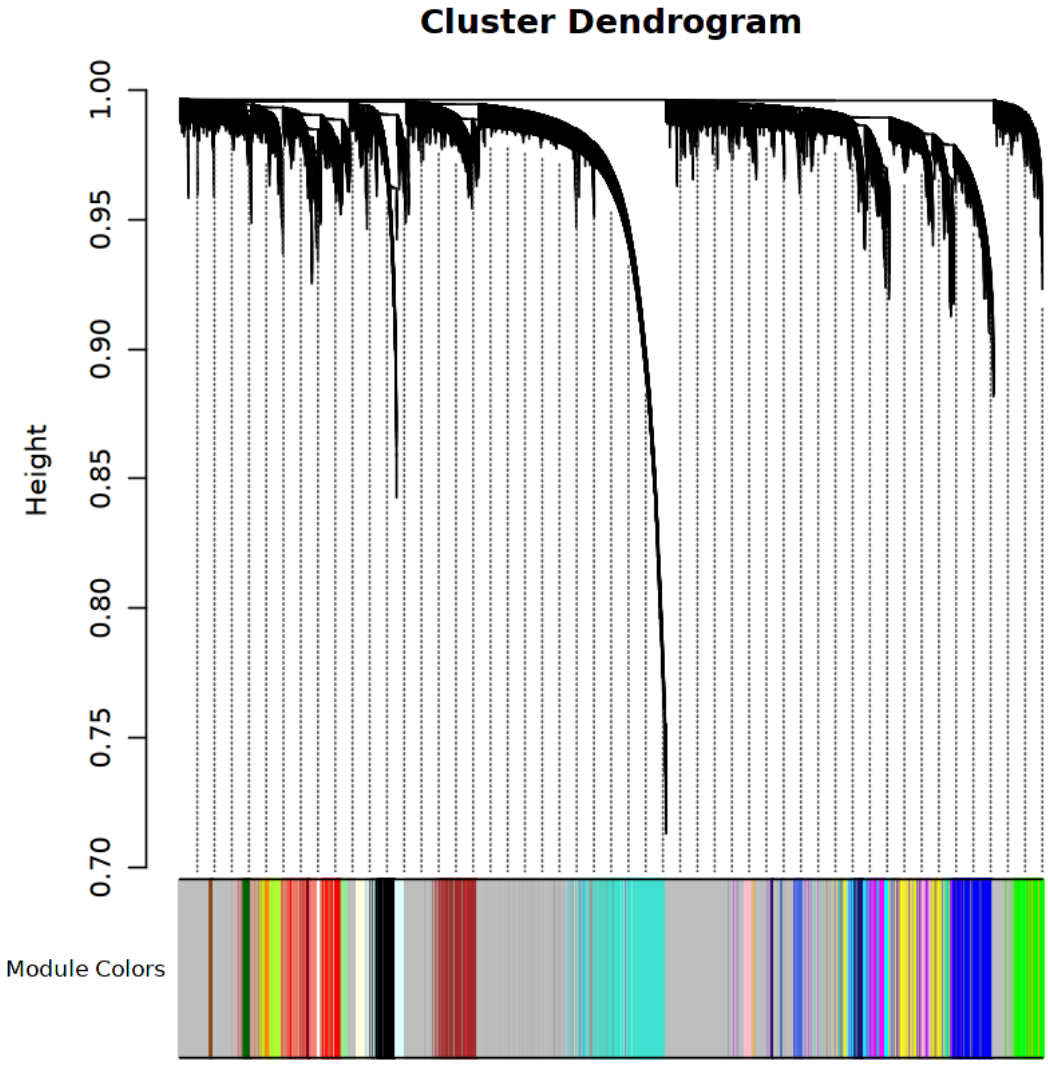
```
27    27   0.9730  -1.44          0.984 4.55e-01  1.80e-02    43.8
28    28   0.9740  -1.41          0.986 3.92e-01  1.22e-02    40.6
29    29   0.9760  -1.39          0.986 3.40e-01  8.41e-03    37.6
30    30   0.9770  -1.38          0.987 2.96e-01  5.79e-03    34.9
Allowing parallel execution with 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 2261 genes from module 1 because their KME is too low.
     ..removing 1620 genes from module 2 because their KME is too low.
     ..removing 169 genes from module 3 because their KME is too low.
     ..removing 185 genes from module 4 because their KME is too low.
     ..removing 179 genes from module 5 because their KME is too low.
     ..removing 102 genes from module 6 because their KME is too low.
     ..removing 118 genes from module 7 because their KME is too low.
     ..removing 103 genes from module 8 because their KME is too low.
     ..removing 71 genes from module 9 because their KME is too low.
     ..removing 168 genes from module 10 because their KME is too low.
     ..removing 93 genes from module 11 because their KME is too low.
     ..removing 61 genes from module 12 because their KME is too low.
     ..removing 5 genes from module 13 because their KME is too low.
     ..removing 178 genes from module 14 because their KME is too low.
     ..removing 12 genes from module 15 because their KME is too low.
     ..removing 35 genes from module 16 because their KME is too low.
     ..removing 95 genes from module 17 because their KME is too low.
     ..removing 11 genes from module 18 because their KME is too low.
     ..removing 37 genes from module 19 because their KME is too low.
     ..removing 1 genes from module 20 because their KME is too low.
     ..removing 3 genes from module 21 because their KME is too low.
     ..removing 12 genes from module 22 because their KME is too low.
     ..removing 24 genes from module 23 because their KME is too low.
     ..removing 9 genes from module 24 because their KME is too low.
     ..removing 1 genes from module 25 because their KME is too low.
     ..removing 5 genes from module 26 because their KME is too low.
     ..removing 7 genes from module 27 because their KME is too low.
```

```
    ..removing 4 genes from module 28 because their KME is too low.
    ..removing 2 genes from module 29 because their KME is too low.
 ..reassigning 244 genes from module 1 to modules with higher KME.
 ..reassigning 80 genes from module 2 to modules with higher KME.
 ..reassigning 119 genes from module 3 to modules with higher KME.
 ..reassigning 53 genes from module 4 to modules with higher KME.
 ..reassigning 21 genes from module 5 to modules with higher KME.
 ..reassigning 13 genes from module 6 to modules with higher KME.
 ..reassigning 12 genes from module 7 to modules with higher KME.
 ..reassigning 31 genes from module 8 to modules with higher KME.
 ..reassigning 39 genes from module 9 to modules with higher KME.
 ..reassigning 3 genes from module 10 to modules with higher KME.
 ..reassigning 8 genes from module 11 to modules with higher KME.
 ..reassigning 20 genes from module 12 to modules with higher KME.
 ..reassigning 25 genes from module 13 to modules with higher KME.
 ..reassigning 11 genes from module 14 to modules with higher KME.
 ..reassigning 6 genes from module 15 to modules with higher KME.
 ..reassigning 9 genes from module 16 to modules with higher KME.
 ..reassigning 11 genes from module 17 to modules with higher KME.
 ..reassigning 29 genes from module 18 to modules with higher KME.
 ..reassigning 8 genes from module 19 to modules with higher KME.
 ..reassigning 5 genes from module 20 to modules with higher KME.
 ..reassigning 4 genes from module 21 to modules with higher KME.
 ..reassigning 1 genes from module 22 to modules with higher KME.
 ..reassigning 5 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.
 ..reassigning 2 genes from module 26 to modules with higher KME.
 ..reassigning 7 genes from module 27 to modules with higher KME.
 ..reassigning 3 genes from module 28 to modules with higher KME.
 ..reassigning 2 genes from module 29 to modules with higher KME.
 ..reassigning 2 genes from module 31 to modules with higher KME.
 ..reassigning 1 genes from module 33 to modules with higher KME.
..merging modules that are too close..
    mergeCloseModules: Merging modules whose distance is less than 0.15
      Calculating new MEs…
```



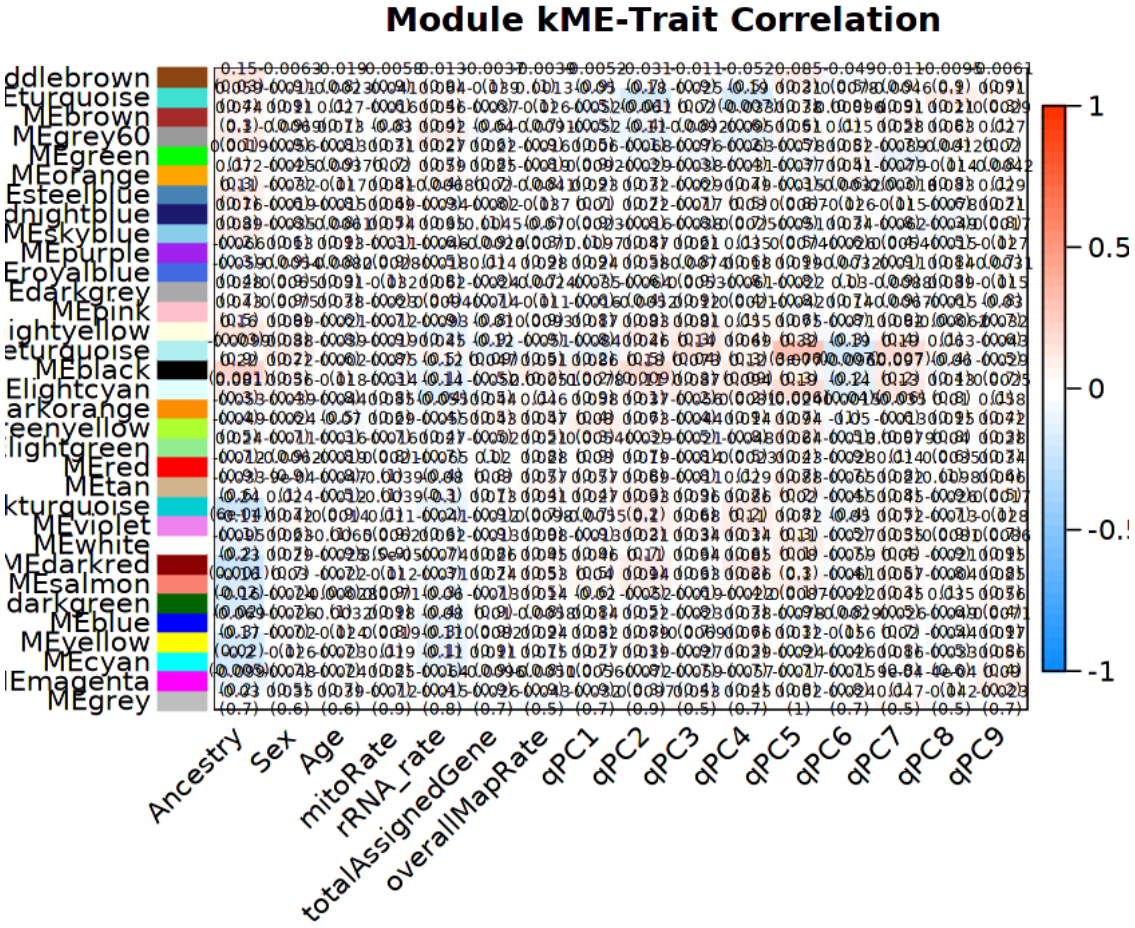
[14]:
```
#3 - TOM Dendogram
plot_cluster_dendrogram()
```

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



[15]:
```
#4 - Module Eigenvalue Correlation with sample's traits
correlate_with_traits()
export_eigengene_tables()
```

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



1.9 Repreducibility Information

[16]:
```
Sys.time()
proc.time()
options(width = 120)
sessioninfo::session_info()
```

```
[1] "2021-07-12 11:41:57 EDT"
```

```
    user   system  elapsed
5164.615 2010.673  859.634
```

```
 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     2021-07-12

 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)
GO.db            3.12.1   2021-04-08 [1] Bioconductor
gridExtra        2.3      2017-09-09 [1] CRAN (R 4.0.2)
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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          1.6.2    2021-05-17 [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)
uuid             0.1-4    2020-02-26 [1] CRAN (R 4.0.2)
vctrs            0.3.8    2021-04-29 [1] CRAN (R 4.0.3)
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 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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