

WGCNA – Intersected Genes Line Plot

```
1  #!/usr/bin/Rscript --vanilla
2  rm(list=ls())
3
4  library(jpeg)
5  library(dplyr)
6  library(tidyr)
7  library(tibble)
8  library(stringr)
9  library(ggplot2)
```

```
26 #####
27 # Constants/Variables
28 #####
29
30 b73_selected_module <- "yellow"
31 o2_selected_module <- "turquoise"
32
33
34 #####
35 # Output folder
36 #####
37 output_path <- file.path(
38   "/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output/2021_07_05_plot_intersected_genes_line_plot"
39 )
40
41 if(!dir.exists(output_path)){
42   dir.create(output_path, showWarnings=FALSE, recursive=TRUE)
43   if(!dir.exists(output_path)){
44     quit(status=1)
45   }
46 }
```

```
49 #####
50 # Read in input file
51 #####
52
53 folder_path = file.path("/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output")
54
55 selected_genotype <- "B73"
56 lnames = load(
57   file = file.path(
58     folder_path,
59     paste0("2021_06_10_", selected_genotype, "_step_by_step_network_construction"),
60     paste0(selected_genotype, "-networkConstruction-stepByStep.RData")
61   )
62 )
63 print(lnames)
64
65 # Replace B73 realted variable names
66 b73Expr = datExpr
67
68 index <- match(sub("^ME", "", colnames(MEs)), moduleColors)
69
70 colnames(MEs) <- paste0("ME", moduleLabels[index])
71
72 b73MEs = orderMEs(MEs, greyName = "ME0")
73 b73Labels = moduleLabels
74 b73Colors = moduleColors
75 b73Tree = geneTree
```

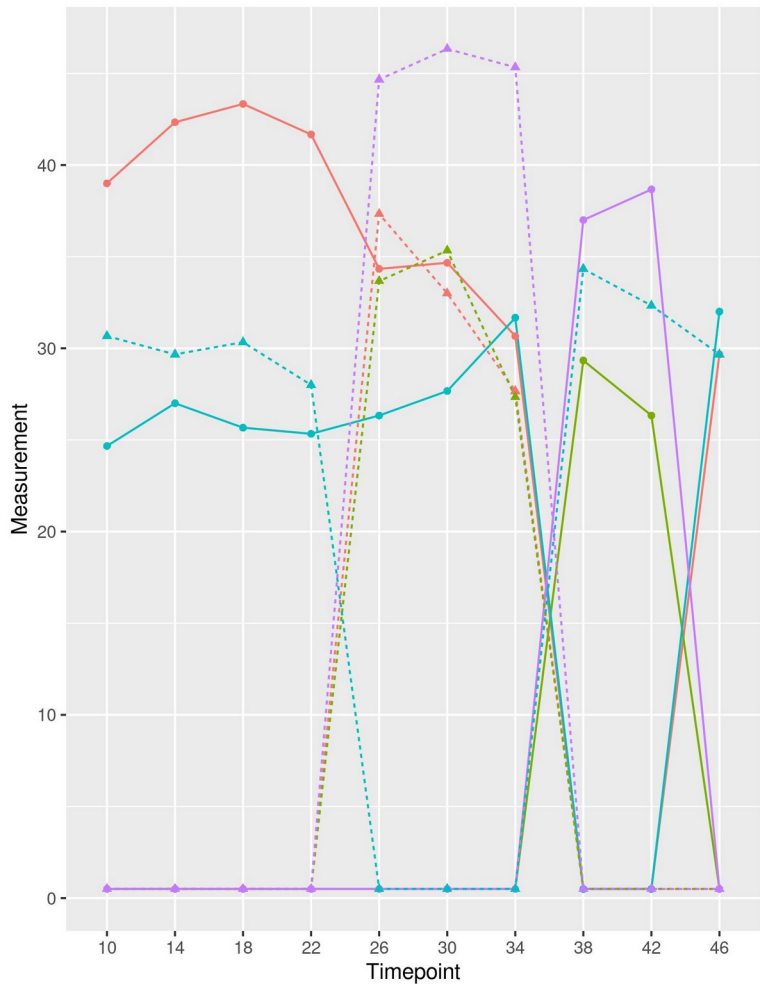
```
83 selected_genotype <- "02"
84 lnames = load(
85   file = file.path(
86     folder_path,
87     paste0("2021_06_10_", selected_genotype, "_step_by_step_network_construction"),
88     paste0(selected_genotype, "-networkConstruction-stepByStep.RData")
89   )
90 )
91 print(lnames)
92
93
94 # Replace 02 related variable names
95 o2Expr = datExpr
96
97 index <- match(sub("^ME", "", colnames(MEs)), moduleColors)
98
99 colnames(MEs) <- paste0("ME", moduleLabels[index])
100
101 o2MEs = orderMEs(MEs, greyName = "ME0")
102 o2Labels = moduleLabels
103 o2Colors = moduleColors
104 o2Tree = geneTree
```

```
126 #####
127 # Overlap modules
128 #####
129
130 b73_genes_colors_df <- data.frame(
131   "Gene" = colnames(b73Expr),
132   "Color" = b73Colors,
133   stringsAsFactors = FALSE
134 )
135
136 o2_genes_colors_df <- data.frame(
137   "Gene" = colnames(o2Expr),
138   "Color" = o2Colors,
139   stringsAsFactors = FALSE
140 )
141
142
143 b73_genes_colors_df <- b73_genes_colors_df %>%
144   filter(Color == b73_selected_module) %>%
145   as.data.frame(stringsAsFactors = FALSE)
146
147 o2_genes_colors_df <- o2_genes_colors_df %>%
148   filter(Color == o2_selected_module) %>%
149   as.data.frame(stringsAsFactors = FALSE)
150
151 print(head(b73_genes_colors_df))
152 print(head(o2_genes_colors_df))
```

```
155 genes_colors_df <- b73_genes_colors_df %>%
156   inner_join(o2_genes_colors_df, by = "Gene") %>%
157   as.data.frame(stringsAsFactors = FALSE)
158
159 print(head(genes_colors_df))
160
161
162 b73Expr <- b73Expr[, genes_colors_df$Gene] %>%
163   rownames_to_column(var = "Sample") %>%
164   separate(Sample, c("Sample", "Timepoint"), sep = "\\_(?=[^\\_]+)$", extra = "drop", fill = "right") %>%
165   pivot_longer(!c("Sample", "Timepoint"), names_to = "Genotype", values_to = "Measurement") %>%
166   as.data.frame(stringsAsFactors = FALSE)
167 o2Expr <- o2Expr[, genes_colors_df$Gene] %>%
168   rownames_to_column(var = "Sample") %>%
169   separate(Sample, c("Sample", "Timepoint"), sep = "\\_(?=[^\\_]+)$", extra = "drop", fill = "right") %>%
170   pivot_longer(!c("Sample", "Timepoint"), names_to = "Genotype", values_to = "Measurement") %>%
171   as.data.frame(stringsAsFactors = FALSE)
172
173
174 expr <- rbind(b73Expr, o2Expr)
175
176 expr$Sample_Genotype <- paste(expr$Sample, expr$Genotype, sep = "_")
177
178 print(head(expr))
179 print(tail(expr))
```

```
182 #####
183 # Plot expression of genes
184 #####
185
186 expr$Timepoint <- factor(expr$Timepoint, levels = unique(expr$Timepoint))
187 expr$Genotype <- factor(expr$Genotype, levels = unique(expr$Genotype))
188 expr$Sample <- factor(expr$Sample, levels = unique(expr$Sample))
189 expr$Sample_Genotype <- factor(expr$Sample_Genotype, levels = unique(expr$Sample_Genotype))
190
191 p <- ggplot(data=expr, mapping=aes(x=Timepoint, y=Measurement, group=Sample_Genotype, color=Genotype, linetype=Sample, shape=Sample)) +
192   geom_line()+
193   geom_point()
194
195 ggsave(
196   filename=paste0(b73_selected_module, "_", o2_selected_module, "_line_plot.jpg"),
197   plot=p,
198   path=output_path
199 )
```


B73-Red : O2-Brown



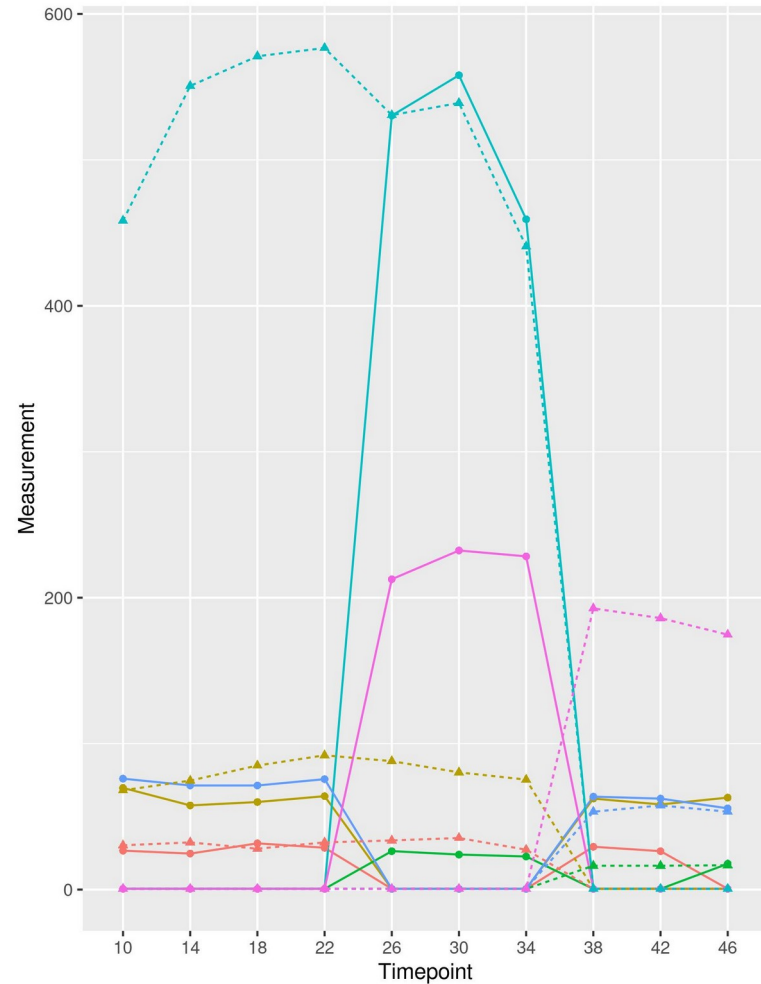
Genotype

- Zm00001d007900
- Zm00001d010618
- Zm00001d010867
- Zm00001d018979

Sample

- B73
- O2

B73-Yellow : O2-Turquoise



Genotype

- Zm00001d012513
- Zm00001d015992
- Zm00001d021018
- Zm00001d034773
- Zm00001d048253
- Zm00001d054043

Sample

- B73
- O2

