WGCNA – Intersected Genes Line Plot

```
#!/usr/bin/Rscript --vanilla
rm(list=ls())

library(jpeg)
library(dplyr)
library(tidyr)
library(tibble)
library(stringr)
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  }
```

```r
##################################################
# Read in input file
##################################################

folder_path = file.path("/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output")

selected_genotype <- "B73"
lnames = load(
  file = file.path(
    folder_path,
    paste0("2021_06_10_", selected_genotype, "_step_by_step_network_construction"),
    paste0(selected_genotype, "-networkConstruction-stepByStep.RData")
  )
)
print(lnames)

# Replace B73 realted variable names
b73Expr = datExpr

index <- match(sub("^ME", "", colnames(MEs)), moduleColors)

colnames(MEs) <- paste0("ME", moduleLabels[index])

b73MEs = orderMEs(MEs, greyName = "ME0")
b73Labels = moduleLabels
b73Colors = moduleColors
b73Tree = geneTree
```

```r
selected_genotype <- "O2"
lnames = load(
  file = file.path(
    folder_path,
    paste0("2021_06_10_", selected_genotype, "_step_by_step_network_construction"),
    paste0(selected_genotype, "-networkConstruction-stepByStep.RData")
  )
)
print(lnames)


# Replace O2 realted variable names
o2Expr = datExpr

index <- match(sub("^ME", "", colnames(MEs)), moduleColors)

colnames(MEs) <- paste0("ME", moduleLabels[index])

o2MEs = orderMEs(MEs, greyName = "ME0")
o2Labels = moduleLabels
o2Colors = moduleColors
o2Tree = geneTree
```

```r
##################################################
# Overlap modules
##################################################

b73_genes_colors_df <- data.frame(
  "Gene" = colnames(b73Expr),
  "Color" = b73Colors,
  stringsAsFactors = FALSE
)

o2_genes_colors_df <- data.frame(
  "Gene" = colnames(o2Expr),
  "Color" = o2Colors,
  stringsAsFactors = FALSE
)


b73_genes_colors_df <- b73_genes_colors_df %>%
  filter(Color == b73_selected_module) %>%
  as.data.frame(stringsAsFactors = FALSE)

o2_genes_colors_df <- o2_genes_colors_df %>%
  filter(Color == o2_selected_module) %>%
  as.data.frame(stringsAsFactors = FALSE)

print(head(b73_genes_colors_df))
print(head(o2_genes_colors_df))
```

```r
genes_colors_df <- b73_genes_colors_df %>%
  inner_join(o2_genes_colors_df, by = "Gene") %>%
  as.data.frame(stringsAsFactors = FALSE)

print(head(genes_colors_df))


b73Expr <- b73Expr[, genes_colors_df$Gene] %>%
  rownames_to_column(var = "Sample") %>%
  separate(Sample, c("Sample", "Timepoint"), sep = "\\_(?=[^\\_]+$)", extra = "drop", fill = "right") %>%
  pivot_longer(!c("Sample", "Timepoint"), names_to = "Genotype", values_to = "Measurement") %>%
  as.data.frame(stringsAsFactors = FALSE)
o2Expr <- o2Expr[, genes_colors_df$Gene] %>%
  rownames_to_column(var = "Sample") %>%
  separate(Sample, c("Sample", "Timepoint"), sep = "\\_(?=[^\\_]+$)", extra = "drop", fill = "right") %>%
  pivot_longer(!c("Sample", "Timepoint"), names_to = "Genotype", values_to = "Measurement") %>%
  as.data.frame(stringsAsFactors = FALSE)


expr <- rbind(b73Expr, o2Expr)

expr$Sample_Genotype <- paste(expr$Sample, expr$Genotype, sep = "_")

print(head(expr))
print(tail(expr))
```

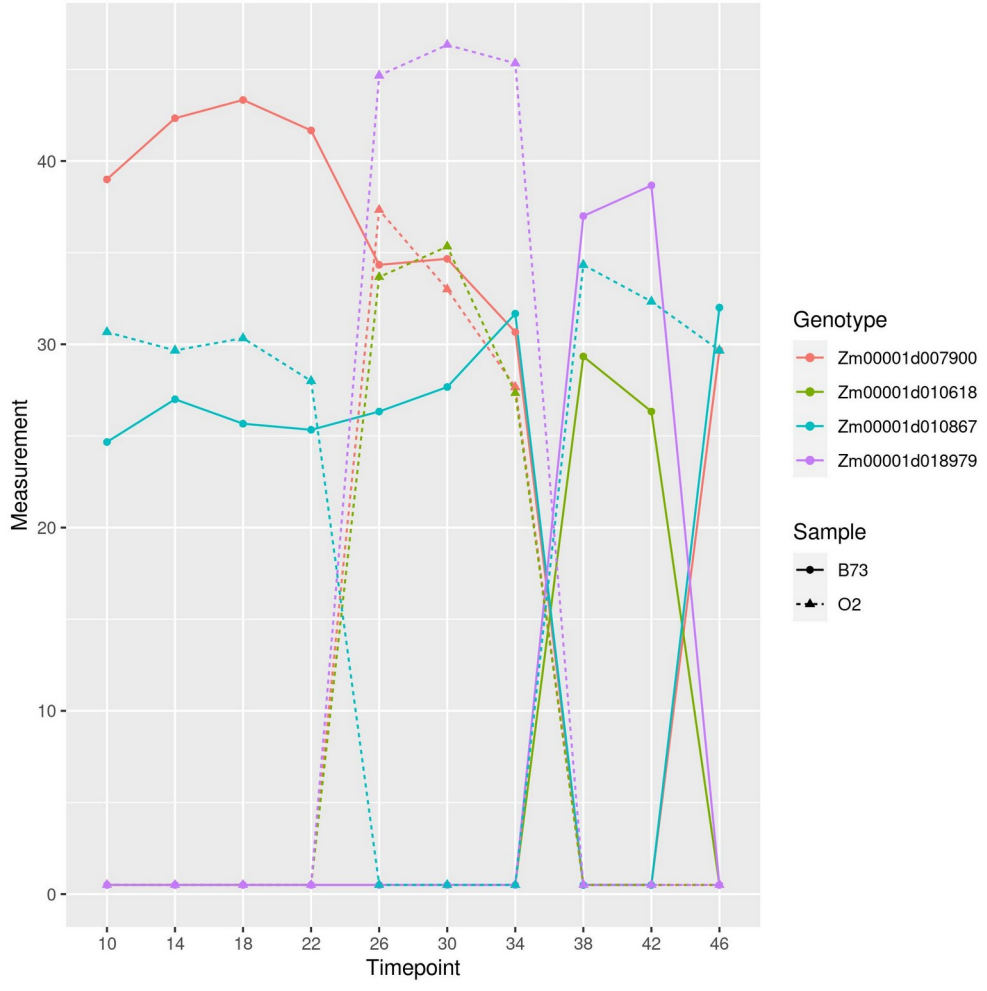
```r
##################################################
# Plot expression of genes
##################################################

expr$Timepoint <- factor(expr$Timepoint, levels = unique(expr$Timepoint))
expr$Genotype <- factor(expr$Genotype, levels = unique(expr$Genotype))
expr$Sample <- factor(expr$Sample, levels = unique(expr$Sample))
expr$Sample_Genotype <- factor(expr$Sample_Genotype, levels = unique(expr$Sample_Genotype))

p <- ggplot(data=expr, mapping=aes(x=Timepoint, y=Measurement, group=Sample_Genotype, color=Genotype, linetype=Sample, shape=Sample)) +
  geom_line()+
  geom_point()

ggsave(
  filename=paste0(b73_selected_module, "_", o2_selected_module, "_line_plot.jpg"),
  plot=p,
  path=output_path
)
```

B73-Red : O2-Brown



B73-Yellow : O2-Turquoise