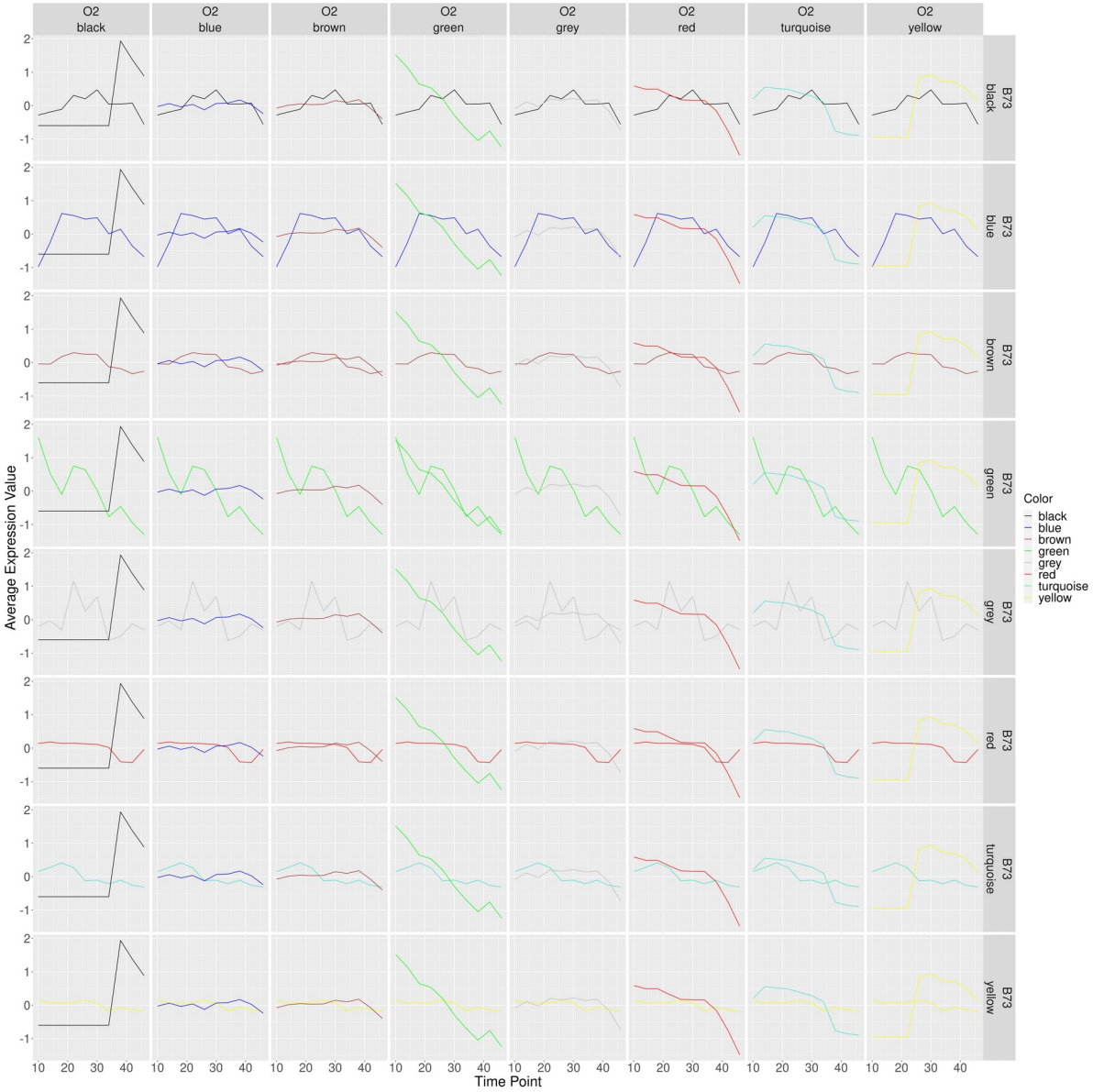
WGCNA – Average Expression Plot for B73 and O2

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

library(jpeg)
library(dplyr)
library(tidyr)
library(tibble)
library(stringr)
library(ggplot2)

set.seed(1)


######################################################
# Constants/Variables
######################################################


######################################################
# Output folder
######################################################
output_path <- file.path("/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output/2021_06_23_B73_O2_average_expression_plot"

if(!dir.exists(output_path)){
  dir.create(output_path, showWarnings=FALSE, recursive=TRUE)
  if(!dir.exists(output_path)){
    quit(status=1)
  }
}
```

```r
##################################################
# Read in input files
##################################################
b73_dat = read.csv(
  file = file.path("/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output/2021_06_10_B73_step_by_step_network_construction
  header = TRUE,
  row.names = 1,
  check.names = FALSE,
  stringsAsFactors = FALSE
)

o2_dat = read.csv(
  file = file.path("/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output/2021_06_10_O2_step_by_step_network_construction/
  header = TRUE,
  row.names = 1,
  check.names = FALSE,
  stringsAsFactors = FALSE
)
```

```r
dat <- b73_dat %>%
  dplyr::left_join(o2_dat, by = "Time", suffix = c(".B73", ".O2")) %>%
  as.data.frame(stringsAsFactors = FALSE)

print(head(dat))
print(tail(dat))
print(dim(dat))


##################################################
# Plot average expression plot
##################################################
p <- ggplot(data = dat, mapping = aes(x = Time, y = Measurement.B73)) +
  ggplot2::geom_line(mapping = ggplot2::aes(x = Time, y = Measurement.B73, group = Module.B73, color = Module.B73)) +
  ggplot2::geom_line(mapping = ggplot2::aes(x = Time, y = Measurement.O2, group = Module.O2, color = Module.O2)) +
  facet_grid(Sample.B73 + Module.B73 ~ Sample.O2 + Module.O2, scales = "free") +
  labs(x = "Time Point", y = "Average Expression Value", color="Color") +
  scale_color_manual(values=unique(c(dat$Module.B73, dat$Module.O2)))


ggsave(
  filename = "average_expression.png",
  plot = p,
  path = output_path,
  width = 20,
  height = 20
)
```


O2 black
O2 blue
O2 brown
O2 green
O2 grey
O2 red
O2 turquoise
O2 yellow
B73 black
B73 blue
B73 brown
B73 green
B73 grey
B73 red
B73 turquoise
B73 yellow
Average Expression Value
Time Point
Color
black
blue
brown
green
grey
red
turquoise
yellow