R Notebook

Correlation (log2FC) - Density plot - 12166 genes

```
library(ggplot2)

data = read.delim('~/DEGs_Infected_vs_Control_Combined.csv')

data = data[,4:7]
class = c('Adults', 'Children', 'Mice - LN', 'Mice - Feet')
colnames(data) = class
method = c('pearson', 'spearman')

for (i in class){
  for (j in class){
    for (k in method) {
      x = as.vector(data[,i])
      y = as.vector(data[,j])

      ## Pearson correlation test
      Rp <- cor.test(x, y, method = k)
      if (Rp$p.value == 0) {Pp <- Rp$p.value}
      else { Pp <- formatC(Rp$p.value, format = "e", digits = 2)}
      Pe <- round(Rp$estimate, 5)

      text_x <- max(x)-1
      text_y <- max(y)-1
      text = paste("R = ",Pe,"\nP-value = ",Pp)

      d = densCols(x, y, colramp = colorRampPalette(rev(rainbow(10, end = 4/6))))

      plot <- ggplot(data=data, aes(x= x, y = y, col =d)) +
        ggtitle(paste(k, "correlation")) +
        ylab(paste('Relative expression', j)) +
        xlab(paste('Relative expression', i)) +
        stat_smooth(method = "lm", size=1, color="black",linetype ="dashed",alpha=0.5) +
        geom_point() +
        annotate("text", x = text_x, y = text_y, size=7, label = text) +
        theme(axis.text=element_text(size=12), axis.title=element_text(size=20))+
      scale_color_identity() +
      theme_bw()

      png(file = paste0('correlation_relative_expression_',i,'.vs.',j,'_',k,'_12166_genes.png'),width=1

      print(plot)

      dev.off()
    }
  }

}
```

```
## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
```

```
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties
```

Correlation (log2FC) - Density plot - Only DEGs - Union

```r
library(ggplot2)

data = read.delim('~/DEGs_Infected_vs_Control_Combined.csv')

data = data[,c(4:7,16:19)]
class = c('Adults', 'Children', 'Mice - LN', 'Mice - Feet')
```

```r
deg = colnames(data[,5:8])
colnames(data) = c(class, deg)
method = c('pearson', 'spearman')

for (i in 1:4){
  for (j in 1:4){
    for (k in method) {
      x = as.vector(data[data[,i+4] != 'NO' | data[,j+4] != 'NO',i])
      y = as.vector(data[data[,i+4] != 'NO' | data[,j+4] != 'NO',j])

      ## Pearson correlation test
      Rp <- cor.test(x, y, method = k)
      if (Rp$p.value == 0) {Pp <- Rp$p.value}
      else { Pp <- formatC(Rp$p.value, format = "e", digits = 2)}
      Pe <- round(Rp$estimate, 5)

      text_x <- max(x)-1
      text_y <- max(y)-1
      text = paste("R = ",Pe,"\nP-value = ",Pp)

      d = densCols(x, y, colramp = colorRampPalette(rev(rainbow(10, end = 4/6))))

      plot <- ggplot(data=data[data[,i+4] != 'NO' | data[,j+4] != 'NO',], aes(x= x, y = y, col =d)) +
        ggtitle(paste(k, "correlation")) +
        ylab(paste('Relative expression', class[j])) +
        xlab(paste('Relative expression', class[i])) +
        stat_smooth(method = "lm", size=1, color="black",linetype ="dashed",alpha=0.5) +
        geom_point() +
        annotate("text", x = text_x, y = text_y, size=7, label = text) +
        theme(axis.text=element_text(size=12), axis.title=element_text(size=20))+
      scale_color_identity() +
      theme_bw()

      png(file = paste0('correlation_relative_expression_',class[i],'.vs.',class[j],'_',k,'_DEGs_union.p

      print(plot)

      dev.off()
    }
  }

}
```

```
## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties
```

```
## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties
```

Correlation (log2FC) - Density plot - Only DEGs - Intersection

```r
library(ggplot2)

data = read.delim('~/DEGs_Infected_vs_Control_Combined.csv')

data = data[,c(4:7,16:19)]
class = c('Adults', 'Children', 'Mice - LN', 'Mice - Feet')
deg = colnames(data[,5:8])
colnames(data) = c(class, deg)
method = c('pearson', 'spearman')

for (i in 1:4){
  for (j in 1:4){
    for (k in method) {
      x = as.vector(data[data[,i+4] != 'NO' & data[,j+4] != 'NO',i])
      y = as.vector(data[data[,i+4] != 'NO' & data[,j+4] != 'NO',j])
```

```
      ## Pearson correlation test
      Rp <- cor.test(x, y, method = k)
      if (Rp$p.value == 0) {Pp <- Rp$p.value}
      else { Pp <- formatC(Rp$p.value, format = "e", digits = 2)}
      Pe <- round(Rp$estimate, 5)

      text_x <- max(x)-1
      text_y <- max(y)-1
      text = paste("R = ",Pe,"\nP-value = ",Pp)

      d = densCols(x, y, colramp = colorRampPalette(rev(rainbow(10, end = 4/6))))

      plot <- ggplot(data=data[data[,i+4] != 'NO' & data[,j+4] != 'NO',], aes(x= x, y = y, col =d)) +
        ggtitle(paste(k, "correlation")) +
        ylab(paste('Relative expression', class[j])) +
        xlab(paste('Relative expression', class[i])) +
        stat_smooth(method = "lm", size=1, color="black",linetype ="dashed",alpha=0.5) +
        geom_point() +
        annotate("text", x = text_x, y = text_y, size=7, label = text) +
        theme(axis.text=element_text(size=12), axis.title=element_text(size=20))+
      scale_color_identity() +
      theme_bw()

      png(file = paste0('correlation_relative_expression_',class[i],'.vs.',class[j],'_',k,'_DEGs_interse

      print(plot)

      dev.off()
    }
  }

}
```

```
## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties
```

```
## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties

## Warning in cor.test.default(x, y, method = k): Cannot compute exact p-value
## with ties
```