

# Analysis

Charlotte Dawson

31/07/2020

## Fake analysis

A fake analysis which uses packages from CRAN (ggplot2), Bioconductor (limma), and github (ggprism).

## Load libraries

```
library(ggplot2)
library(ggprism)
library(limma)

set.seed(1)
```

## Output figures

Generate an MA plot.

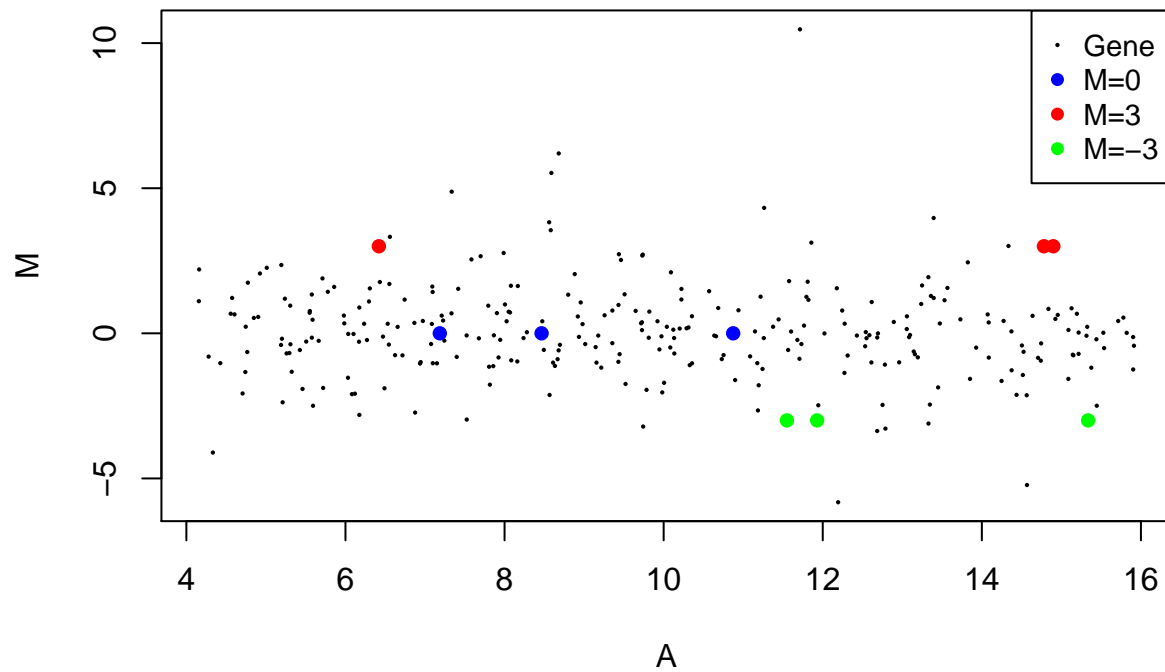
```
MA <- new("MAList")
MA$A <- runif(300, 4, 16)
MA$M <- rt(300, df = 3)

# Spike-in values
MA$M[1:3] <- 0
MA$M[4:6] <- 3
MA$M[7:9] <- -3

status <- rep("Gene", 300)
status[1:3] <- "M=0"
status[4:6] <- "M=3"
status[7:9] <- "M=-3"
values <- c("M=0", "M=3", "M=-3")
col <- c("blue", "red", "green")

# base plot with limma
plotMA(MA, main="MA-Plot with 12 spiked-in points",
       status=status, values=values, hl.col=col)
```

## MA-Plot with 12 spiked-in points



```
# ggplot with ggprism theme
MA.df <- data.frame(MA$M, MA$A, status, colour = status != "Gene")

ggplot(MA.df, aes(x = MA.A, y = MA.M, colour = colour)) +
  geom_point() +
  theme_prism() +
  scale_color_prism("colorblind_safe")
```

