```r
# xy = matrix(runif(10000), ncol = 2)
# xy = xy[xy[,1] < 0.1 | xy[,2] < 0.1,]
# xy = xy %*% matrix(c(1, 0.4, 0.4, 1), ncol = 2)
# xy = xy[xy[,1] <= 1 & xy[,2] <= 1,]

xyc = read.csv("synthetic_data.csv")
xy = xyc[,1:2]

set.seed(1234)
subset = sample.int(nrow(xy), 300)

library(fastICA)
library(NMF)

## Loading required package:  methods
## Loading required package:  pkgmaker
## Loading required package:  registry
## Loading required package:  rngtools
## Loading required package:  cluster
## NMF - BioConductor layer [OK] | Shared memory capabilities [OK]
## | Cores 2/2

fit.pca = prcomp(xy, center = TRUE, scale = FALSE)

temp = replicate(1000, fastICA(xy, 2, method = "C"), simplify = FALSE)
temp2 = sapply(temp, function(x) shapiro.test(x$S)$statistic)
fit.ica = temp[[which.max(temp2)]]

fit.nmf = nmf(t(xy[subset,]), rank = 2, nrun = 20, method = "snmf/r")
```

```r
library(NMF)
library(RColorBrewer)
library(ggplot2)
library(grid)

pal = brewer.pal(3, "Set2")[c(2, 3, 1)]
pal = sapply(pal, function(col) do.call(rgb, c(as.list(col2rgb(col)/255), alpha = 0.5)))
syms = c(19, 4, 21)
col = pal[xyc[,3]]
pch = syms[xyc[,3]]

# plot(0 ~ 0, type = "n", xlab = "Gene 1", ylab = "Gene 2", xlim = c(0, 1), ylim = c(0, 1),
# # arrows(
# #   x0 = c(0, 0),
# #   y0 = c(0, 0),
```

```r
# #   x1 = c(0.5, 1),
# #   y1 = c(1, 0.45),
# #   col = "lightgrey", lwd = 5)
# points(xy[subset,1], xy[subset,2], col = "black", pch = pch[subset])
# legend("topright", legend = c("State A", "State B", "Transition State"), pch = syms[c(3,

# for (spec in list(list(fit.pca$rotation, colMeans(xy)), list(fit.ica$A, colMeans(xy)), lis
# {
#  plot(xy[subset,1], xy[subset,2], col = rgb(0, 0, 0, 0.5), pch = pch[subset], xlab = "",
#  temp = spec[[1]]
#  temp = t(t(temp) / sqrt(colSums(temp^2)) / 2)
#  arrows(
#  x0 = spec[[2]][1],
#  y0 = spec[[2]][2],
#  x1 = temp[1,] + spec[[2]][1],
#  y1 = temp[2,] + spec[[2]][2],
#  col = "black", lwd = 5)
# }

ggplot(data.frame(x = xyc[,1], y = xyc[,2], State = as.factor(c("B", "Transition", "A")[xyc
        geom_point() +
        coord_fixed(xlim = c(0, 1), ylim = c(0, 1), ratio = 1) +
        theme_bw() +
        xlab("Gene 1") + ylab("Gene 2") +
        theme(axis.ticks = element_blank(), axis.text.x = element_blank(), axis.text.y = ele
        scale_shape_manual(values = c(21, 19, 4))
```
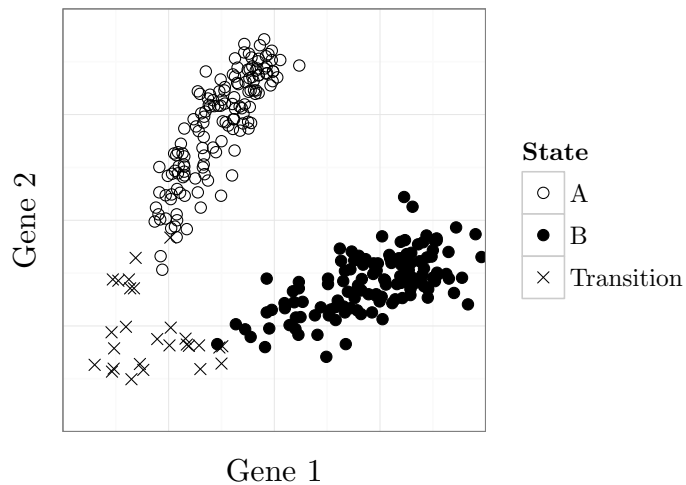


```r
baseplot = ggplot(data.frame(x = xyc[,1], y = xyc[,2], State = as.factor(c("B", "Transition'
        geom_point(col = "grey") +
```

```
        coord_fixed(xlim = c(0, 1), ylim = c(0, 1), ratio = 1) +
        theme_bw() +
        theme(axis.ticks = element_blank(), axis.text.x = element_blank(), axis.text.y = ele
        scale_shape_manual(values = c(21, 19, 4)) +
        theme(legend.position="none")


for (spec in list(list(fit.pca$rotation, colMeans(xy)), list(fit.ica$A, colMeans(xy)), list(
{
        temp = spec[[1]]
        temp = t(t(temp) / sqrt(colSums(temp^2)) / 2)
        thisplot = baseplot +
                geom_segment(x = spec[[2]][1], xend = temp[1,1] + spec[[2]][1], y = spec[[2]
                        arrow = arrow(length = unit(0.5, "cm")), size = 1.5, colour = "black
                geom_segment(x = spec[[2]][1], xend = temp[1,2] + spec[[2]][1], y = spec[[2]
                        arrow = arrow(length = unit(0.5, "cm")), size = 1.5, colour = "black
        print(thisplot)
}
```