SVD Example

2022-08-30

This example is due to Dr Hua Zhou (UCLA biostatistcs) from my computing course. These are two handwritten 3's. We want to align one 3 on top of the other.

```r
X <- read.csv("~/Course to teach/Computing/SVD example/X.txt", header=FALSE)

Y <- read.csv("~/Course to teach/Computing/SVD example/Y.txt", header=FALSE)

X <- as.matrix(X)
Y <- as.matrix(Y)

plot(X, type='b', col=1, xlim=range(c(X[,1], Y[,1])), ylim=range(c(X[,2], Y[,2])))
points(Y, type='b', col=2)
```
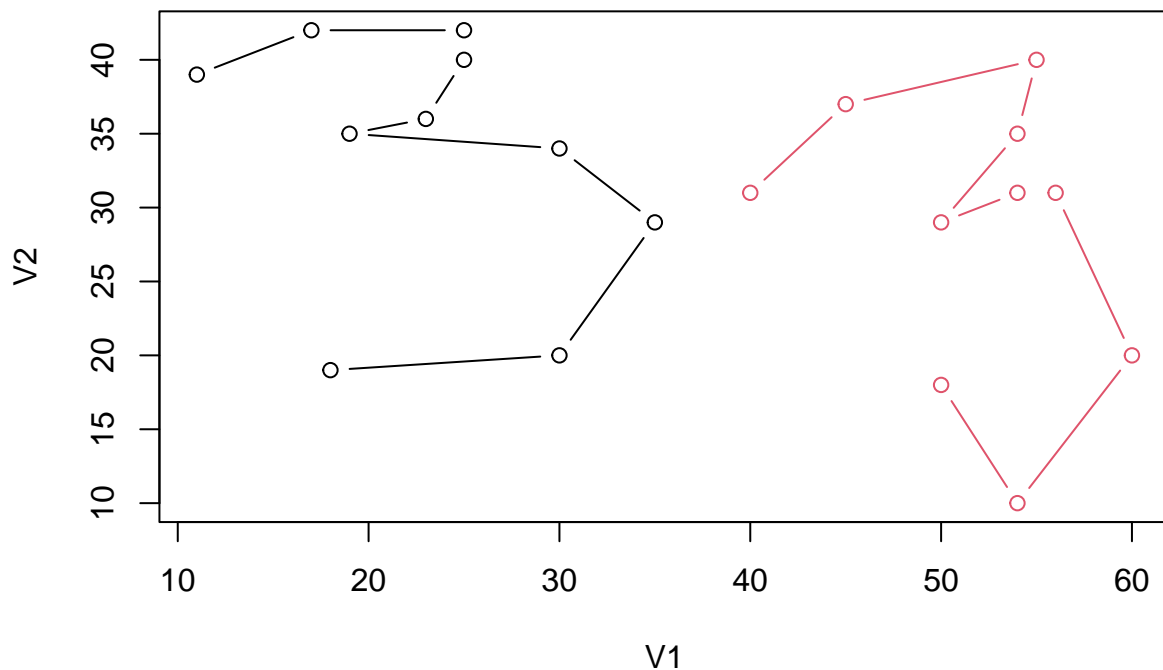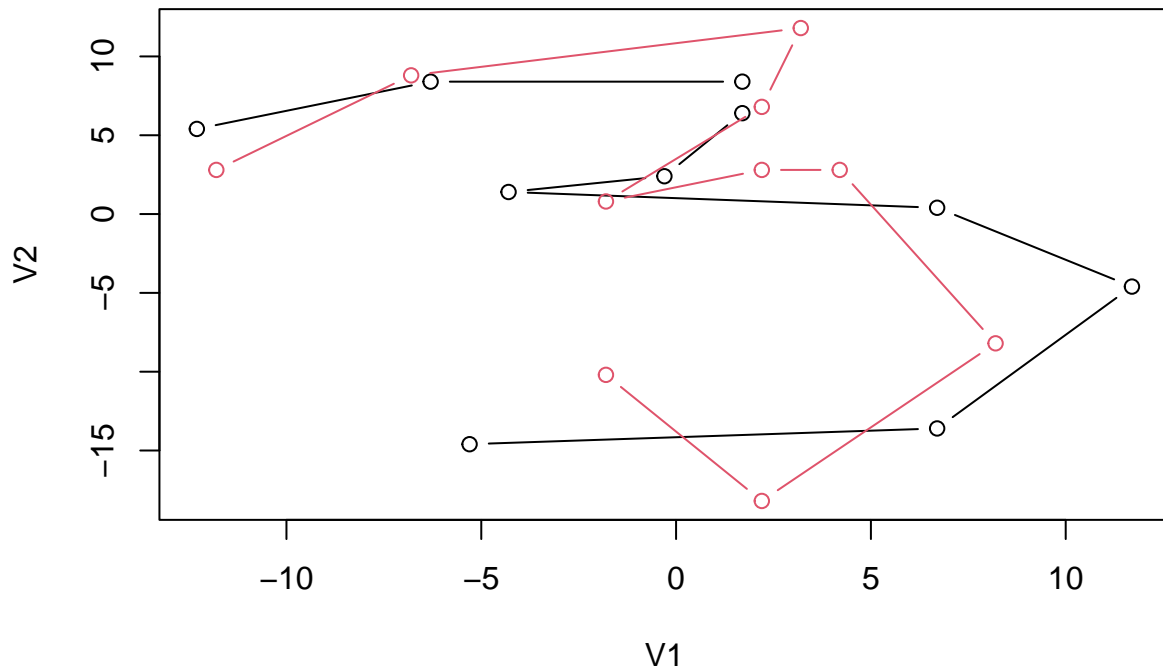

We first mean center the two images and visualize.

```r
X1 <- X - matrix(colMeans(X), nrow(X), 2, byrow = T)
Y1 <- Y - matrix(colMeans(Y), nrow(Y), 2, byrow = T)
```

1

```
plot(X1, type='b', col=1, xlim=range(c(X1[,1], Y1[,1])), ylim=range(c(X1[,2], Y1[,2])))
points(Y1, type='b', col=2)
```
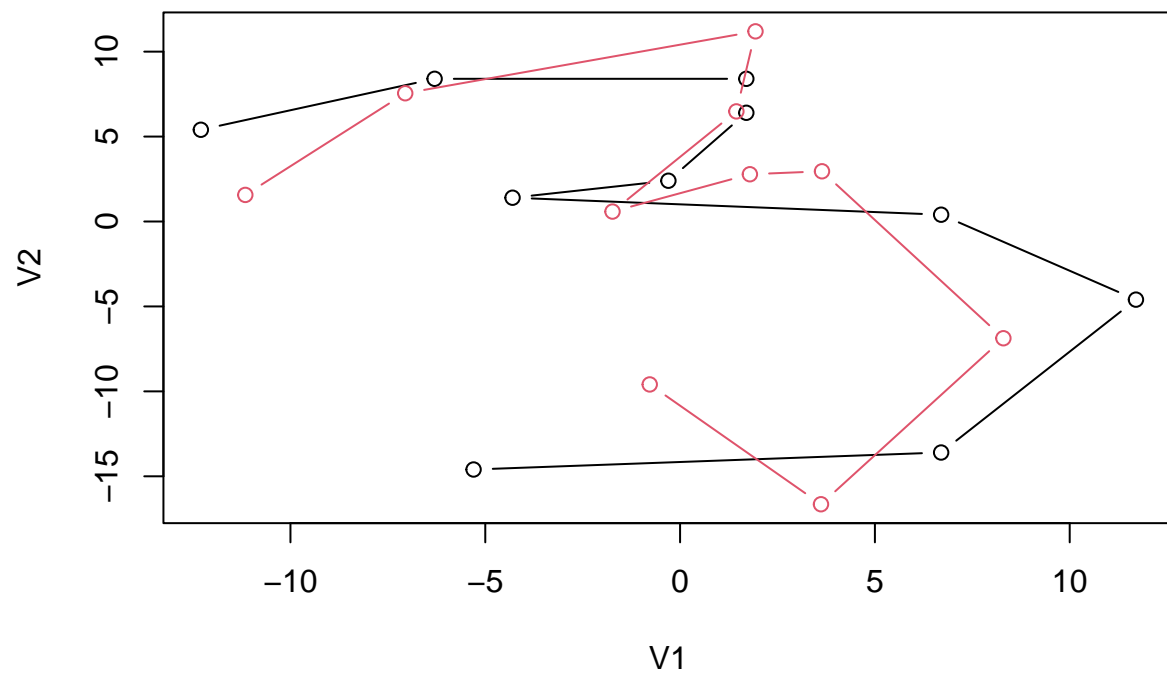

The difference between images is

```
sum((X1-Y1)^2)
```

```
## [1] 180.9
```

We now align the two images on top of the other using SVD and also compute a scalar factor, specifically we solve $\min_{\beta,\mathbf{O}} \|X_1 - \beta Y_1 \mathbf{O}\|_F^2$, where $\mathbf{O}$ is an orthogonal matrix and β is a scalar.

```
crosscov <- t(X1)%*%Y1
crosscovSV <- svd(crosscov) #SVD helps o get crosscov = crosscovSV$u%*%diag(crosscovSV$d)%*%t(crosscovS

O <- crosscovSV$v %*% t(crosscovSV$u)

Y2 <- Y1 %*% O

fit <- lm(array(X1)~array(Y2)-1)
beta <- fit$coefficients

X1hat <- beta*Y2

plot(X1, type='b', col=1, xlim=range(c(X1[,1], X1hat[,1])), ylim=range(c(X1[,2], X1hat[,2])))
points(X1hat, type='b', col=2)
```

The difference between images after above transformation is

```
sum((X1-X1hat)^2)
```

```
## [1] 166.5321
```

Note that the error is reduced after the transformation.