

Self-Organizing Map

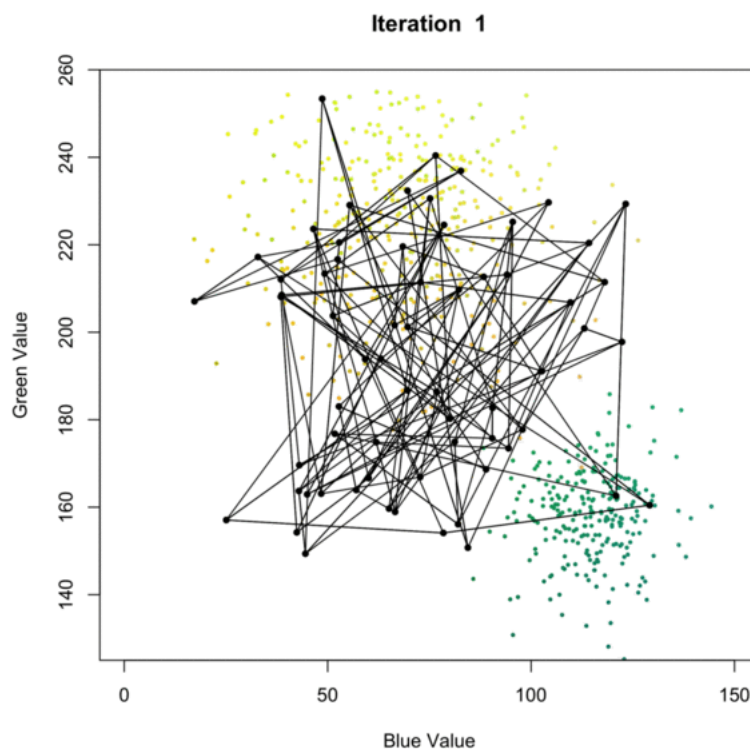
Ruoqing Zhu

Last Updated: December 05, 2021

Self-Organizing Map

Basic Concepts

I found the best demonstration of the Self-Organizing Map algorithm is the following graph that displays it over iterations. It is available at this website (<https://annalyzin.wordpress.com/2017/11/02/self-organizing-map/>):



Let's understand this by pairing it with the algorithm. There are several different algorithms available, but one of the most popular ones is proposed by @kohonen1990self. Here, we present a SOM with a 2-dimensional output. The following are the inputs:

- $\{x_i\}_{i=1}^n$ is a set of n observations, with dimension p (the yellow and green dots in the figure).
- w_{ij} , $i = 1, \dots, p$, $j = 1, \dots, q$ are a grid of centers (the connected black dots). They are similar to the centers in a k-mean algorithm. However, they also preserve some geometric relationships among w_{ij} 's, meaning that w_{ij} 's are closer if their indices i, j are closer (connected in the figure).
- α this is a learning rate between $[0, 1]$. This controls how fast the w_{ij} 's are updated.

- r is also a tuning parameter. This controls how many w_{ij} 's will be updated at each iteration

Now, we look at the algorithm. This is different from k -means because we do not use all the observations immediately. The algorithm works by stream-in the observations one-by-one. Whenever a new observation x_k , $k = 1, \dots, n$ comes in, we will update the centers w_{ij} 's by the following:

- For all w_{ij} , calculate the distance between each w_{ij} and x_k . Let $d_{ij} = \|x_k - w_{ij}\|$. By default, we use Euclidean distance.
- Select the closest w_{ij} , denoted as w_*
- Update each w_{ij} based on the fomular $w_{ij} = w_{ij} + \alpha h(w_*, w_{ij}, r) \|x_k - w_{ij}\|$

After each iteration (updating with one more observation), we will decrease the value of α and r . In the kohonen package, the α starts at 0.05, and gradually decreases to 0.01, while r is chosen to be 2/3 of all cluster means at the first iteration.

Example: Handwritten Digit Data

Using the kohonen package, we perform a SOM on the Handwritten Digit Recognition Data. The heatmap shows how each w_{ij} is away from it's neighboring w_{ij} 's. The extreme bright one means that the center is quite isolated by itself.

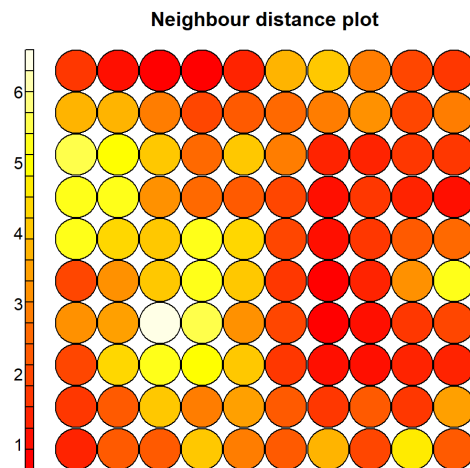
Hide

```
library(kohonen)
## Warning: package 'kohonen' was built under R version 4.1.2

# Handwritten Digit Recognition Data
library(ElemStatLearn)

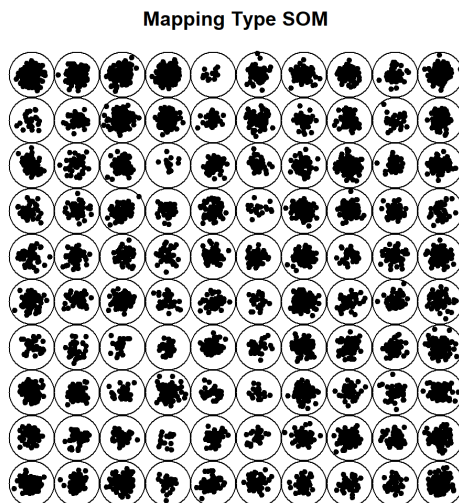
# the first column is the true digit
dim(zip.train)
## [1] 7291 257

# for speed concern, I only use a few variables (pixels)
zip.SOM <- som(zip.train[, seq(2, 257, length.out = 10)],
               grid = somgrid(10, 10, "rectangular"))
plot(zip.SOM, type = "dist.neighbours")
```



Hide

```
plot(zip.SOM, type = "mapping", pchs = 20,
     main = "Mapping Type SOM")
```



Hide

```
# plot(zip.SOM, main = "Default SOM Plot")

# you can try using all the pixels
# zip.SOM <- som(zip.train[, 2:257],
#               grid = somgrid(10, 10, "rectangular"))
# plot(zip.SOM, type = "dist.neighbours")
```

We could also look at the class labels (digits) coming out of the SOM. Particularly the plot on the right-hand side shows the proportion of subjects with each label for the subjects in each cluster (using a pie chart).

Hide

```

set.seed(1)
zip.SOM2 <- xyf(zip.train[, seq(2, 257, length.out = 10)],
               classvec2classmat(zip.train[, 1]),
               grid = somgrid(10, 10, "hexagonal"), rlen = 300)
par(mfrow = c(1, 2))
plot(zip.SOM2, type = "codes", main = c("Codes X", "Codes Y"))
zip.SOM2.hc <- cutree(hclust(dist(zip.SOM2$codes[[2]])), 10)
add.cluster.boundaries(zip.SOM2, zip.SOM2.hc)

```

