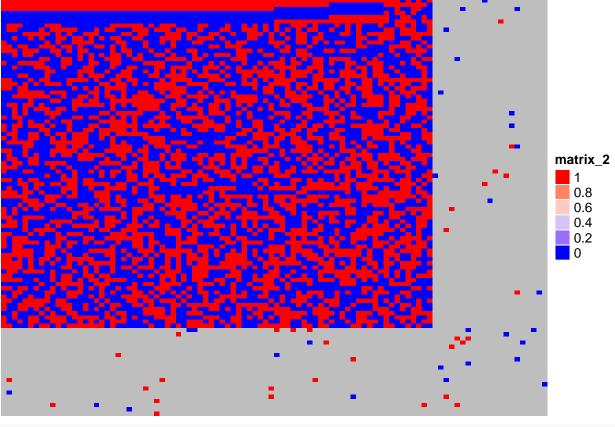
## sparse Data Simulation

```
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
library(ComplexHeatmap)
## Loading required package: grid
## Make a synthetic sparse data matrix
x \leftarrow sample(c(1, 0), 100 * 100, replace = T) %>% matrix(ncol = 100, nrow = 100)
Heatmap(x, cluster_rows = F, cluster_columns = F)
                                                                                    matrix_1
                                                                                       8.0
                                                                                       0.6
                                                                                       0.4
                                                                                       0.2
                                                                                       0
## 30*100+30*100-30*30=5100. Keep 60 values and make others NA => 5040 NA
x[80:100, ] \leftarrow NA
x[, 80:100] \leftarrow NA
for (i in 1:30) {
```

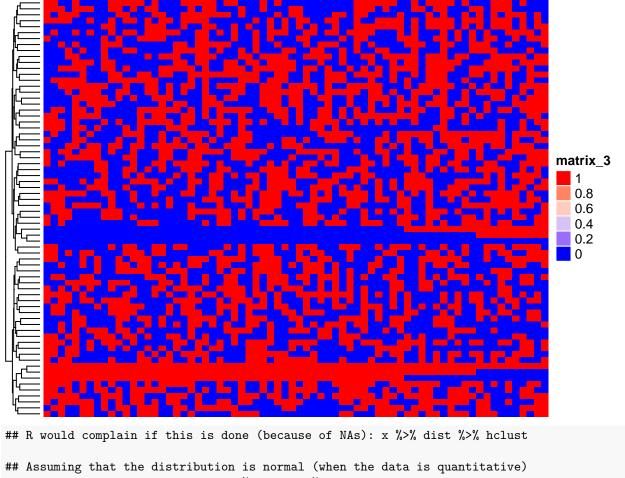
```
x[sample(80:100, 1), sample(1:100, 1)] <- sample(c(1, 0), 1)
    x[sample(1:100, 1), sample(80:100, 1)] <- sample(c(1, 0), 1)
}

## Add 5 imaginary, highly correlated strains (Will use euclidean distance
## instead of pcc)
x[1, 1:70] <- rep(1, 70)
x[2, 1:70] <- c(rep(1, 60), rep(0, 10))
x[3, 1:70] <- c(rep(1, 50), rep(0, 20))
x[4, 1:70] <- rep(0, 70)
x[5, 1:70] <- c(rep(0, 60), rep(1, 10))
x[6, 1:70] <- c(rep(0, 50), rep(1, 20))

## Visualize the result:
Heatmap(x, cluster_rows = F, cluster_columns = F)</pre>
```



Heatmap(x[1:70, 1:70], cluster\_columns = F)



```
## R would complain if this is done (because of NAs): x %>% dist %>% hclust

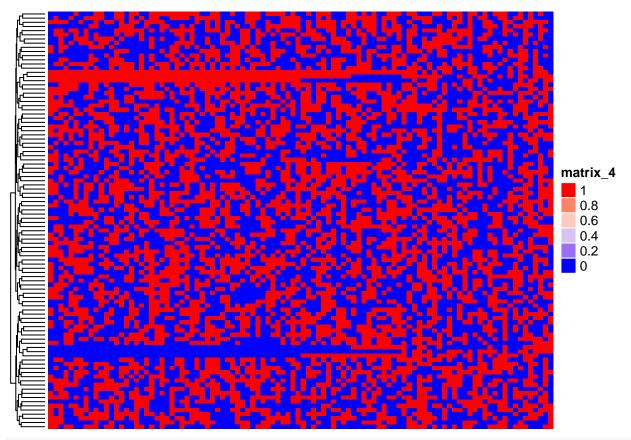
## Assuming that the distribution is normal (when the data is quantitative)

## => the imputed data would be 50% 0 and 50% 1

for (i in 1:dim(x)[1]) {
    for (j in 1:dim(x)[2]) {
        if (is.na(x[i, j]) == T) {
            x[i, j] <- sample(c(1, 0), 1)
        }
    }
}

## Visualize the result:

Heatmap(x, cluster_columns = F)</pre>
```



# The next step would be: By knowing more and more of the unknown data
# (which were imputed), what will be interesting? How can the fixed sparse
# data give us more info?