Heatmap simulation

Purpose

Simulation heatmaps. Goal is to be similar to ChIP-seq data, in order to make cartoons for publication/presentation schematics.

Loading Libraries

```
heatmap_sim <- function(
    nrows,
    nbins,
    p_geom = 0.1,
    se_norm = 10,
    jitter_factor = 3,
    jitter_amount = 5
    ){


    require(ComplexHeatmap)

    ## Simulating Data

    # init df
    sim.df <- data.frame(matrix(NA, nrow = nrows, ncol = nbins))

    # Populating with random data.
    # For each row, first a random mean is picked from the geometric
    # distribution with probabiltiy p
    # Then a number of observations equal to nbins / 2 is chosen by from
    # normal distribution given by this mean and se
    # The resulting vector is sorted left to right.
    # The process is then repeated for the right side, using the same
    # parameters, but sorting right to left (so the
    # highest scores are in the center and lowest on the edges).
    # Then any negative numbers are removed and set equal to 0.
    # Finally some jitter noise is added

    # simulating data
    for (i in 1:nrow(sim.df)) {
        m = rgeom(1, p_geom)
        left = sort(rnorm((nbins/2), m, se_norm), decreasing = FALSE)
        right = sort(rnorm((nbins/2), m, se_norm), decreasing = TRUE)
        left[left < 0] = 0
        right[right < 0] = 0
```

```
        sim.df[i,] <-
            c(
                jitter(left, jitter_factor, jitter_amount),
                jitter(right, jitter_factor, jitter_amount)
                )
    }

    # Sorting by row sums
    sim.df <- sim.df[order(rowSums(sim.df), decreasing = TRUE),]

    # Plotting Heatmap
    hm <- Heatmap(
        as.matrix(sim.df),
        cluster_columns = F,
        cluster_rows = F,
        show_row_names = FALSE,
        show_column_names = FALSE
    )
    return(hm)
}
```

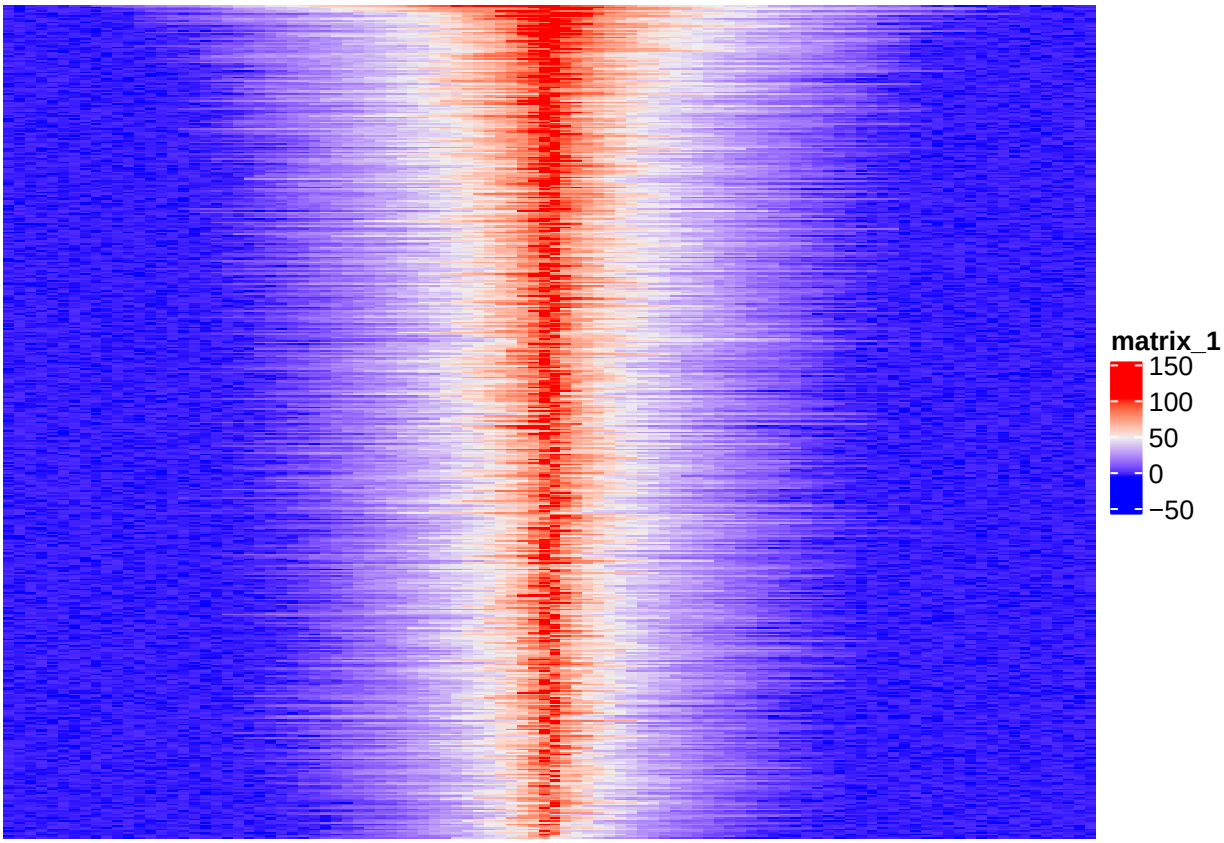
```
hm <- heatmap_sim(
    nrows = 500,
    nbins = 100,
    p_geom = 0.13,
    se_norm = 40,
    jitter_factor = 1,
    jitter_amount = 3
)
```

```
## Loading required package: ComplexHeatmap
```

```
## Loading required package: grid
```

```
## ========================================
## ComplexHeatmap version 2.0.0
## Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
## Github page: https://github.com/jokergoo/ComplexHeatmap
## Documentation: http://jokergoo.github.io/ComplexHeatmap-reference
##
## If you use it in published research, please cite:
## Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional
##   genomic data. Bioinformatics 2016.
## ========================================
```

```
hm
```


matrix_1
150
100
50
0
−50