

Data from a microarray experiment is provided in a CSV file. Create a heatmap with a hierarchical clustering dendrogram using this data.

Use the `heatmap()` function of R. Check the documentation for this function:

<https://www.rdocumentation.org/packages/stats/versions/3.6.2/topics/heatmap>

Use only a part of this data as explained here:

**a)** Use the first ten samples (from X1005 to X12012).

**b)** Use only ten genes – from Row\_1 to Row\_2.

Row\_1 = Last Two digits of your roll number, and Row\_2 = Row\_1 + 9.

For example – for Roll number 180106012: Row\_1 = 12 and Row\_2 = 21.

The genes should be along the vertical axes of the heatmap, and samples in the horizontal axes. In other words, rows should be genes, and samples are columns.

Genes should be clustered using hierarchical clustering. The dendrogram must be shown. Do not cluster the samples.

For each sample, the gene expression data must be scaled.

The heatmap must be suitably labeled.

**Submit the following:**

a) Your R script for this task.

b) A report in MS Word. The report should have the following:

1) Name:

2) Roll number:

3) Row\_1 and Row\_2 values

4) Image of the heatmap with dendrogram. Do not insert a Screenshot. In R, you can export graphs as images. Export the image and insert the exported image in the report.