

UCI SOMatic Browser

Goal: to allow navigation of highly dimensional data sets by way of Self-Organizing Maps (SOMs)

Link: <http://crick.bio.uci.edu/SOMatic>

Tutorial Steps:

Download the latest version:

```
$ wget http://crick.bio.uci.edu/SOMatic/SOMatic_Latest.tgz
```

Installing:

Be sure that gcc version>2.8.2 is loaded by running:

```
$ g++ --version
```

Untar the SOMatic folder and go inside the bin directory:

```
$ tar -zxf SOMatic_Latest.tgz
$ cd SOMatic/bin
```

Run make:

```
$ make
```

Building website:

To test the program, go to SOMatic/scripts and run the following:

```
$ ./buildsite.sh -SOMName ExampleWebsite -Matrix ../examples/example.matrix -Rows 30 -Cols
50 -SampleList ../examples/sample.list -Timesteps 4000000 -Trials 3
```

(Optional) Add gene overlay:

Start in the SOMatic directory, download the gtf file from Ensembl, and unzip it:

```
$ wget ftp://ftp.ensembl.org/pub/release-
80/gtf/mus_musculus/Mus_musculus.GRCm38.80.gtf.gz

$ gzip -d Mus_musculus.GRCm38.80.gtf.gz
```

Run the following in the SOMatic/scripts directory:

```
$ ./getgenes.sh -SOMName ExampleWebsite -Rows 30 -Cols 50 -GTFFile
../Mus_musculus.GRCm38.80.gtf -AddToChrom chr
```

(Optional) Add GO overlay:

Start in the SOMatic directory, download the gene2go and gene_info files from ncbi, and unzip them:

```
$ wget ftp://ftp.ncbi.nih.gov/gene/DATA/gene2go.gz
$ gzip -d gene2go.gz
$ wget ftp://ftp.ncbi.nih.gov/gene/DATA/GENE_INFO/Mammalia/Mus_musculus.gene_info.gz
$ gzip -d Mus_musculus.gene_info.gz
$ wget http://geneontology.org/ontology/go.obo
```

Run the following in the SOMatic/scripts directory:

```
$ ./getGOGenomic.sh -SOMName ExampleWebsite -Rows 30 -Cols 50 -Gene2GO ../gene2go -
GeneInfo ../Mus_musculus.gene_info -GOFile ../go.obo
```