Instructions to run the examples

CellRouter is a computational platform implemented in Java and R. The Java source code contains the Flow Network implementations required for trajectory identification. The R code uses results generated by the Java core engine to systematically dissect complex differentiation trajectories.

Overall, the following softwares are required   :
- Oracle Java Development Kit (JDK) (tested using the Java version 1.8)
- R/Bioconductor (tested using R version 3.3.1)
- RStudio

Many R packages are required and should be properly installed. They may be installed by using the following commands:

```
list.of.packages <-
c('reshape','reshape2','pheatmap','clusterProfiler','ReactomePA','plotrix','tsne','igraph','ggplot2,
"DESeq",'mclust','grid','scde','gplots','genefilter', 'Rtsne', 'DESeq2')
new.packages <- list.of.packages[!(list.of.packages %in% installed.packages()[,"Package"])]
if(length(new.packages)) install.packages(new.packages, repos=c("http://cran.rstudio.com/",
"https://bioconductor.org/biocLite.R"))
```

During the CellRouter analysis, n case of a missing package after running the steps above, please install them by typing:

```
source('http://bioconductor.org/biocLite.R')
biocLite('package_name')
```

The folder *CellRouter* contains .jar files with flow network implementation of CellRouter and additional libraries required. Each script has a variable named *libdir* which should correctly point to this folder.

In addition, the working directory, defined by the R command *setwd(),* should be updated accordingly. The algorithm assumes that a folder named *path* inside a folder *results exists*. The directory structure of folders containing the examples already contains the folder *results* and *paths*.

The script *StemID_BM_CellRouter.R* contains the source code required to reproduce the analysis in Figure 1.

The script *CellRouter_BloodNet.R* contains the source code required to reproduce the analysis in Figure 2.

The scripts *CellRouter_MixedStates.R* and *CellRouter_Mesoderm.R* contain the source code required to reproduce the analysis in Supplementary Note 4. *CellRouter_MixedStates.R* contains code to reproduce the analysis in Supplementary Figure N4 and N5.

CellRouter_Mesoderm.R contains code to reproduce the analysis in Supplementary Figure N6 and N7.