**RAW DATASETS:**

* **ScRNA-Seq count matrix of pediatric GBM patients from Neftel et al. (2019) are found in:**

[**https://singlecell.broadinstitute.org/single\_cell/study/SCP393/single-cell-rna-seq-of-adult-and-pediatric-glioblastoma#study-summary**](https://singlecell.broadinstitute.org/single_cell/study/SCP393/single-cell-rna-seq-of-adult-and-pediatric-glioblastoma#study-summary)

* **Pediatric brain tumor Proteomics data from the (Mass spectrometry- relative abundance matrix) is found in:**

Pediatric Brain Cancer Pilot Study – Proteome (PDC Study Identifier: PDC000180). Download the Prot. Asm (protein abundance matrix) text files from:

[**https://cptac-data-portal.georgetown.edu/study-summary/S047**](https://cptac-data-portal.georgetown.edu/study-summary/S047)

Extract the abundance count matrix from the text file “Gygi\_TCMP\_HMS\_Proteome.tmt11.txt” found in the downloaded folder.

* **ALL Histone PTM co-modifications’ mass spectrometry- relative abundance matrix is found in:**

The CCLE chromatin profiling dataset can be downloaded from the link below: <https://depmap.org/portal/download/api/download?file_name=ccle%2Fccle_2019%2FCCLE_GlobalChromatinProfiling_20181130.csv&bucket=depmap-external-downloads>

Additional metadata (e.g., tumor subtype/histology, donor age/sex/race, etc.) can be retrieved from here: <https://depmap.org/portal/download/api/download?file_name=ccle%2Fccle_2019%2FCell_lines_annotations_20181226.txt&bucket=depmap-external-downloads>

Use the metadata to extract only the MS relative abundance counts from the n=32 ALL patients data to reproduce the network seen in Figure 3.

**SEURAT CLUSTERING GUIDED-TURORTIAL**

**Follow the tutorial in R using the scRNA-Seq count matrix obtained** from Neftel et al. (2019). Only the pediatric GBM samples’ counts were used in this study (n=8 patients, N= 1943 cells) (SCP393). Seurat and BigSCale were used to identify differential markers in the GBM cell fate clusters and infer the GRN from the Bayesian network algorithm (AR1MA1-VBEM).

<https://satijalab.org/seurat/articles/pbmc3k_tutorial.html>

**BIGSCALE ALGORITHM GUIDED TUTORIAL**

[**https://github.com/iaconogi/bigSCale2#bigscale-2-gene-regulatory-networks-tutorial**](https://github.com/iaconogi/bigSCale2#bigscale-2-gene-regulatory-networks-tutorial)

**CELLROUTER ALGORITHM GUIDED TUTORIAL**

Download GitHub code and execute as instructed in the GitHub page using the scRNA-Seq counts matrix. Guided tutorial is provided below.

[**https://github.com/edroaldo/cellrouter**](https://github.com/edroaldo/cellrouter)

**https://github.com/edroaldo/cellrouter/blob/master/Myeloid\_Progenitors/CellRouter\_Paul\_Tutorial.md**

**AR1MA1-VBEM (BAYESIAN NETWORK INFERENCE)**

Download the GitHub code master-folder, and run the script using the gene expression count matrix (scRNA-Seq counts)

[**https://github.com/mscastillo/GRNVBEM**](https://github.com/mscastillo/GRNVBEM)

**CODES FOR PARTIAL INFORMATION DECOMPOSITION (PID) NETWORKS**

The raw data matrices for the pediatric brain tumors’ proteomic (mass spectrometry) network and the ALL Histone PTM networks (CCLE data- histone tail mass spectrometry) is provided in the ‘Datasets’ folder. Their computed PID networks are also found in the folder. Below are the codes to execute to infer the PID networks from the raw data matrix and infer their network structure and dynamics/information flow (Centrality measures).

**PID NETWORK INFERENCE** (to be executed in Julia)

using NetworkInference

infer\_network("/Users/15145/Desktop/ALL.txt", PIDCNetworkInference())

nodes = get\_nodes("/Users/15145/Desktop/ALL.txt")

inferred\_network = InferredNetwork(PIDCNetworkInference(), nodes)

write\_network\_file("/Users/15145/Desktop/ALL\_PID.txt",inferred\_network)

**NETWORK CENTRALITY MEASURES AND COMMUNITY STRUCTURE DETECTION (to be executed in R)**

setwd("C:/Users/15145/Desktop") #Set Directory with PID Data matrix saved as a CSV file (See Dataset folder in GitHub for formatting)

data <- read.csv(file = "ALL\_PID.csv")

library(igraph)

#To Infer the Network Topology and perform Louvain Community Detection

edges <- as.data.frame(data)

colnames(edges) <- c("from", "to", "weight")

g <- graph\_from\_data\_frame(edges, directed = FALSE)

lc <- cluster\_louvain(g)

membership(lc)

plot(lc, g)

betweenness.cent <- betweenness(g)

plot (betweenness.cent)

graph.strength(g)

eigen\_centrality(g)

Transitivity(g) #clusteringcoefficient

**TUTORIALS FOR NETWORK ANALYSIS**

<https://www.datacamp.com/community/tutorials/centrality-network-analysis-R>

<https://www.r-bloggers.com/2018/12/network-centrality-in-r-an-introduction/>