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

**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) with the top 100 differential markers pooled from the top 10 PCA components in the Seurat and BigSCale clustering space.

[**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 Bayesian GRN (from pediatric GBM datasets) is provided in the ‘Datasets’ folder. The Bayesian network’s gene markers were further subjected to the PID network analysis, wherein the normalized scRNA-Seq counts of the 17 markers identified by the Bayesian network were selected and subjected to the PID network inference. Their computed PID networks data files 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/Proteome\_Raw\_Data.txt", PIDCNetworkInference())

nodes = get\_nodes("/Users/15145/Desktop/Proteome\_Raw\_Data.txt")

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

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

#Similarly, for the GRN inference, use the “Bayesian\_GRN.txt” file as the raw data and the outputted PID network is provided in the Dataset folder as GRN\_PID.txt.

**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 = "Proteome\_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/>