Forest of Imputation Trees (FITs) is a method to impute highly sparse and noisy data-sets from single cell epigenome profiling. It has been tested on single cell open-chromatin profiles as well as single RNA-seq profile.

Download FITs

Standalone executable code for Linux

Python code

Matlab code

Help

FITs work in two phases. It has been made so to handle very large read-count matrixes and to get better imputation. In phase-1 it builds multiple imputation trees and from every tree it extract 1 or 2 imputed version original read-count matrix. One can run phase-1 of FITs in parallel processing mode also, where multiple trees can be build on several processors. After phase-1, the phase-2 part of FITs is used to accumulate the most relevant imputed version for every cell.

Tested dataset

Contact: kumarv1@gis.a-s