

Pre-adipogenesis gene regulatory network analysis

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September 18, 2019

1 Overview

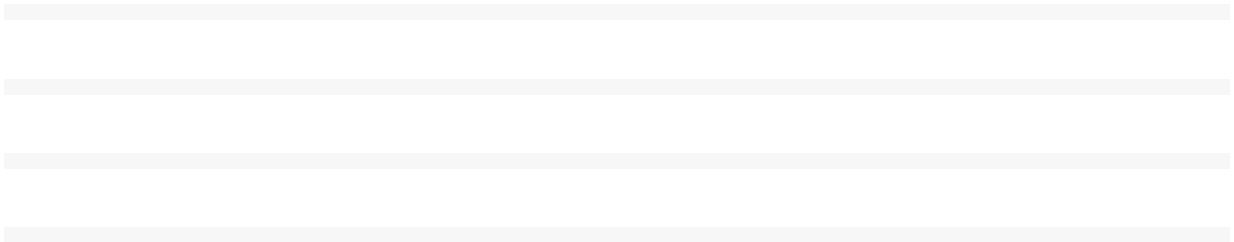
This vignette describes methods for gene regulatory network identification based on time-series ATAC-seq and PRO-seq data. Details will be updated later

2 Differential expression analyses

Differentially expressed transcripts and open chromatin peaks are identified using *pro_time_deg_20190501.R* and *atac_time_deg_20190501.R*.

3 Network inference analysis

The network inference code can be found in *netInfer_20190520.R*. This code relies on functions in *net_infer_functions.R*.



4 References