À lire absolument : article Bolteau

À lire en bonus :

Plan de la présentation : (chacun remplit ce qu’il/elle a compris)

1. But de de l’étude (partie biologie)
2. Outils mathématiques utilisés pour l’étude afin de modéliser
3. Liens entre les outils

Article Bolteau

Inferring Boolean Networks from Single-Cell Human Embryo Datasets

goal : develop a framework for inferring computational models that distinguish between two developmental stages

understand the chain of events regulating human preimplantation development leading to an implantation-competent embryo

Our method selects pseudo perturbations from scRNAseq data

computational challenges with normalization and \zero-inflation", complicating network models

These pseudo-perturbations consist of input-output discretized expressions, for a limited set of genes and cells

By combining these pseudo-perturbations with prior-regulatory networks, we can infer Boolean networks that accurately align with scRNAseq data for each developmental stage

PKN reconstruction

graphe unique ?, check pyBRAvo, check github

Experimental design construction

pseudo-perturbations

binarized expression values for input and intermediate genes in chosen cells whose value is identical in both cell classes

normalized expression values for readout genes in the chosen cells of both cell classes

logic program maximizing nb of diff pseudo perturbation for k genes (fixed)

readout observations

BN inference

check Caspo

PKN + experimental design → BN family

data preprocessing

the PKN, our dataset comprised 125 genes (111 input and intermediates, and 14 readouts).

n\_ij = min = 0

Problem formulation.

= pseudo-perturbations construction and cell groups

conditions taken in different works ?