

Understanding Tumor Heterogeneity and Plasticity Through the Lens of Cancer Stem Cell Model and Mathematical Modeling

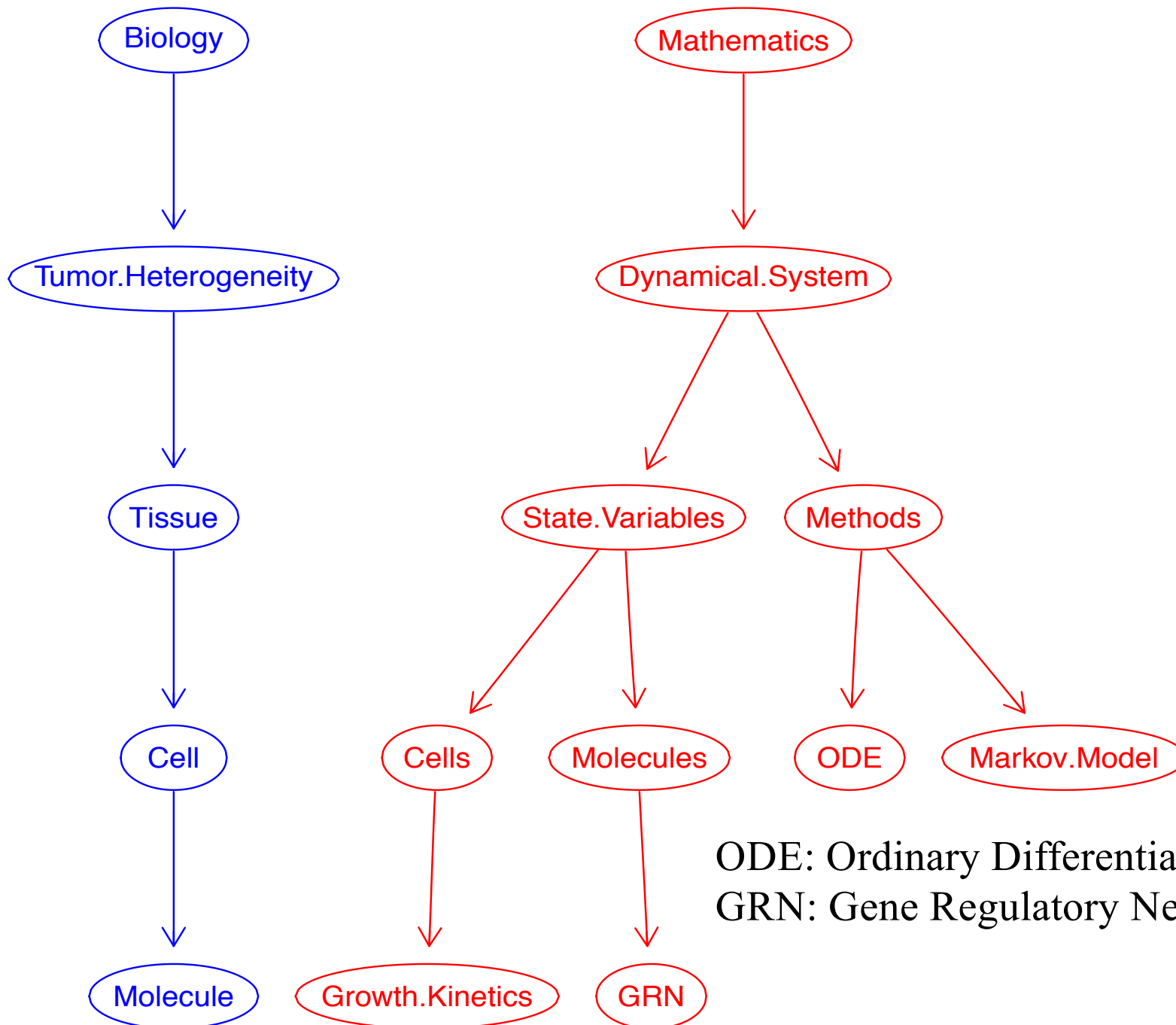
Cell Fate Decision Determined by Gene Regulatory Network (GRN)

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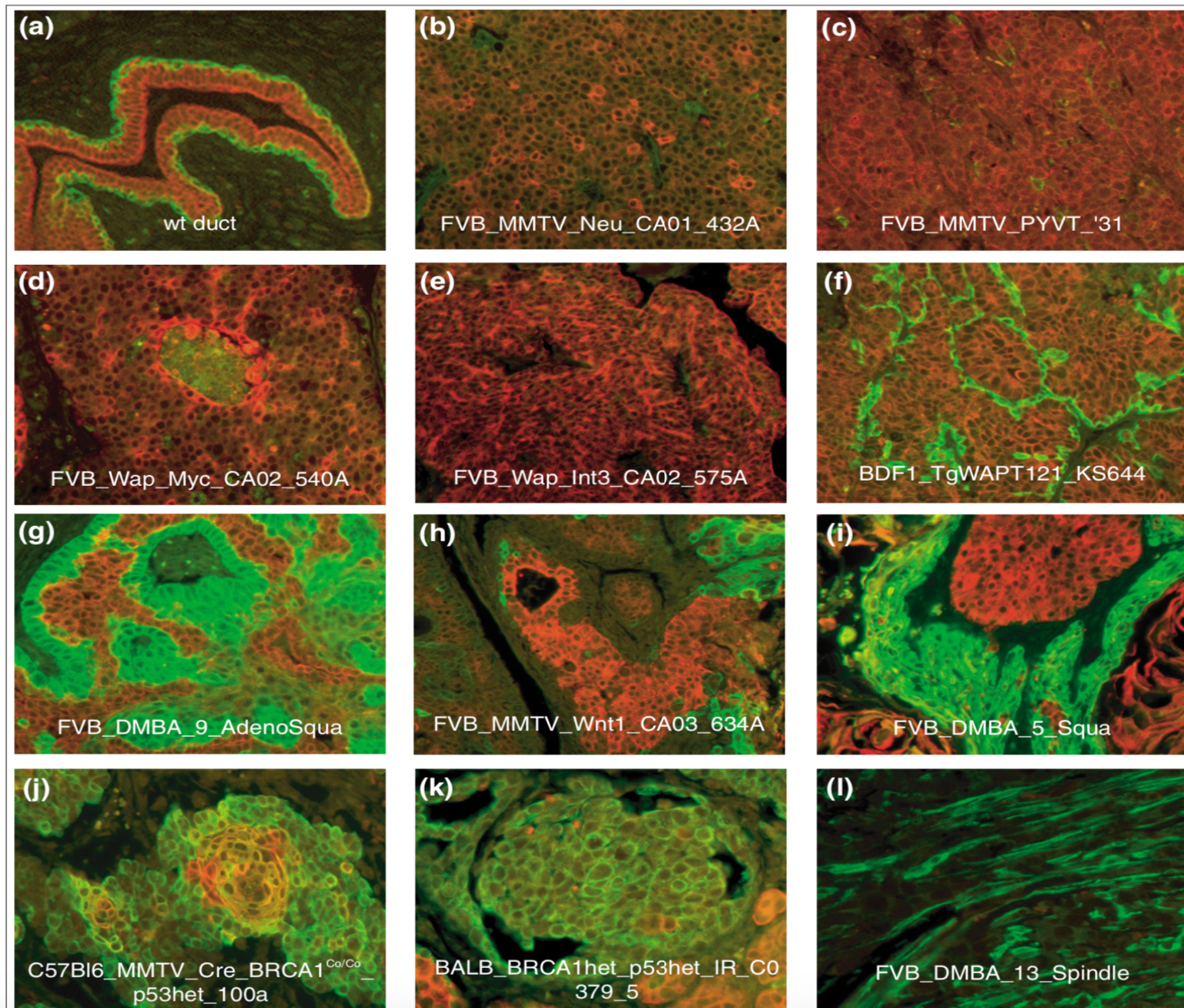
April 26, 2021

Understanding Biology with Mathematical Modeling



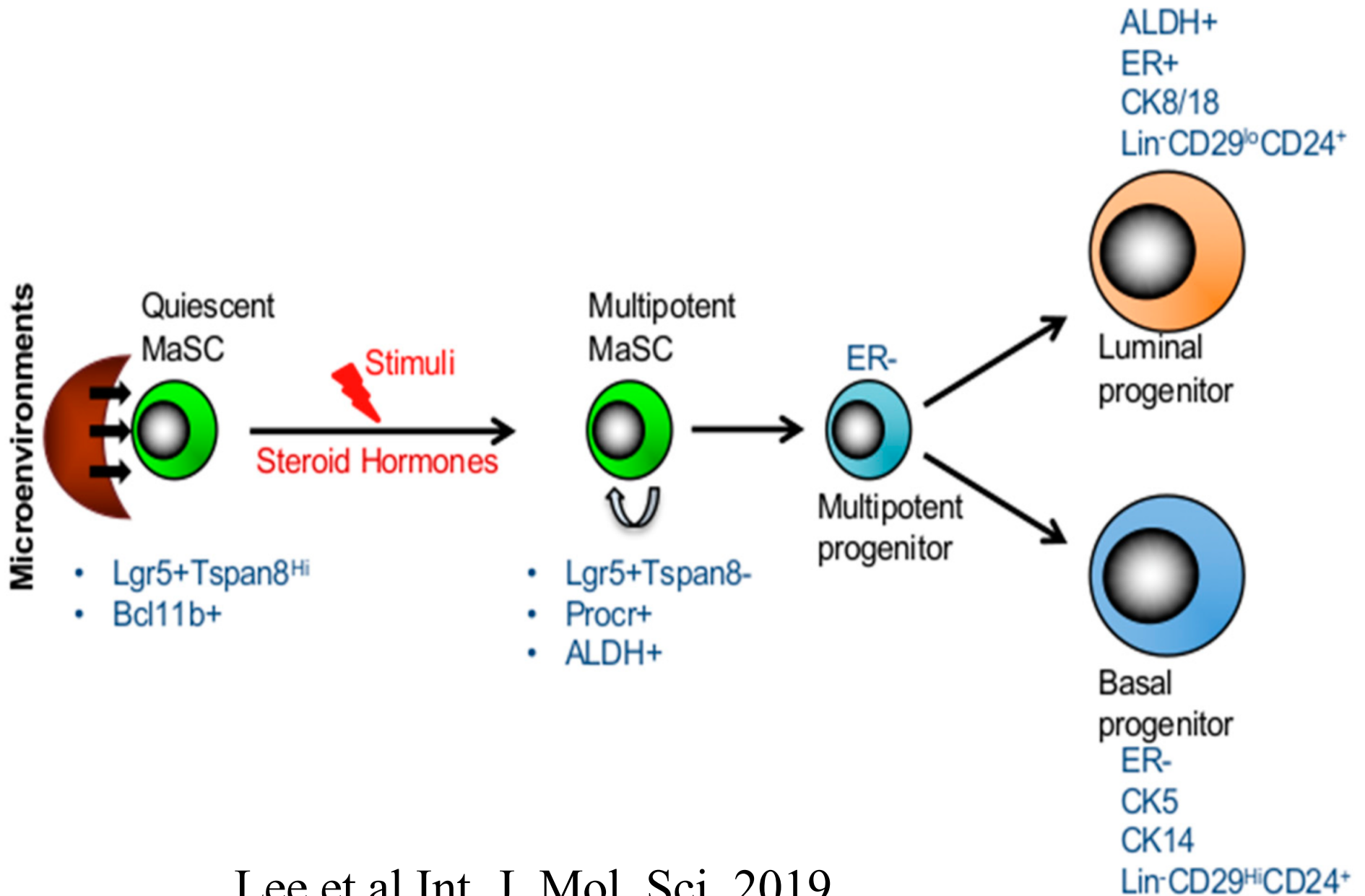
ODE: Ordinary Differential Equation
GRN: Gene Regulatory Network

Heterogeneity of Mouse Mammary Tumors



Keratins 8/18 Keratin 5 Herschkowitz, ..., Perou Genome Biology 2007

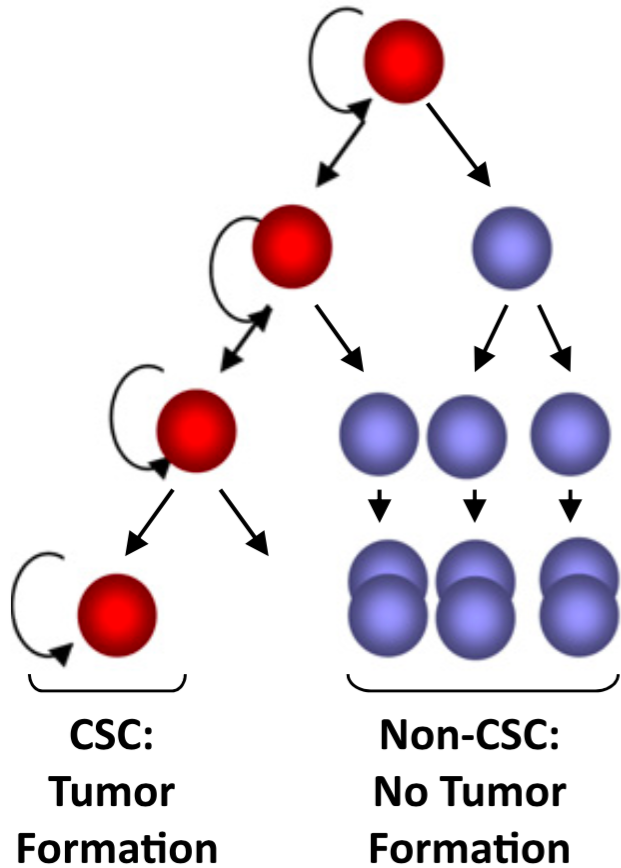
Mammary Stem Cell Model



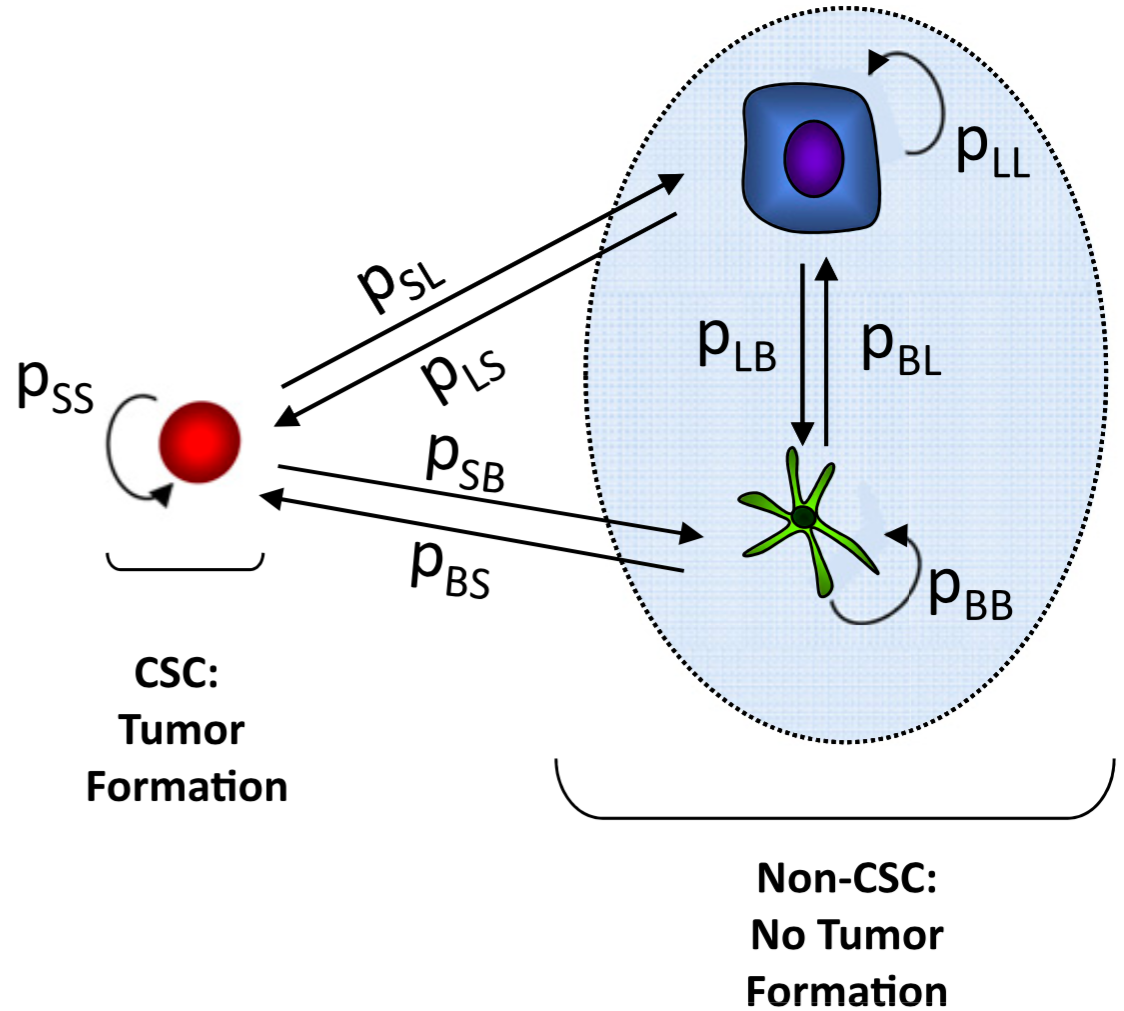
Lee et al Int. J. Mol. Sci. 2019

Cancer Stem Cell Model

CSC model I



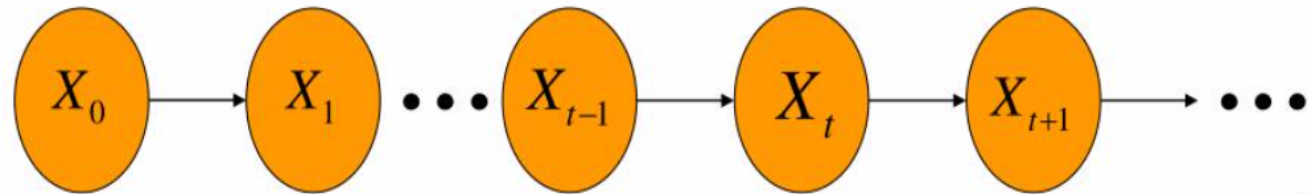
CSC model II



Markov Process for Cancer Stem Model

$$\mathbf{x} = \begin{bmatrix} x_1 \\ x_2 \\ \vdots \\ x_n \end{bmatrix}$$

x_i : frequency of cell type i



$$P = \begin{bmatrix} p_{11} & p_{12} & \dots & p_{1n} \\ p_{21} & p_{22} & \dots & p_{2n} \\ \dots & \dots & \dots & \dots \\ p_{n1} & p_{n2} & \dots & p_{nn} \end{bmatrix}$$

transition probability matrix

$$p_{ij} \geq 0$$

$$\sum_j p_{ij} = 1$$

$$\mathbf{x}^{t+1} = \mathbf{x}^t P$$

$$\mathbf{x}^* = \mathbf{x}^* P \quad \text{at steady state}$$

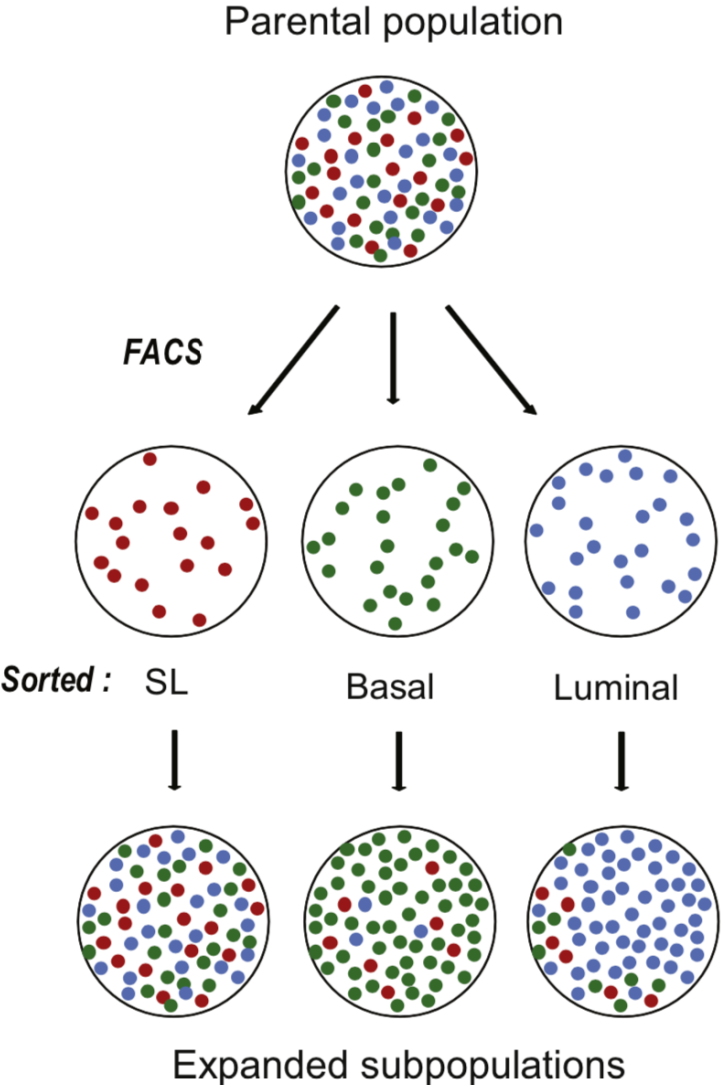
\mathbf{x}^* is the left eigen vector of matrix P

Its eigen value is 1, which is the largest eigen value

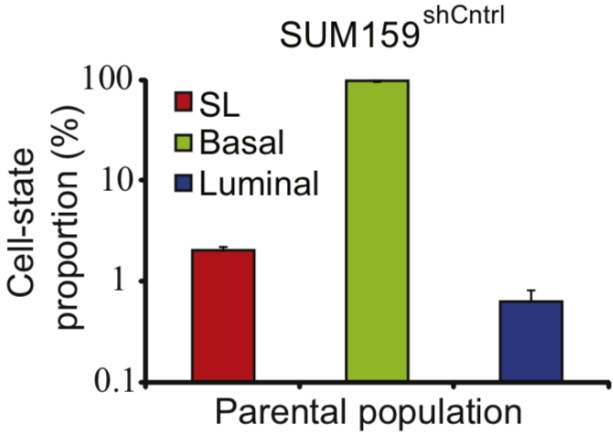
Conversion Between Cancer Stem Cell and Non-stem Cells

SL: stem-like

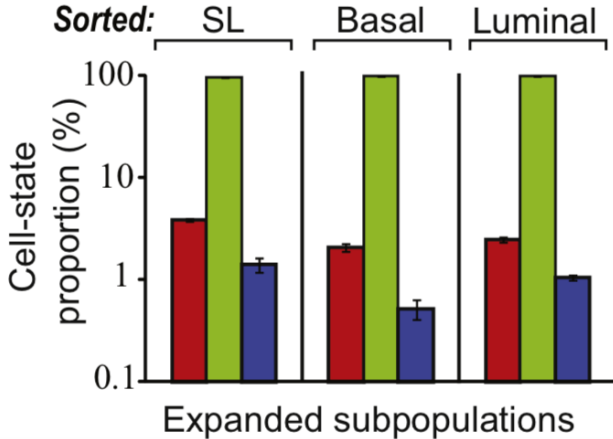
A



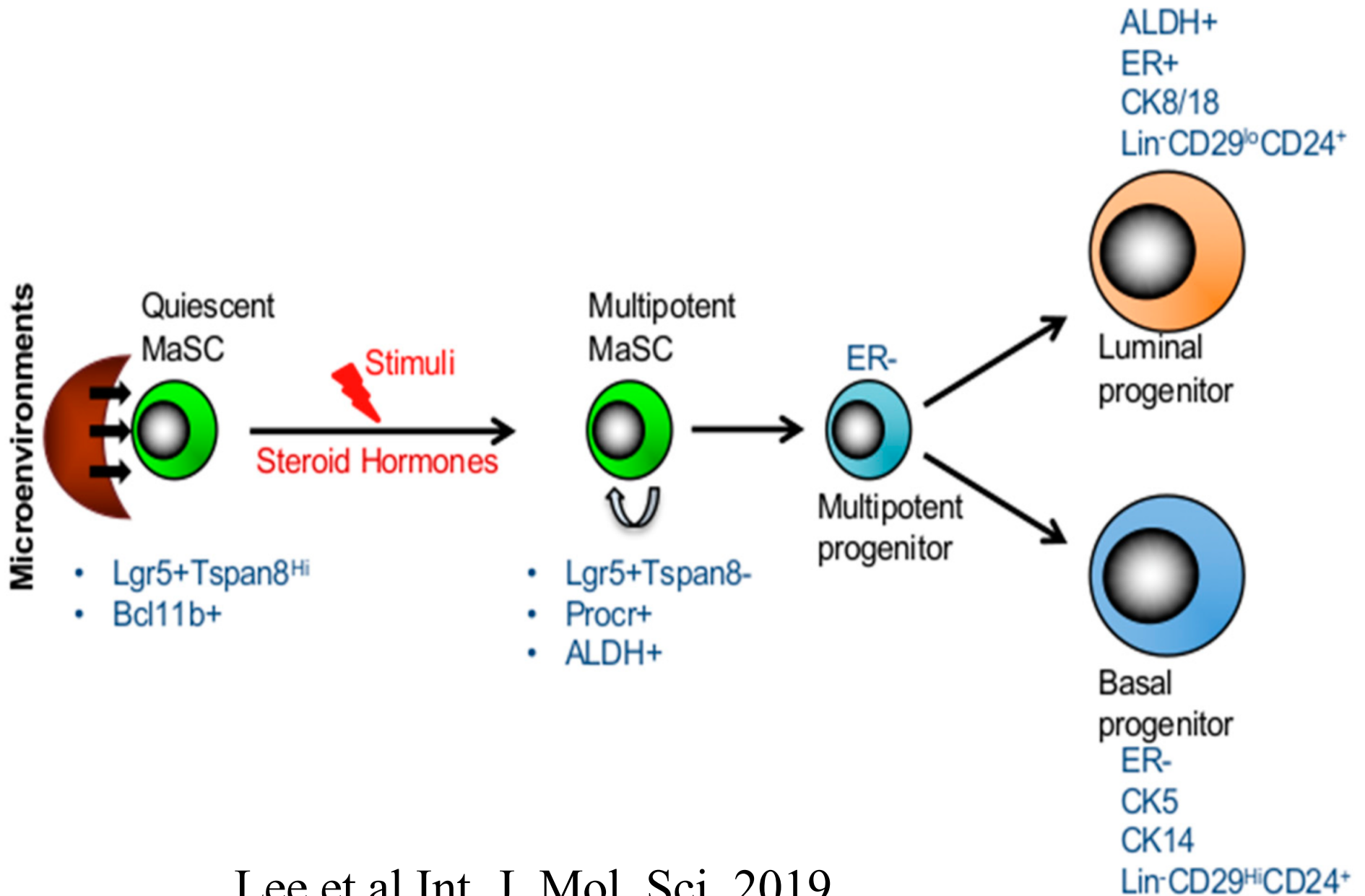
B



C

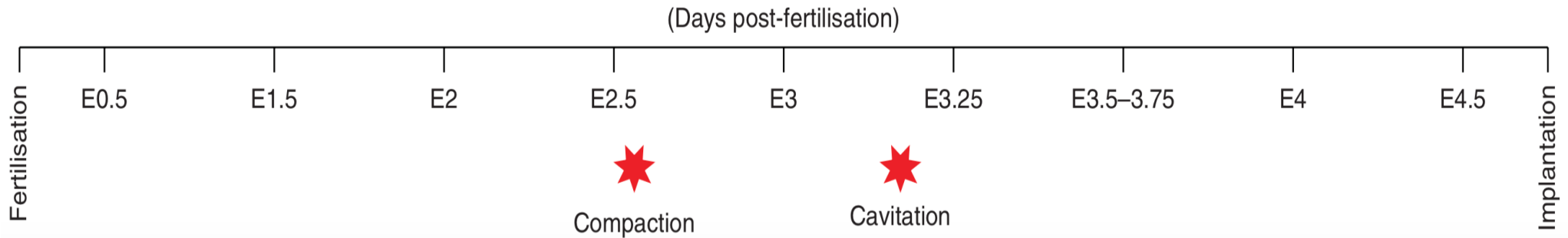
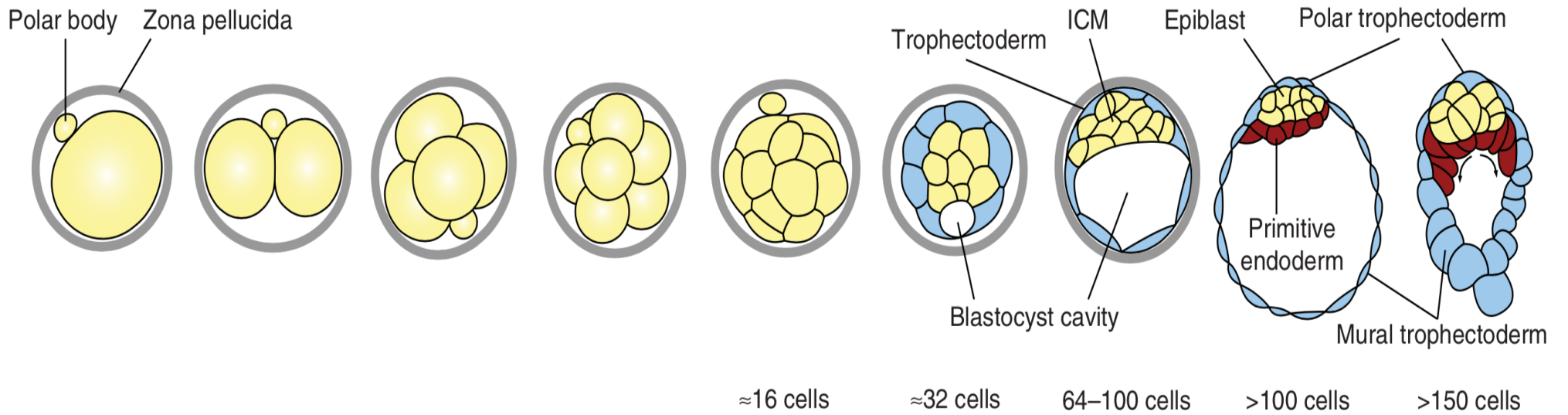
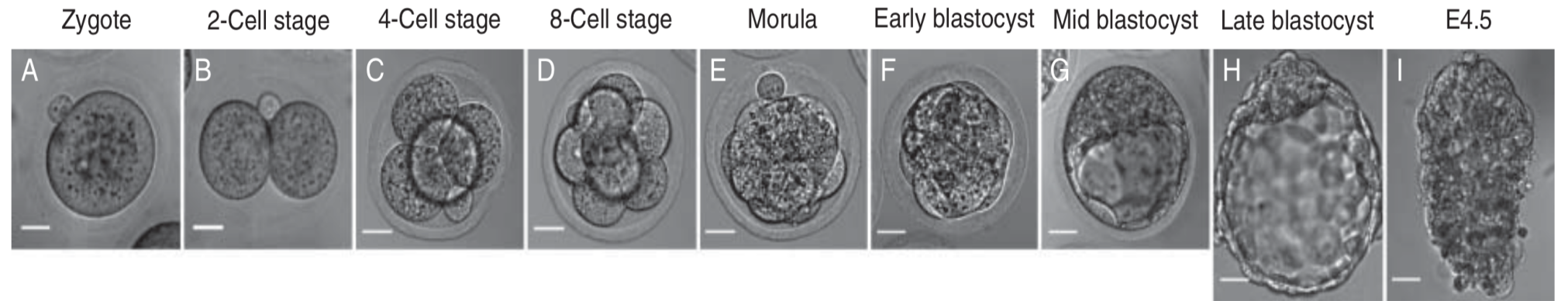


Mammary Stem Cell Model



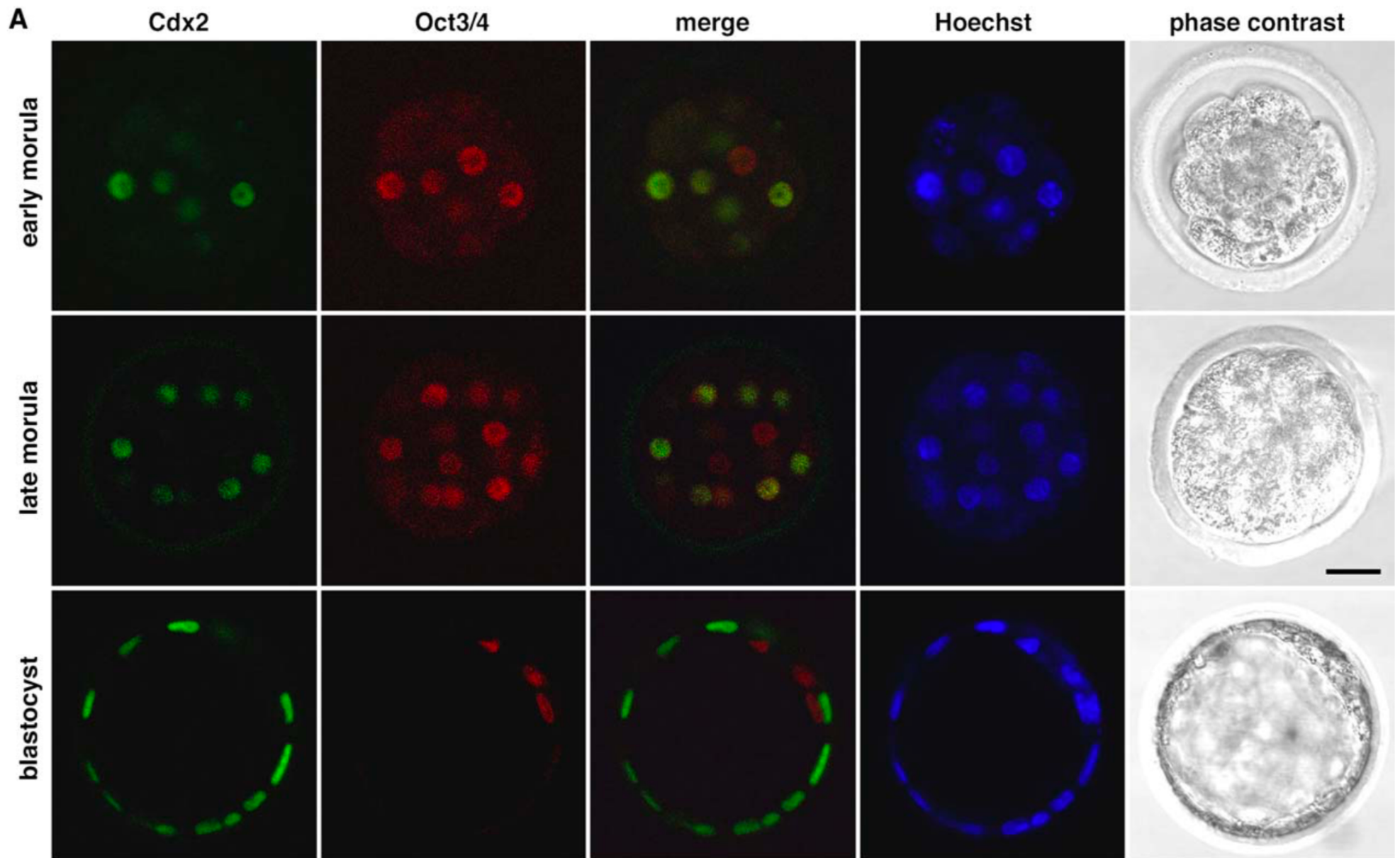
Lee et al Int. J. Mol. Sci. 2019

Mouse Embryo Developmental Stages

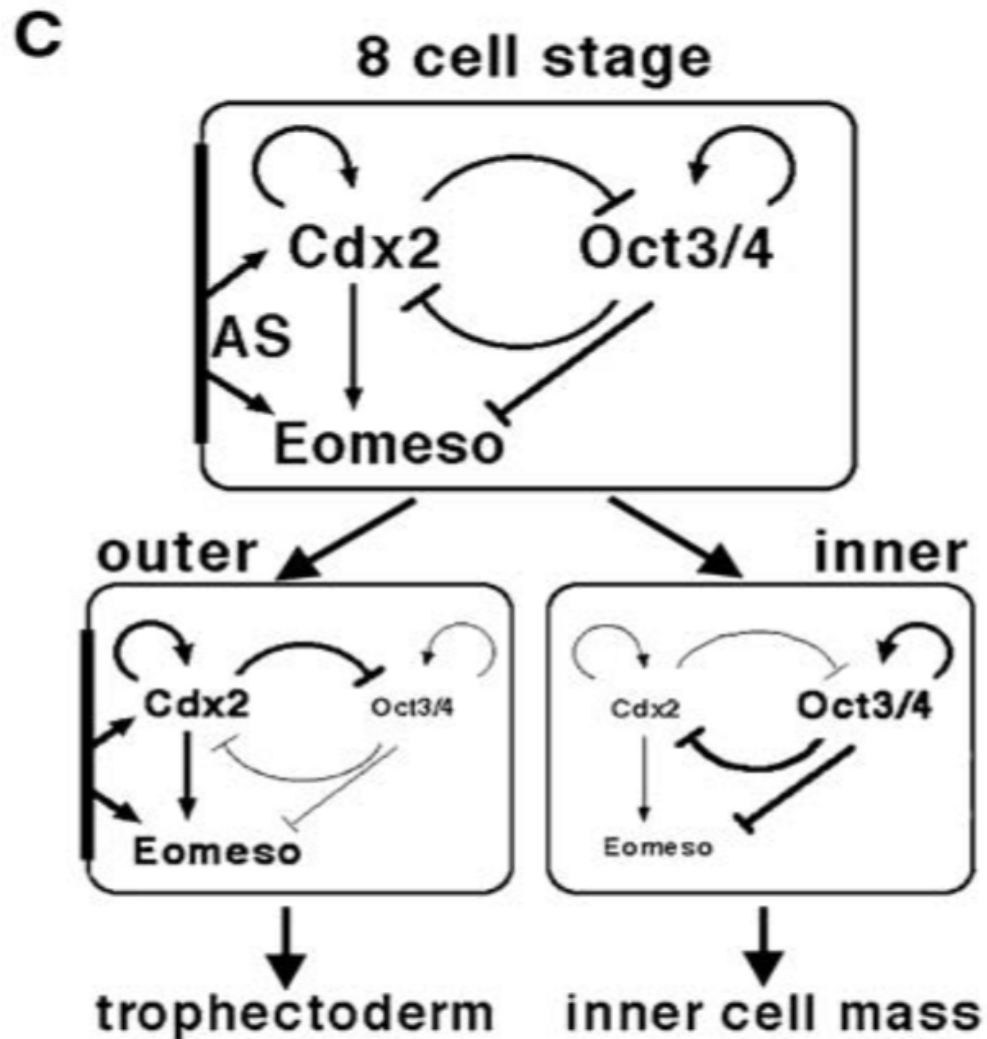


Saiz et al Reproduction 2013

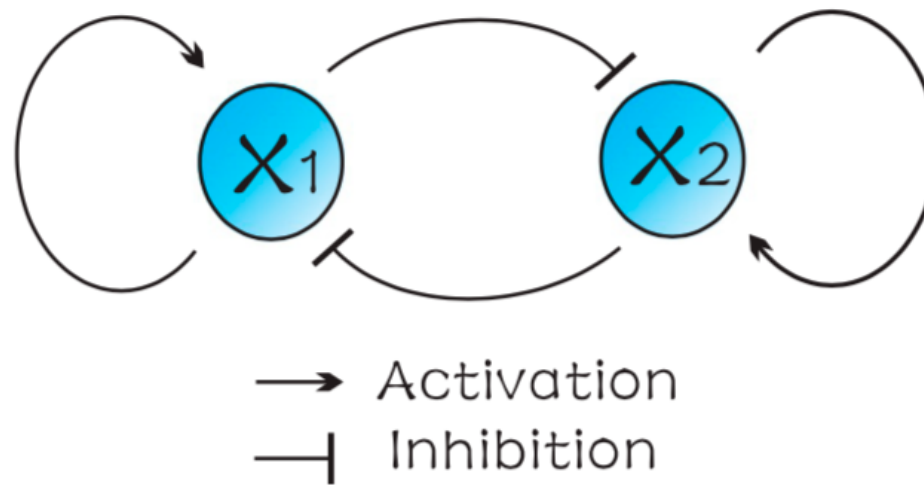
Interaction Between Oct3/4 and Cdx2 Expression Determines Trophectoderm Differentiation



Gene Regulatory Network of Oct3/4 and Cdx2 Determines Trophectoderm vs. Inner Cell Mass (ICM) Lineage



Toggle Switch Gene Regulatory Network (GRN)

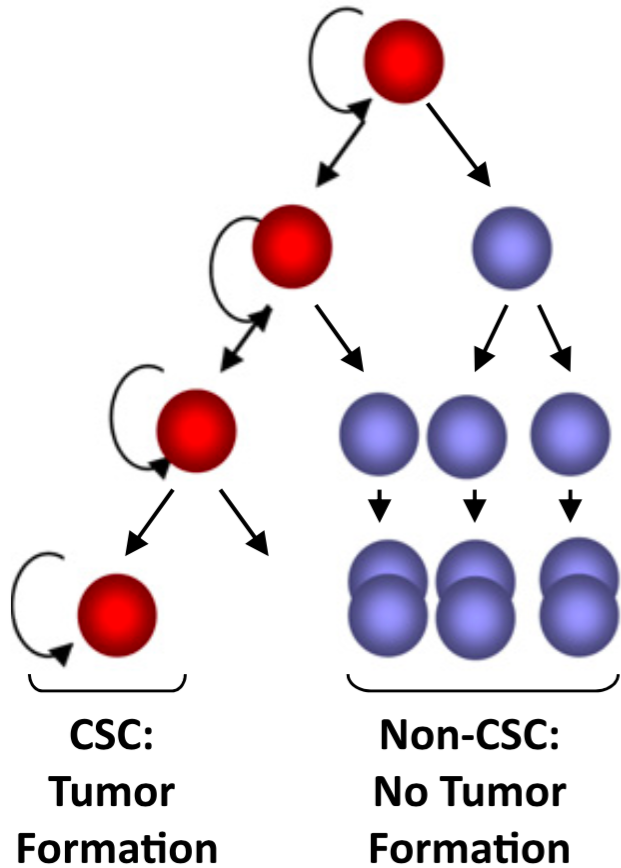


Gardner et al Nature 2000, 403:339

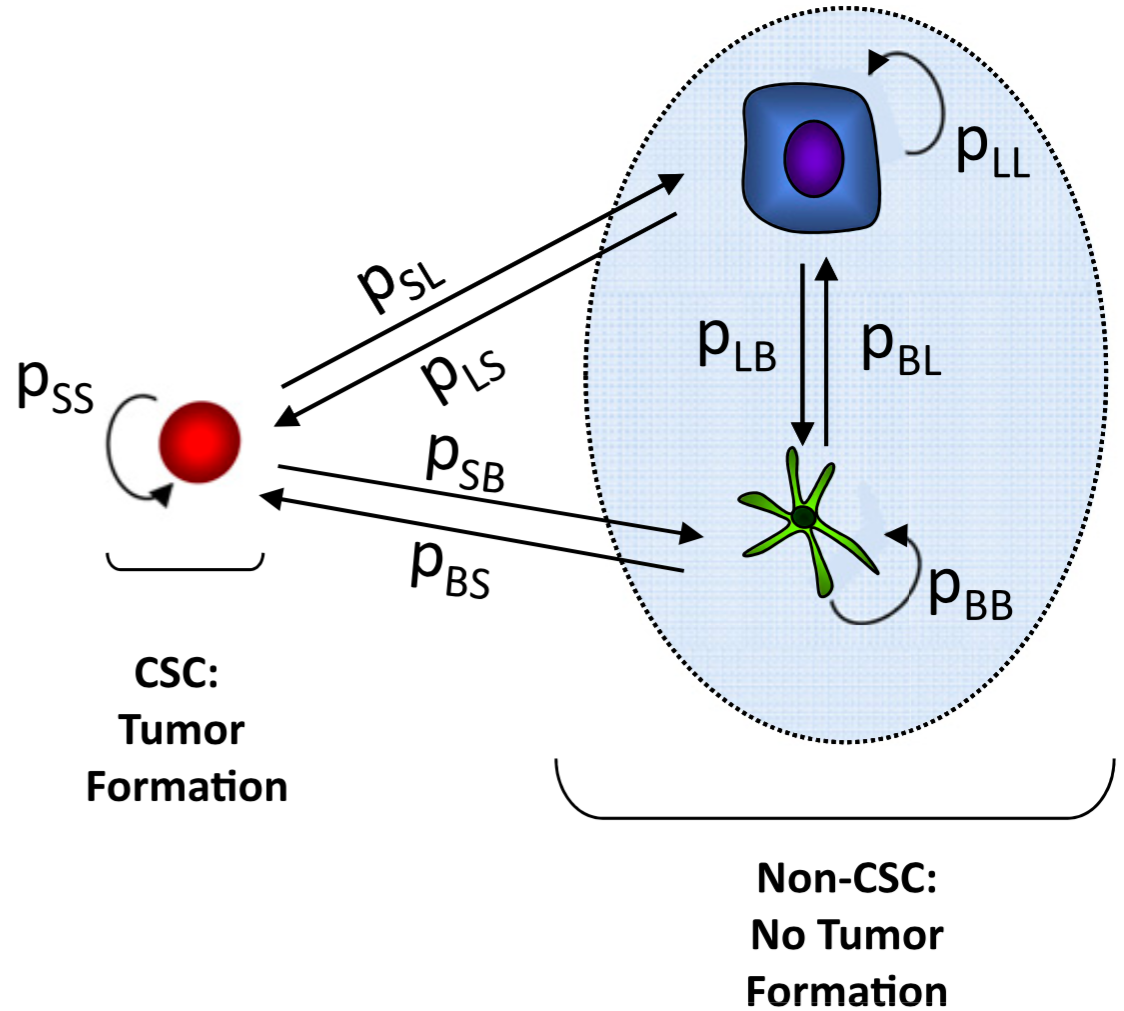
Wang et al PNAS 2011, 108:8257

Cancer Stem Cell Model

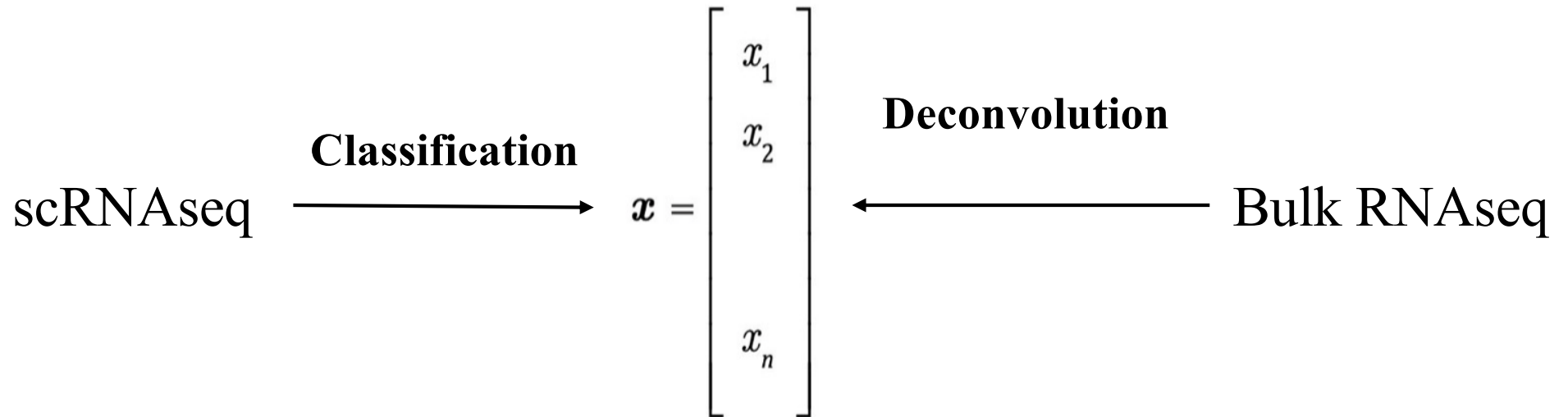
CSC model I



CSC model II

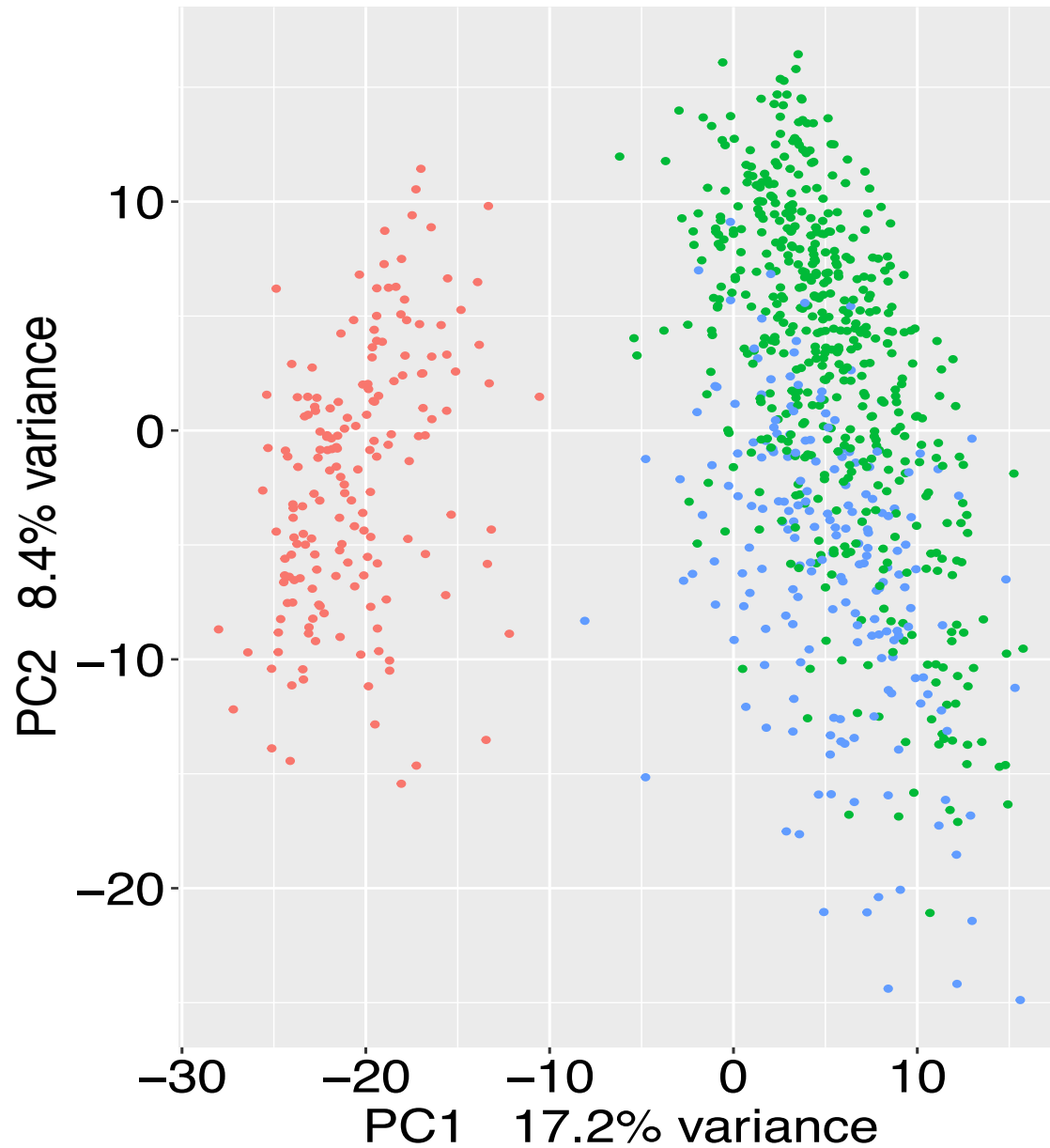


Two Complementary Approaches to Study Tumor Heterogeneity



TCGA BRCA Pam50 subtypes

BRCA: breast cancer



Basal	173
LumA	500
LumB	193

subtype



Deconvolution of Bulk RNAseq Data

y : gene expression of a sample
 n genes

$s_1 \dots s_p$ are gene signature

$$\begin{bmatrix} y_1 & s_{11} & s_{12} & \dots & s_{1p} \\ y_2 & s_{21} & s_{22} & \dots & s_{2p} \\ \cdot & & & & \cdot \\ \cdot & & & & \cdot \\ y_n & s_{n1} & s_{n2} & \dots & s_{np} \end{bmatrix}$$

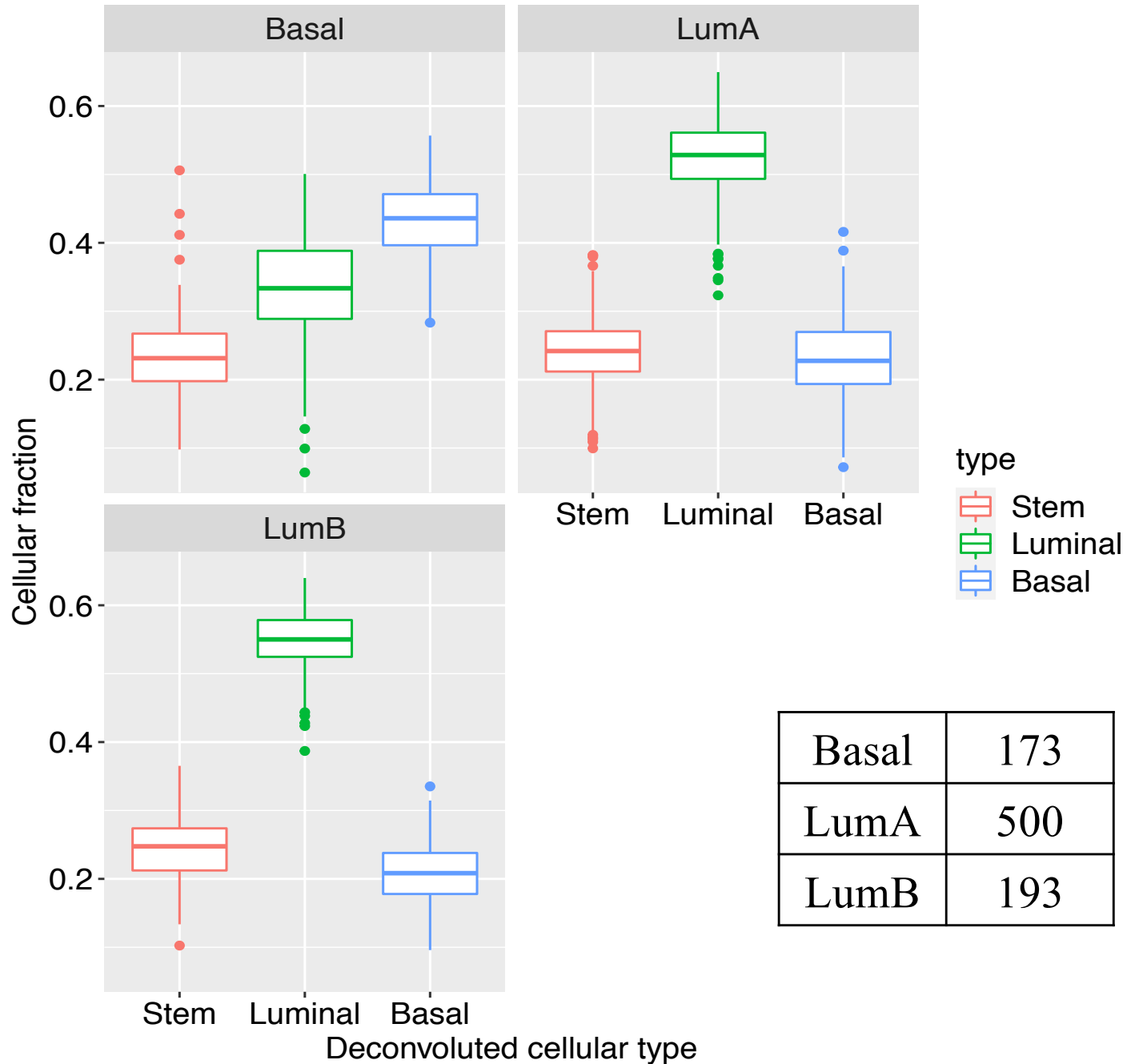
$$\min(|\mathbf{S}\mathbf{x} - \mathbf{y}|^2)$$

$$\sum x_i = 1$$

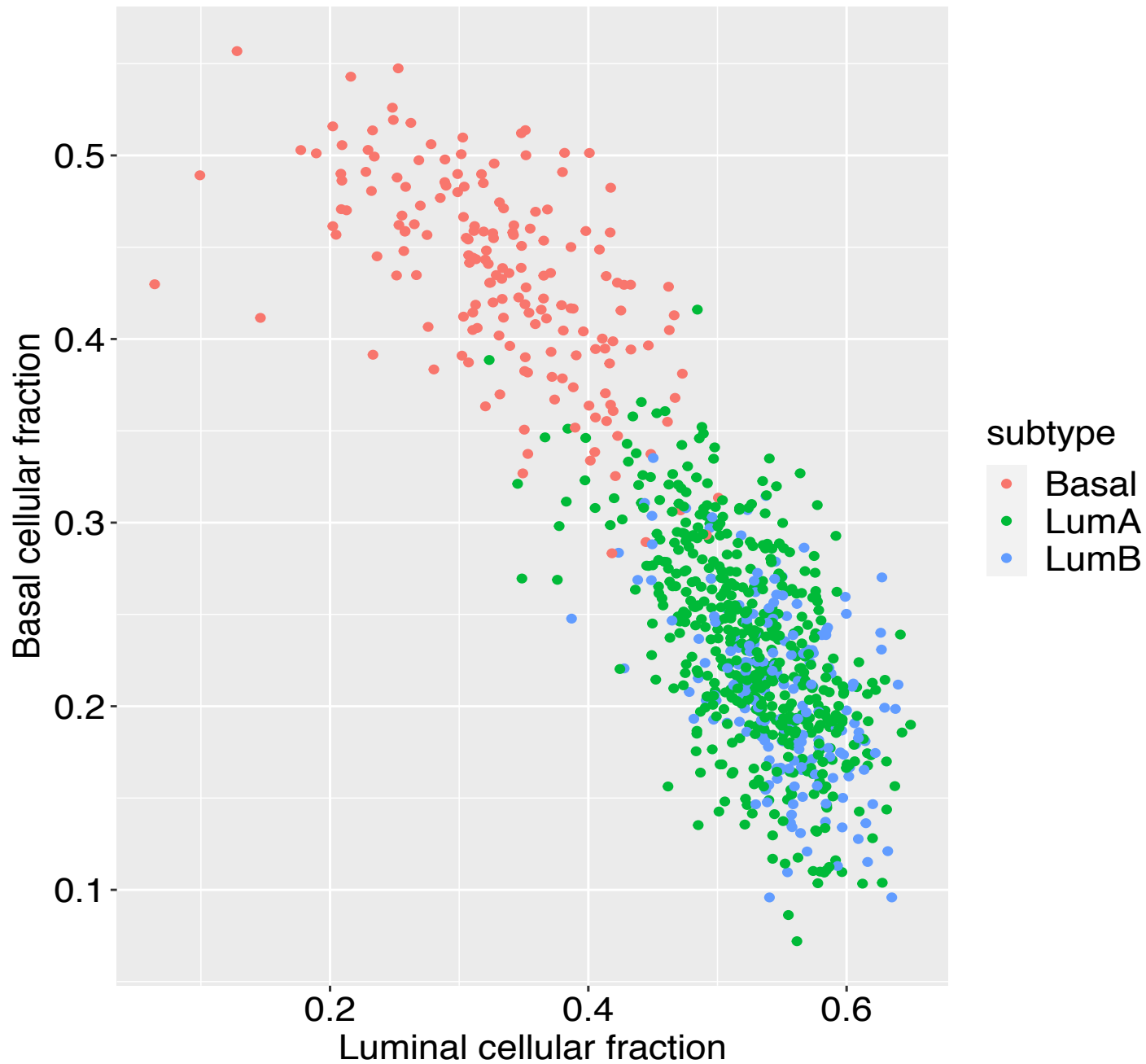
$$x_i \geq 0 \ \& \lt 1$$

Deconvolution with mixture model
using R package DeconRNASeq

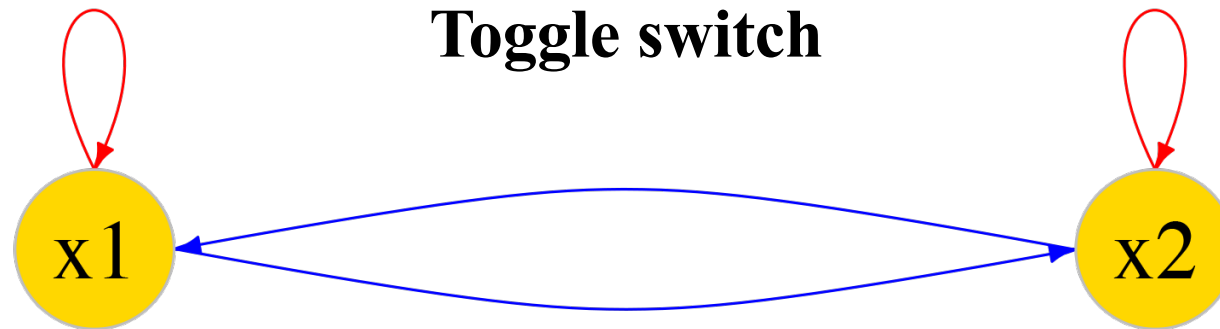
Deconvolution of TCGA BRCA Tumors



Deconvolution of TCGA BRAC Tumors



Differential Equation Model of Gene Regulatory Network (GRN)



$$\frac{dx_1}{dt} = \frac{a_1 x_1^n}{S^n + x_1^n} + \frac{b_1 S^n}{S^n + x_2^n} - k_1 x_1$$

$$\frac{dx_2}{dt} = \frac{a_2 x_2^n}{S^n + x_2^n} + \frac{b_2 S^n}{S^n + x_1^n} - k_2 x_2$$

b_1 and b_2 are weights for mutual inhibition

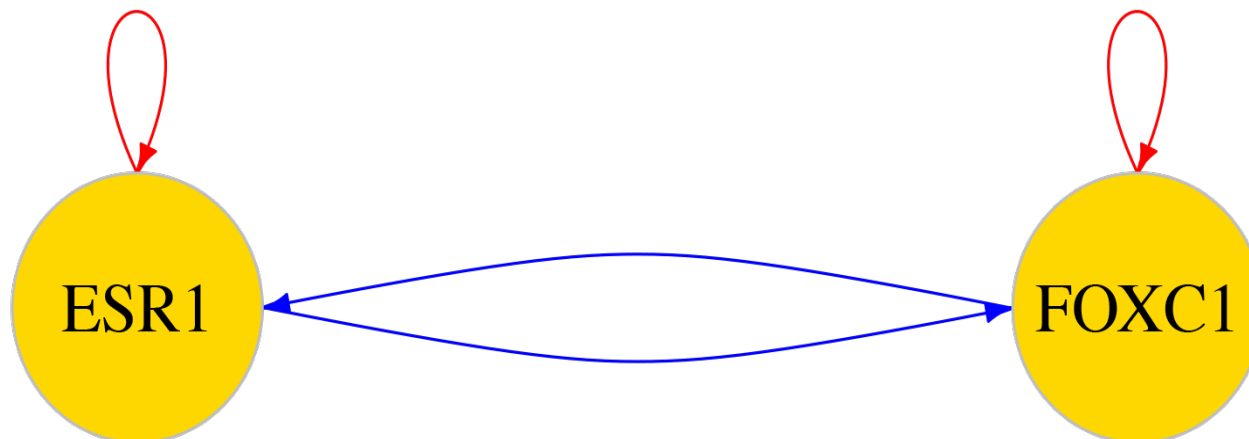
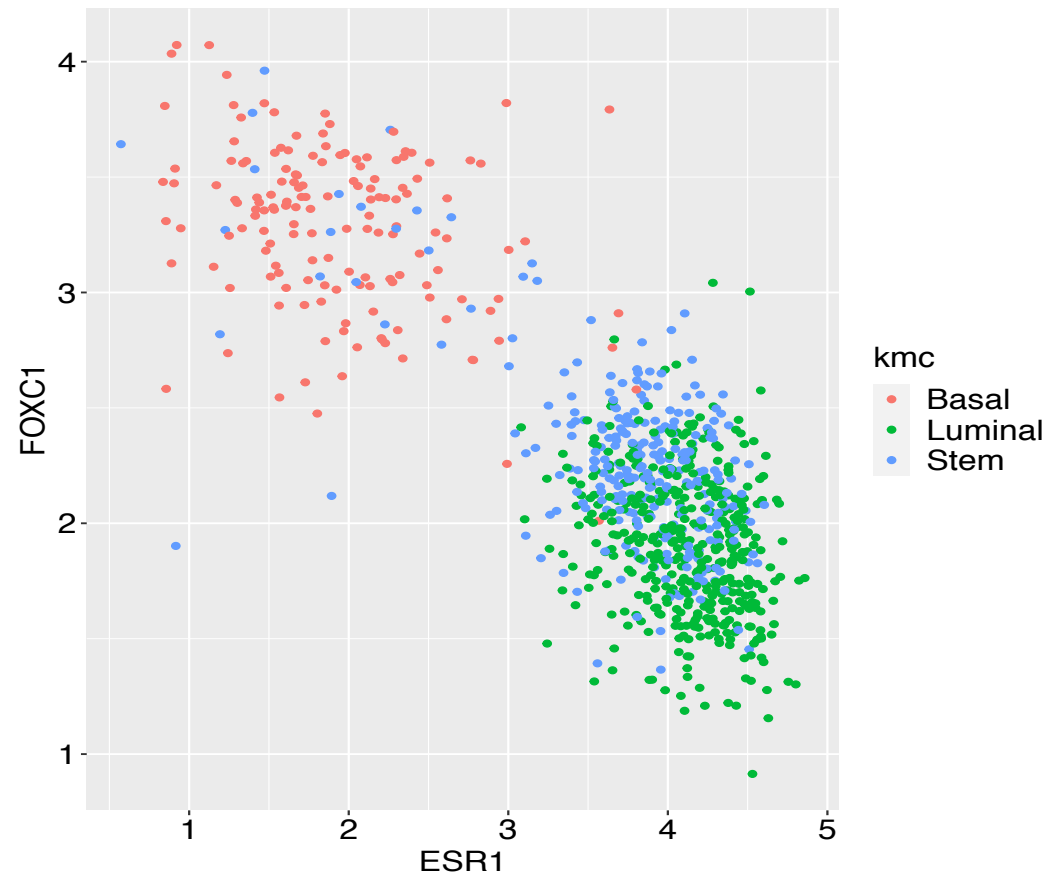
a_1 and a_2 are weights for auto-activation

k_1 and k_2 are weights for degradation

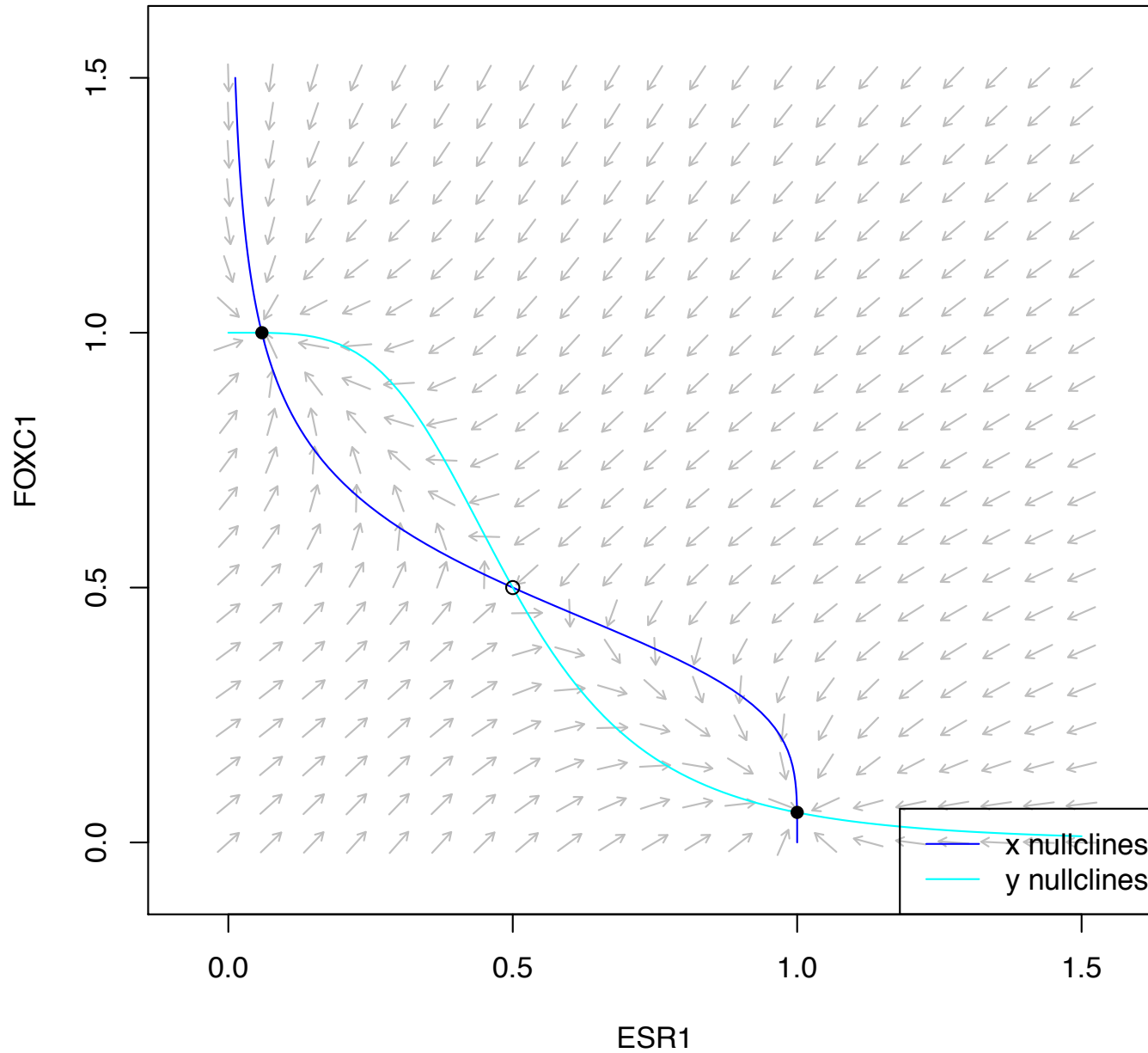
n is Hill Coefficient

S is threshold of Hill function

GRN of Luminal and Basal States

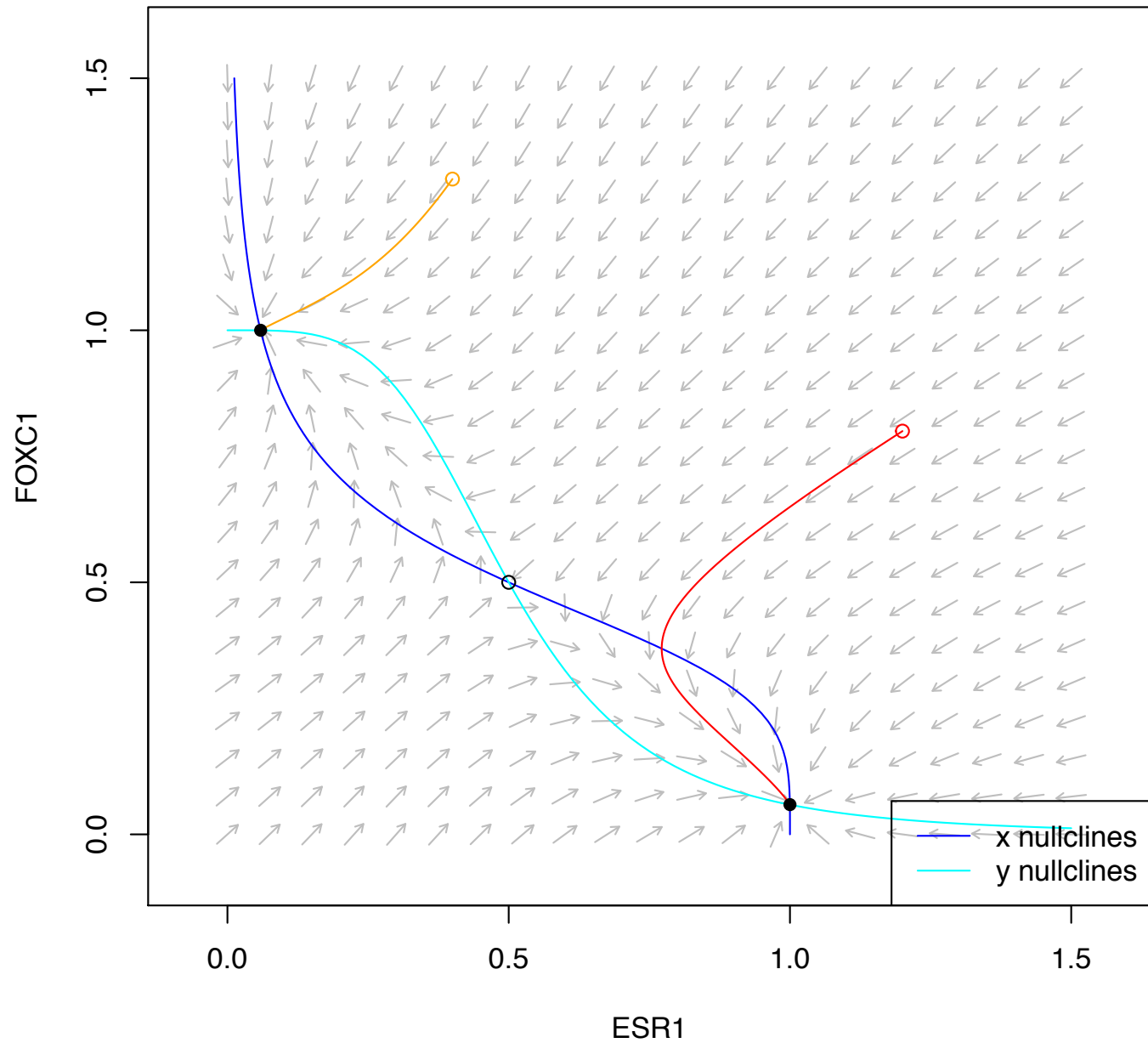


Flow Diagram of Toggle Switch GRN



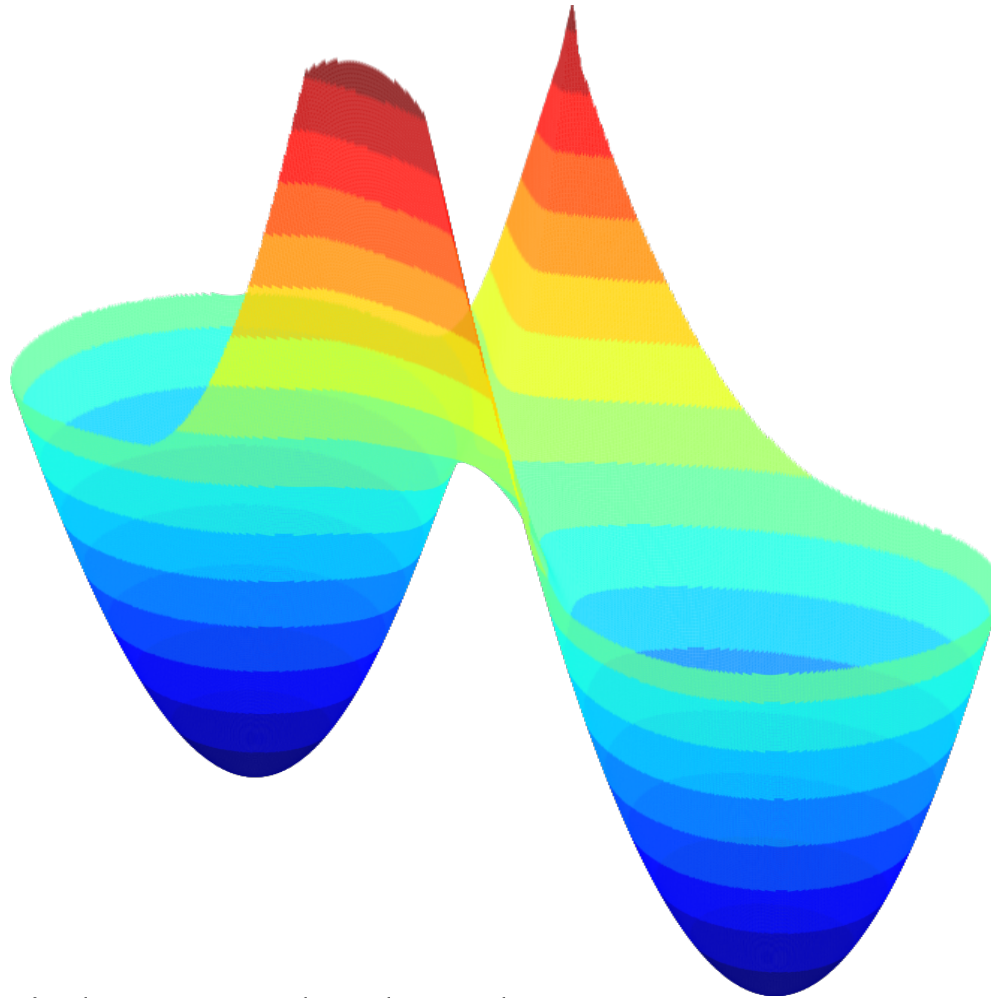
$a1=a2$	0
$b1=b2$	1
$k1=k2$	1
n	4
S	0.5

Flow Diagram of Toggle Switch GRN



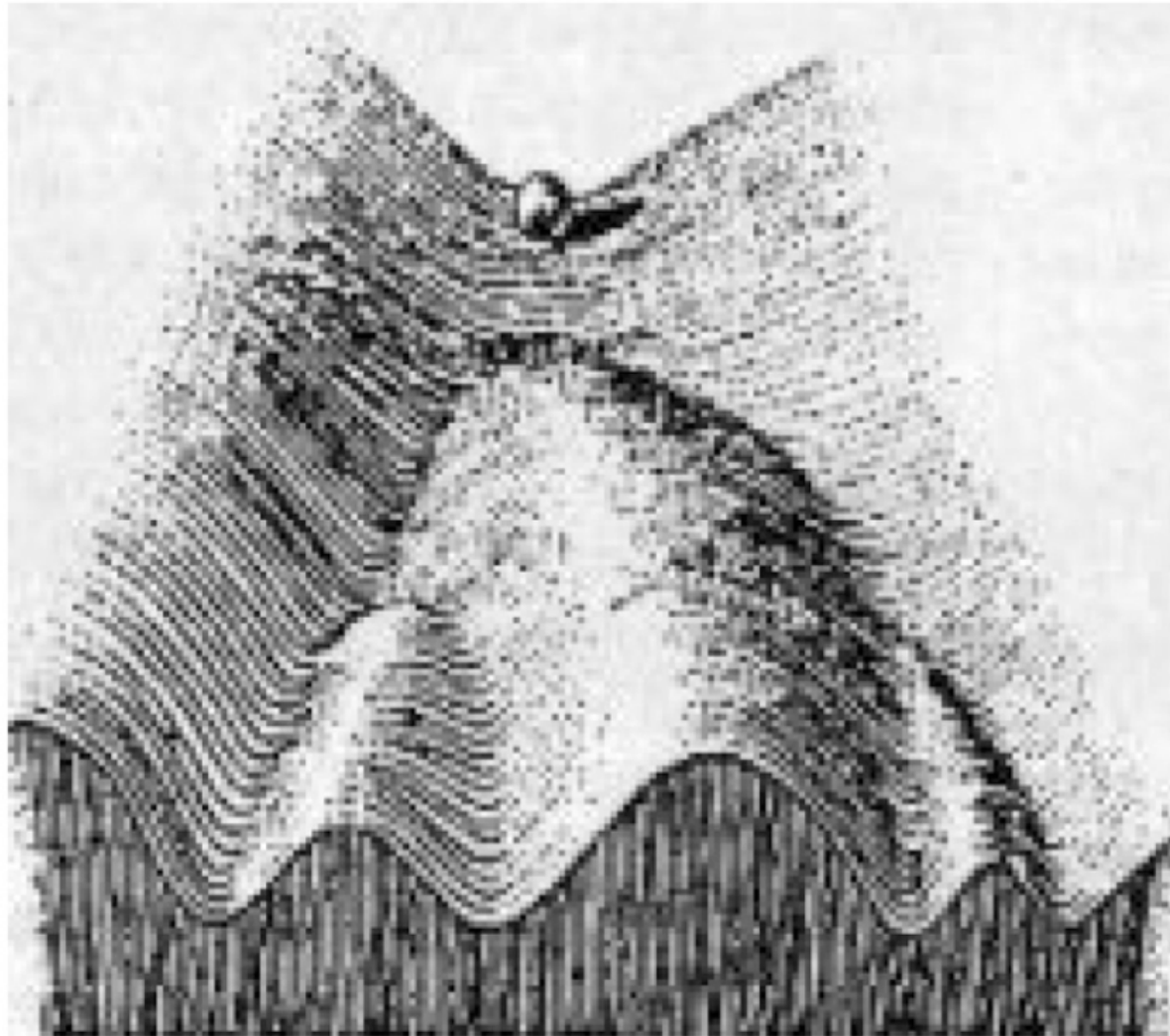
$a1=a2$	0
$b1=b2$	1
$k1=k2$	1
n	4
S	0.5

Quasi-Potential of GRN

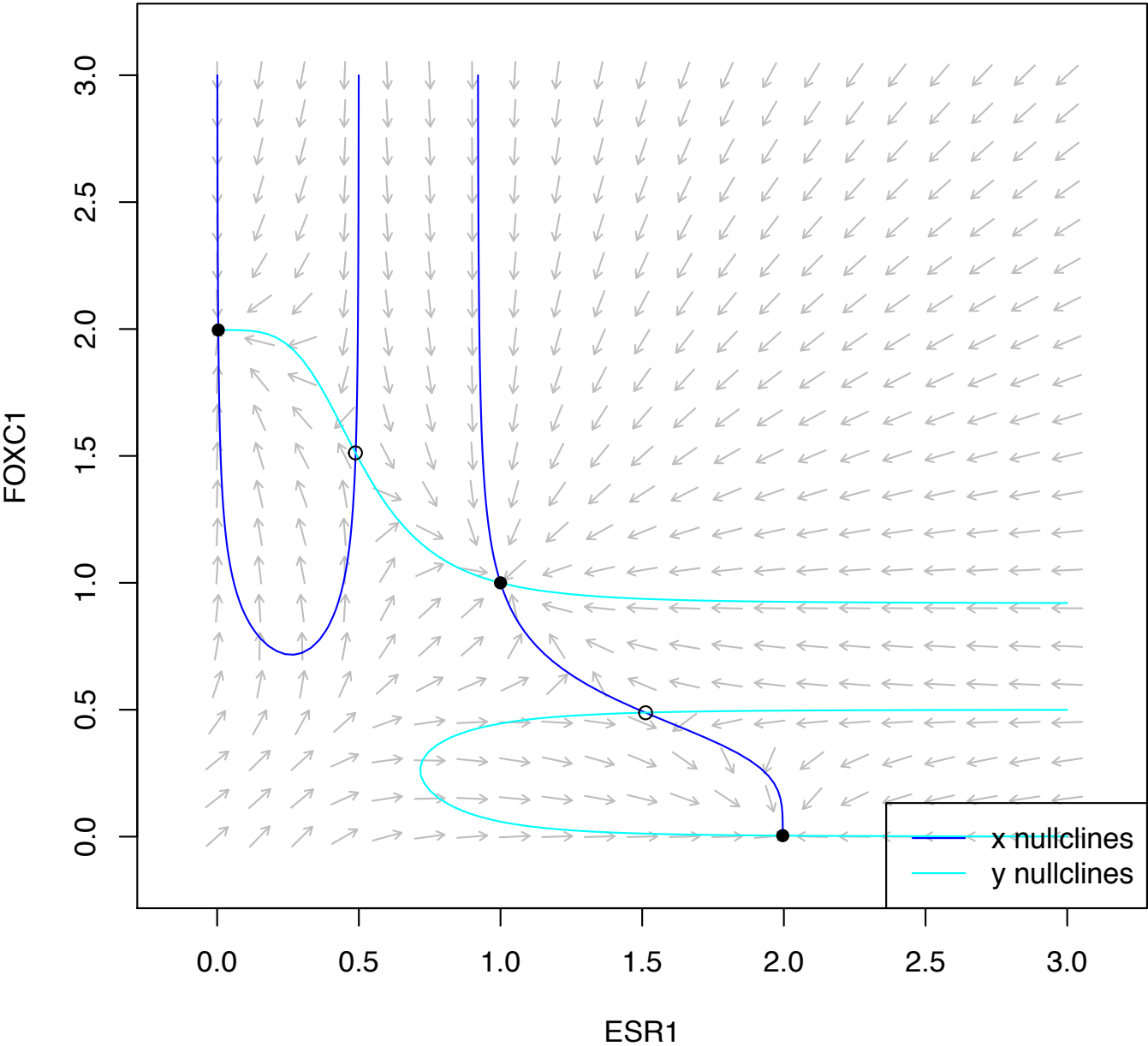


Quasi-potential was calculated
with R package QPot

Waddington's Epigenetic Landscape

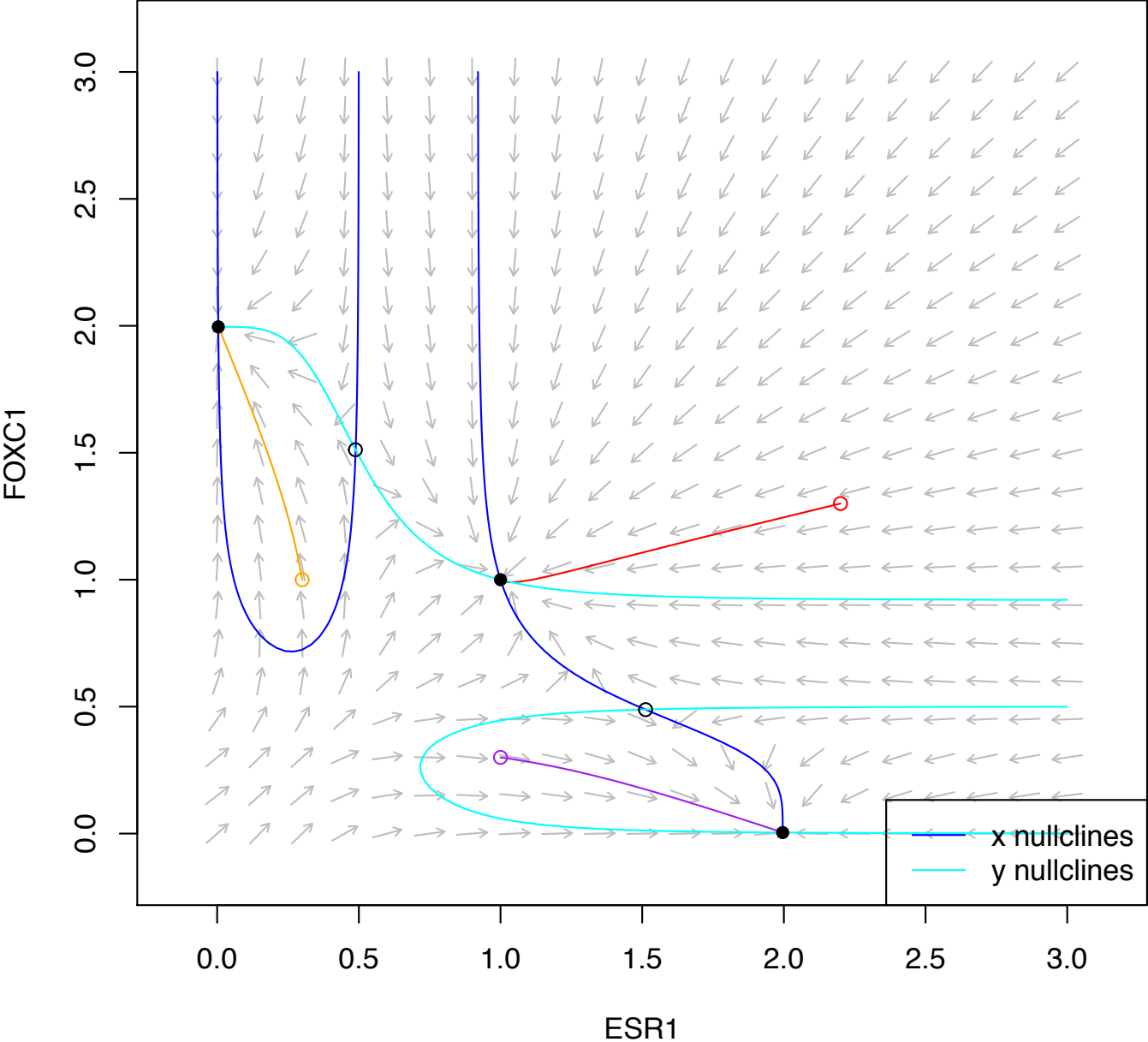


Toggle Switch GRN with Auto-Activation



$a1=a2$	1
$b1=b2$	1
$k1=k2$	1
n	4
S	0.5

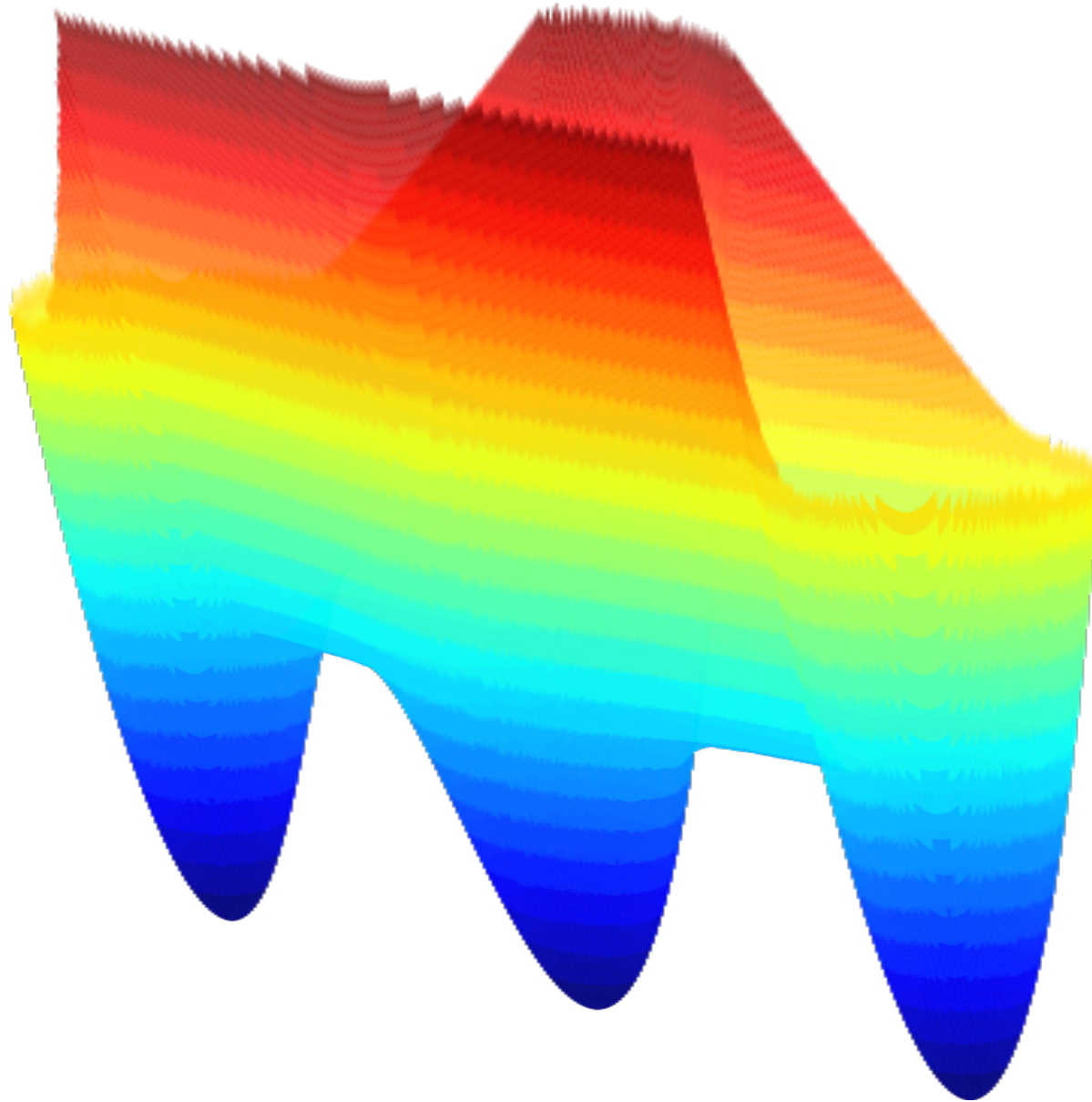
Toggle Switch GRN with Auto-Activation



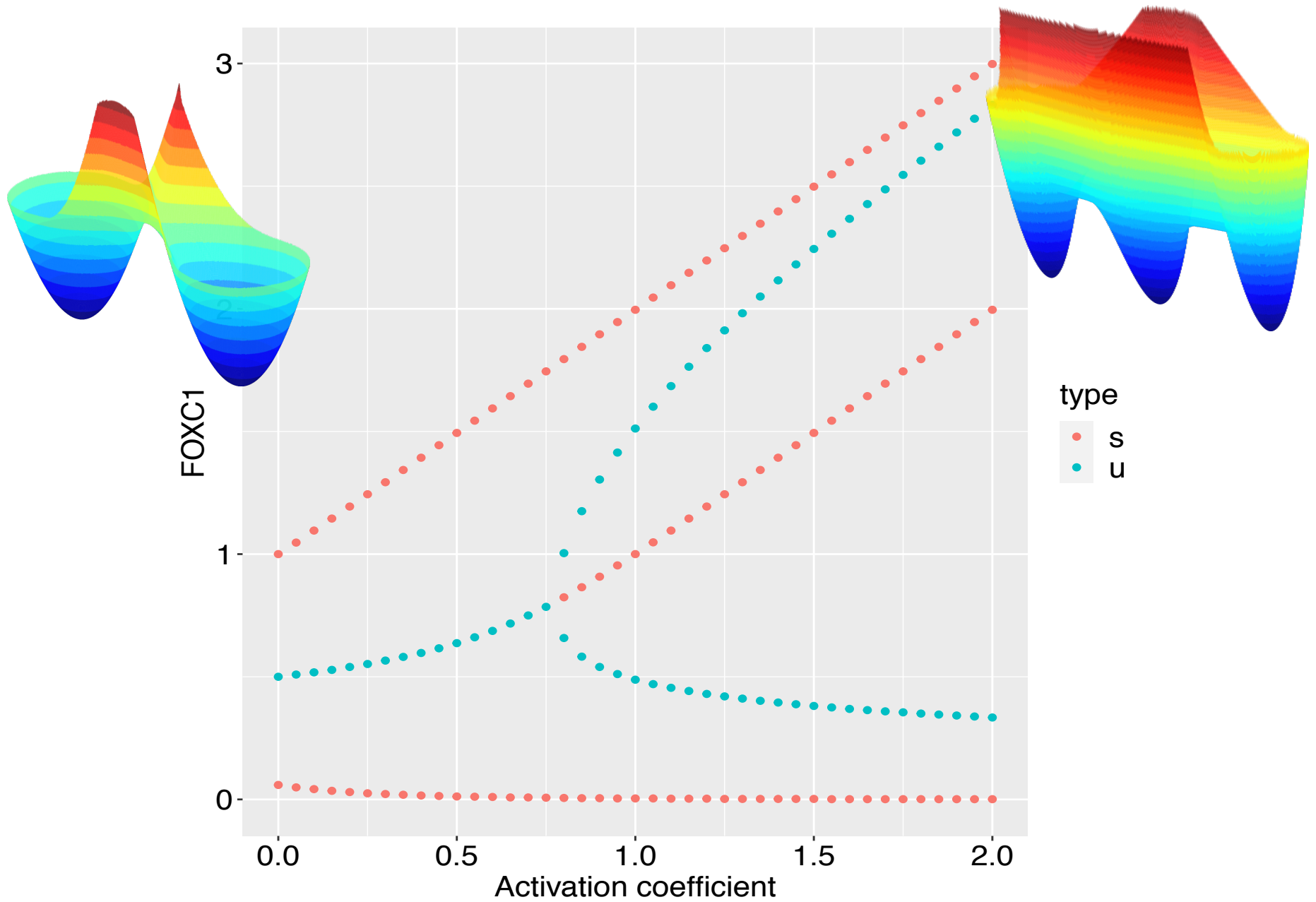
$a1=a2$	1
$b1=b2$	1
$k1=k2$	1
n	4
S	0.5

— x nullclines
— y nullclines

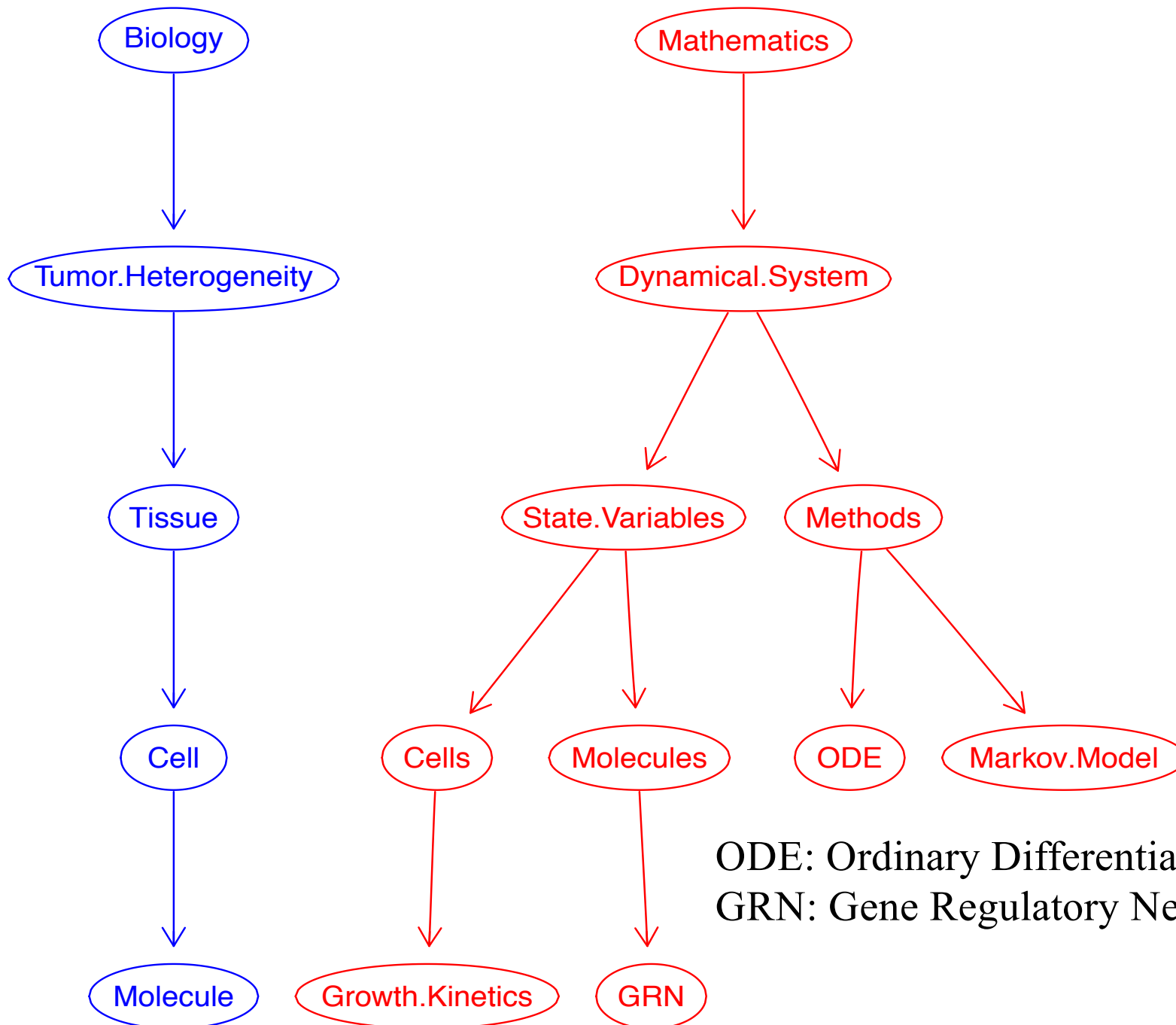
Quasi-Potential of GRN



Bifurcation diagram



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GRN: Gene Regulatory Network