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# **Dynamical Crossover of Clone Size Statistics in** a Stochastic Model of Stem Cell Differentiation

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### **Critical Statistics of Clonal Population**

Stem Cells (SCs) support tissue homeostasis





## **Previous Models of Cell Fate Decision**

**Critical Birth-Death Process (CBD)** 

prob. 1/2

Voter Model (VM)

- Proliferating Cell (PC) Differentiated Cell
- $\alpha = 1 \qquad \Phi(X) = e^{-X}$

**exp.:** epithelial (sheet) tissues



basal layer

#### *in vivo* Lineage Tracing

Tracking the labeled population of progenies of single SCs to unravel how cells choose their fate and maintain tissue

#### **Clone Size Statistics**

Universal scaling form of cumulative distribution

 $C_n(t) \simeq \Phi(n/n_{\text{surv}}(t))$ 

collapse onto a single scaling function  $\Phi(X)$ 

Average clone size grows!!  $n_{surv}(t) \sim t^{\alpha}$ 

A.M.Klein and B. D. Simons, Development 138, (2011).



## **Problems & Research Questions**

with **finely-tuned** probabilities

✓ Fine-tuning is required in the previous models.

 $\rightarrow$  A theoretical model without fine-tunings is desirable.

 $\checkmark$  CBD and VM are not discussed in the equal foot point.

 $\rightarrow$  Can we treat the two models in a unified framework?

#### Self-replicating Langevin System: Many-Body Langevin + Birth-Death Process **Self-replication Process** : Local Density Dependent Spatial cell-cell Interaction : Cell Adhesion $\frac{d}{dt}\vec{r}_{j}(t) = -\vec{\nabla}_{j}U(\{\vec{r}_{i}(t)\}) + \sqrt{2T}\vec{\xi}_{j}(t) \qquad j = 1, 2, ..., N(t)$ Differentiation Proliferation $w^-( ho_L)$ $\langle \mathcal{E}^{\mu}_{\cdot}(t) \rangle = 0$

interaction range 2L



Negative feedback via local density  $\rho_L(\vec{r})$ 

 $w^{\pm}(\rho)$  are balanced at an attractive fixed point  $\rho = \rho^*$ 

$$U(\{\vec{r}_i\}) = \sum_{j=1}^{N} \sum_{k>j} u(\vec{r}_j - \vec{r}_k) \frac{\langle \zeta_j(t) \rangle = 0}{\langle \xi_j^{\mu}(t) \xi_k^{\nu}(t') \rangle} = \delta_{j,k} \delta^{\mu,\nu} \delta(t - t')$$

$$= 1$$

$$u(\vec{x} - \vec{y}) = \frac{1}{2} K(|\vec{x} - \vec{y}| - l_0)^2$$
for  $\vec{x}, \vec{y}$ : neighboring pairs
$$l_0$$
: typical length scale of a single cell



#### **Scaling Hypothesis** Slope: 1/2 Scaling form $10^{1}$ $(l(t) - l_0)/L$ $t \ll t_c(L),$ $t \gg t_c(L).$ Slope: 🕻 $\frac{l(t) - 1}{L} = f\left(\frac{t}{t_c(L)}\right) \begin{cases} \simeq \frac{t}{t_c(L)} \\ \sim \left(\frac{t}{t_c(L)}\right)^{1/2} \end{cases}$ $10^{0}$ L = 10 L = 20 L = 30 L = 40Crossover Time $t_c(L) = 2\lambda^{-1}(L-1)$ $t / t_{c}(L)$ A simple scenario: competition between l(t) and L $L = l(t) \simeq (1 + \lambda t_c/2)$ l(t) Average clone size



## **Remark: Clustering of Cells**

Large interaction range

Unphysical clustering of cells

#### **Linear Stability Analysis** $\rho(k;t) \sim e^{\nu(k)t}$ Uniform distribution is unstable if $\frac{\beta}{\alpha L^2} \lesssim 0.012$ time scale of cell division $\overline{\alpha L^2}$ $\overline{\lambda L^2} = \overline{\text{time scale of spatial interaction}}$



## **Summary of Current Study**

In this study, we propose a model of cell fate decision with cell-cell interaction

✓ Fine-tuning is avoided ✓ CBD and VM are unified by the interaction range : A unified framework to study interacting cell population ✓ Dynamical crossover of clone size statistics for 1 dim