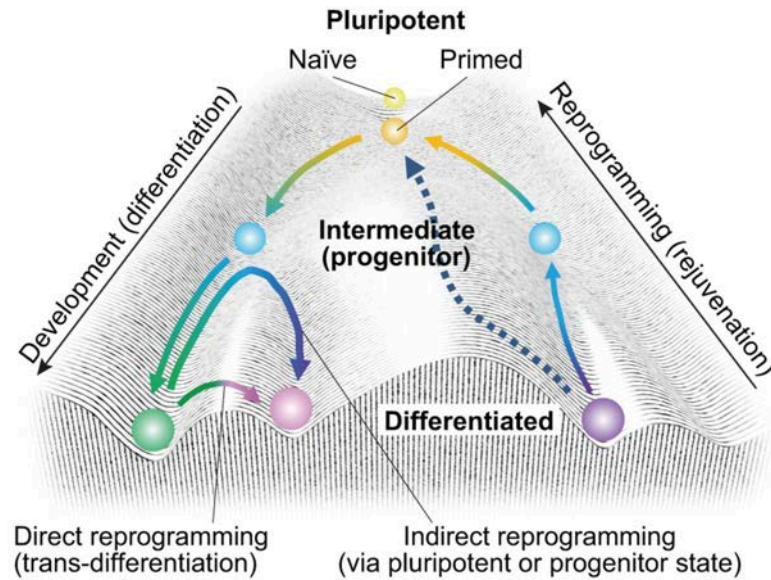


Statistical mechanics of stem cells

SIDHARTHA GOYAL
Physics
University of Toronto



UNIVERSITY OF
TORONTO



Origin of stem cells

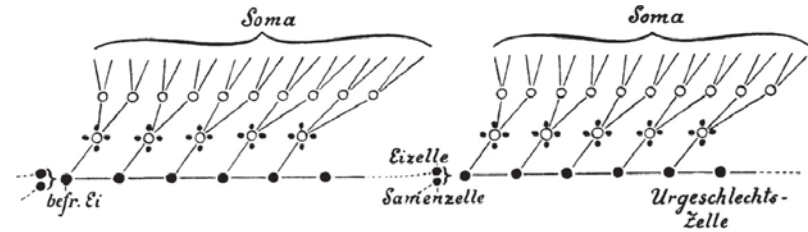
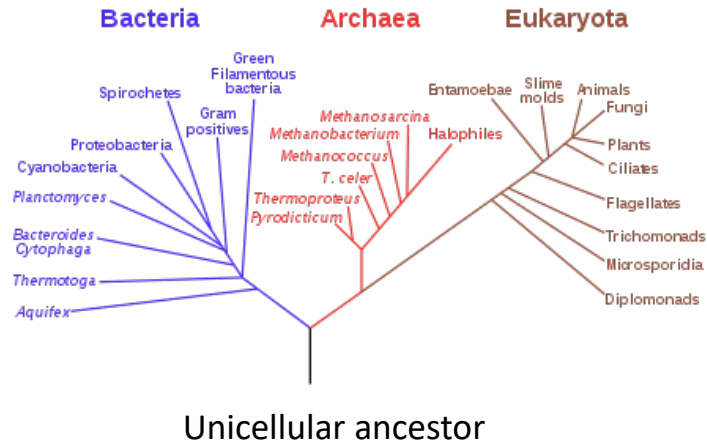
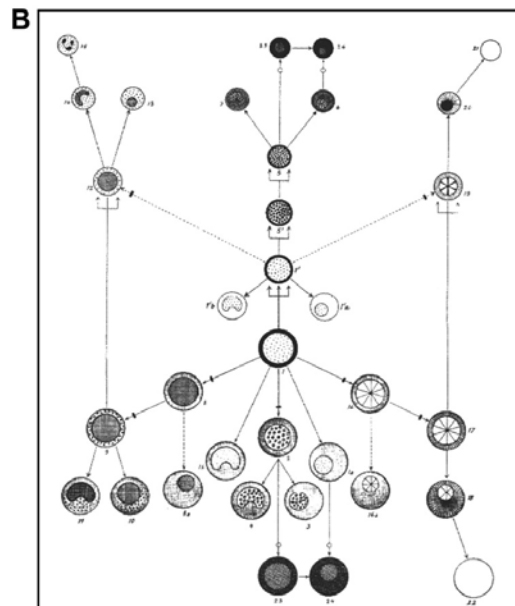


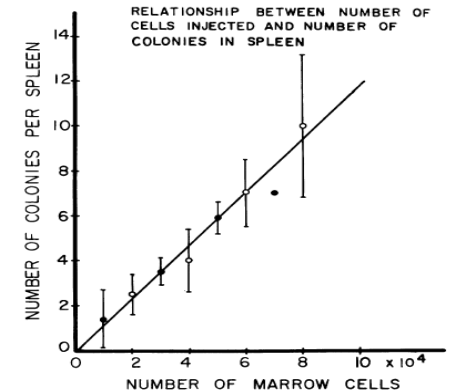
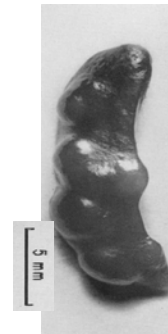
Fig. 1.

Fertilized egg (1870's)



Progenitor of blood cells
(1905)

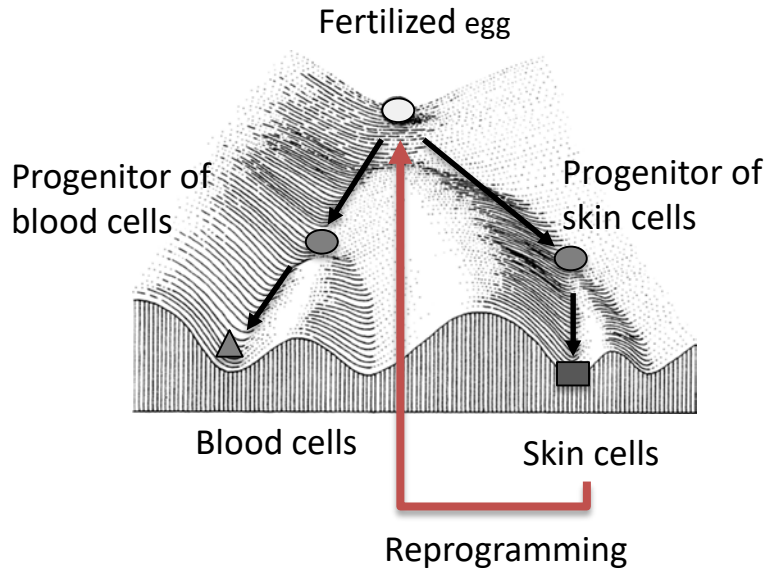
Precursor of tumors
(1920's)



- Self-renew
- Generate other types of cells

Radiation Research, 1961
Till and McCulloch at
University of Toronto

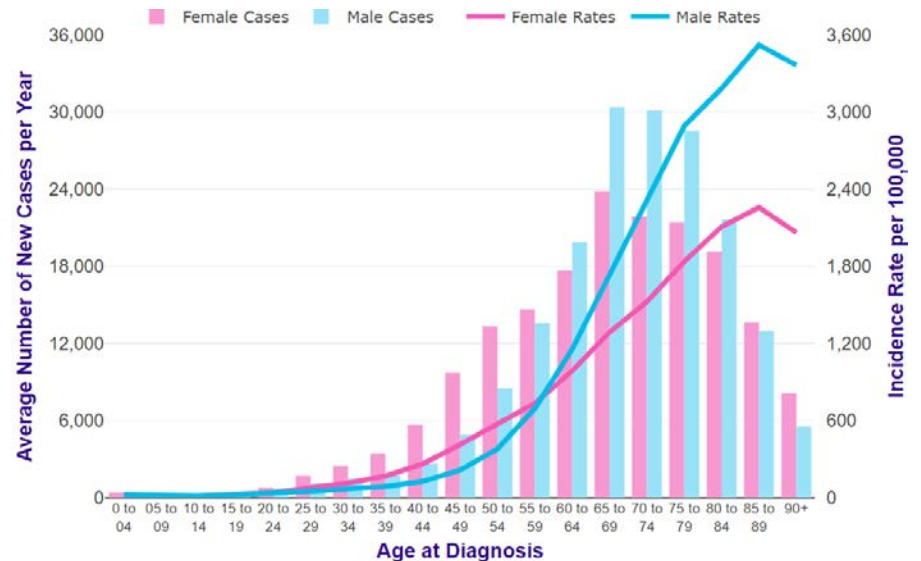
Evolution of stem cells



Genetic changes in stem cells

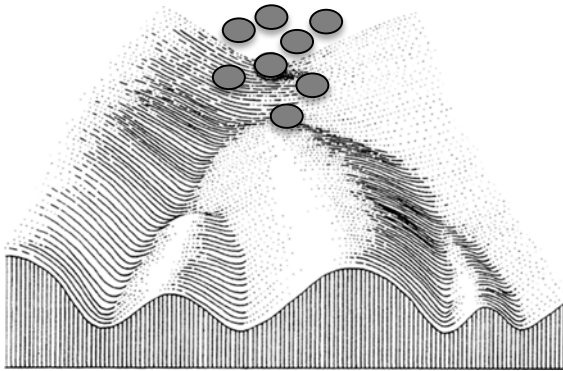
Non-genetic (epigenetic) inheritance (1930-40)

Robustness and response to environment



Population of stem cells

Stems cells



Does epigenetic variability affect stem cell evolution?

How does stem cell function evolve and diversify?

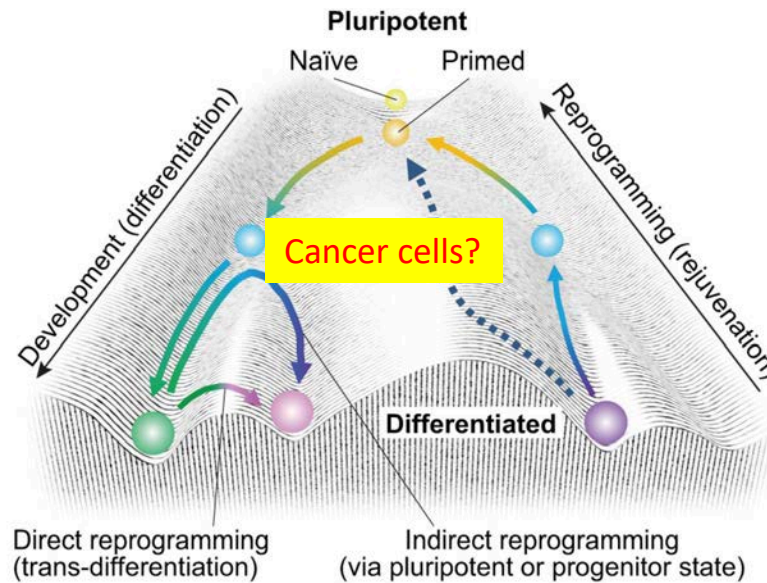
Can we predict stem cell fate, for example which stem cell may lead to a tumor?

Outline

Blood regeneration:
homeostasis and clonality

Tom Chou
Sanggu Kim
UCLA

BMC Biology, 2015



Dominant clones in cellular
reprogramming

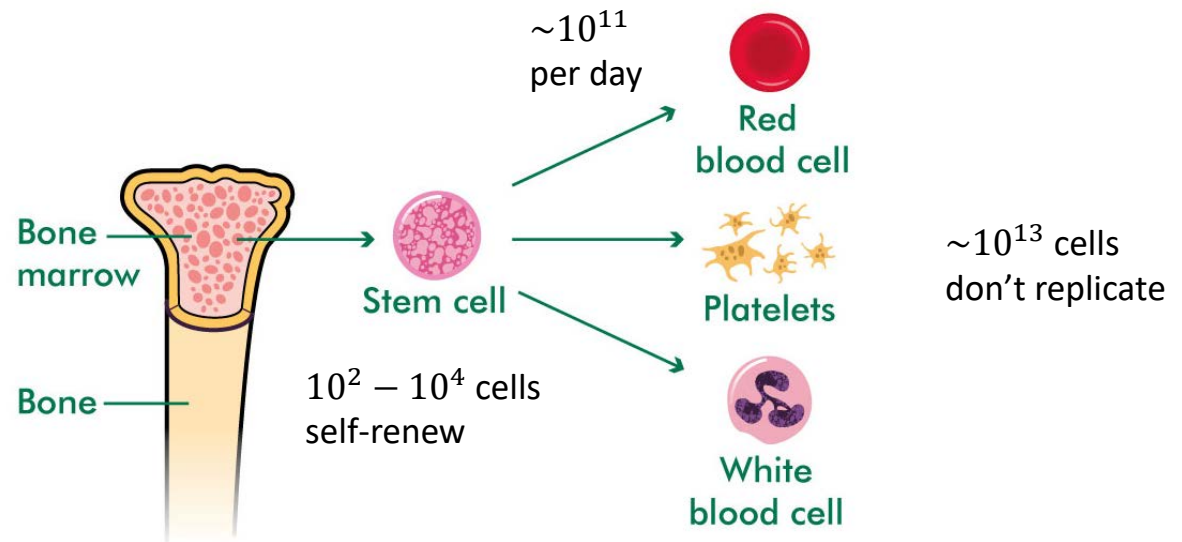
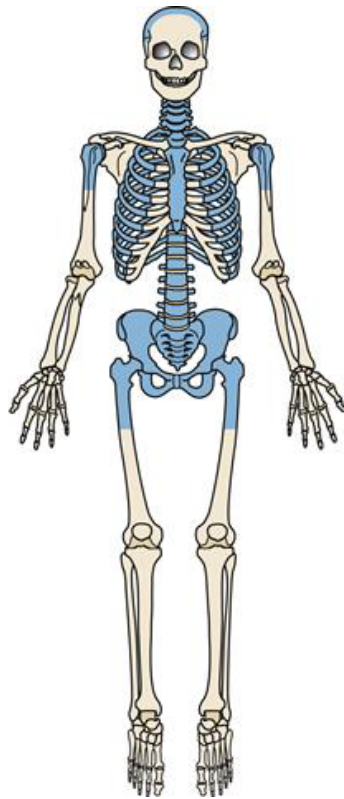
Sophie McGibbon-Gardner
Nika Shakiba
Peter Zandstra
UofT

Science, 2019

Heterogeneity in cancer

Catherine O'Brien
UofT

Blood production

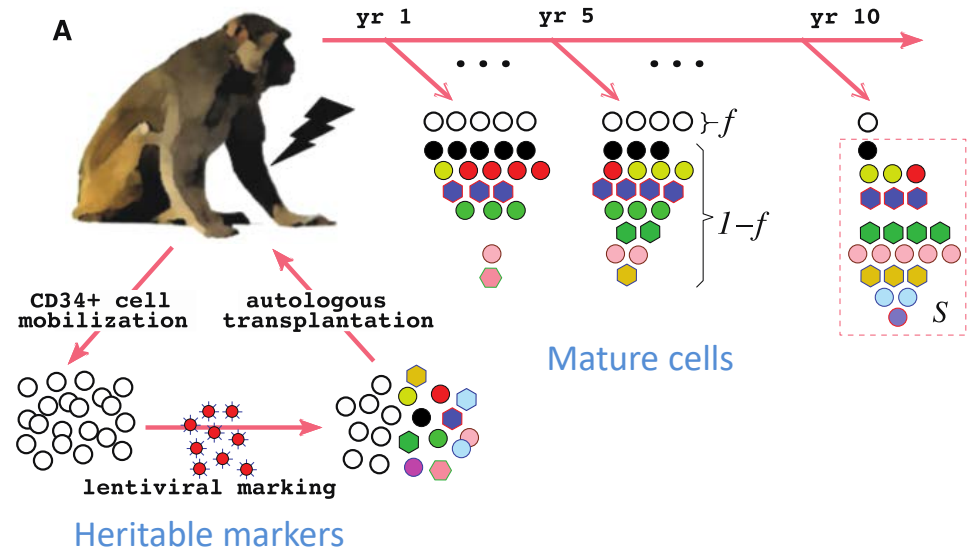
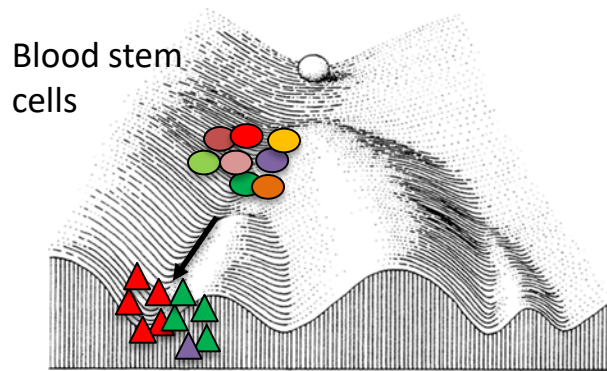


How many stem cells are producing blood?

Are some stem cells better than others?

Are stem cells biased in their output?

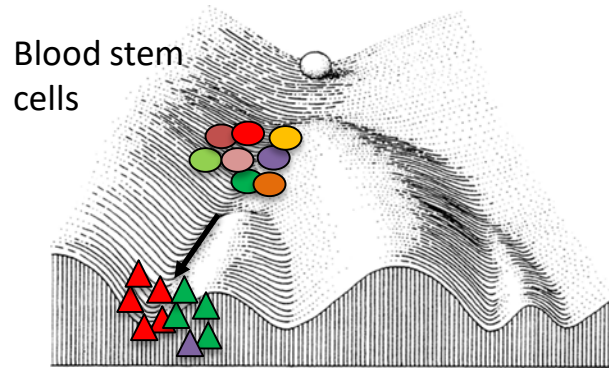
Tracking clonal output



What are the features of long-term, animal-level blood production?

Phenomenology: data -> model -> predictions?

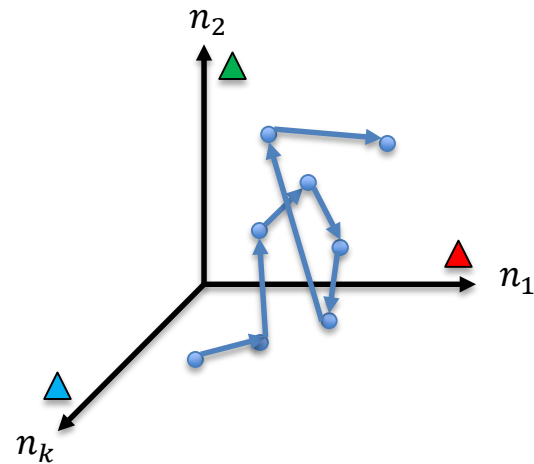
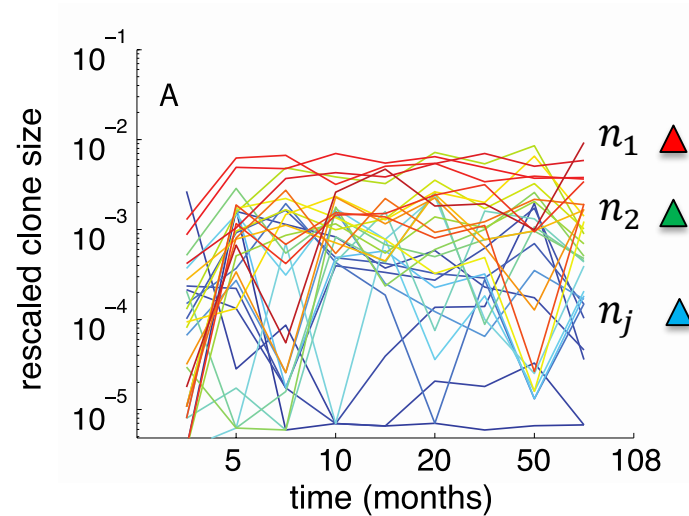
Tracking clonal output



Large variability in stem cell output

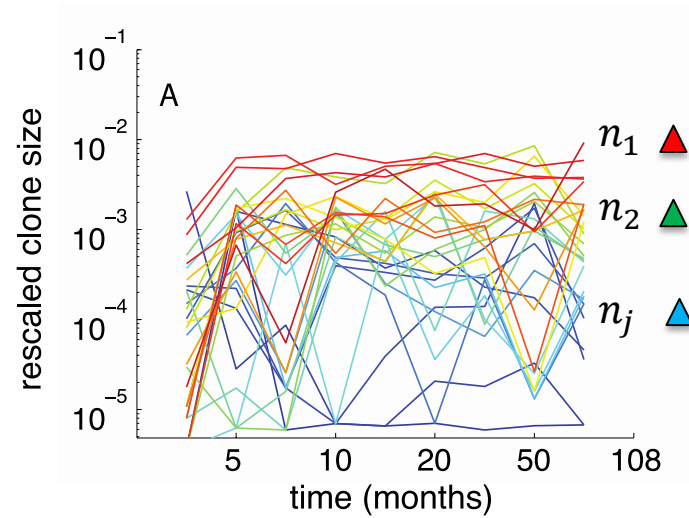
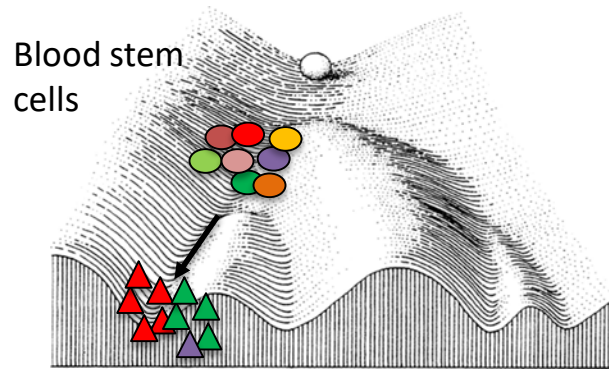
So, are some stem cells better than the others?

Need some “theory” or a model to compare against



Flow in high dimensions

Tracking clonal output

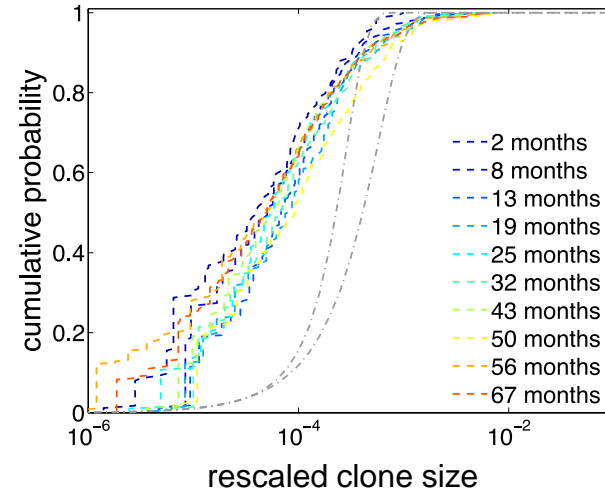
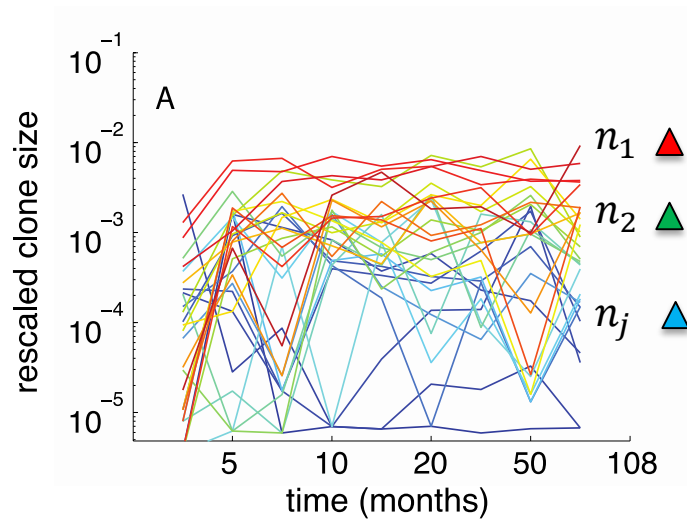


$$p(\{n_1(t), n_2(t), n_3(t), \dots, n_j(t), \dots\})$$

Under sampled distribution

Look for something *simpler*

Density of “states”



$$p(\{n_1(t), n_2(t), n_3(t), \dots, n_j(t), \dots\})$$

Under sampled distribution

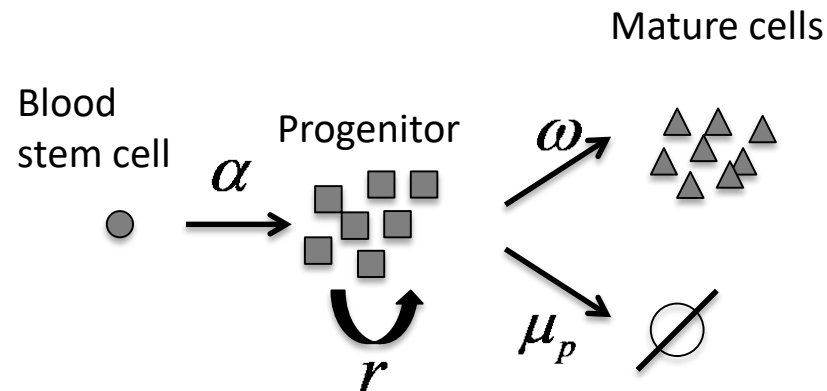
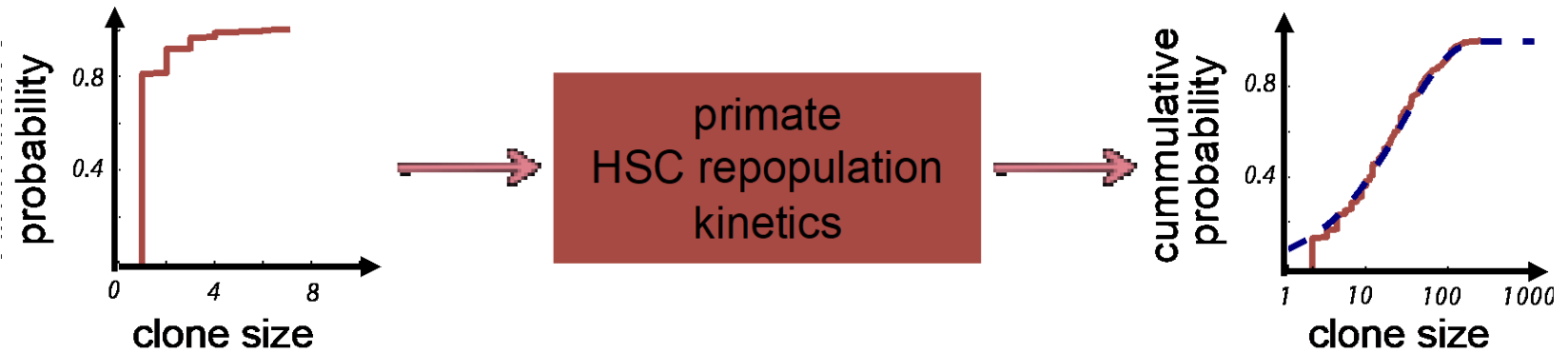
Look for something *simpler*

$$p(s, t) = \left\langle \sum_j \delta(n_k(t) - s) \right\rangle$$

Density of states

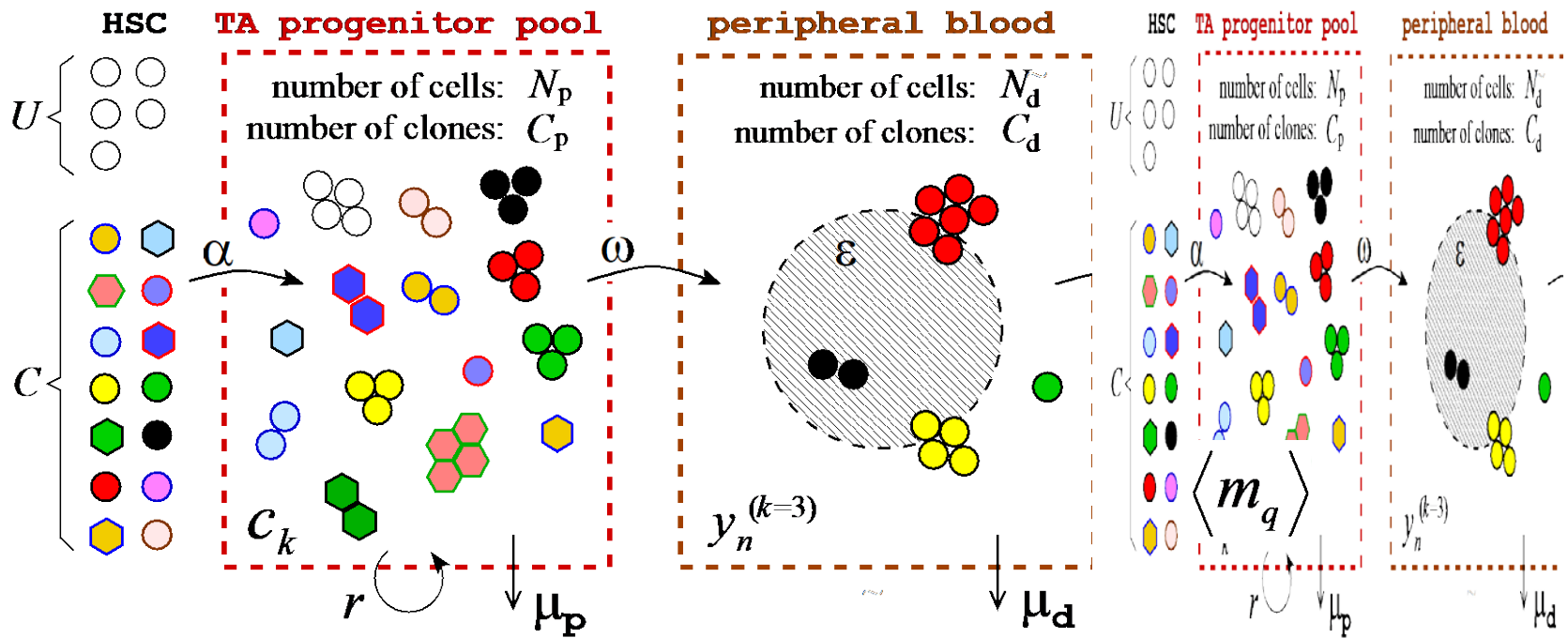
Time-invariant distribution
(conserved quantity)

Reframing the problem



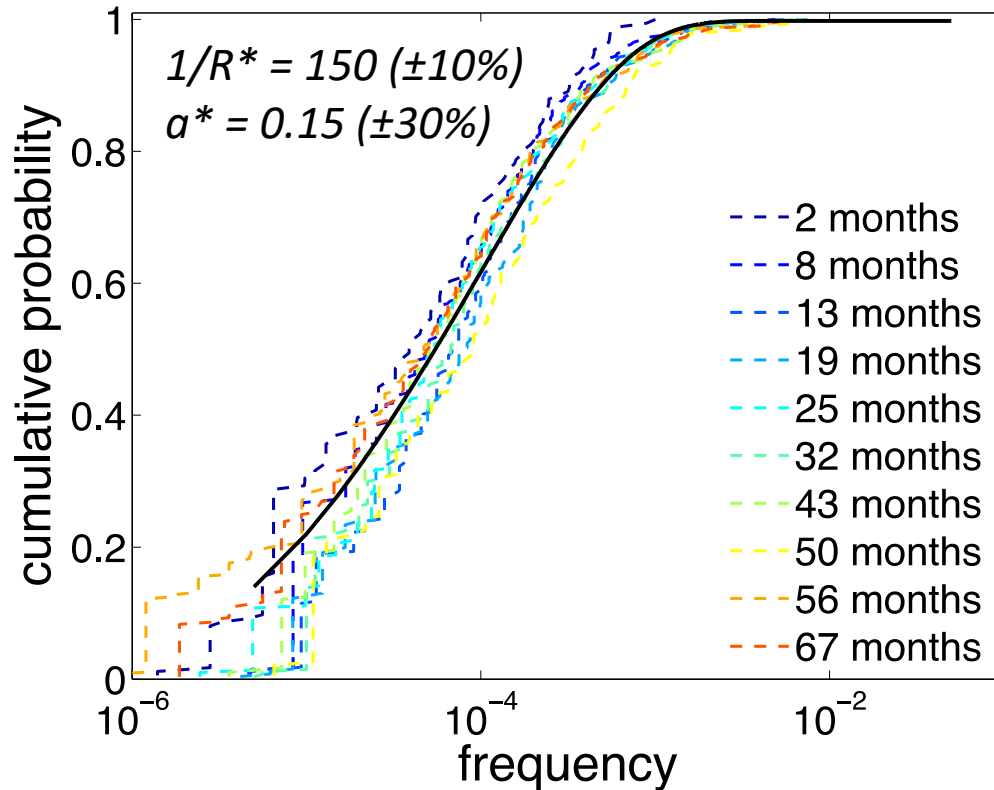
Global feedback on
progenitor growth

Model for tracking clones

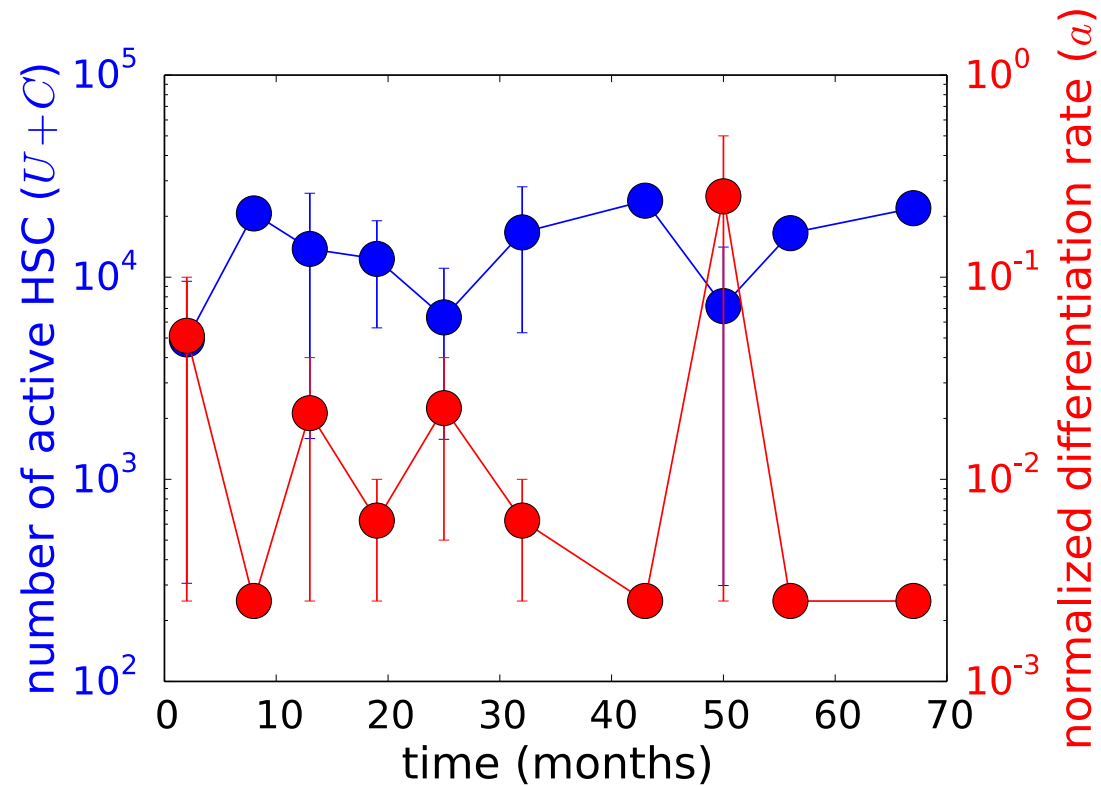


“Neutral” theory explains the data

$$m_{q>0} \approx A[\Gamma(a, (q+1)R) - \Gamma(a, qR)]; \quad R = -\frac{\varepsilon w}{\log \bar{r}}, \quad a = \frac{\alpha}{r}$$



Coming back to biology of blood regeneration

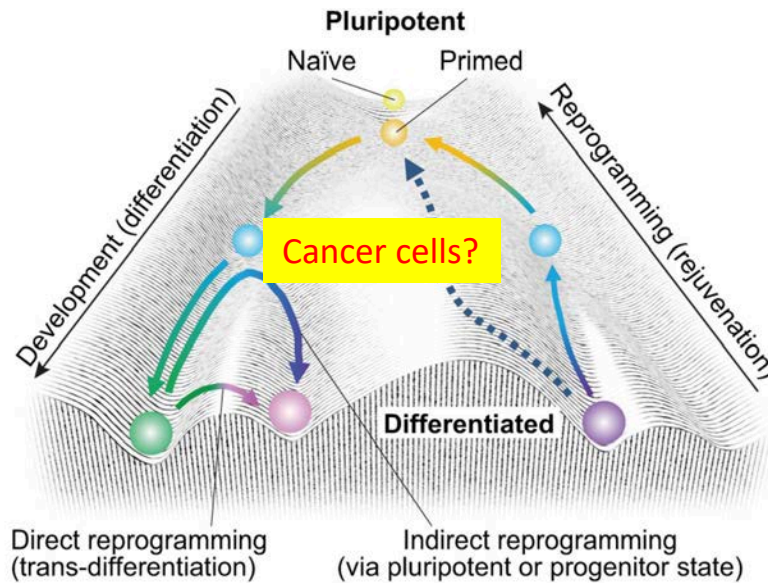


Number of active stem cells at any time is of the order 10K
Differentiation rate \ll progenitor replication rate

Blood regeneration:
homeostasis and clonality

Tom Chou
Sanggu Kim
UCLA

BMC Biology, 2015



Dominant clones in cellular
reprogramming

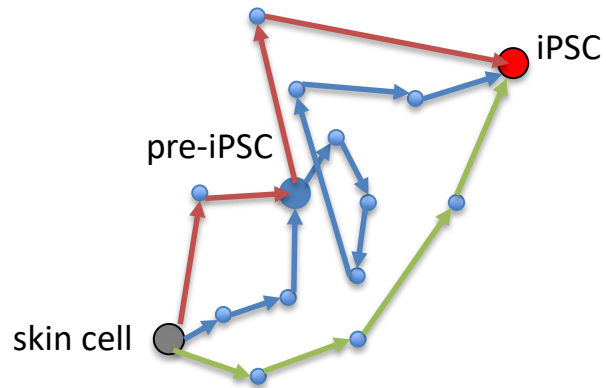
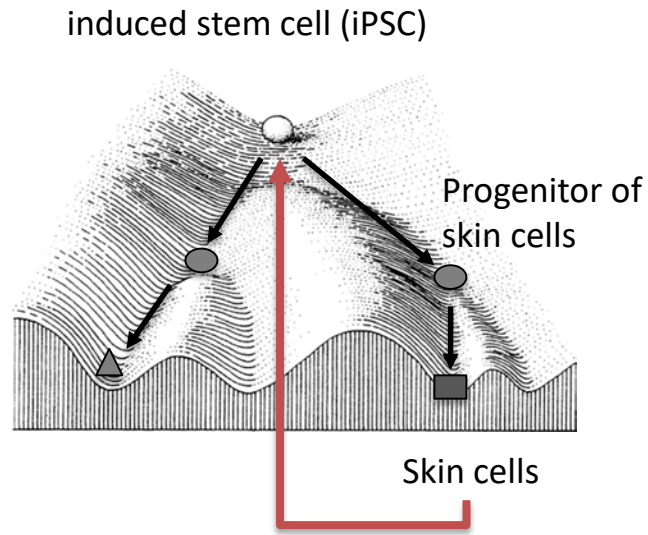
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Heterogeneity in cancer

Catherine O'Brien
UofT

Cellular reprogramming

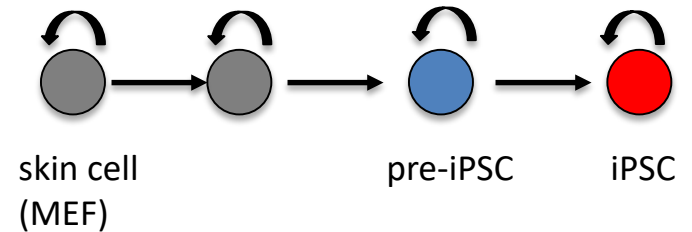


Gene expression space (high dimensional)

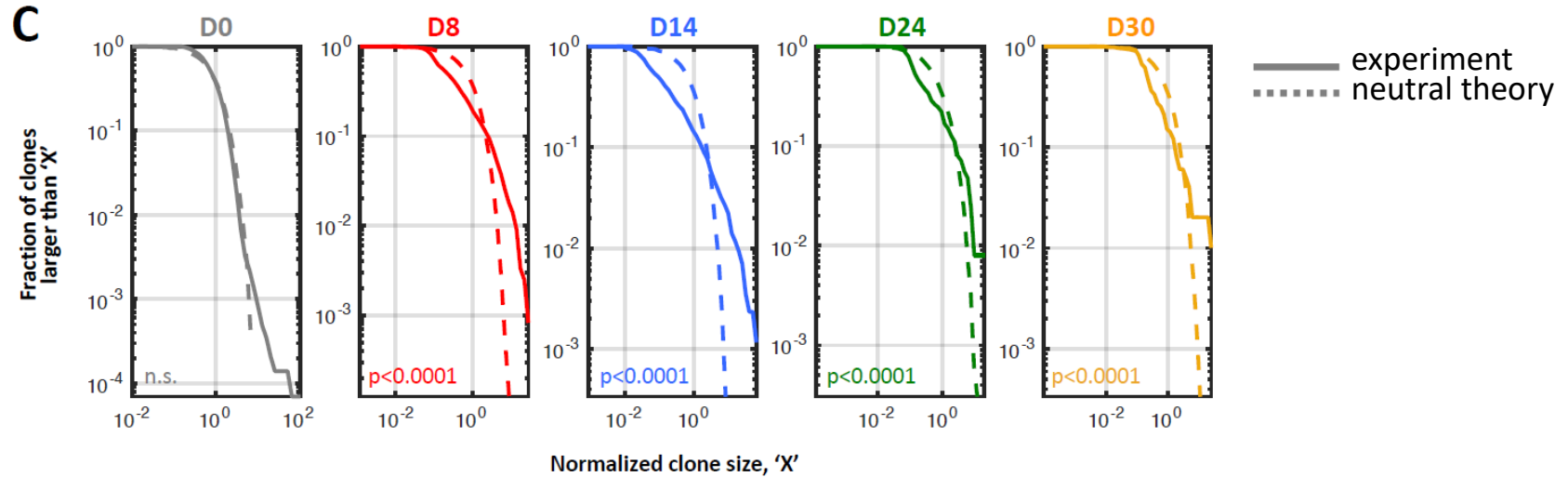
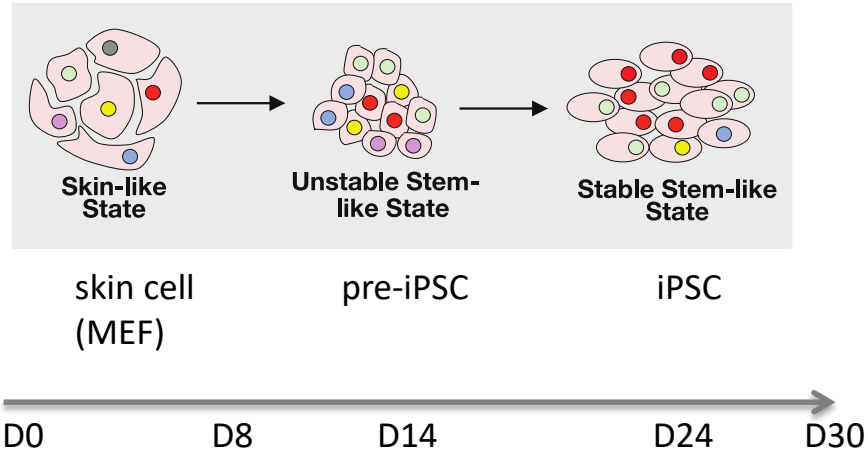
reprogramming landscape vs undirected search

individual cells vs group of cells

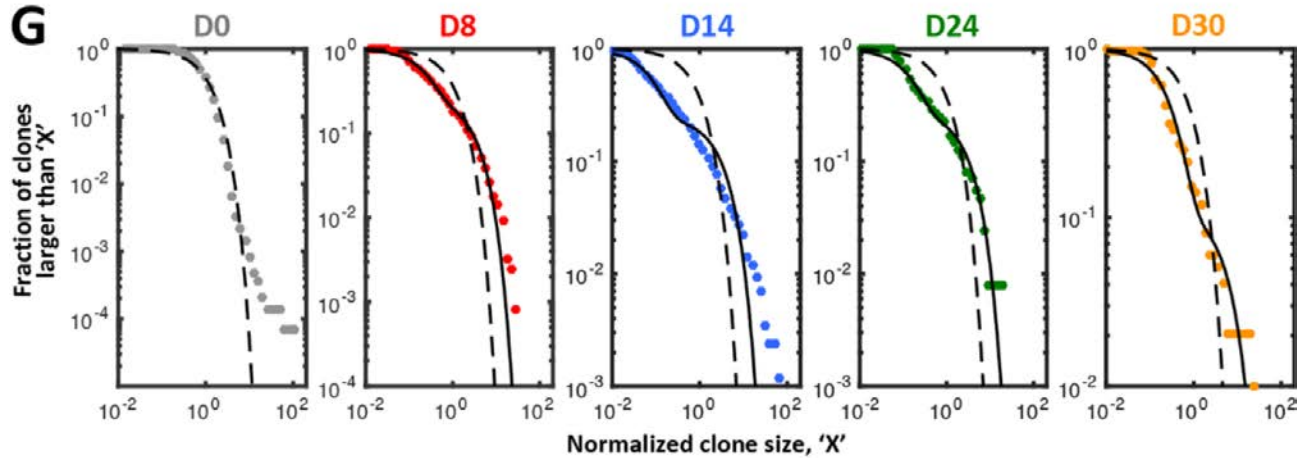
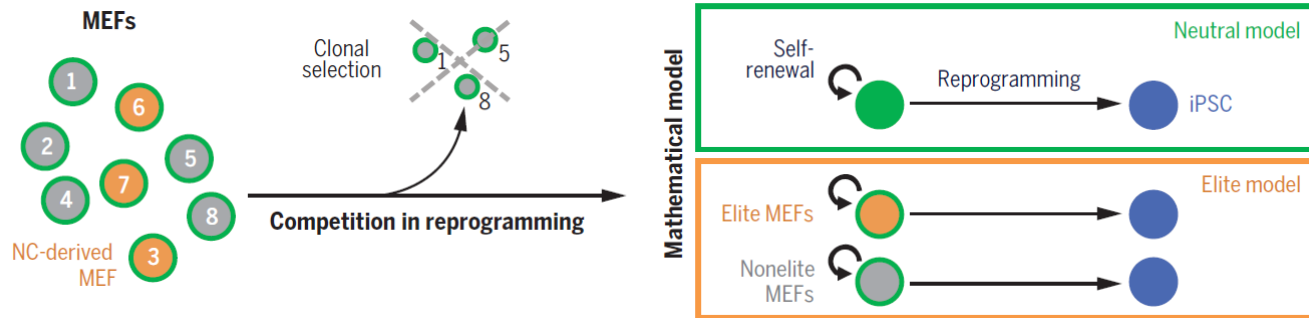
four state model



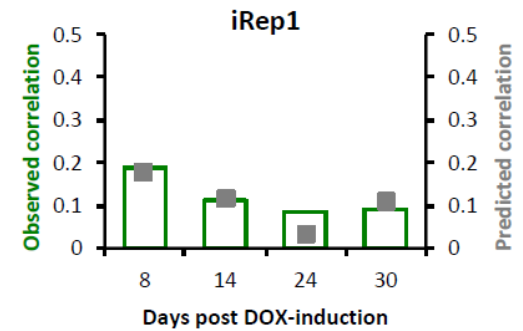
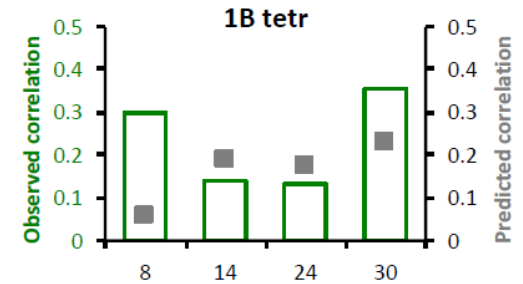
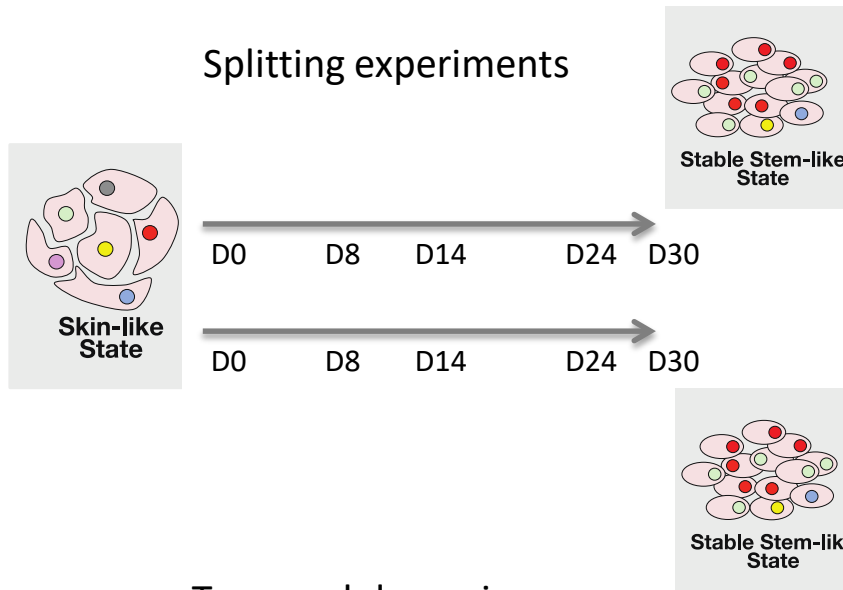
Tracking reprogramming potential



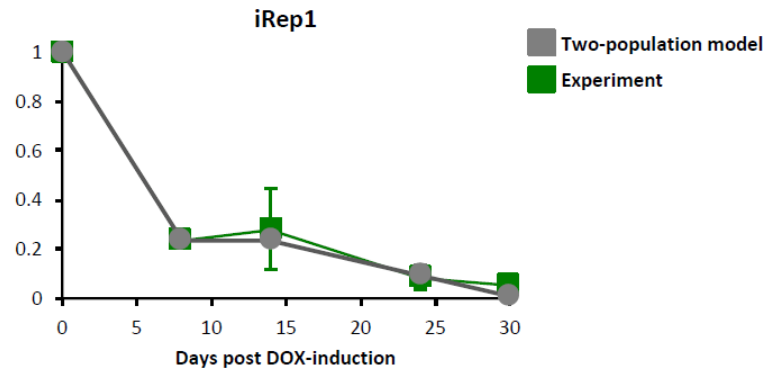
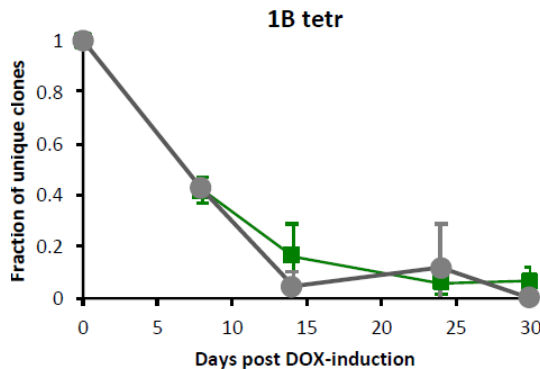
Competition model



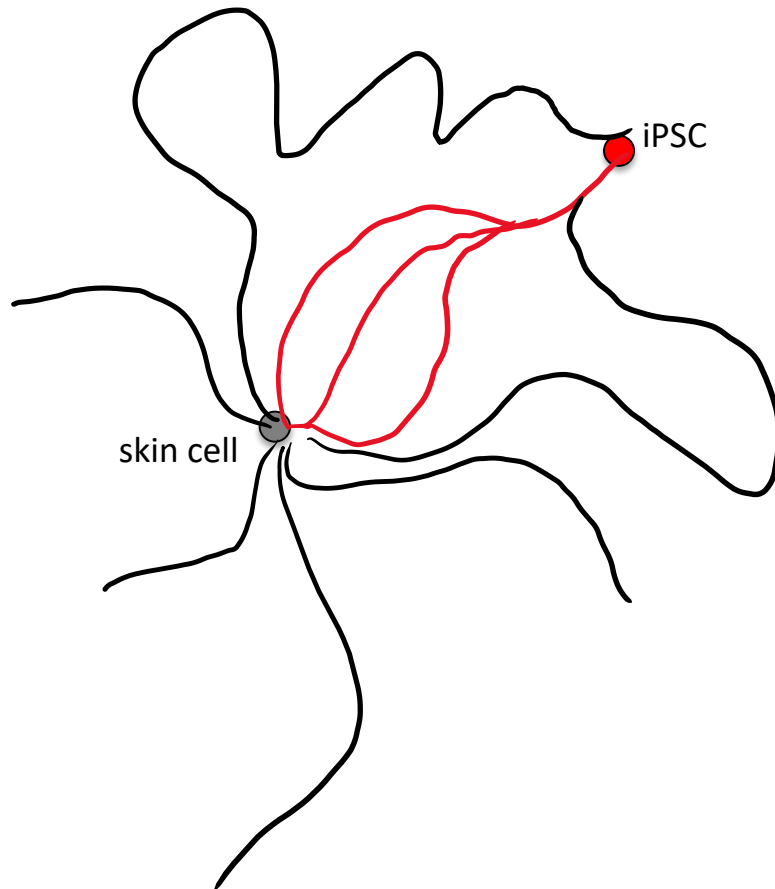
Testing the model



Temporal dynamics



Outlook: Track trajectories of reprogramming cells in gene expression space



How do elite and non-elite trajectories differ?

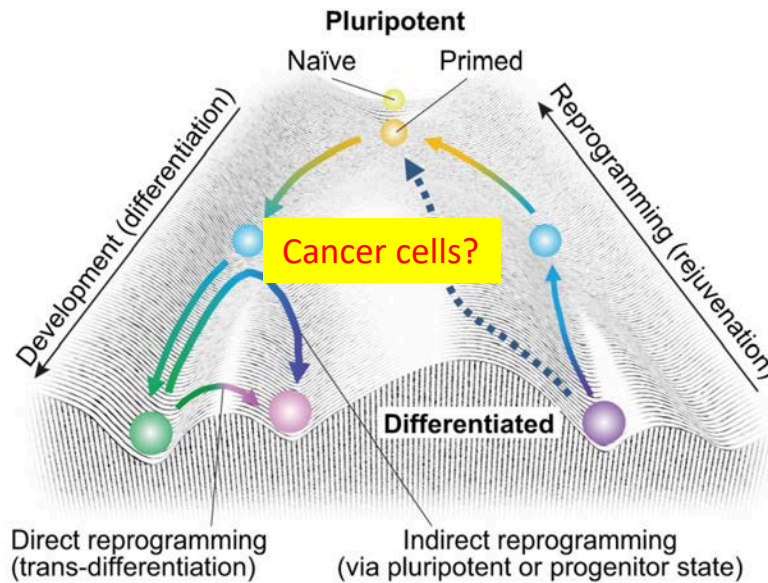
Is there a reprogramming landscape that elite cells utilize?

Are non-elite cells solving a “search” problem

Blood regeneration:
homeostasis and clonality

Tom Chou
Sanggu Kim
UCLA

BMC Biology, 2015



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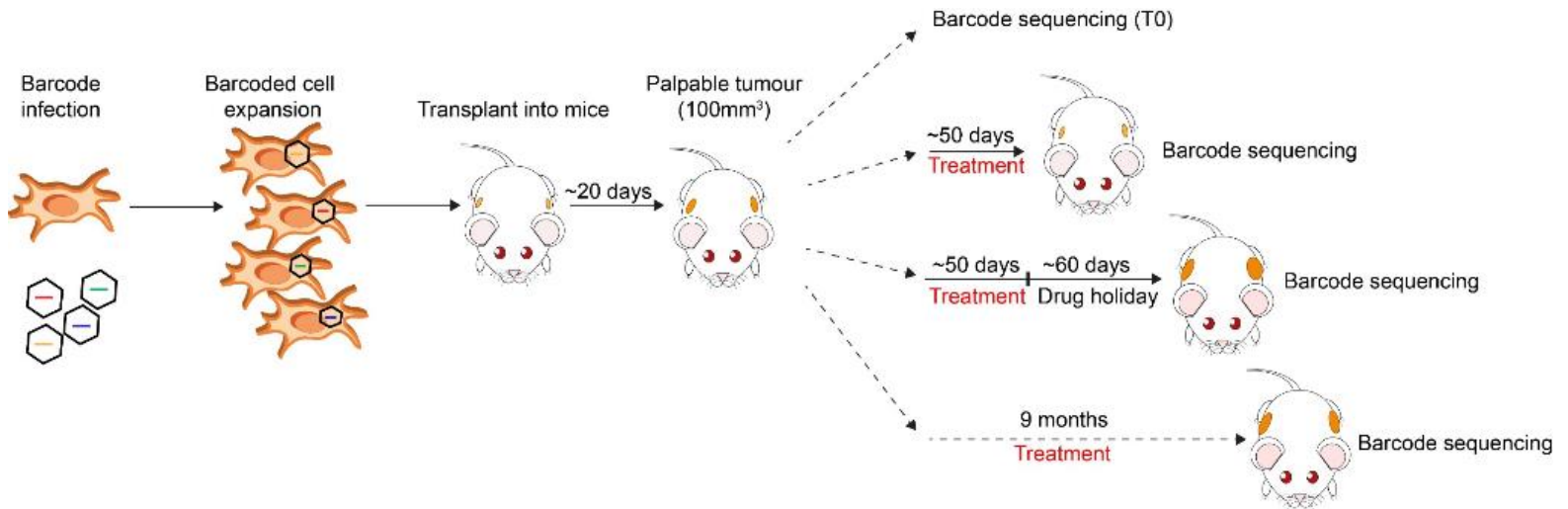
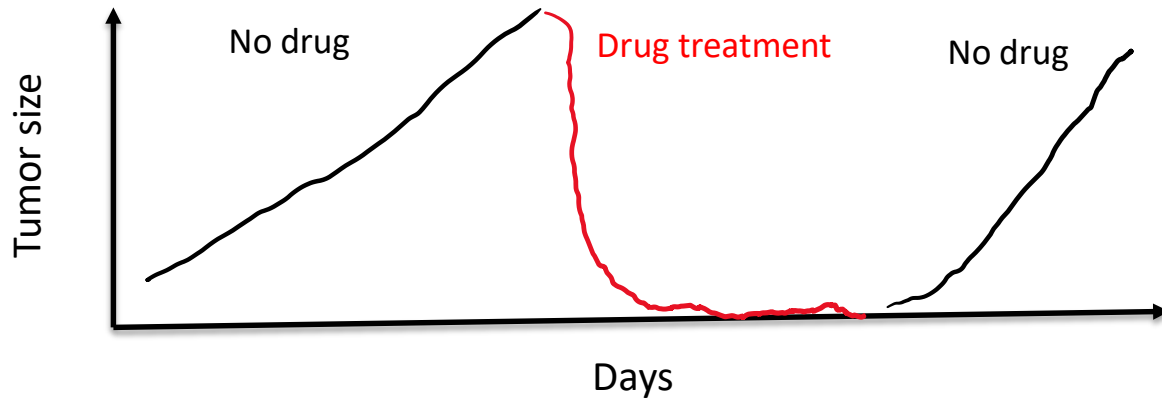
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Peter Zandstra
UofT

Science, 2019

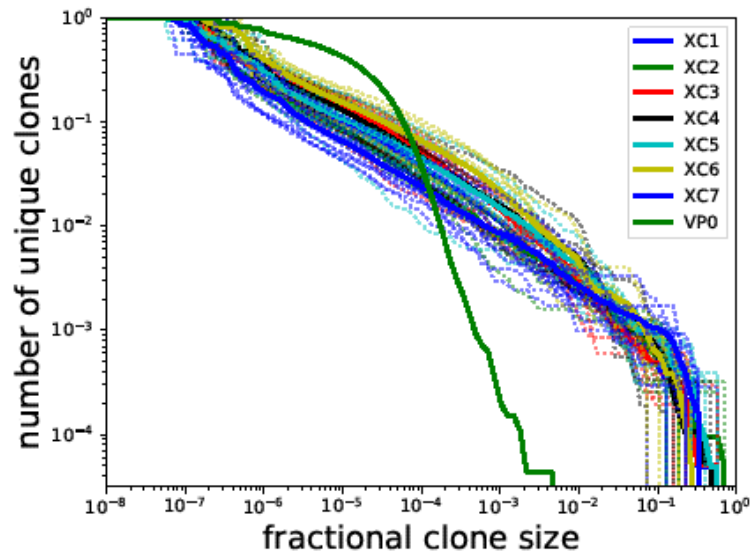
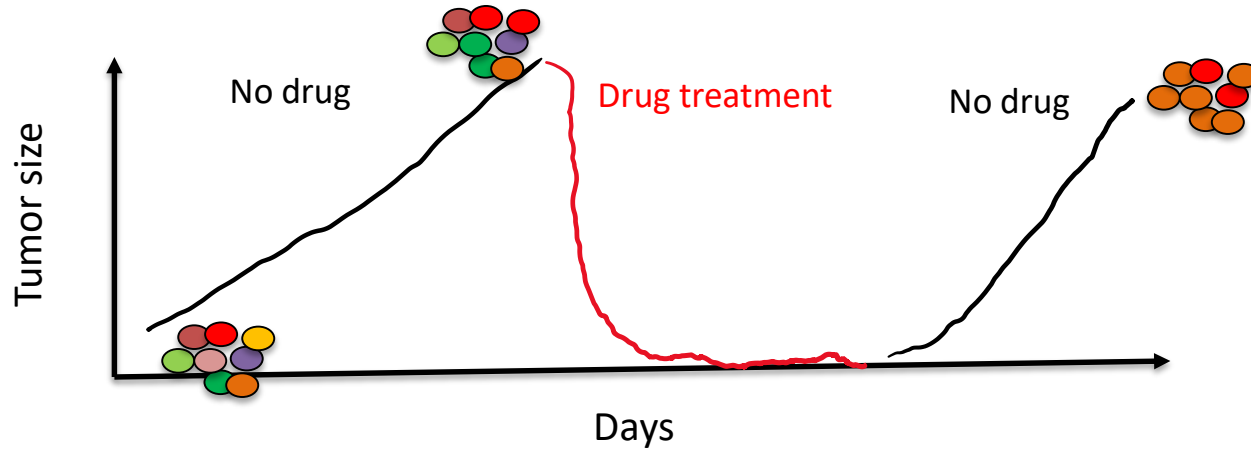
Heterogeneity in cancer

Catherine O'Brien
UofT

Complexity of tumors



Hint of equipotency in cancer



How do all clones survive drugs?

Epigenetic rather than genetic mechanisms?



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