

If cells play dice, can we gamble our way out of cancer ?

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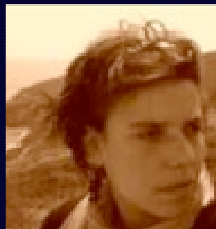
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Biology and Natural Science - DSABNS 2012**

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<http://dl.dropbox.com/u/6053055/2012-02-09-TALK.pdf>

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cancer

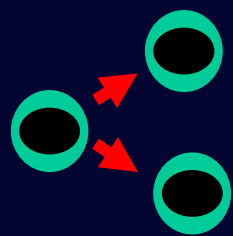
- ❖ cancer is a consequence of multicellularity
 - ❖ cellular genome is under permanent attack
(environmental or metabolic genotoxic agents)
 - ❖ DNA replication machinery is not perfect
- } mutations
- ❖ many mutations are neutral
 - ❖ others → malignant transformation → clonal development
 - ❖ risk of mutation: μ rate, # cells@risk, cell-lifetime

tissue architecture

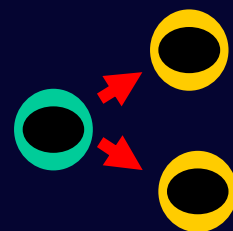
- ❖ tissue architecture has evolved
- ❖ most tissue cells have a ↘ lifetime & a ↗ turnover
 - minimize impact of **mutations**
- ❖ many tissues evolved a hierarchical structure
 - tree-like structure
- ❖ at the root of the tree are the tissue-specific stem-cells

- ❖ example: **hematopoiesis**
- ❖ **stem-cell** concept was developed in hematopoiesis and has
 - ❖ extended to many other tissues
- ❖ tissue **resilience** relies on ↘ # & ↘ turnover of stem cells

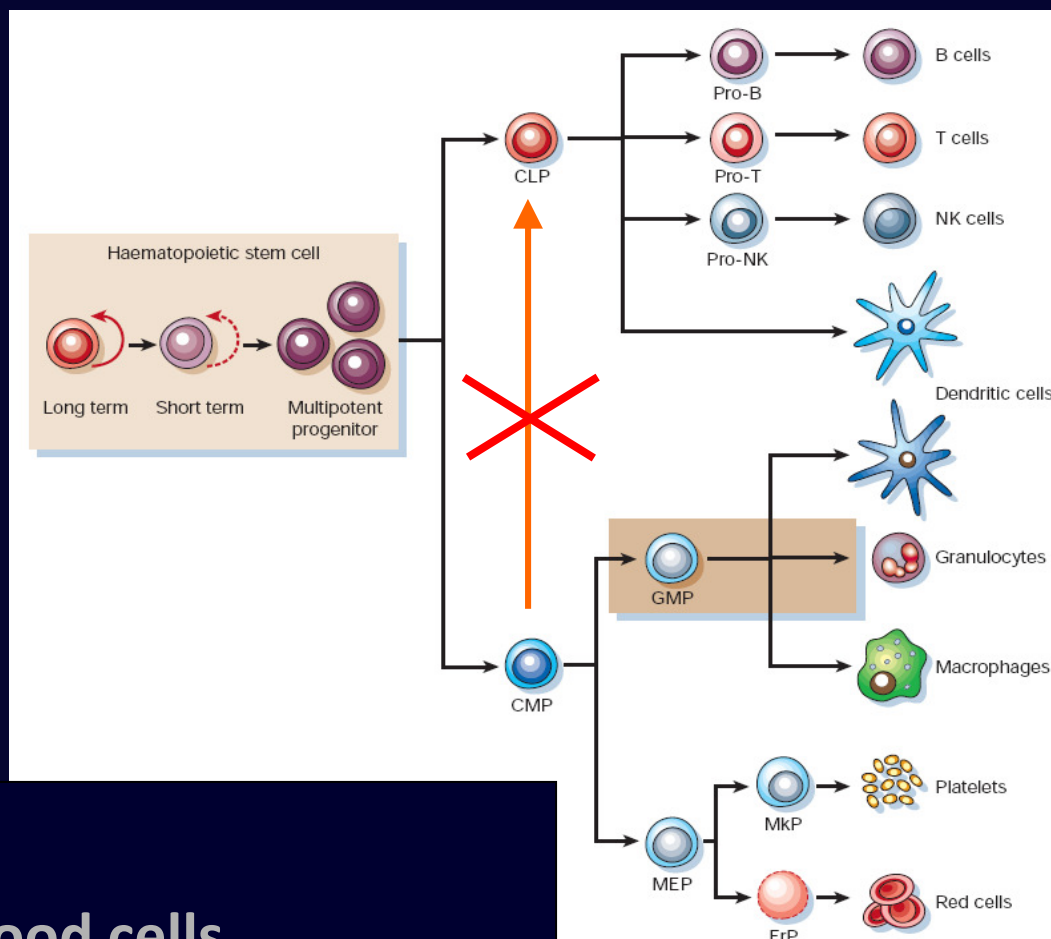
hematopoietic stem cells (HSC)



self-renewal :
for how long ?
(Hayflick hypothesis,
telomere shortening)

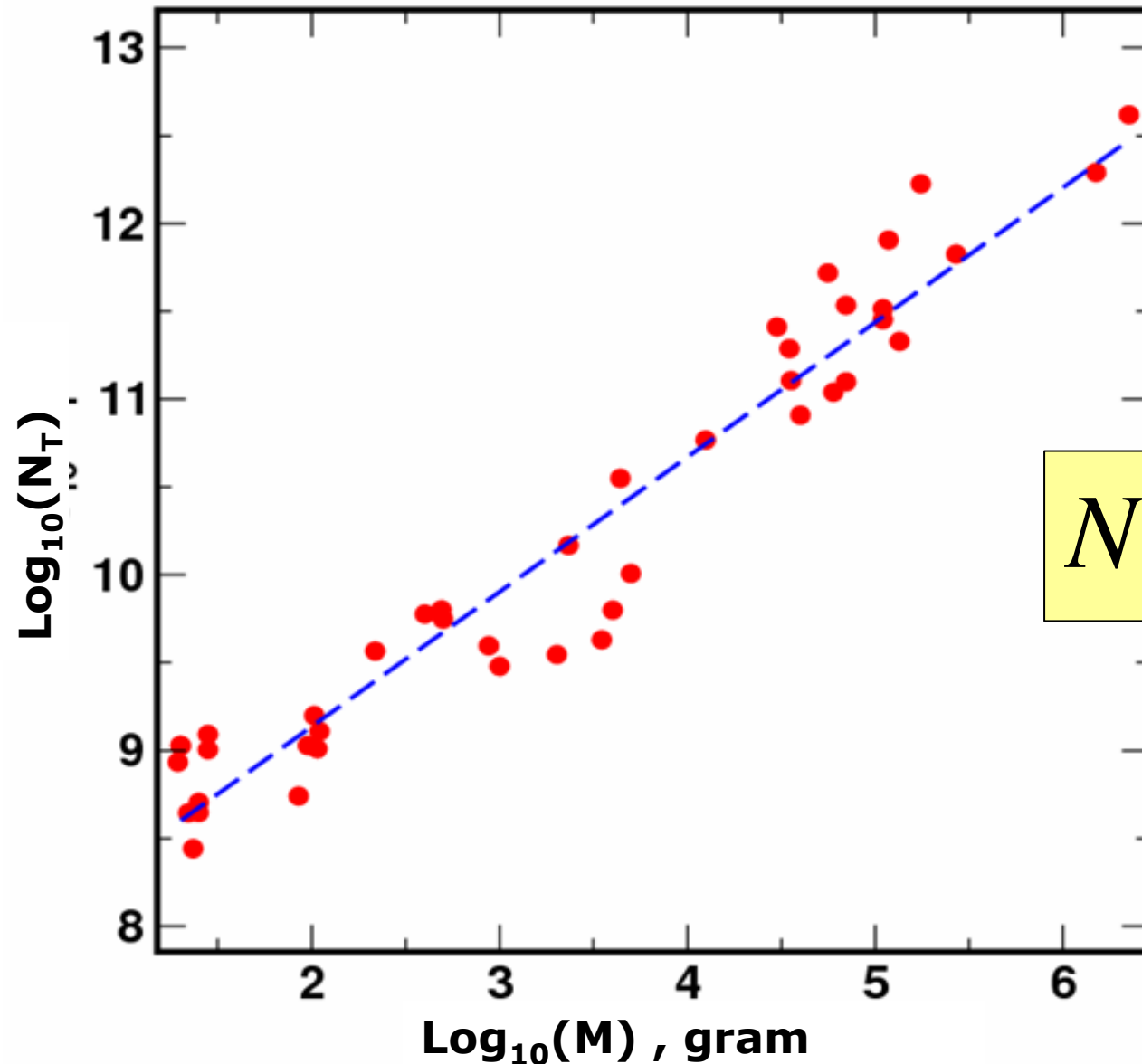


differentiation :
capacity to differentiate
into all other types of blood cells



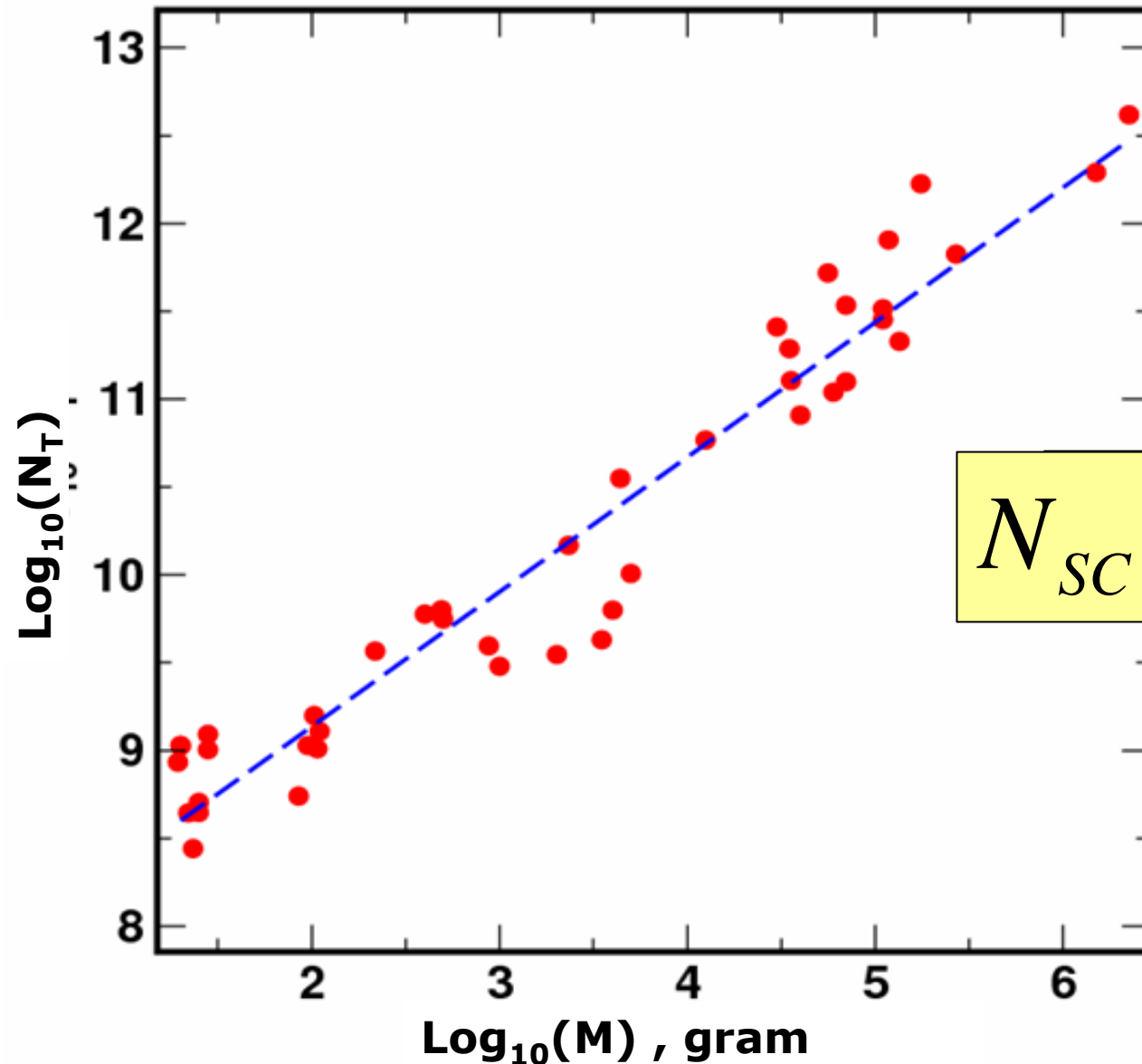
stemness is a matter of degree – you have to stand at the
root of the **hematopoietic tree**

allometric scaling of hematopoiesis in land mammals



$$N_{SC} \sim M^{3/4}$$

allometric scaling of hematopoiesis in land mammals



$$N_{SC} = N_0 M^{3/4}$$

allometric scaling of hematopoiesis in land mammals

use experimental estimates for **cats** for calibration (**fix N_0**):
 under normal conditions, **≥ 40 !** (Abkowitz et al, Blood, 2002)

what	model predictions ×	experimental data
HSC in humans cat = 40	385	~400 (Buescher et al, J Clin Invest, 1985)
rate HSC division cat post-TRX = 8 week ⁻¹	60 week⁻¹	~ 52-104 week⁻¹ (Rufer, et al, J Exp Med, 1999)
human post-transplant cat = 13	111	~ 116 (Nash et al, Blood, 1988)
mouse	1	1 (Abkowitz et al, PNAS , 1995)
rate macaques	23 week⁻¹	23 week⁻¹ (Shepherd et al, Blood , 2007)
rate baboons	36 week⁻¹	36 week⁻¹ (Shepherd et al, Blood , 2007)

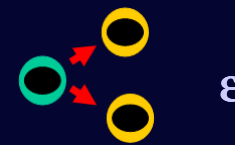
the hematopoietic tree

- ❖ in humans ~ 400 HSC divide each once per year;
- ❖ **but** : daily output of bone marrow $\sim 3.5 \times 10^{11}$ cells !!!

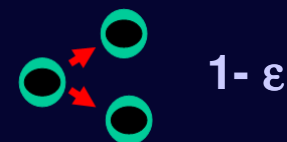
how to explain this enormous amplification given the slow replication rate of HSC ?

- ❖ one must consider :

differentiation

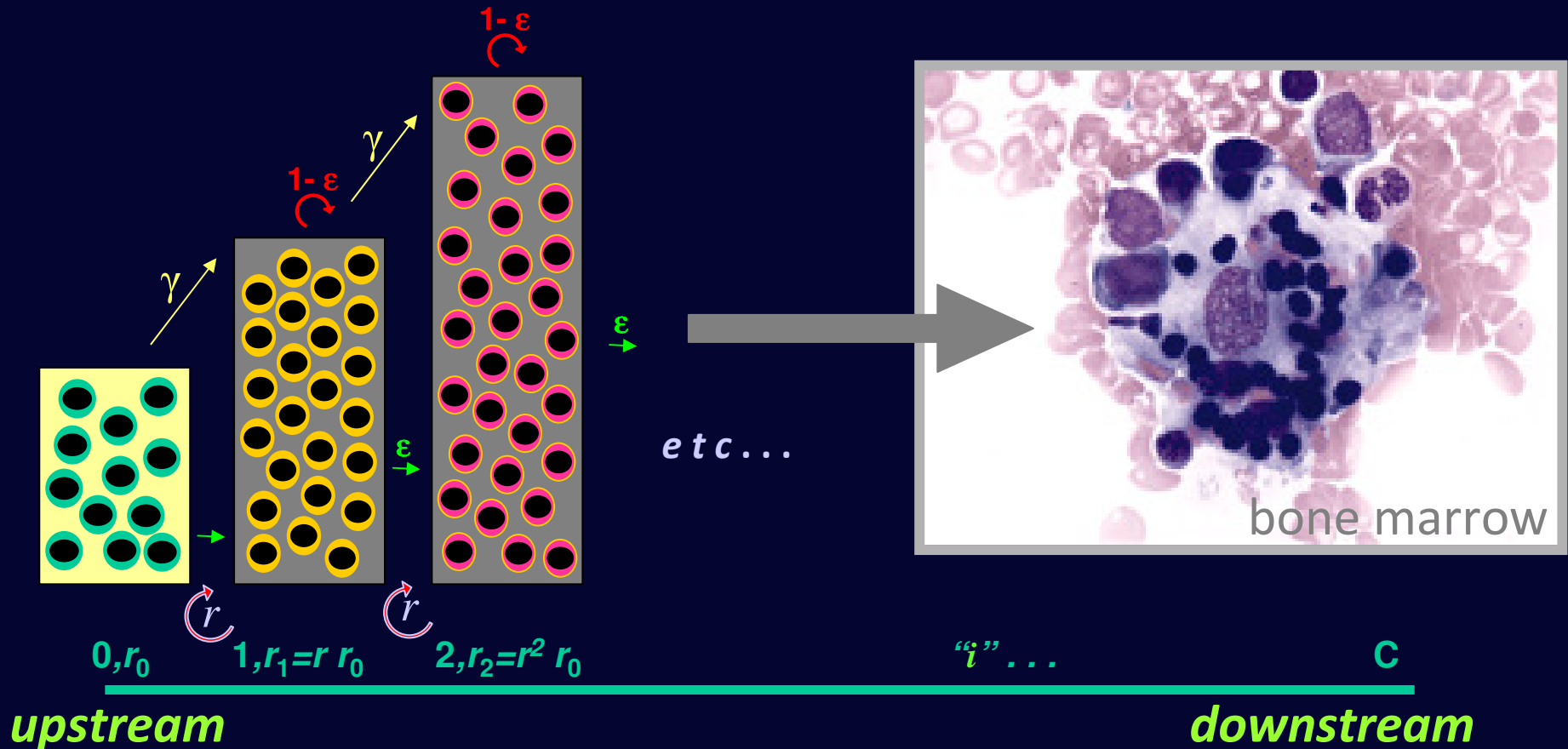


amplification

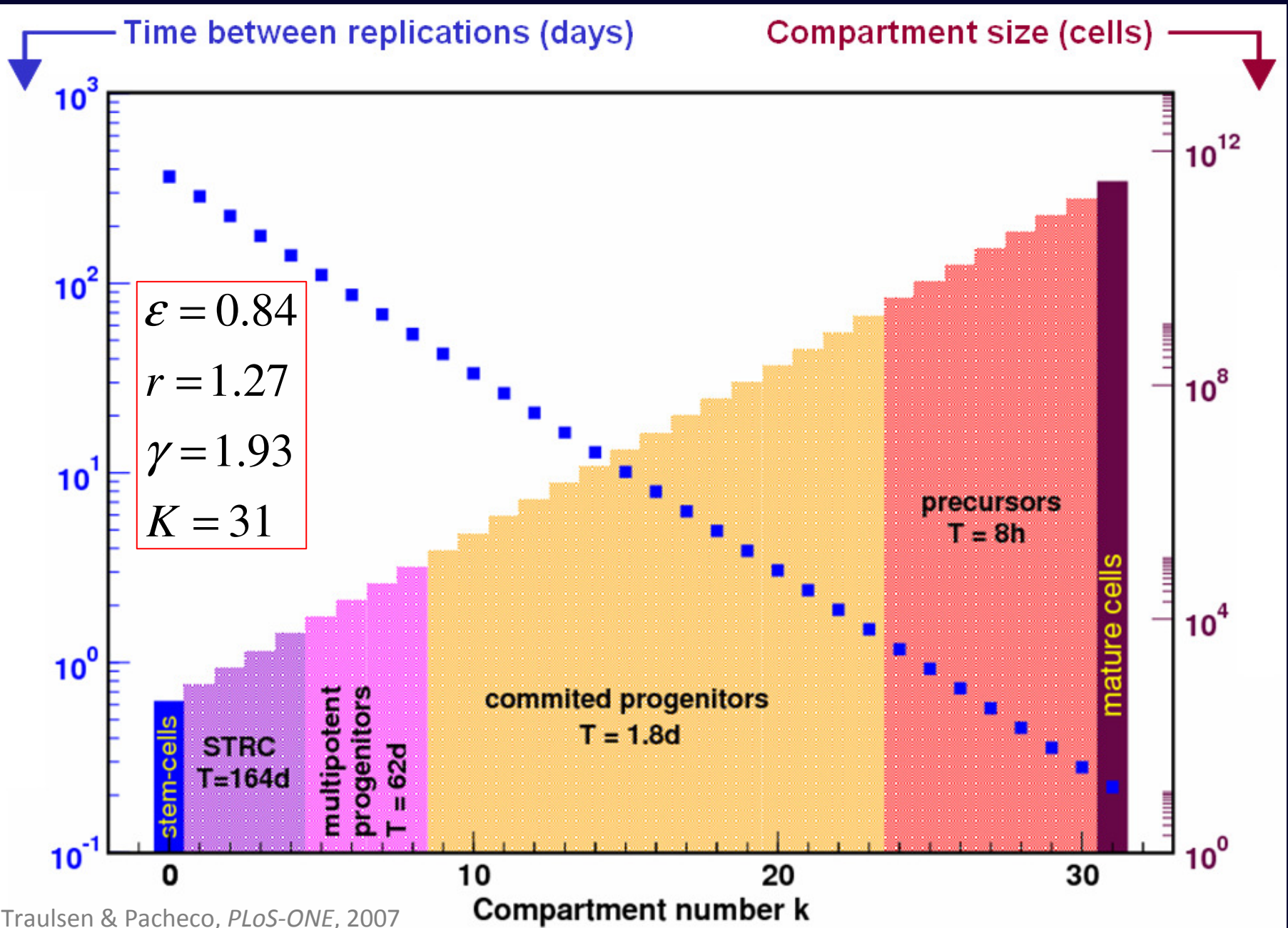


the hematopoietic tree

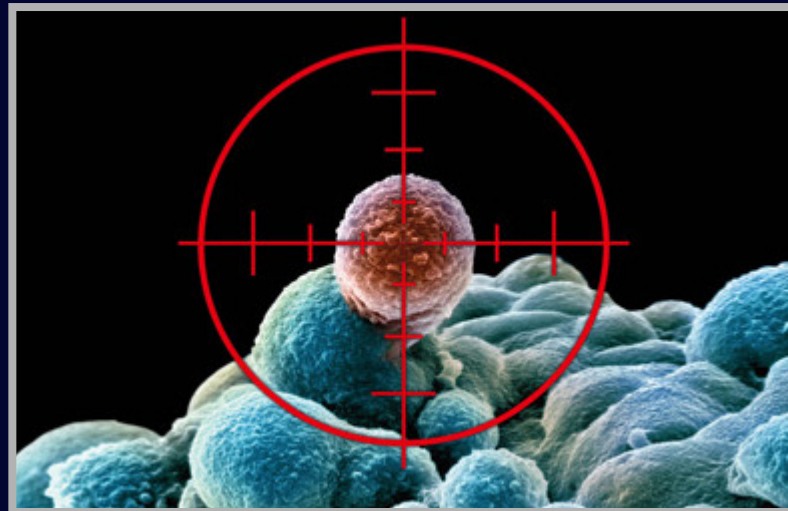
- ❖ we consider a **compartmentalized structure** in which **cells from upstream compartments flow into downstream compartments**, under **stationary flux conditions**;



the hematopoietic tree



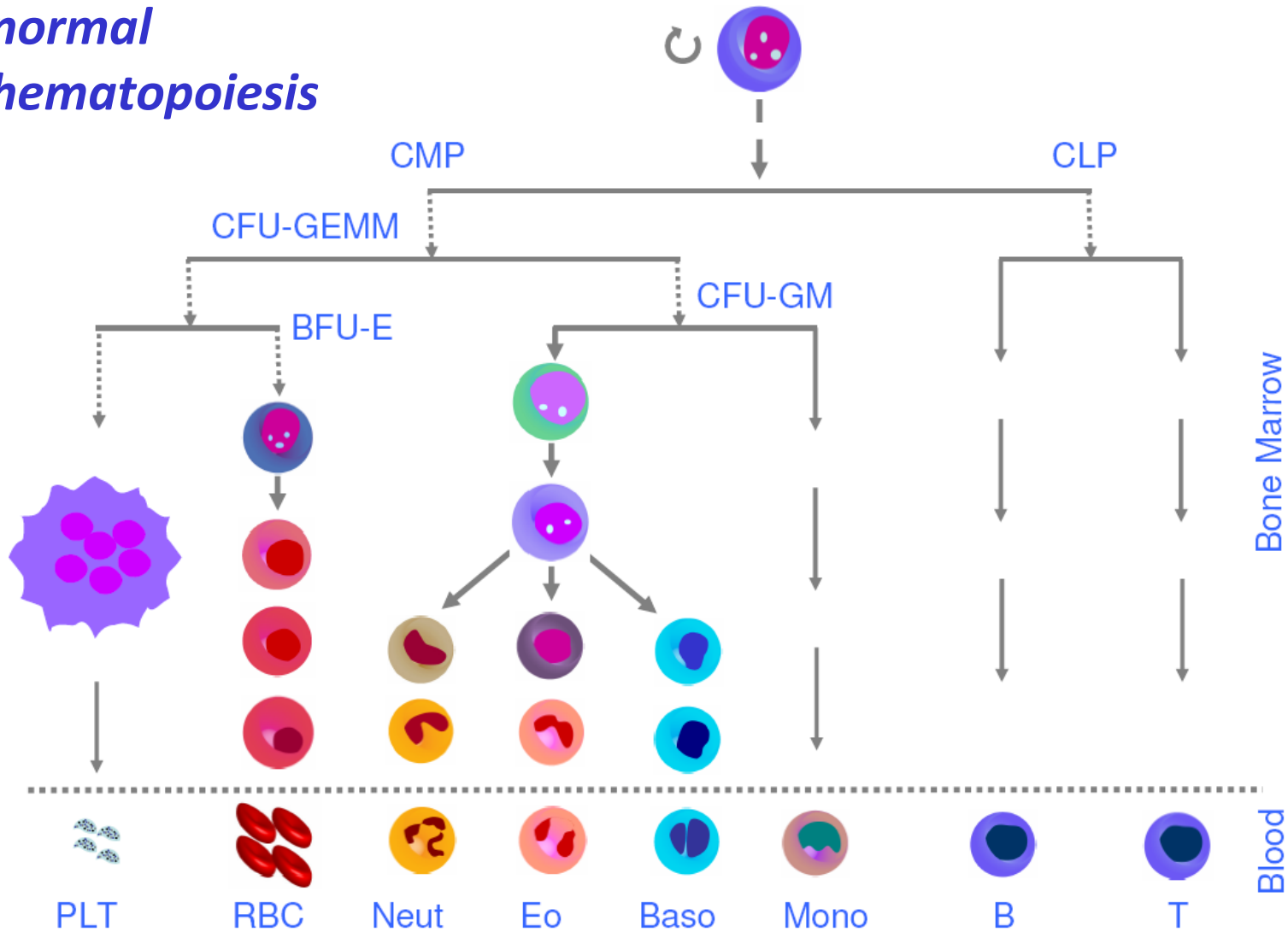
DISEASE



trouble

normal : $10^{-7} < \mu < 10^{-6}$ per cell per replication

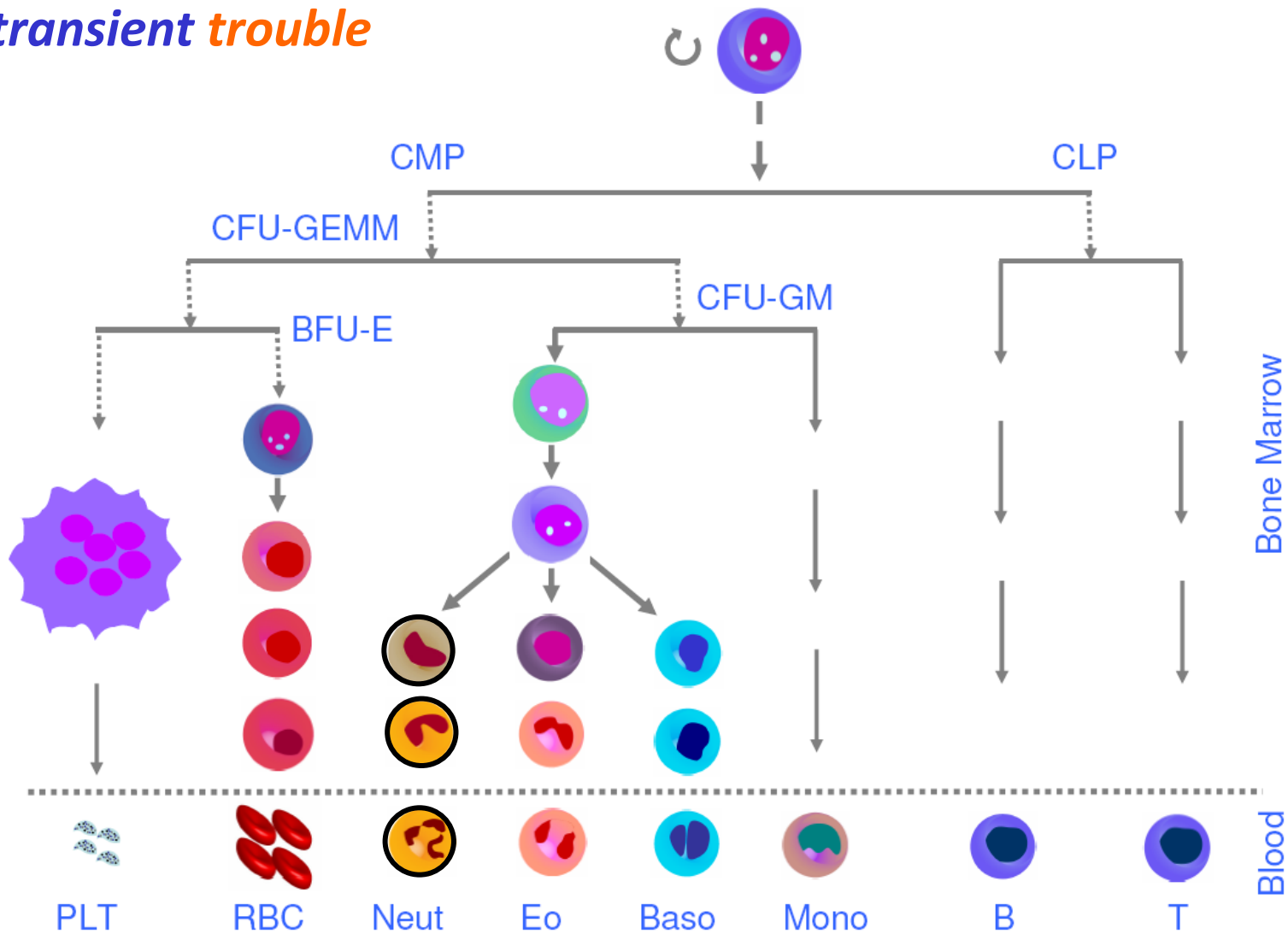
normal hematopoiesis



trouble

normal : $10^{-7} < \mu < 10^{-6}$ per cell per replication

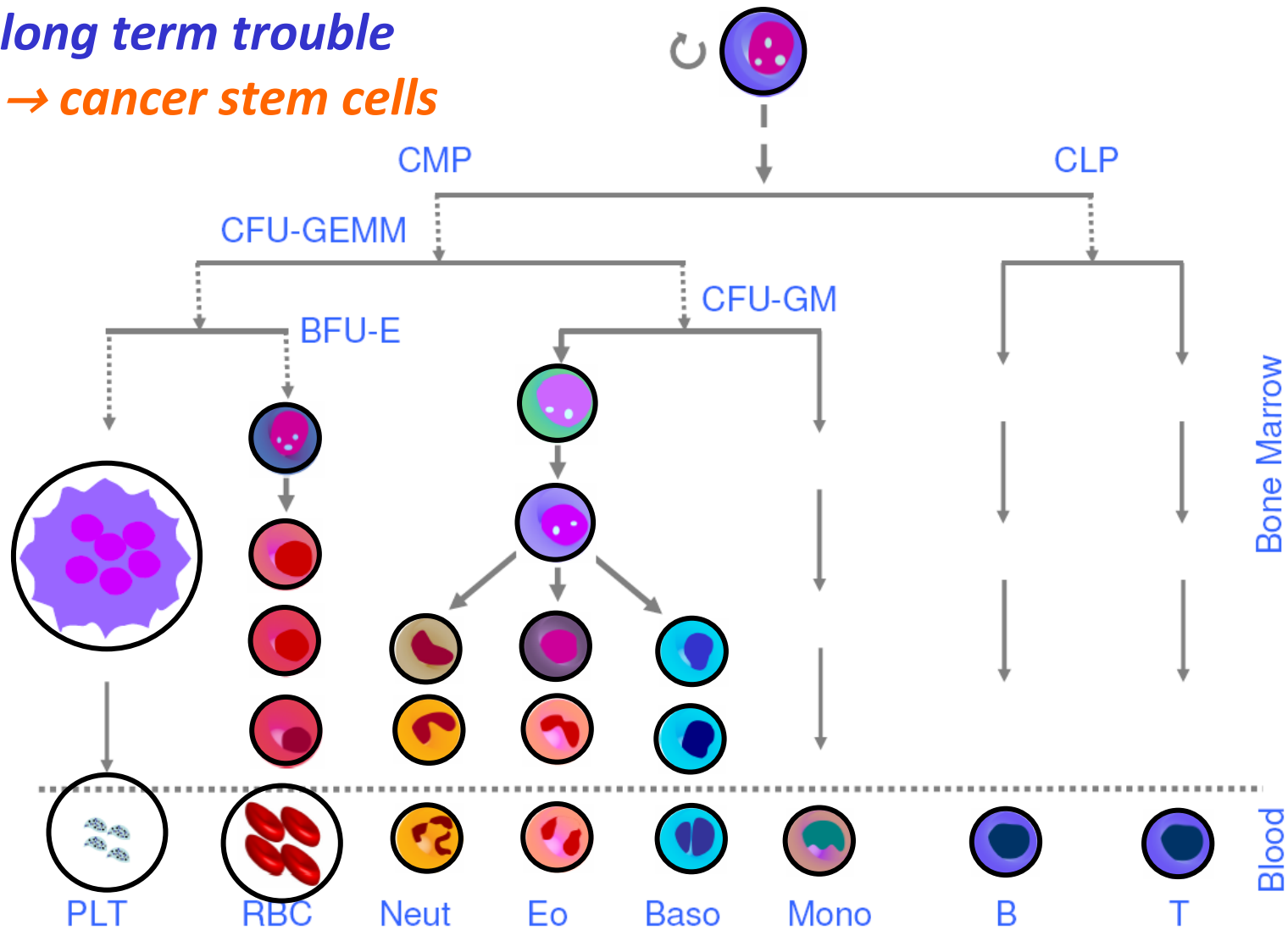
transient trouble



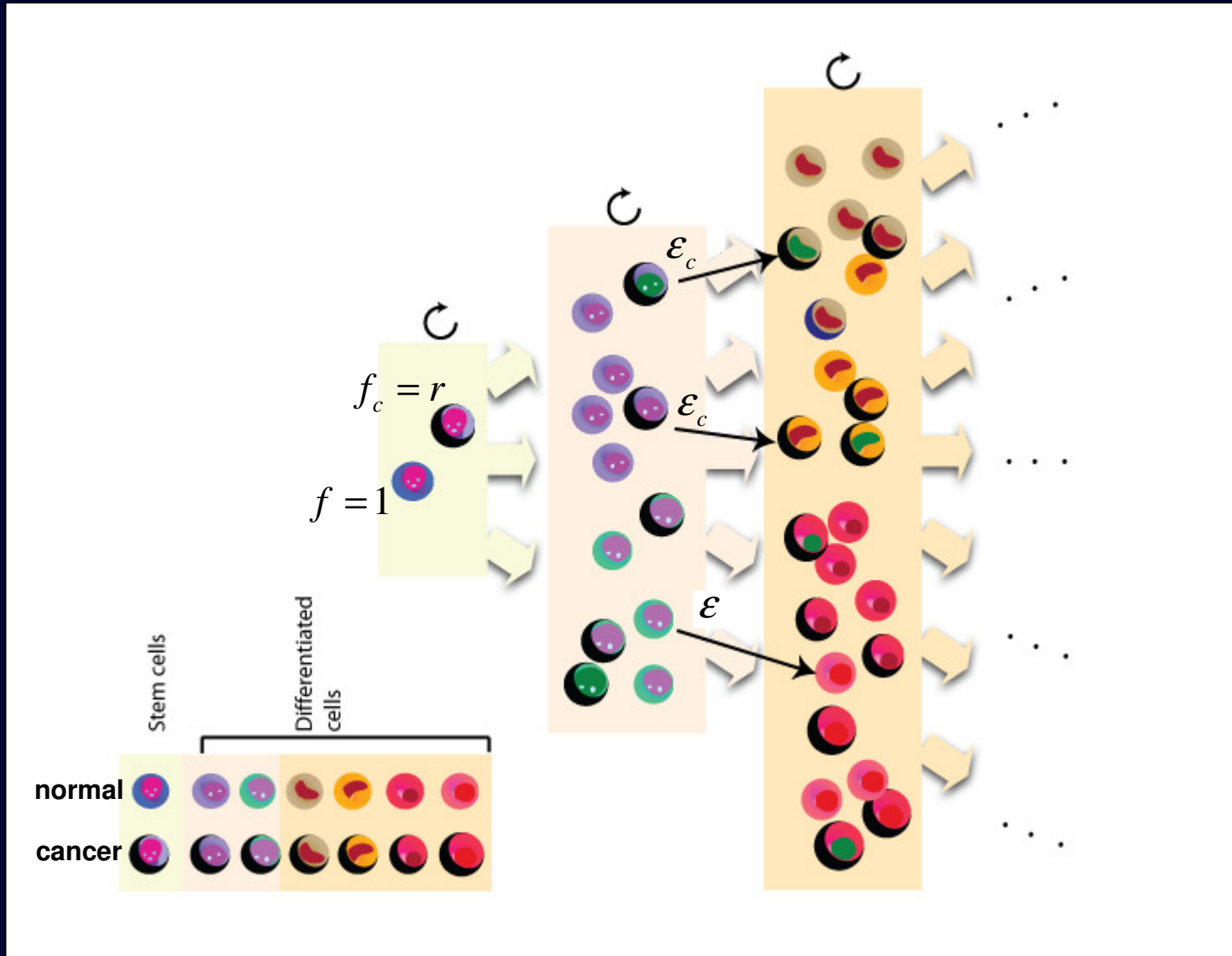
trouble

normal : $10^{-7} < \mu < 10^{-6}$ per cell per replication

long term trouble
→ cancer stem cells



troubled hematopoiesis



cancer dynamics becomes a multi-scale ecology of cell competition

starting upstream with a small number of HSC & CSC and getting downstream into very large numbers of cells of all kinds

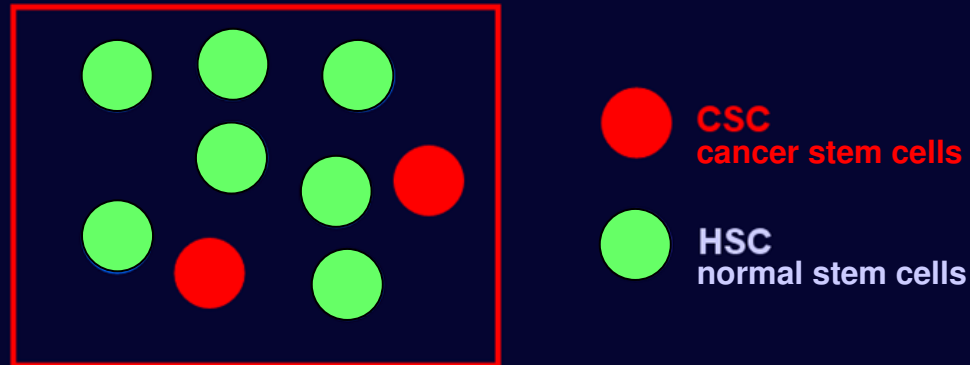
the mathematics of Darwinian cell selection

Dingli, Traulsen & Pacheco, *Cell Cycle*, 2007

Dingli, Traulsen & Pacheco, *PRSB* 275 (2008) 2389

stochastic dynamics of *HSC*

stochastic model for *humans* :



- ❖ *SC population remains constant (400);*
- ❖ *HSC divide at normal rate (once per year);*
- ❖ *CSC divide at rate $r \times$ normal, where $r =$ relative fitness ;*
- ❖ *when a cell divides, gives rise to two new identical cells;*
- ❖ *subsequently, 1 cell is randomly selected for export;*
- ❖ *HSC may suffer mutations and transform into CSC.*

*this stochastic model is known in
mathematics (& population genetics)
as a
Moran (birth-death) process*

in each stochastic discrete event, either :

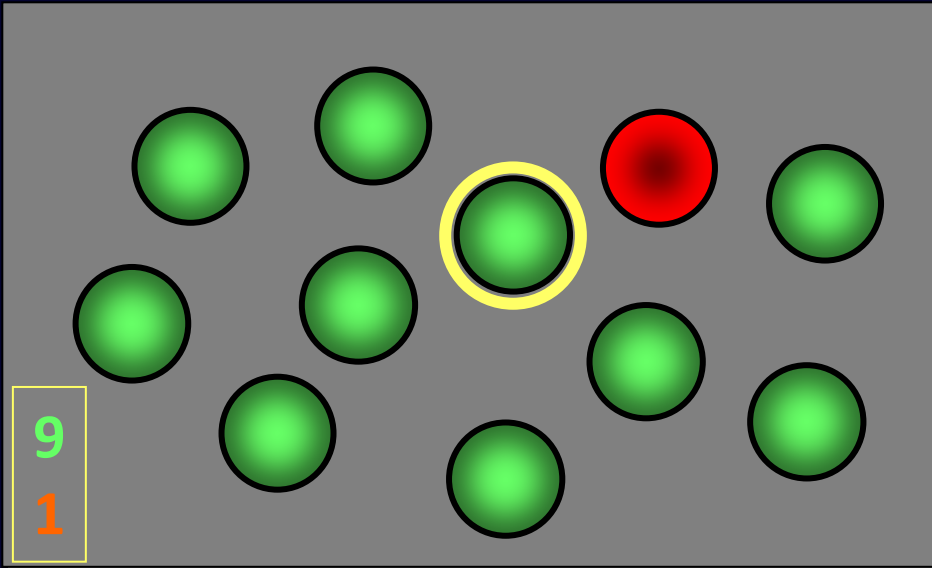
— nothing happens

— the number of cells of one of the types changes by ± 1

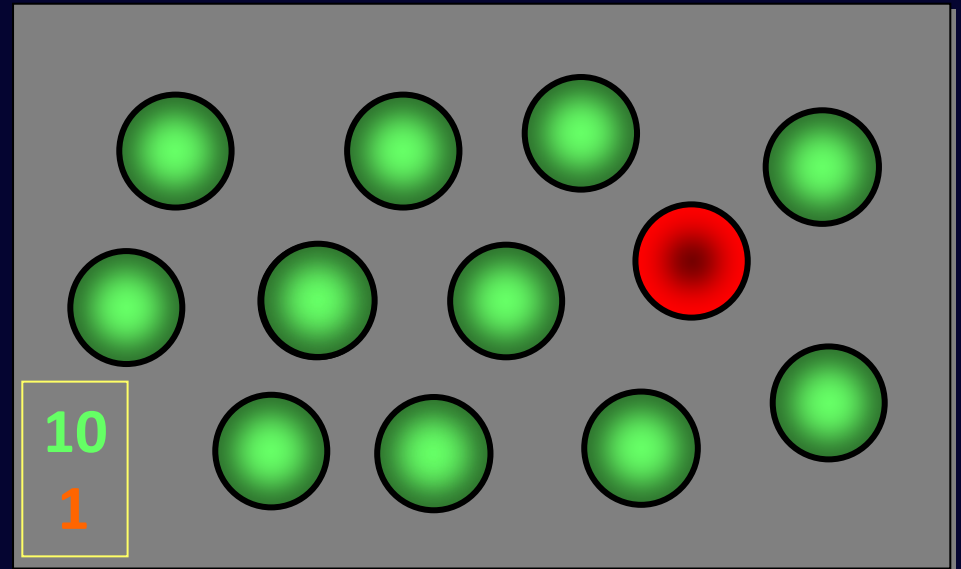
*after **N** events, one time step has elapsed*

example 1: 1 HSC is exported & nothing happens in SC pool

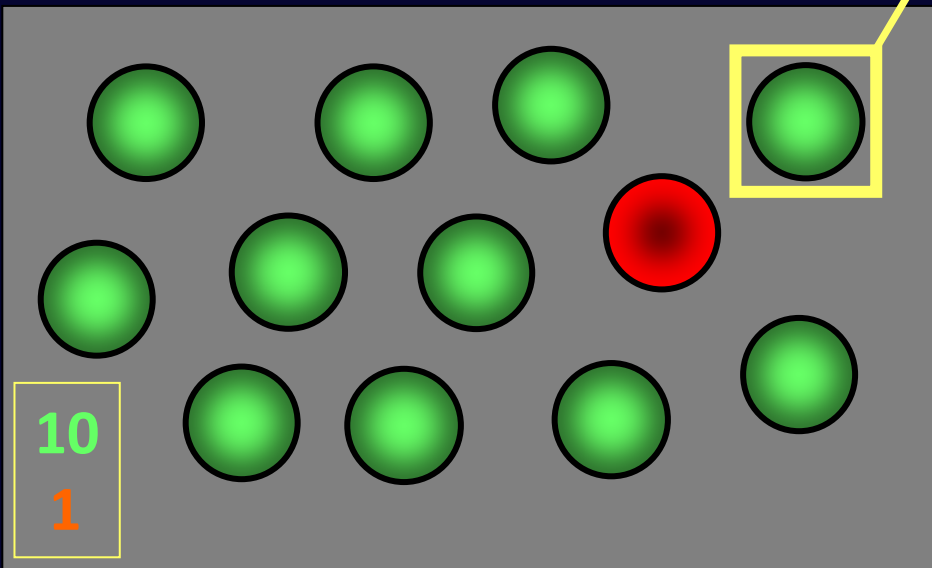
a. select 1 cell proportional to fitness



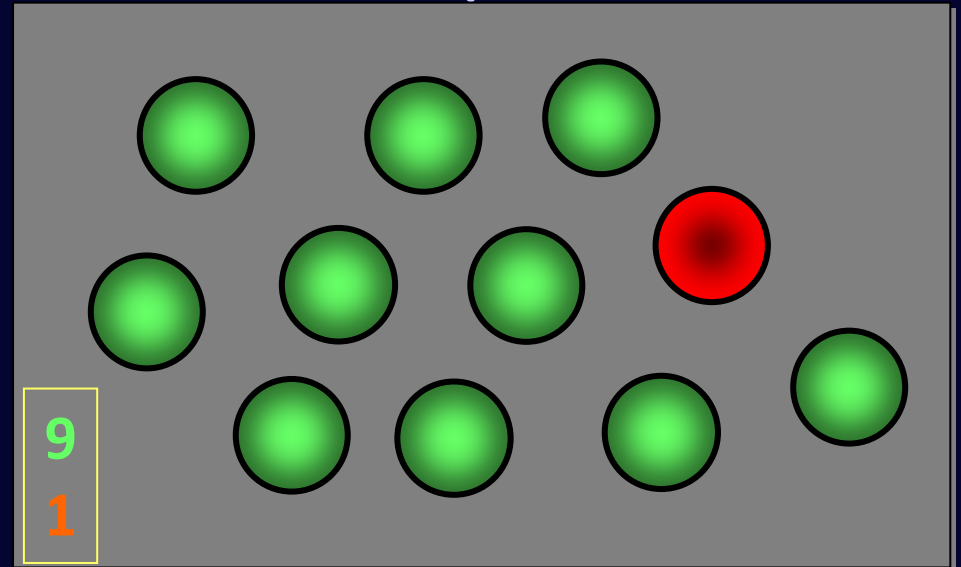
b. chosen cell replicates



c. select 1 cell at random

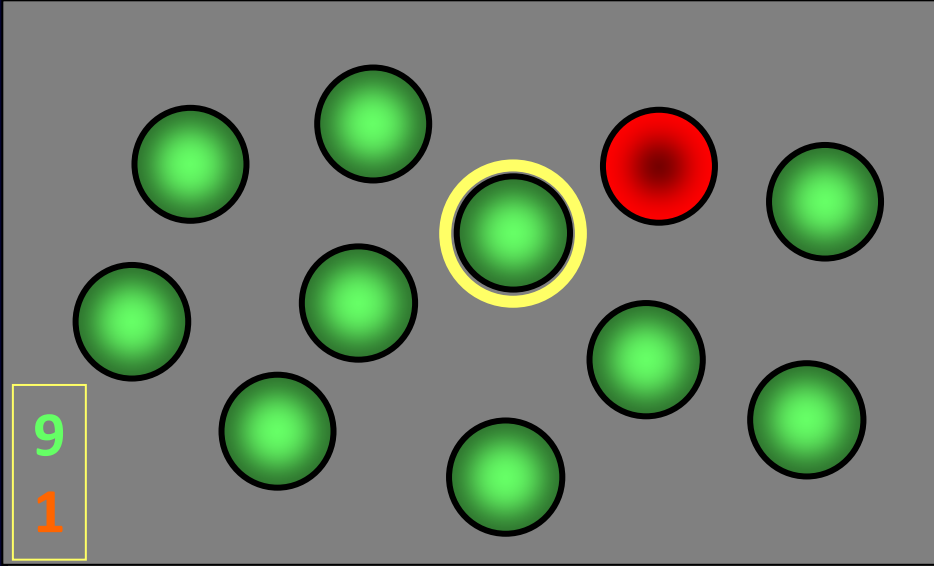


d. chosen cell is exported

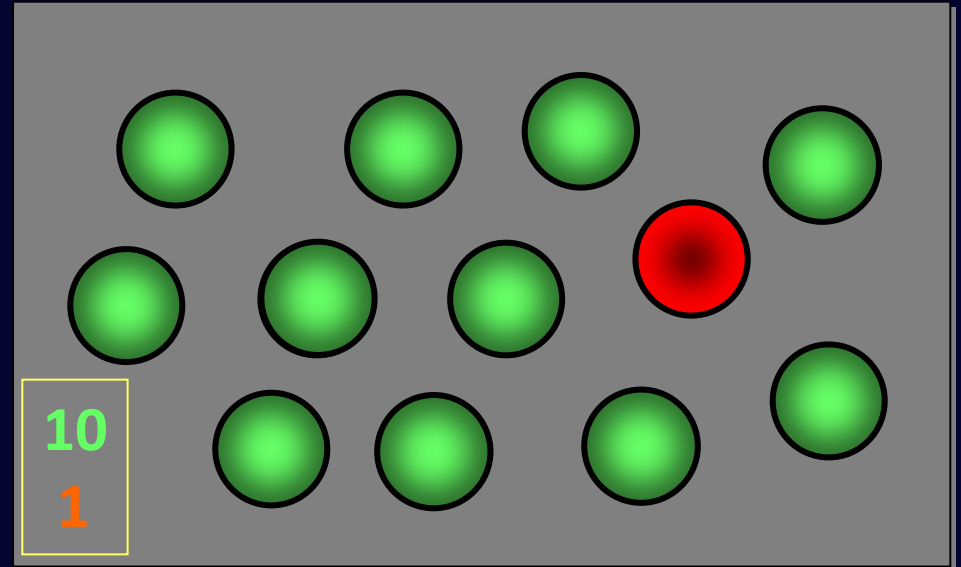


example 2: 1 CSC is exported & CSC-lineage gets extinct

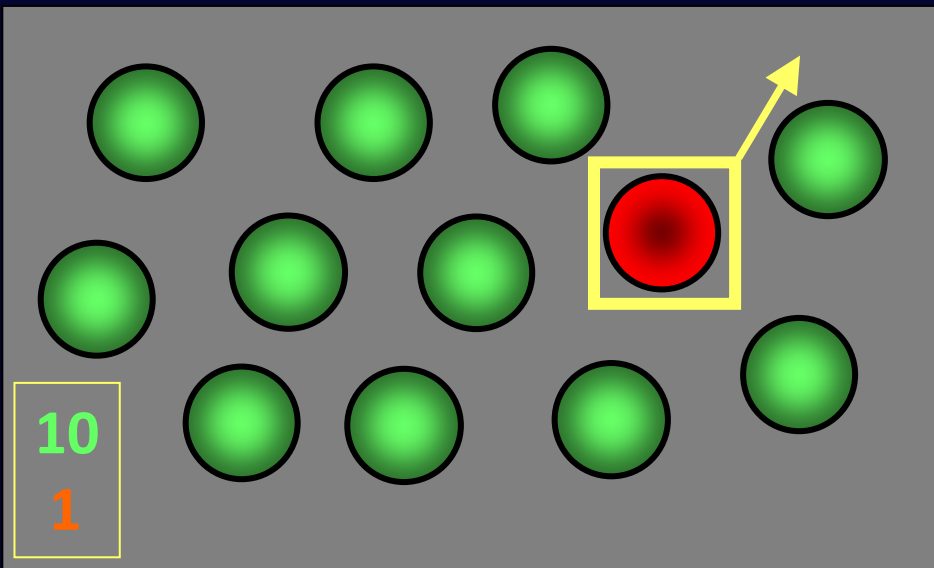
a. select 1 cell proportional to fitness



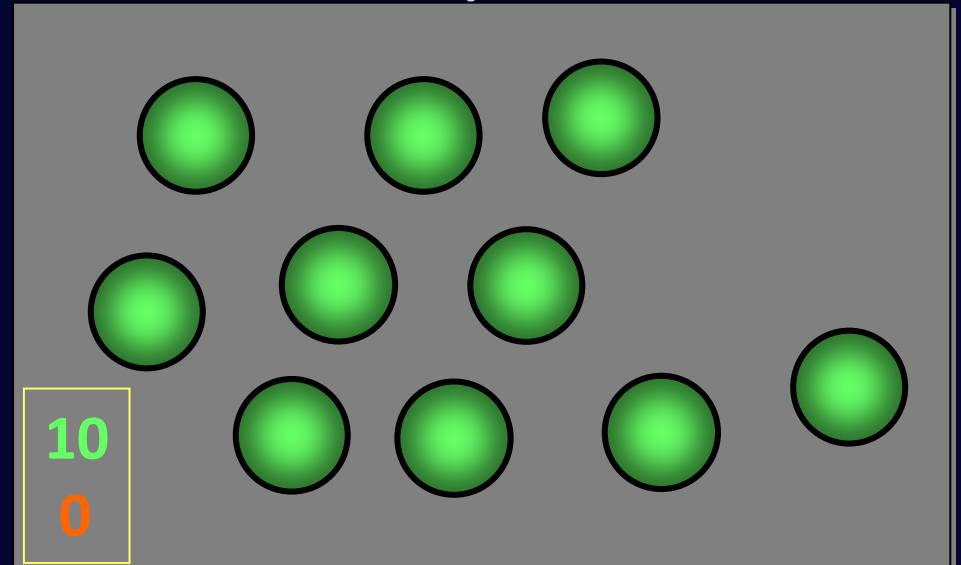
b. chosen cell replicates



c. select 1 cell at random

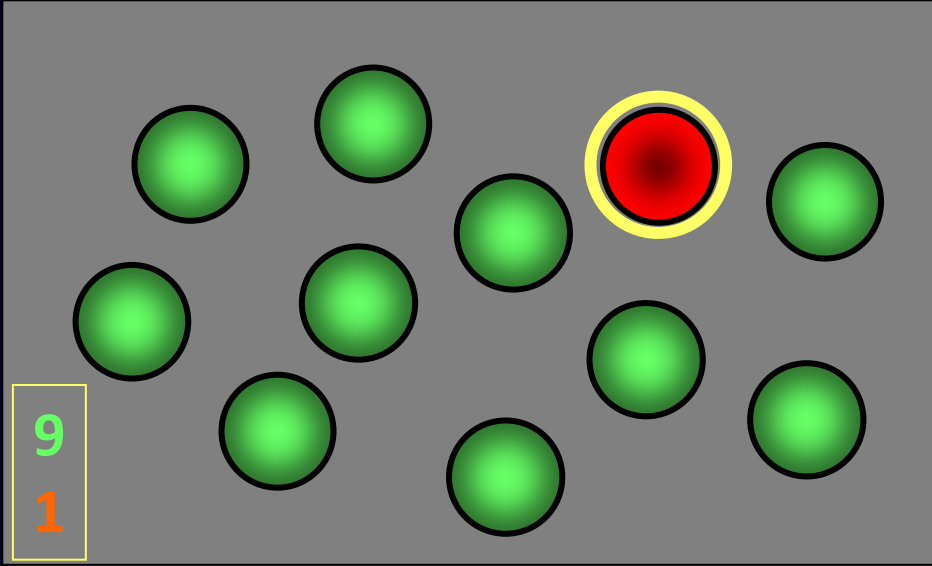


d. chosen cell is exported

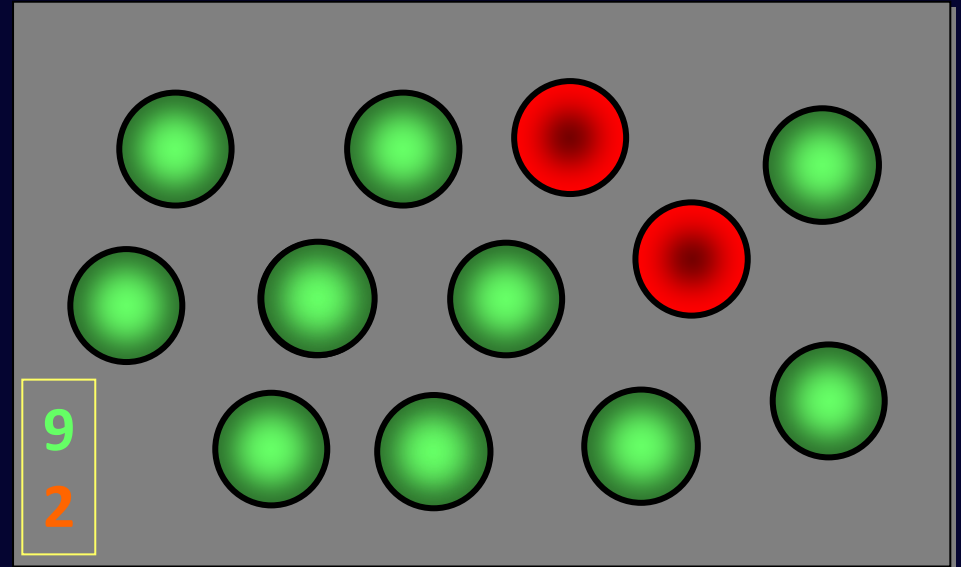


example 3: 1 HSC is exported & CSC number increases by 1

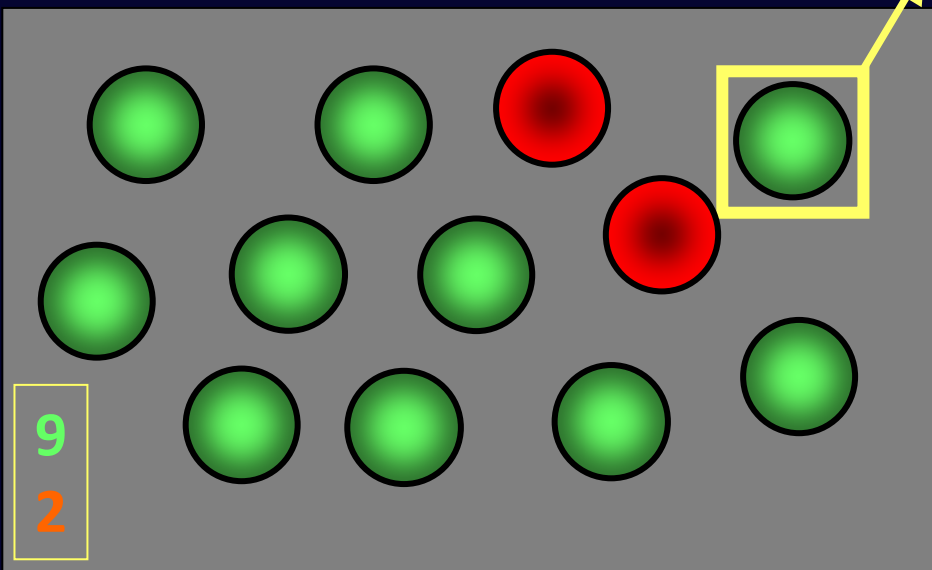
a. select 1 cell proportional to fitness



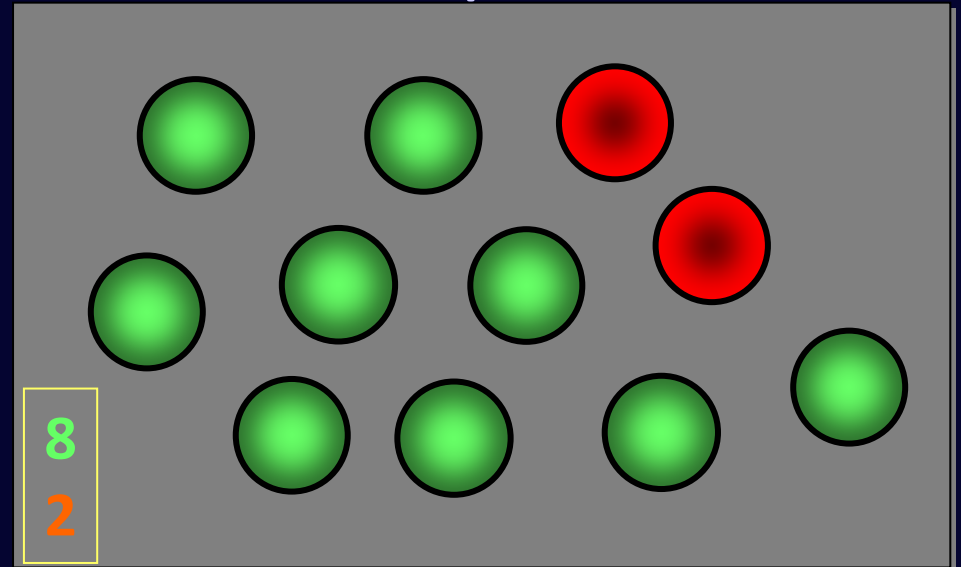
b. chosen cell replicates



c. select 1 cell at random

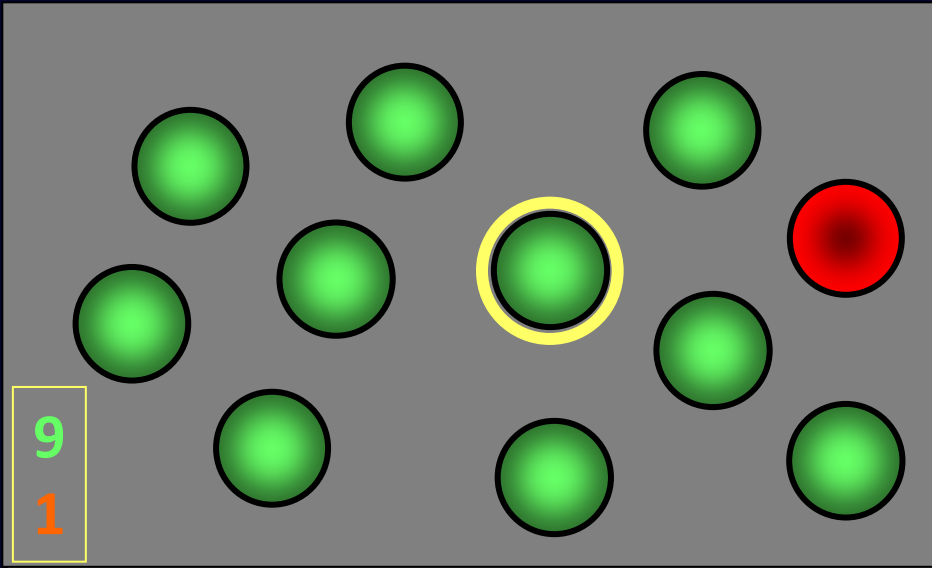


d. chosen cell is exported

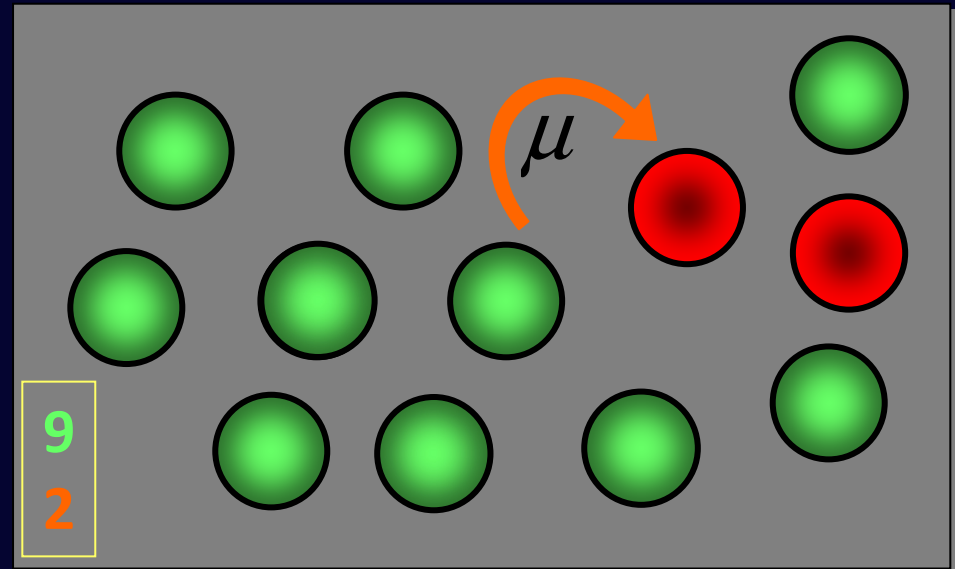


example 4: HSC mutations enter scene to make things worse

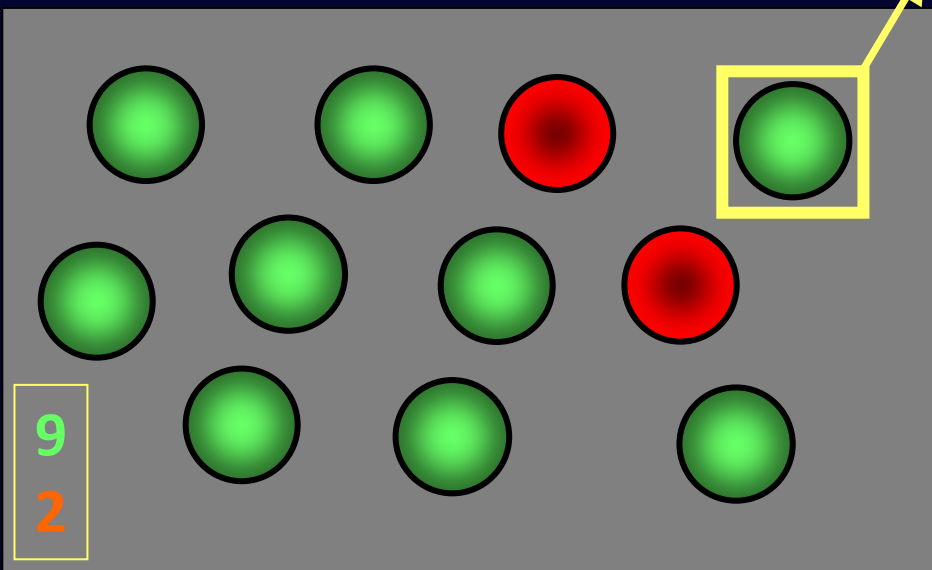
a. select 1 cell proportional to fitness



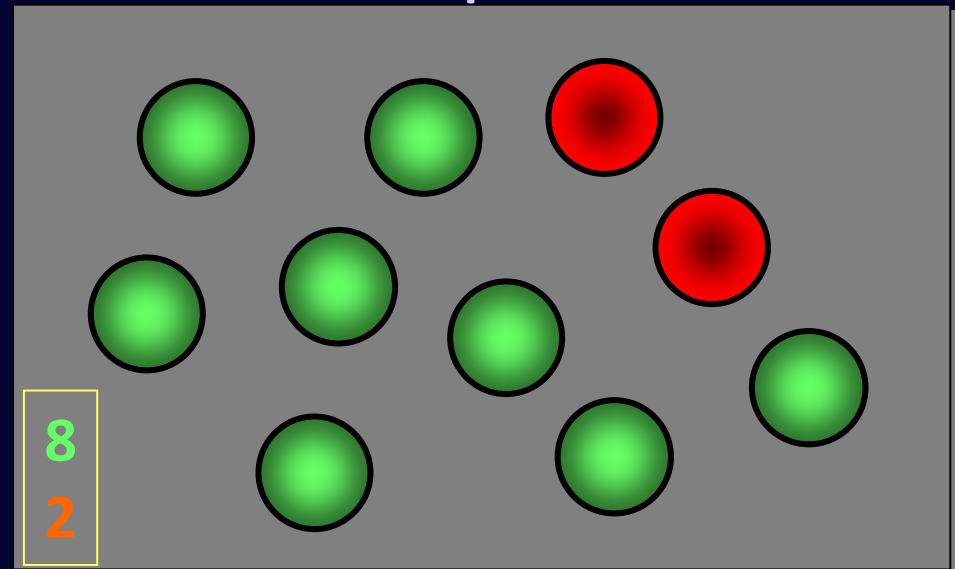
b. chosen cell replicates & mutates



c. select 1 cell at random

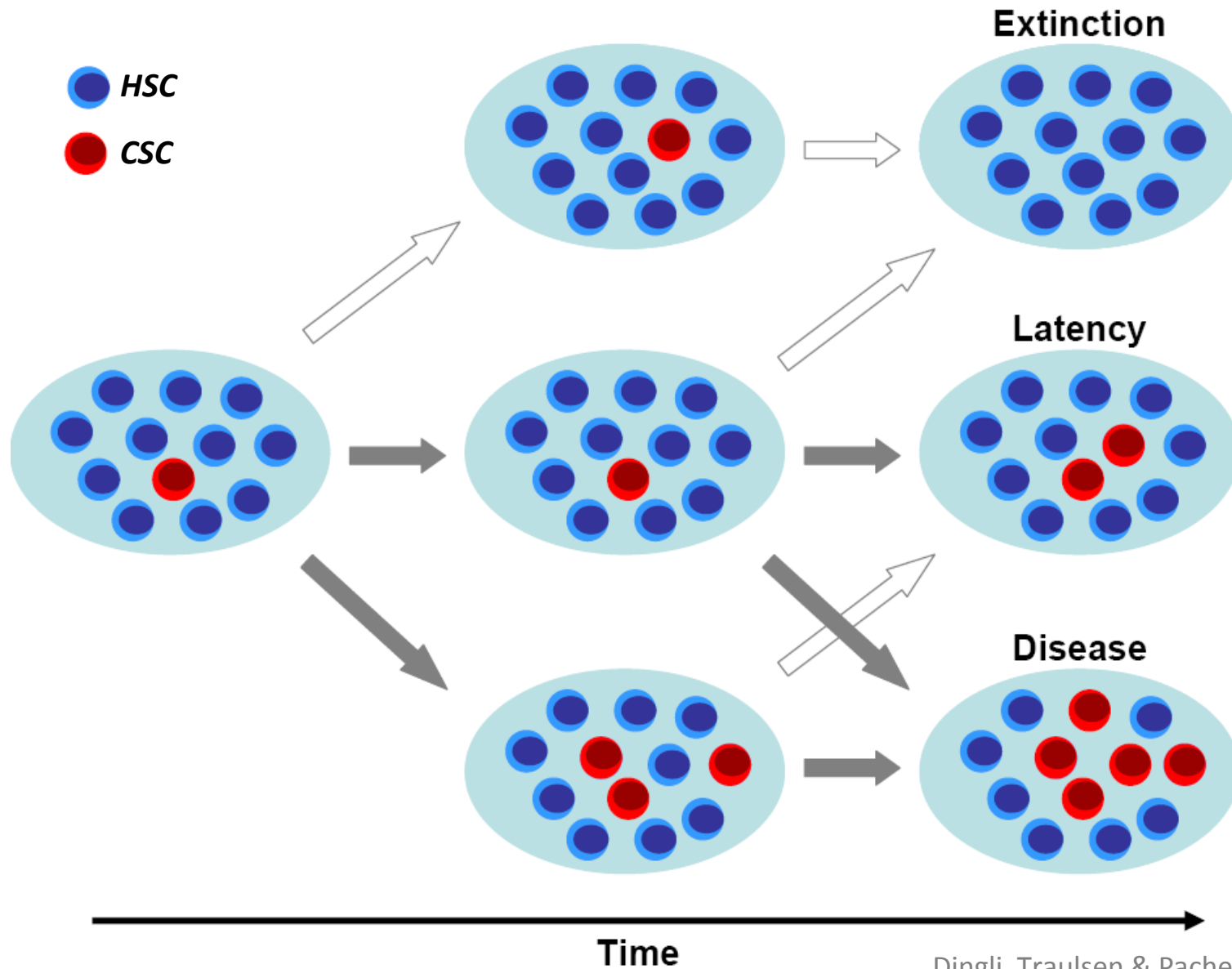


d. chosen cell is exported



stochastic dynamics of *HSC*

several possible scenarios :



is the stochastic dynamics of cells an oddity ?

neutral evolution

&

PAROXYSMAL NOCTURNAL HEMOGLOBINURIA

Dingli, Luzzatto & Pacheco, *PNAS* 105 (2008) 18496



Motoo Kimura (木村 資生 Kimura Motoo, November 13, 1924 - November 13, 1994)

paroxysmal nocturnal hemoglobinuria

what is known :

- ❖ rare disease
- ❖ true stem-cell disorder since :
- ❖ it originates in the PIG-A gene of a HSC
- ❖ rate of PIG-A gene mutation is normal
- ❖ often BMF is later observed

conventional wisdom regarding disease development :

- ❖ a 2nd mutation leads to a fitness advantage of PNH cells → disease expansion (**too rare an event**)

Dingli, Pacheco & Traulsen, *Physical Review E* 77 (2008) 021915

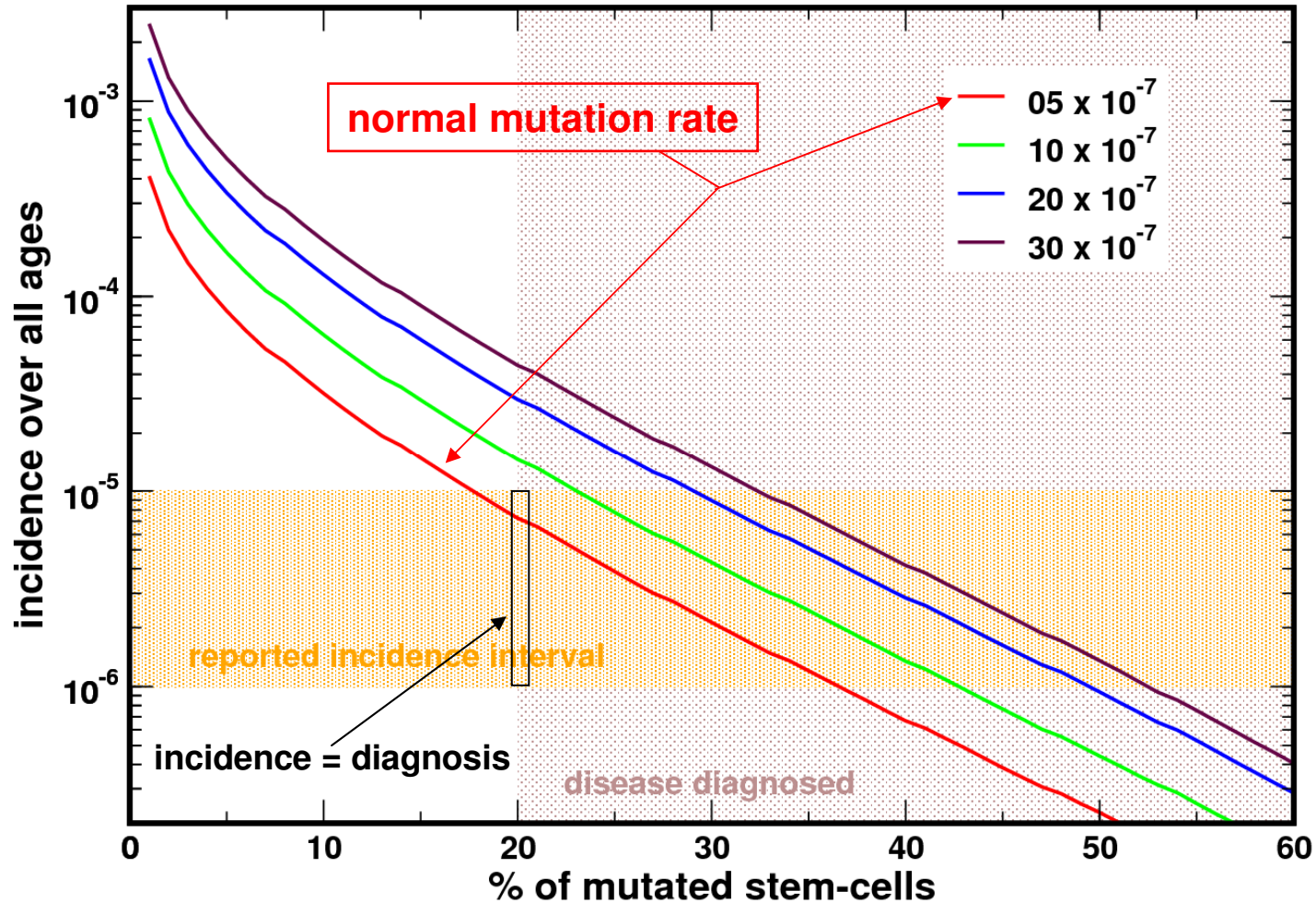
- ❖ *relative fitness advantage* of PNH cells due to an **immune attack to normal HSC** → disease expansion

model features

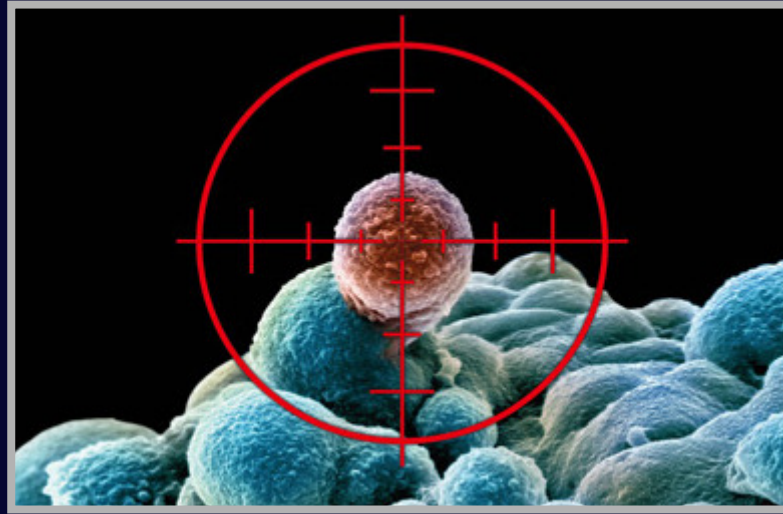
disease development

- ❖ use $N_{sc} = 400$
- ❖ simulate **HSC** activity in virtual USA (10^9 virtual Americans)
- ❖ use normal mutation rate for HSC → PNH transformation
- ❖ assume *neutral drift* ($r=1$) between **HSC** & **PNH** cells
- ❖ fold data with CENSUS 2000 for USA population
- ❖ compare results with incidence data in *USA*

results



results above & other results suggest that **it is not necessary to invoke a relative fitness difference to explain** incidence of PNH



neutral evolution relies on the stochastic nature of cell behavior, & **PNH** shows us that, likely, many individuals suffer the PIG-A mutation but are never diagnosed PNH, as it is more likely for the mutant to become extinct than to evolve into a clone. This, in turn, suggests that the current way of approaching the (now over) 40-year old war-on-cancer, that is,

cure = *kill-every-single-cancer-cell*

is perhaps not always the best; in fact, sometimes it maybe even unnecessary.

progenitor driven **CHRONIC MYELOID LEUKEMIA**

Dingli, Traulsen, Lenaerts & Pacheco,

Clinical Leukemia 2 (2008) 133

BioEssays 32 (2010) 1003

Cancer Letters 294 (2010) 43

Genes and Cancer 1, 4 (2010) 309-315

Haematologica 95 (2010) 900-907

BMC Biology 9(2011) 41

Cell Cycle 10 (2011) 1540

PLoS-CB 7 (2011) e1002290

Chronic Myeloid Leukemia

what is known :

- ❖ Hematopoietic stem cell disorder
- ❖ Initial event: Philadelphia chromosome
- ❖ ? HSC are enough to drive chronic phase ?
- ❖ clonal expansion and myeloproliferation
- ❖ stem cell derived but progenitor cell driven
- ❖ *abl*-kinase inhibitors very effective

CML dynamics

- ❖ Q-RT-PCR data from patients treated with *imatinib*
- ❖ 2 data sets available
 - ❖ Michor *et al*, *Nature*, 2005
 - ❖ Roeder *et al*, *Nature Medicine*, 2006
 - ❖ other data recently available for *nilotinib*
- ❖ **data fitting**

model features

disease development

- ❖ use existing model of hematopoiesis
- ❖ how to get from HSC origin to progenitor driven disease ?
- ❖ bone marrow expansion $\rightarrow \epsilon_{\text{CML}} < \epsilon_0$

treatment

- ❖ how does *imatinib* work ?
- ❖ does *imatinib* induce cell death?
- ❖ how many cells are responding to *imatinib* ?

model constraints

disease development

- ❖ time from initial insult to diagnosis is 3.5 – 6 years
- ❖ progenitor cell expansion >14%
- ❖ total number of active HSC is *not* increased
- ❖ daily bone marrow output is ~ 3 x normal

treatment

- ❖ *imatinib* leads to $\epsilon_{\text{IMAT}} > \epsilon_0 > \epsilon_{\text{CML}}$
- ❖ *imatinib* does not affect HSC
- ❖ at any time a fraction *z* of cells responds to *imatinib*

CML dynamics under *imatinib*

we define (deterministic model . . .)

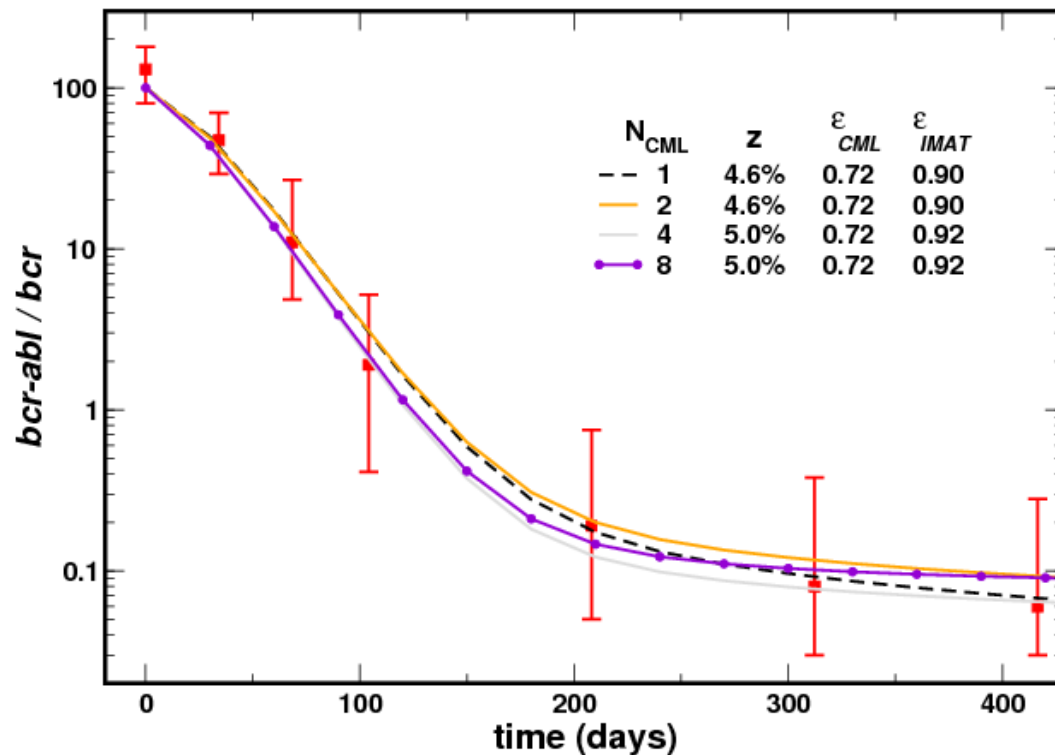
output rate from compartment "i"

$$d_i = (2\varepsilon - 1)r_i$$

input rate from compartment "i-1"

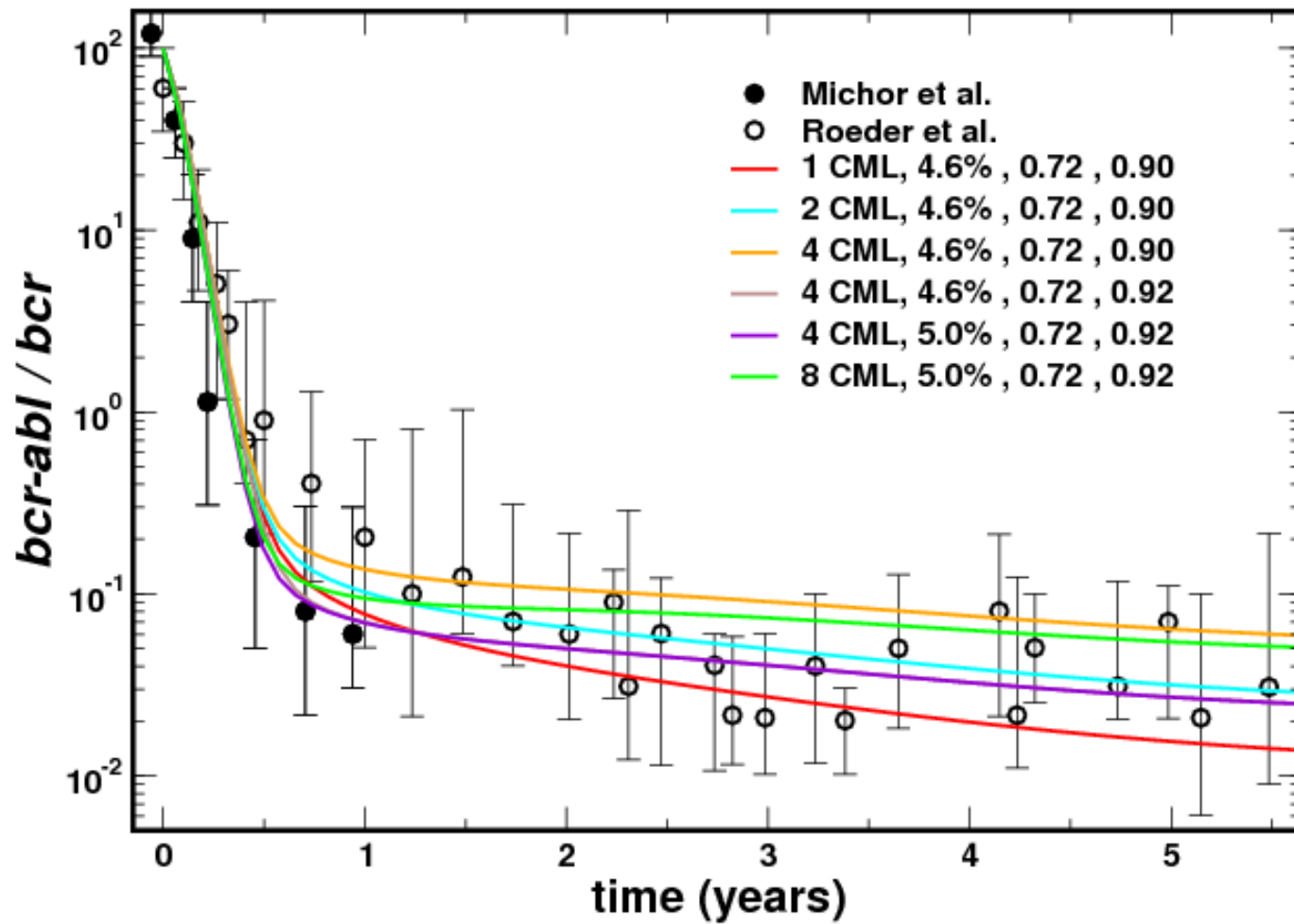
$$b_{i-1} = 2 \cdot \varepsilon \cdot r_{i-1}$$

$$\frac{d}{dt} N_i^{CML} = (1 - z) \cdot [b_{i-1}^{CML} \cdot N_{i-1}^{CML} - d_i^{CML} \cdot N_i^{CML}] + z \cdot [b_{i-1}^{IMAT} \cdot N_{i-1}^{CML} - d_i^{IMAT} \cdot N_i^{CML}]$$



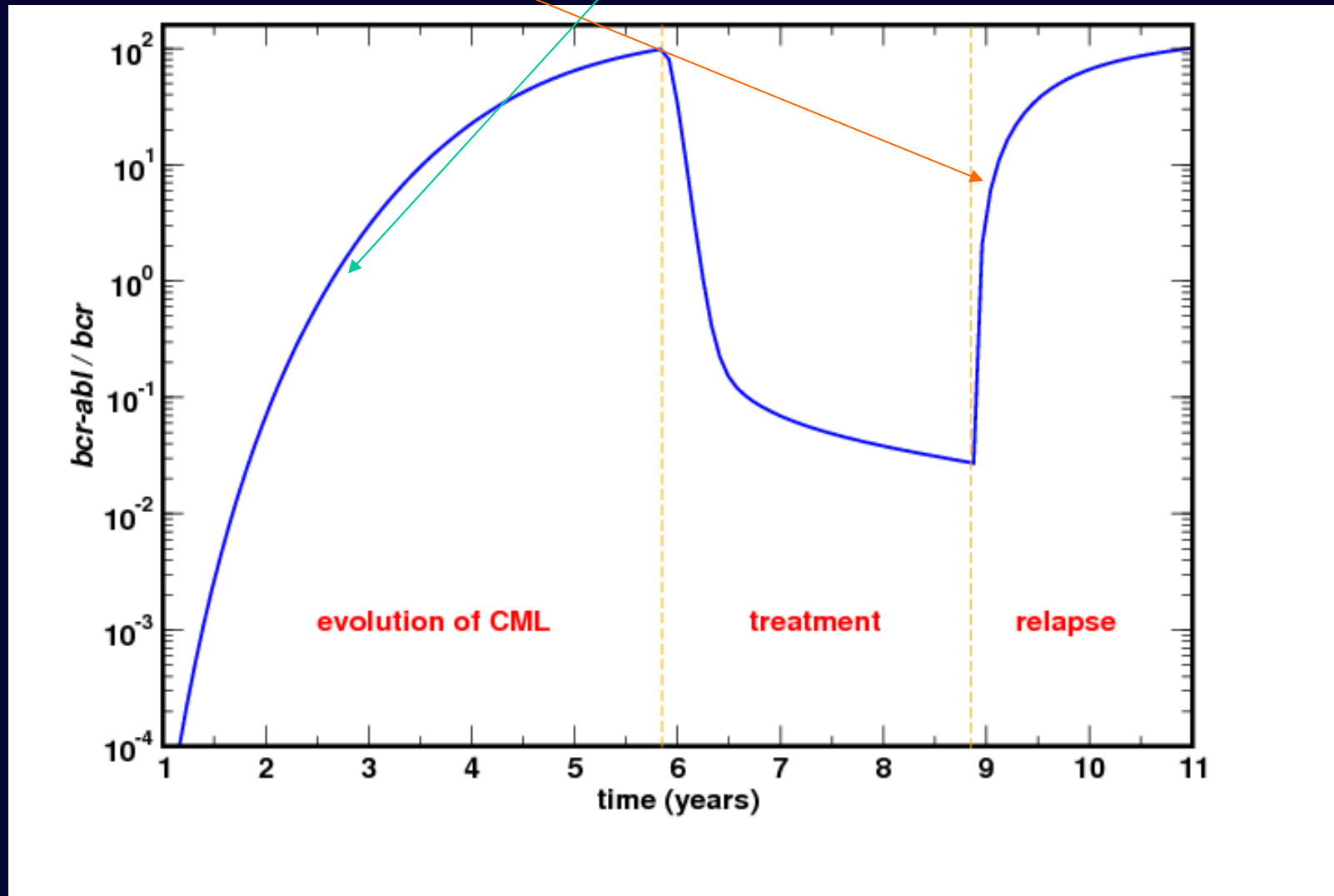
fit to Michor *et al.* data

results

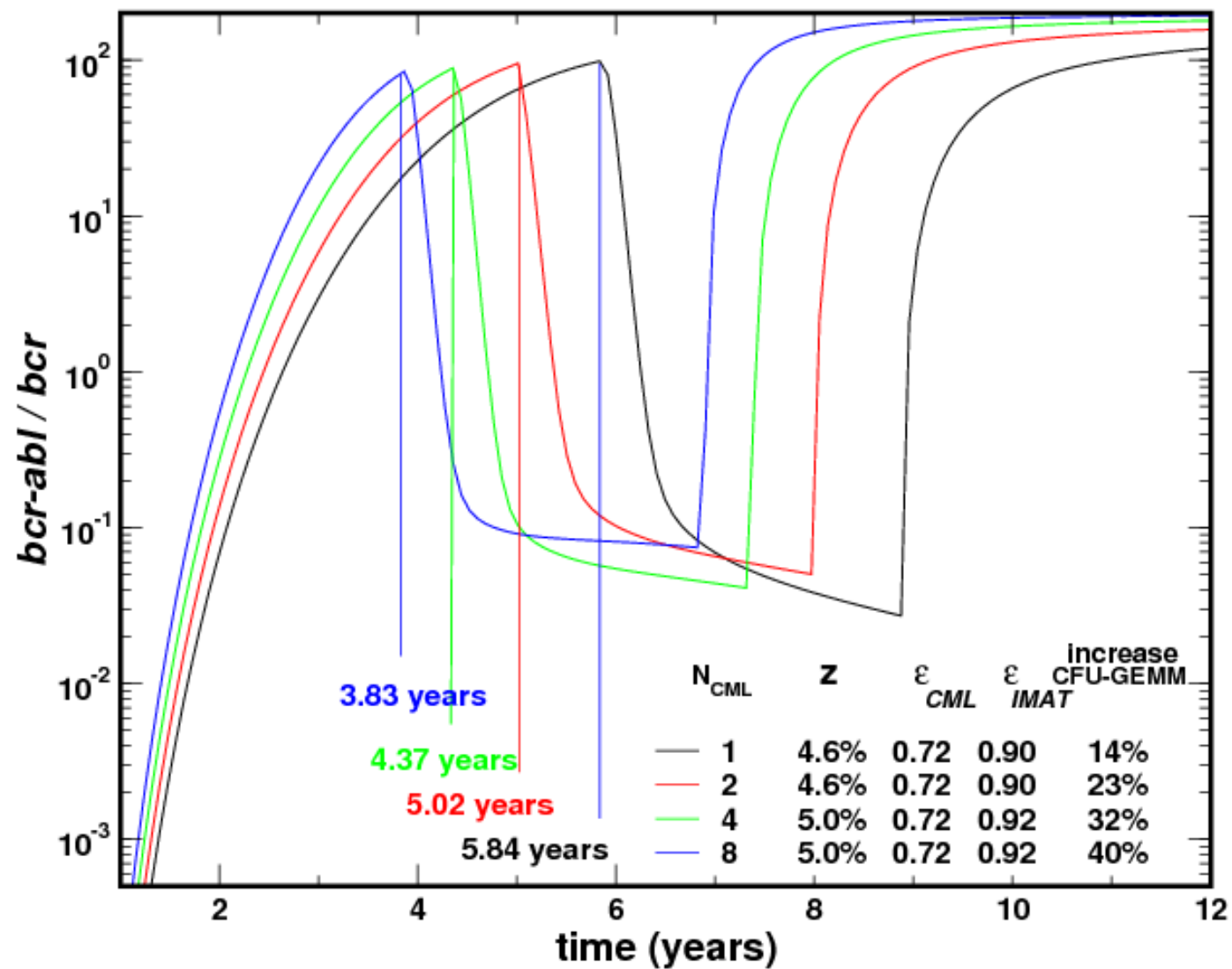


features

up to now, the # HSC driving the disease is constant in time & their dynamics is deterministic; when treatment is stopped, treated cells *wake up* and relapse is much **faster** than **normal** disease progression



features



features of CML

- ❖ CML is driven by a small number of neoplastic stem cells
- ❖ *imatinib* reduces the fitness of the neoplastic cells
- ❖ many CML progenitors persist
- ❖ only a fraction of CML cells are responding to therapy at any time
- ❖ relapse is driven by CML progenitors not just HSC

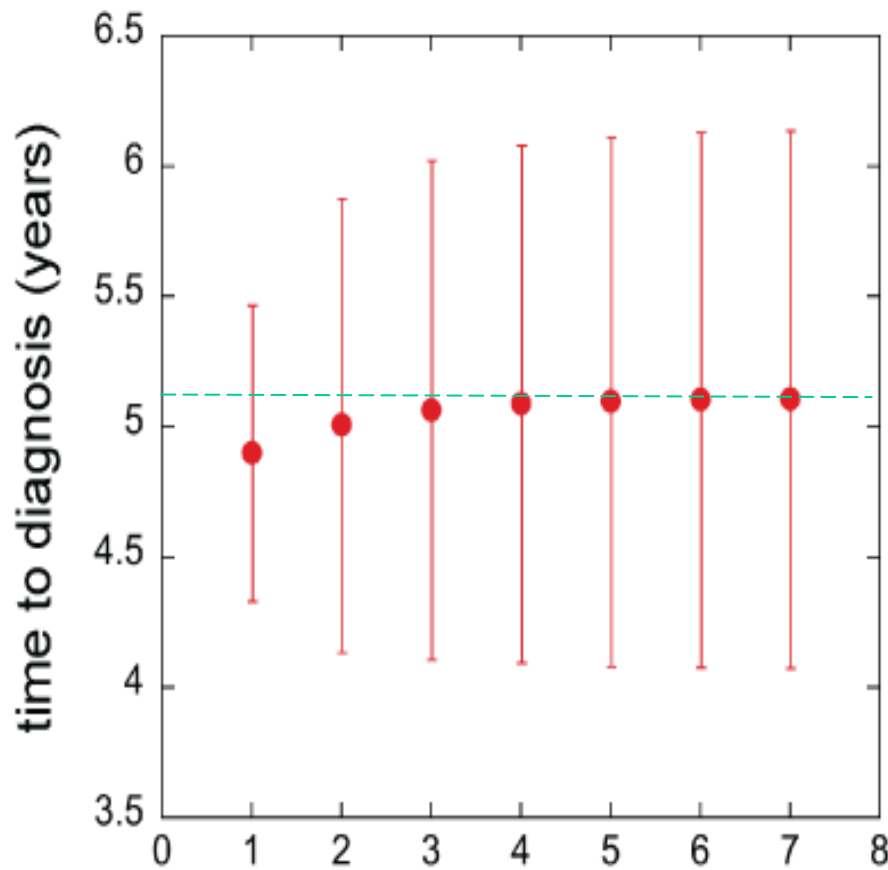
but :

- ❖ hematopoiesis is stochastic in nature, hence

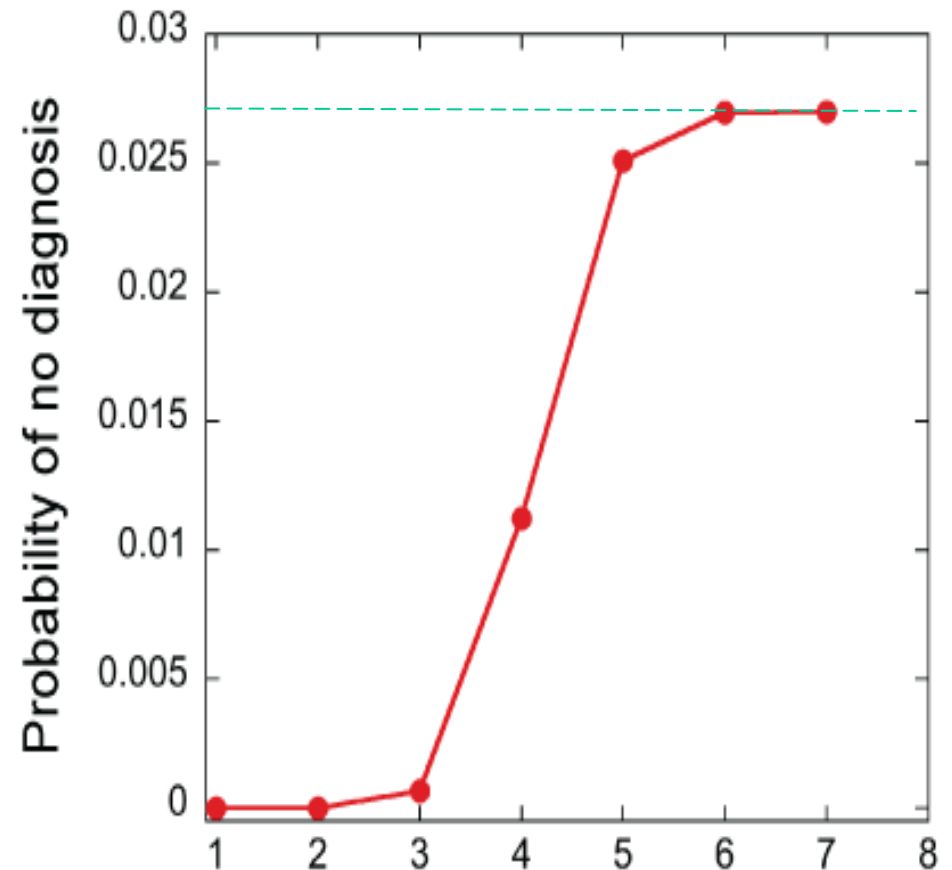
what is the impact of stochastic effects on CML dynamics ?

stochasticity in CML

... stochastic dynamics of 10^{12} cells is unfeasible

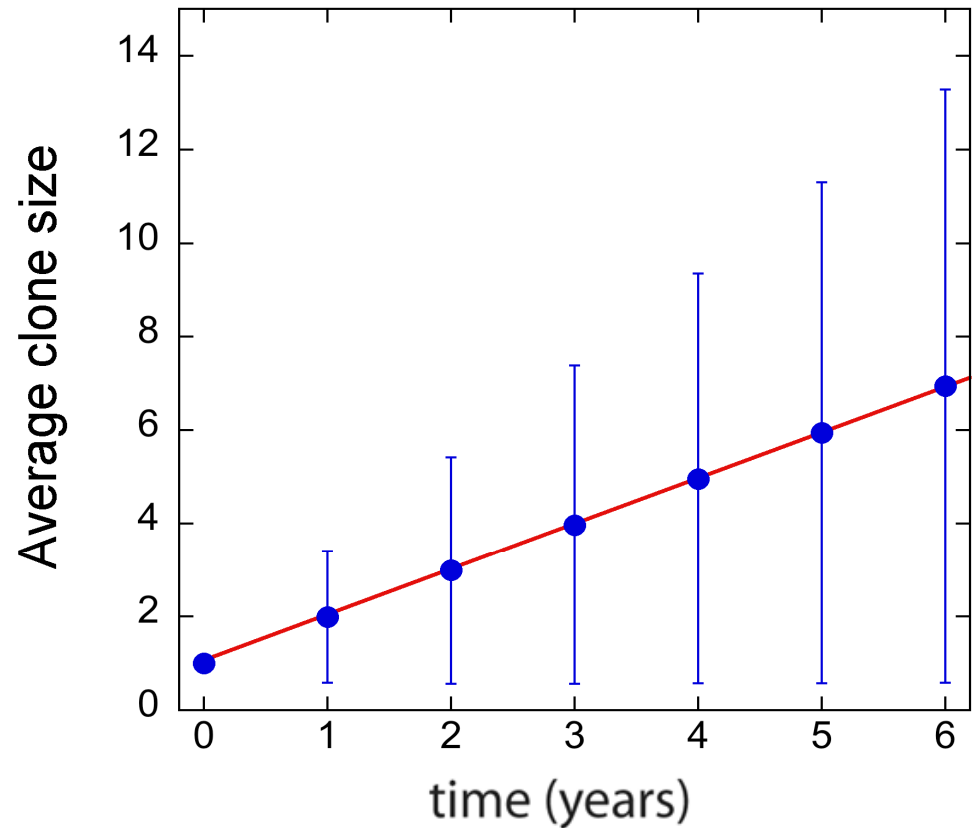
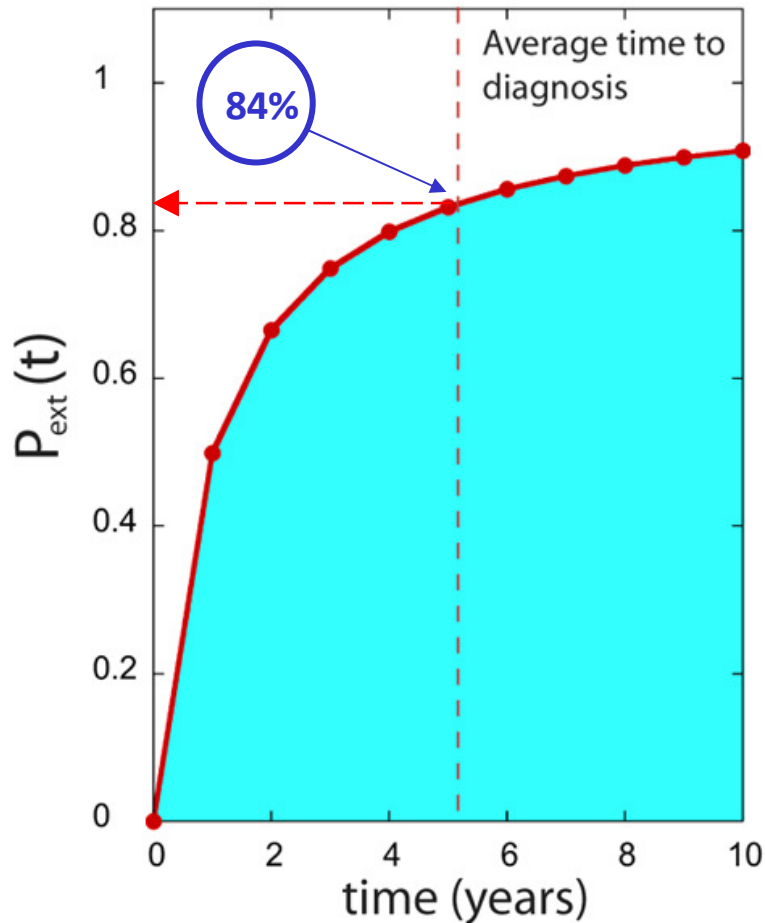


Number of stochastic compartments



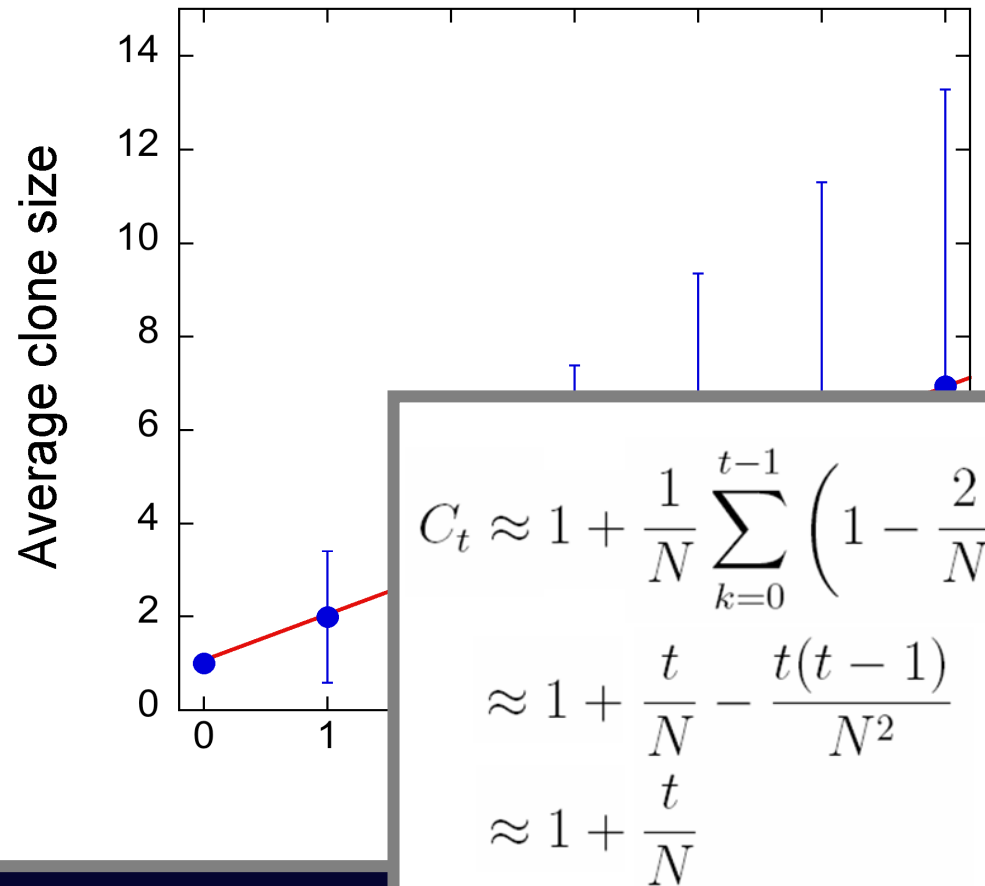
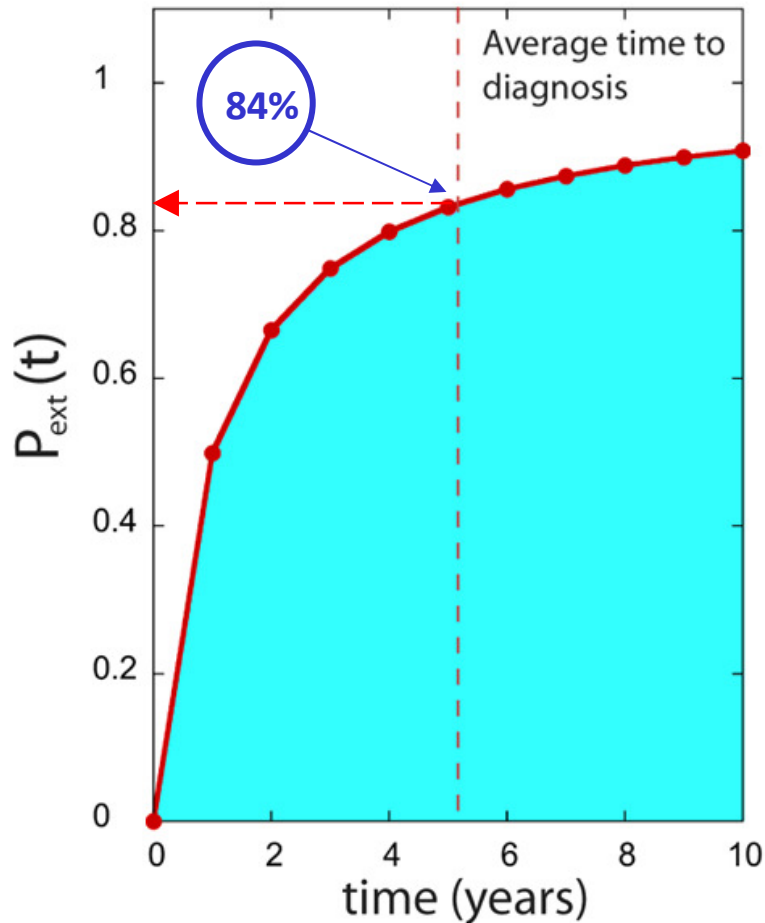
stochasticity in CML

in **84%** of individuals, **CSC** population goes extinct before diagnosis
in **16%** of individuals, **CSC** population grows, on average, 1 per year

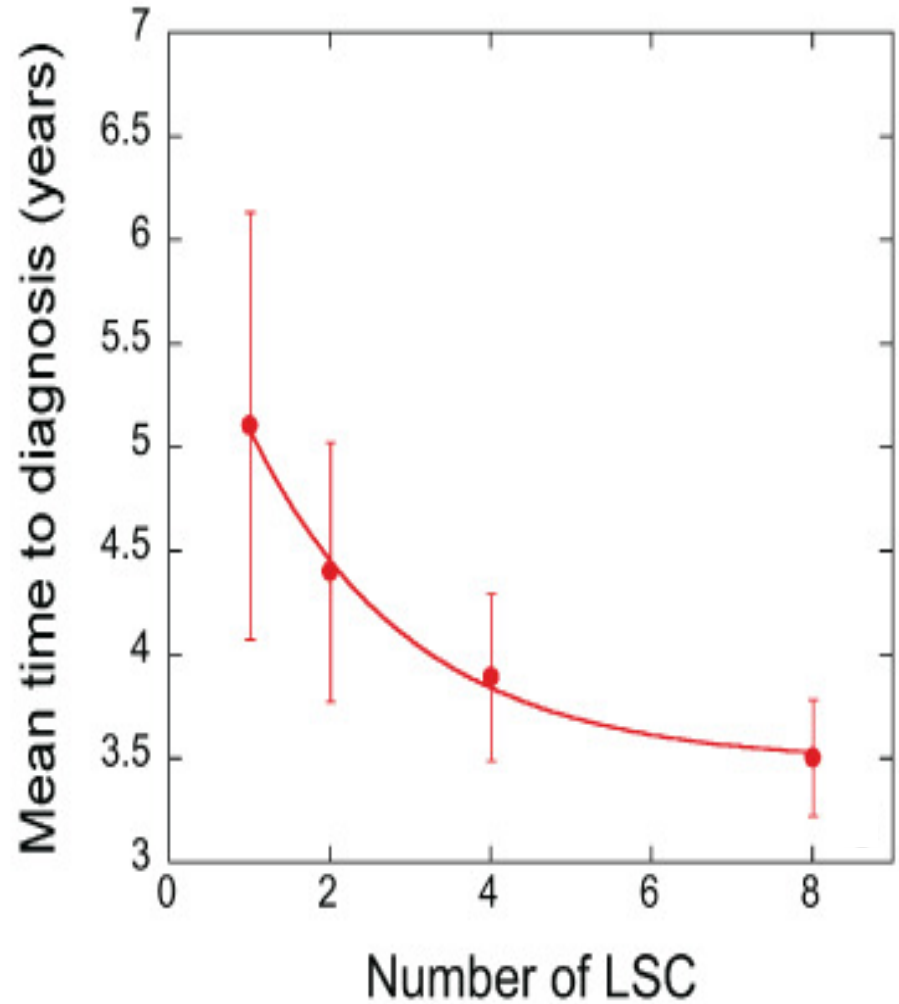
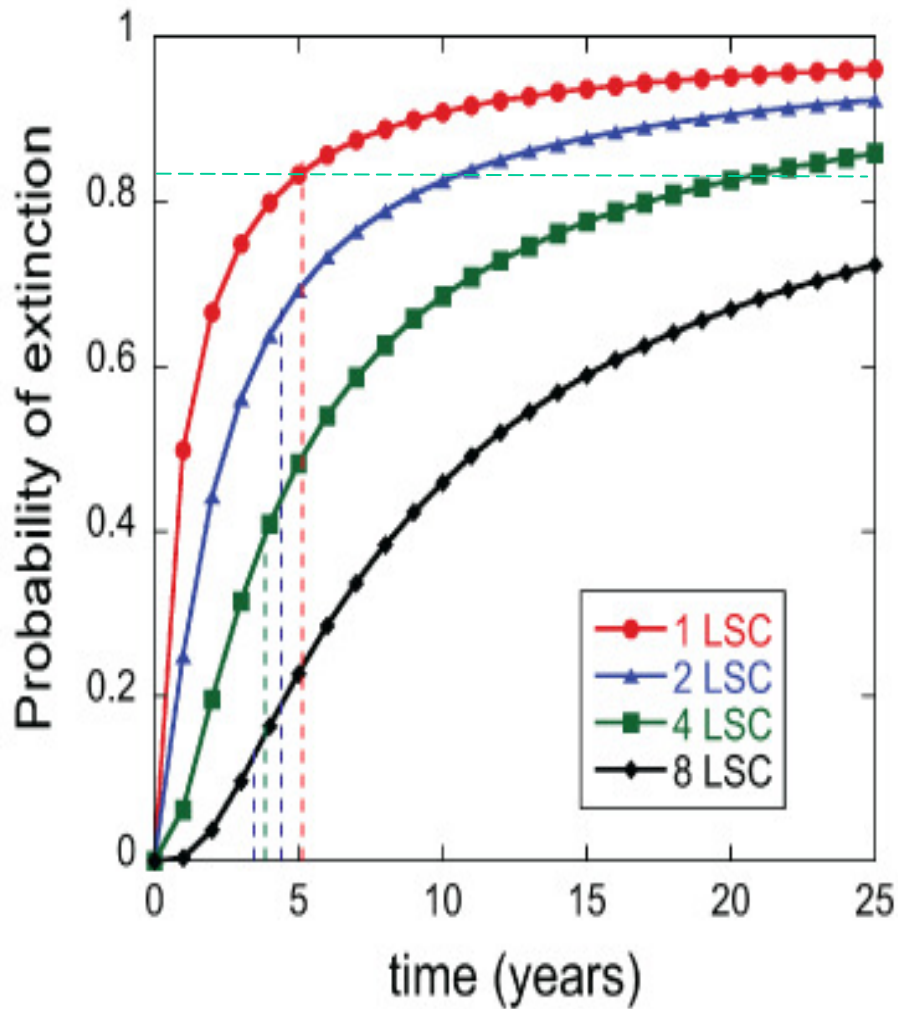


stochasticity in CML

in **84%** of individuals, **CSC** population goes extinct before diagnosis
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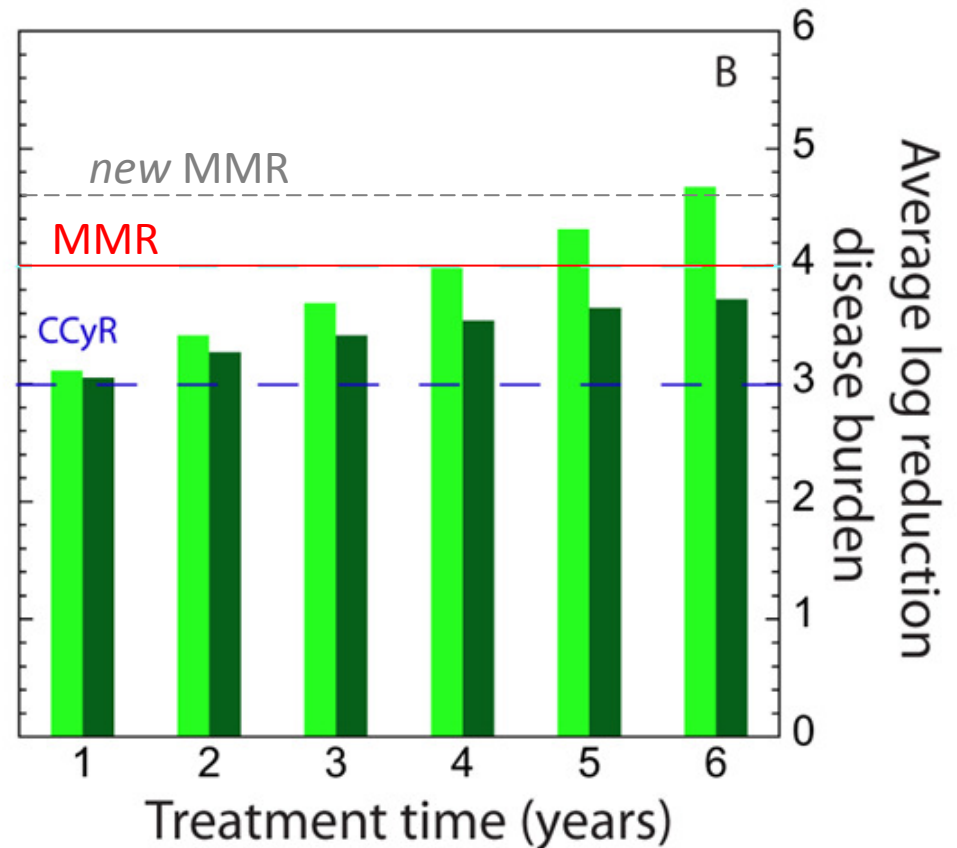
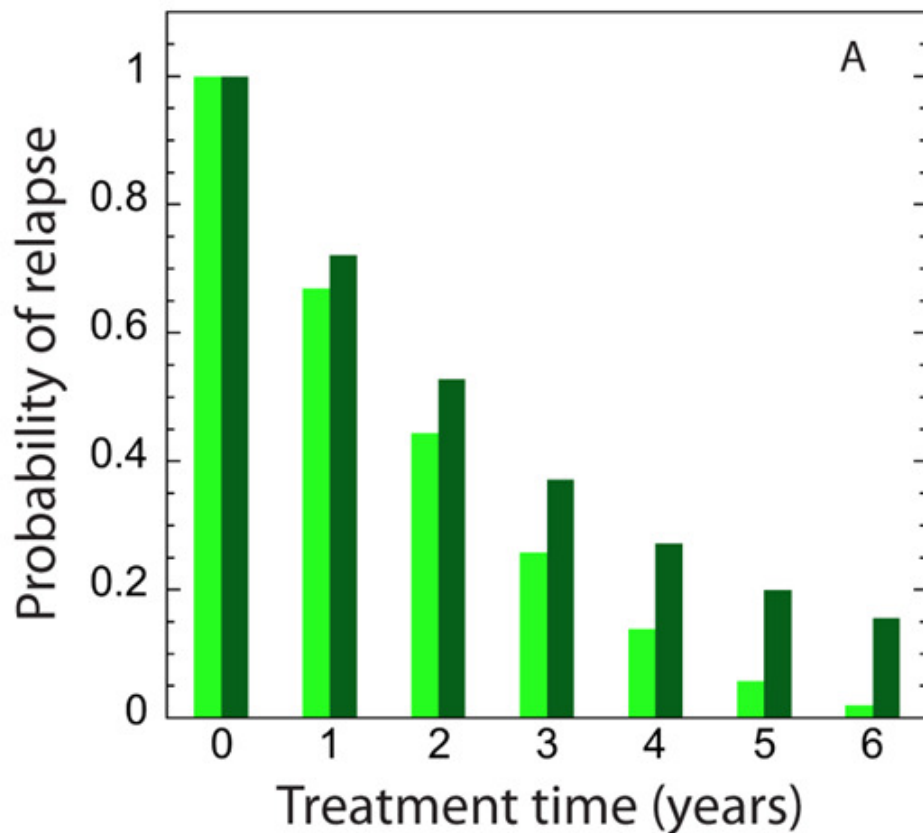
stochasticity in CML



stochasticity in CML

c1 ■ no LSC @ diagnosis

c2 ■ including 16% patients with LSC @ diagnosis



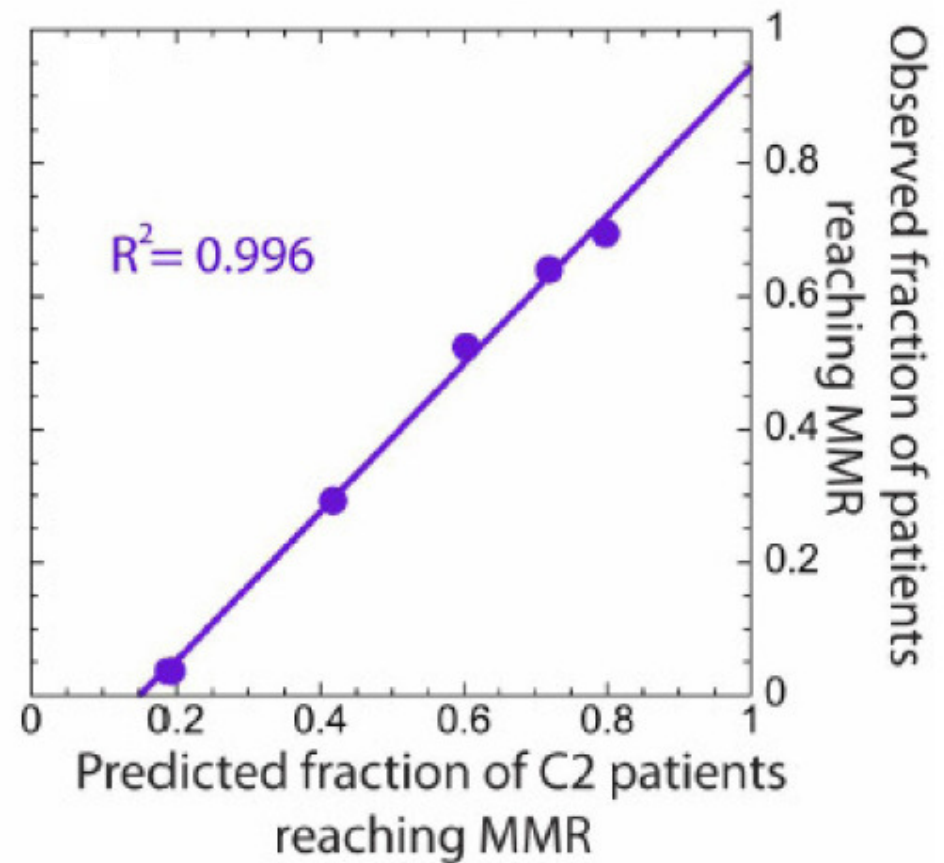
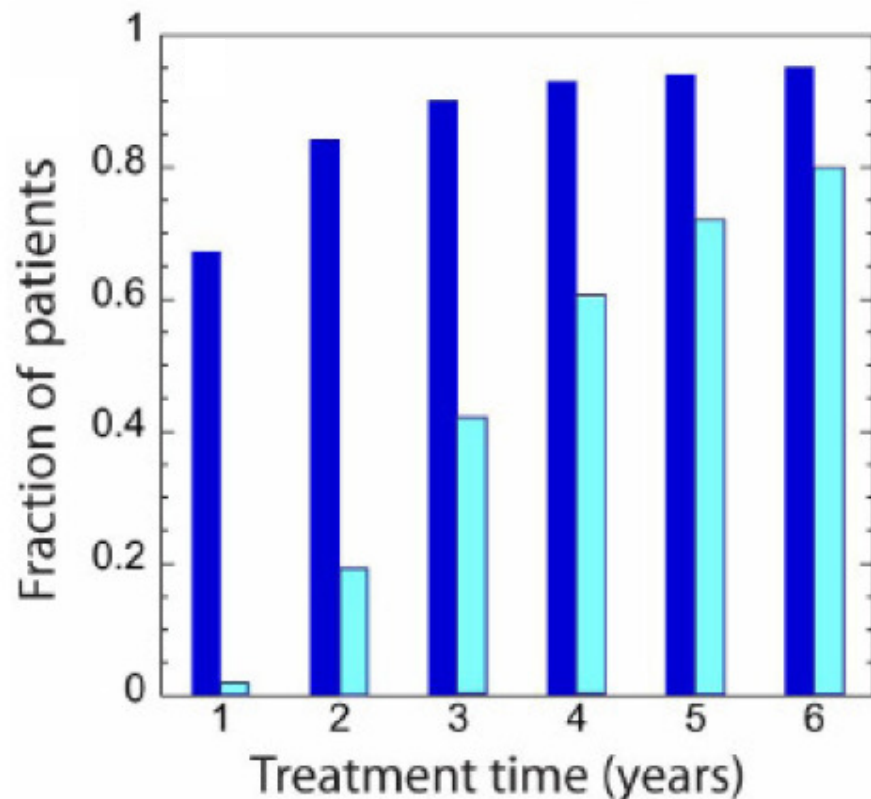
despite **NOT** affecting directly **CSC**,

imatinib + natural selection can cure the majority of **CML** patients

ongoing: development of resistance mutations . . .

stochasticity in CML

treatment with TKI-inhibitors helps an individual to stay alive and live his everyday life while natural selection helps him getting rid of the cause of the disease; however, it takes years for one to gamble his way out of cancer.



■ Complete Cytogenetic Response (CCyR)

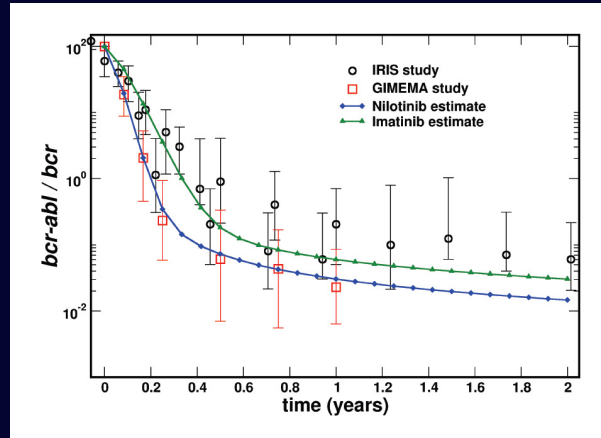
■ Major Molecular Response (MMR)

cancer ecology & CML treatments

Lenaerts *et al.*, Cell Cycle 10 (2011) 1540-1544

different therapeutic power of TKI-inhibitors

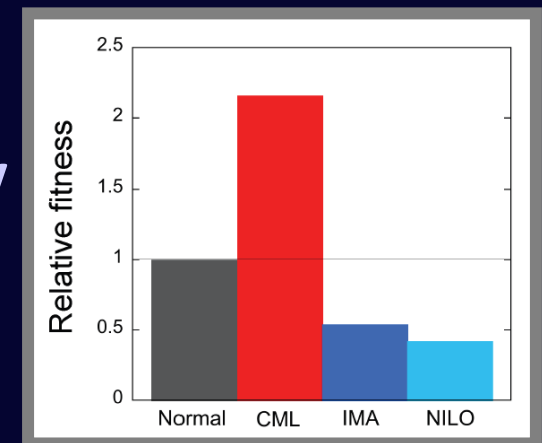
- ❖ CML can be successfully treated with different TKI-inhibitors
- ❖ *imatinib* & *nilotinib* lead to distinct disease progression curves



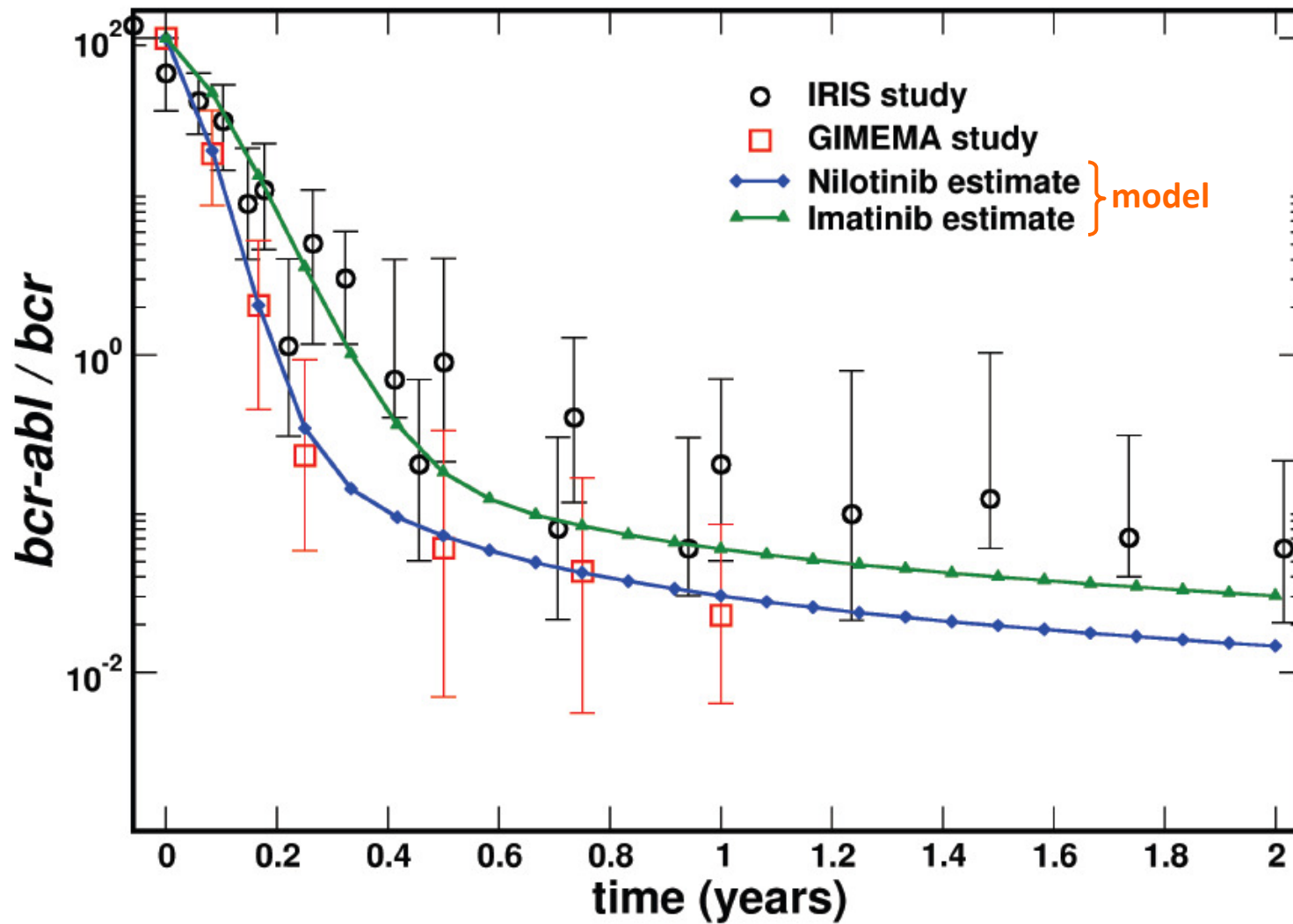
- ❖ however, *in-vitro* studies show no apparent difference between *imatinib* & *nilotinib*

what's going on ?

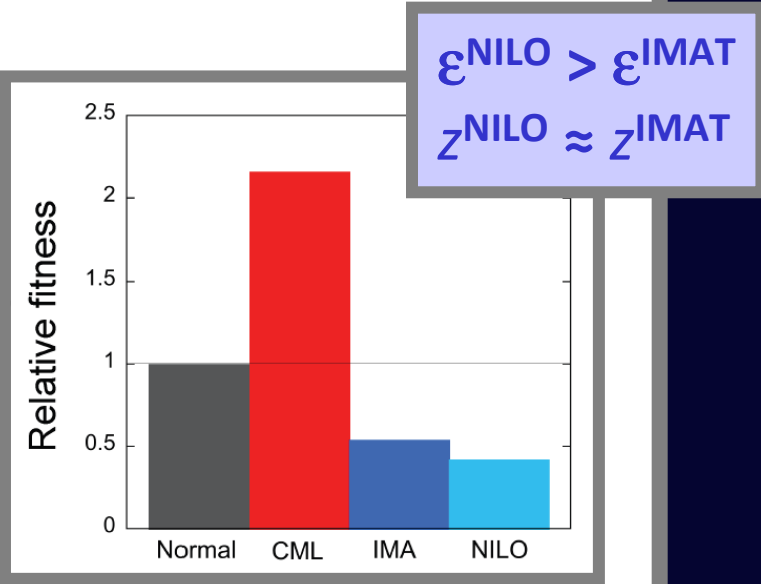
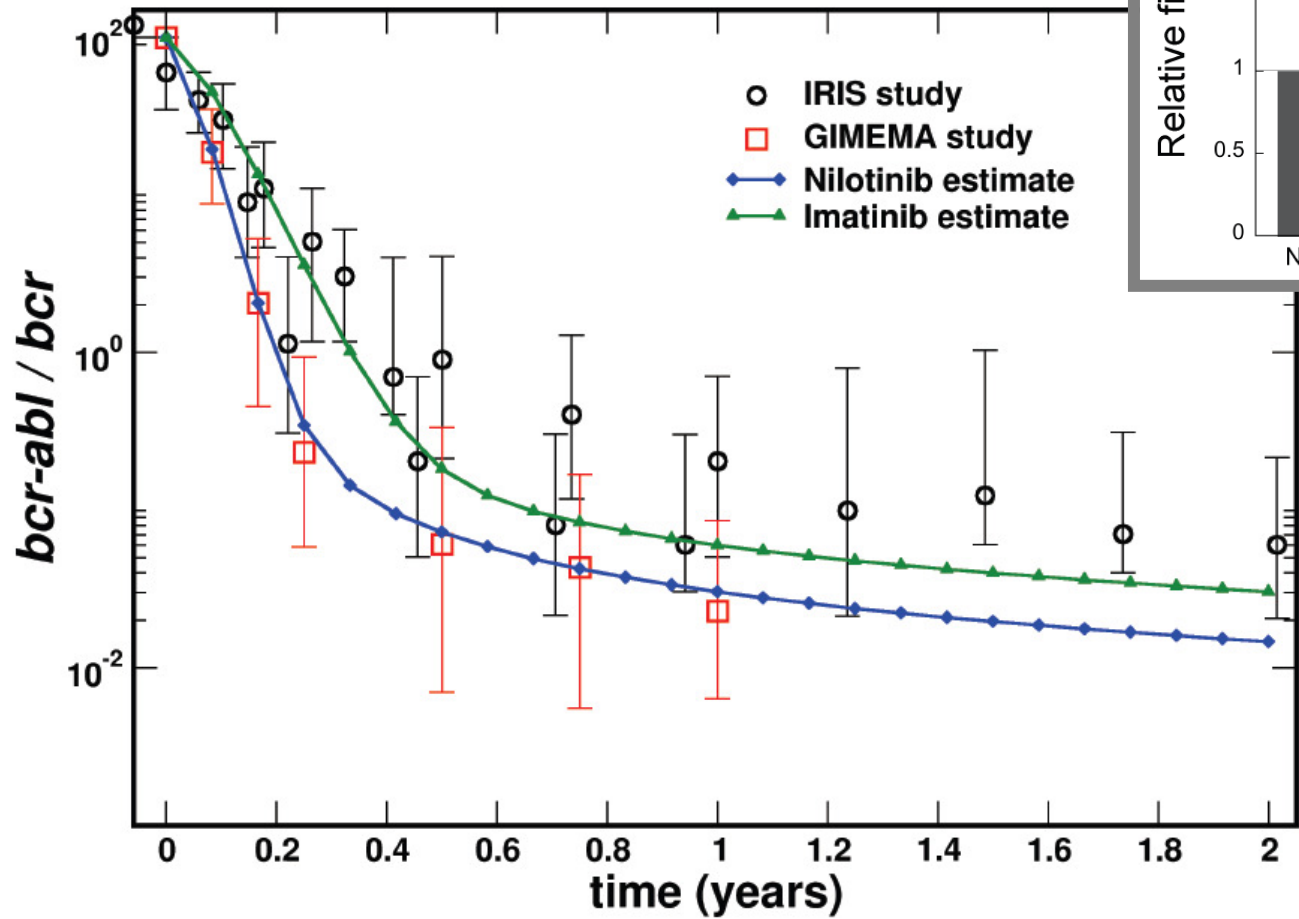
- ❖ *in-vitro* studies do not incorporate the ecology of cell competition that occurs *in-vivo*.



imatinib ⊗ nilotinib



imatinib \otimes nilotinib

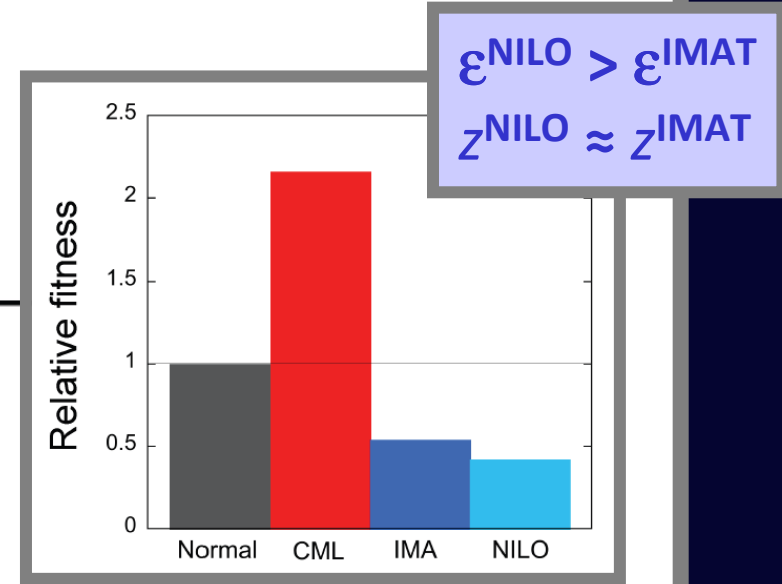
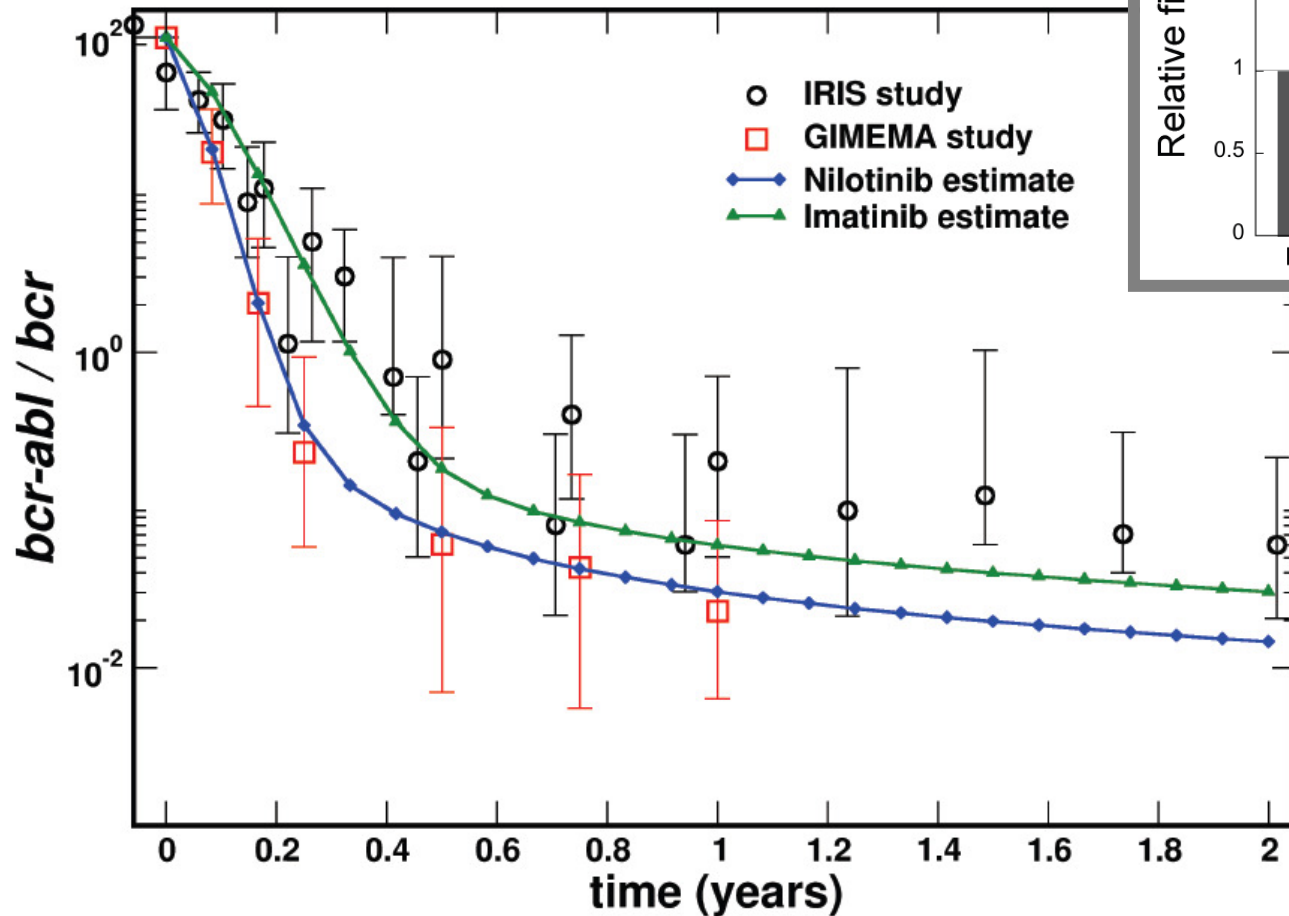


imatinib \otimes nilotinib

in vitro : **no** differences

in vivo : **important** differences

(ecology of cancer cells is important)



conclusions

- ❖ *hematopoiesis results from the slow replication of a limited **number** of active stem-cells which **scales allometrically with** the **mass** of an adult mammal as $N_{sc} \sim M^{3/4}$*
- ❖ *the small number of HSC together with their slow replication rate protect hematopoiesis from long-term trouble.*
- ❖ *the **paradigm** of stochastic behaviour – **neutral evolution** – suggests that **PNH** does not result from any 2nd mutation or immune system attack – it results from the unlikely event of a rare-mutation in a small population at a normal mutation rate.*
- ❖ *stochastic effects have measurable consequences in disease progression, and lead to variabilities in the time to progression of stem-cell derived diseases; in **CML**, and in the **absence of resistance mutations**, stochastic effects let **TKI-inhibitors cure most patients**.*
- ❖ *such a broad vision of hematopoiesis paves the way to study blood diseases (e.g., **PNH**, **CML**, **CN**) as well as the detailed microscopic description of response to therapies, such as those associated with **TKI-inhibitors** (imatinib, nilotinib, dasatinib, etc.) not to mention studying the development of mutations which are resistant to treatment (**ongoing . . .**)*



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allometric scaling of hematopoiesis

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Cyclic neutropenia in mammals

Jorge M. Pacheco, Arne Traulsen, Tibor Antal, David Dingli
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paroxysmal nocturnal hemaglobinuria

scaling considerations

Dingli, Traulsen & Pacheco, *PRSB* 275 (2008) 2389

scaling relations so-far . . .

❖ number of **HSC** in adult mammals :

$$N_{SC} \approx 16.55 M^{3/4}$$

❖ number of **HSC** during human ontogeny :

$$N_{SC} \approx 5.5 m(t)$$

❖ specific basal metabolic rate :

$$B_c \approx 2.9 M^{-1/4} \quad (\text{year}^{-1})$$

❖ average life-span :

$$L \approx 8.6 M^{1/4} \quad (\text{year})$$

([M] = kg)

implications . . .

Hayflick hypothesis (1961):

cells undergo a limited number of divisions during their lifespan

from the scaling relations, each cell divides

$$N \sim \text{rate} \times \text{lifespan} \sim M^{-1/4} \times M^{1/4} \sim M^0$$

that is, constant & independent of the mammalian species :

a mouse-HSC and an elephant-HSC replicate, on average, the same number of times during the ~2-year and the ~70-year lifespans of the mouse and elephant, respectively; humans are the exception, as we live much longer than lifespan estimate.

scaling across mammals

in

CYCLIC NEUTROPENIA

Dingli, Antal, Traulsen & Pacheco, Cell Proliferation (in press)

Pacheco, Traulsen, Antal & Dingli, American Journal of Hematology, 83 (2008) 920

cyclic neutropenia

features

- ❖ rare congenital disorder
- ❖ → oscillations of neutrophil count






model

- ❖ biological defect is the same in mammals
- ❖ architecture of hematopoiesis is invariant across mammals
- ❖ allometric scaling should relate period of oscillations

results :

$$\frac{T_H}{T_D} = \left(\frac{M_H}{M_D} \right)^{1/4}$$



					
species	<i>mouse</i>	<i>macaque</i>	<i>dog</i>	<i>baboon</i>	<i>human</i>
mass (kg)	0.025	5	13	40	70
period (days)	3	10-11	14	17-18	19-21
sampling period (hours)	<18	63	84	105	120

cyclic neutropenia

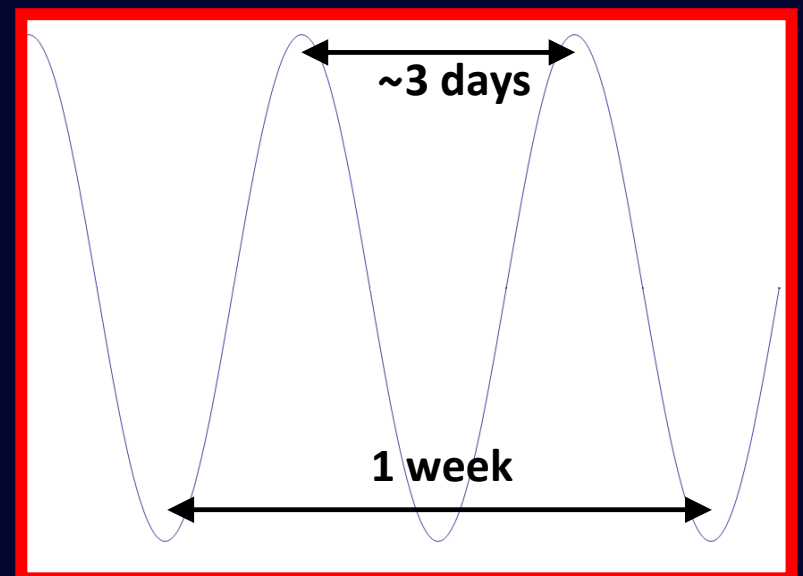
*our model predicts a period of ~3 days for CN in mice
this is a direct consequence of metabolic rate of mice
does CN occur in mice ?*

Grenda *et al.* Blood 100 (2002) 3221–3228

“Mice expressing a neutrophil elastase mutation derived from patients with severe congenital neutropenia have normal granulopoiesis”

- ❖ *there is a study on mice which claims there is **no CN***
- ❖ *is that true ?*
- ❖ *what did they do ?*
- ❖ *they measured neutrophil count every week . . .*

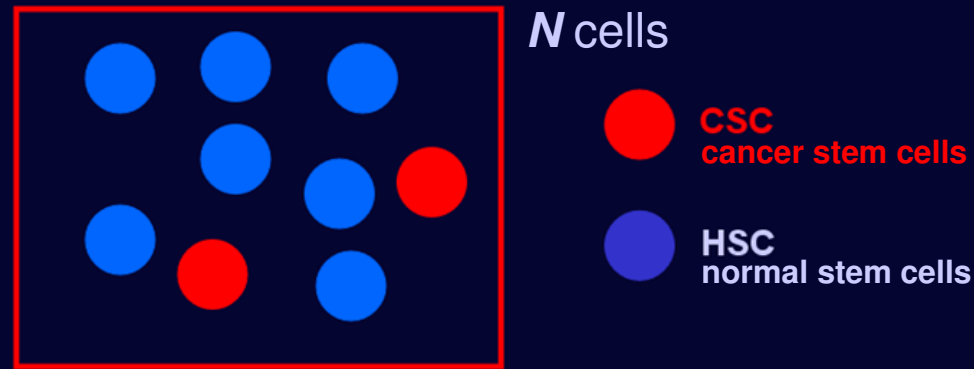
- ❖ *because sampling period is a multiple of CN period, they **ever** observe oscillations*



stochastic protection

THE MOST ROBUST MAMMAL

protection : the *best* of mammals



combine allometric scaling with stochastic dynamics to determine the **mammal which is best protected** against acquired hematopoietic stem-cell disorders.

scaling of lifespan: $L \sim M^{1/4}$

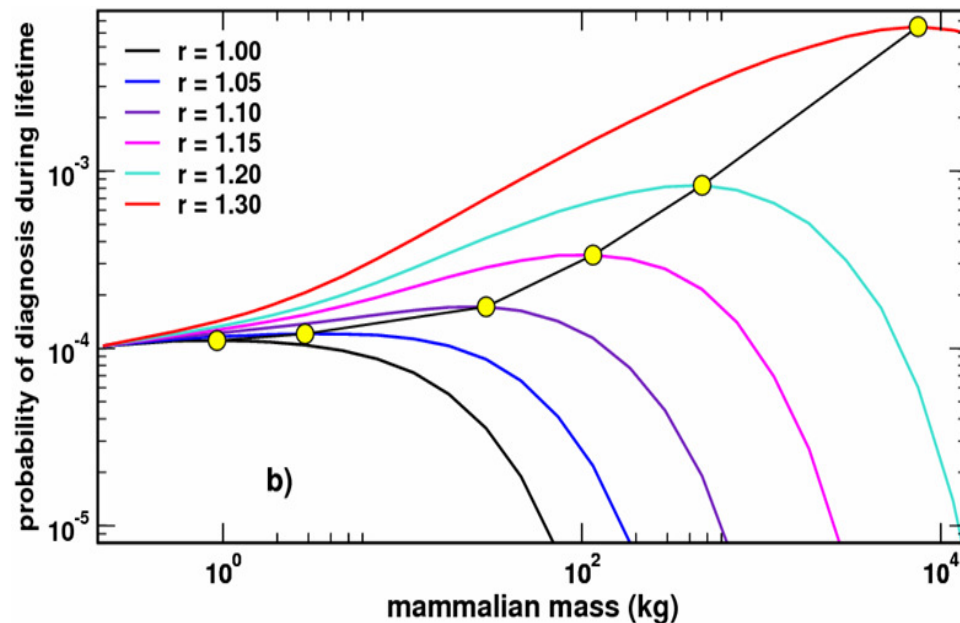
mass specific metabolic rate : $B_c \sim M^{-1/4}$

size of active SC pool : $N_{SC} \sim M^{3/4}$

prob. mutation **HSC** \rightarrow **CSC** : $\mu \sim 10^{-6}$
p/ replication

protection : the *best* of mammals

- ❖ *r* is very difficult to determine experimentally; unfortunately, it is consensual that, in general, *r* is large (>1.5);
- ❖ when $r \sim 1$, large mammals are more protected than small mammals;
- ❖ when $r > 1.3$, small mammals are more protected, since the probability for the organism to acquire cancer mutations is minimized;
- ❖ a small active HSC pool minimizes the risk of mutations; once mutations occur, the path to full blown disease opens up easily (whenever $r > 1$).



$r = 1.05$: $prob(\text{mouse}) = prob(M=18 \text{ kg})$

$r = 1.10$: $prob(\text{mouse}) = prob(M=125 \text{ kg})$

$r = 1.15$: $prob(\text{mouse}) = prob(M=870 \text{ kg})$

$r = 1.20$: $prob(\text{mouse}) = prob(M=5800 \text{ kg})$