Modeling & Simulation (Computational Immunology)

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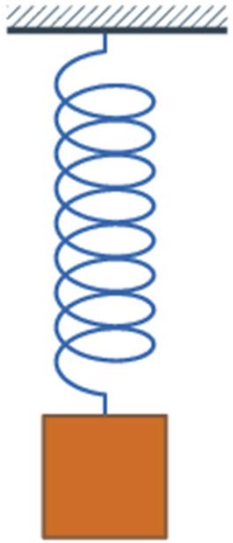
What is a mathematical model?

Uses mathematical language to describe a system

A mathematical model consists of a collection of variables and rules governing their values.

Models are **based on assumptions** inspired by observing some real phenomena in the hope that the model behavior resembles the real behavior.



Mathematical modeling is process of constructing, testing, and improving mathematical models

Advantages of the modeling approach in biology

"Essentially, all models are wrong, but some are useful."
-George Box, University of Wisconsin

- Concise summary of present knowledge of operation of a particular system
- Predict outcomes of modes of operation not easily studied experimentally in a living system
- Provide diagnostic tools to test theories about the site of suspected pathology or effect of drug treatment
- Clarify / simplify complex experimental data
- Suggest new experiments to advance understanding of a system

Limitations of the modeling approach

"Essentially, all models are wrong, but some are useful."
-George Box, University of Wisconsin

- Models often require many simplifying assumptions
  - beware of garbage in, garbage out
- Validation of model predictions is essential
  - examination of behavior under known limiting conditions
  - experimental validation
  - limits of model can point out what we don't understand

The Immune System

Science that began with Jenner in 1796

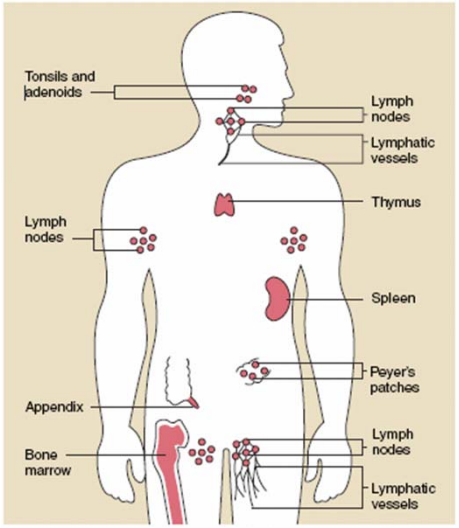
- A network of cells, tissues, and organs that work together to defend the body against attacks by "foreign" invaders (antigens).
  - Primarily microbes (germs)—tiny, infection-causing organisms such as bacteria, viruses, parasites, and fungi.
- Provides basis for vaccines (e.g., flu shot)
- But also implicated in disease:
  - Autoimmune (Lupus, MS, Rheumatoid Arthritis)
  - Respond to harmless foreign substance (ragweed pollen) produces allergy
  - Sepsis, Cancer
- Understanding will lead to better diagnostics & therapies

Organs of immune system = "lymphoid organs", since home to lymphocytes (small white blood cells that are key players in the immune system)

Why Model the Immune System?

Experiments provide only a static window onto the real dynamics of immunity

- Immune response involves the collective and coordinated response of $\approx 10^{12}$ cells and molecules
- Spatially-distributed system
  - blood, lymph nodes, spleen, thymus, bone marrow, etc.



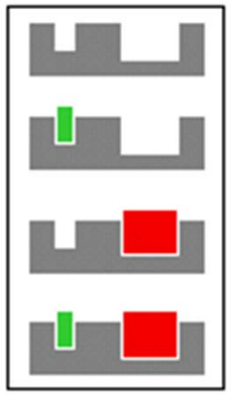
- Feedback loops and non-linear dynamics
- Experiments often require artificial constructs

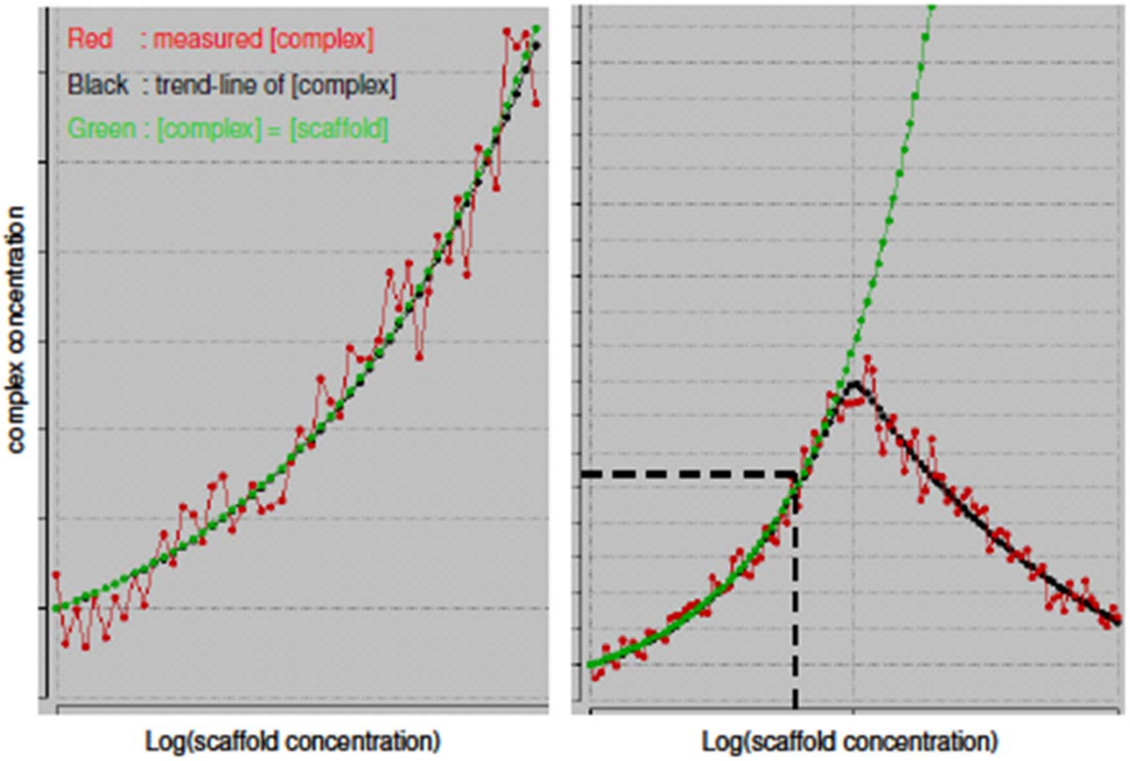
Models can help understand the source(s) of variability between experiments

Mechanistic modeling vs. curve fitting

Only mechanistically correct models extrapolate reliably

Gene transcriptionally activated by complex of three proteins, and one acts as scaffold





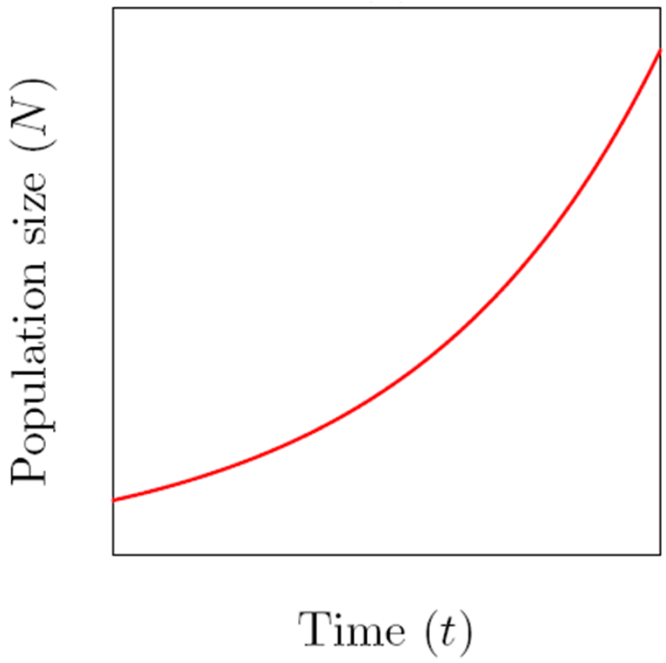
Figures from: Hamid Bolouri

Interpolation (i.e. within sample predictions) vs.
Extrapolation (i.e. out of sample predictions, as in the right panel)

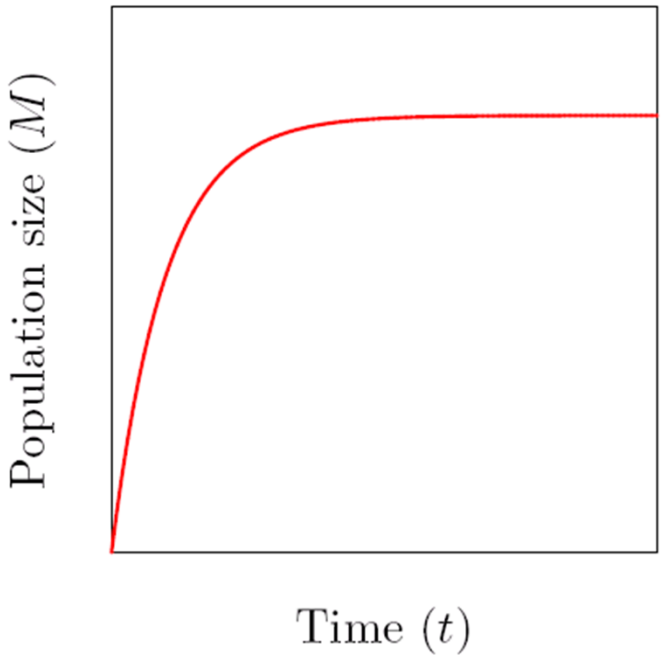
Dynamic vs. Static modeling

A dynamic model accounts for the element of time,
while a static model does not

Exponential growth of virus



White blood cells produced
by bone marrow



Dynamic equations can be simulated to study system behavior

Types of Dynamic Models

Choosing the type of model is an important first step

- **Continuous**: time or state variables (often called 'density')
  - Ordinary differential equations
- **Discrete**: time or state variables
  - assume a small set of qualitative states e.g. active or inactive
  - changes in state are given by discrete (logical) rules

- **Deterministic**: no randomness is involved in the development of future states of the system
  - Given model structure, parameter values, and initial conditions, there is no variation in output
- **Stochastic**: the next state of is not fully determined by the previous state – probability is involved
  - can take into account the fluctuations in mRNA/protein/cell numbers and external noise

Spatial structure can also important

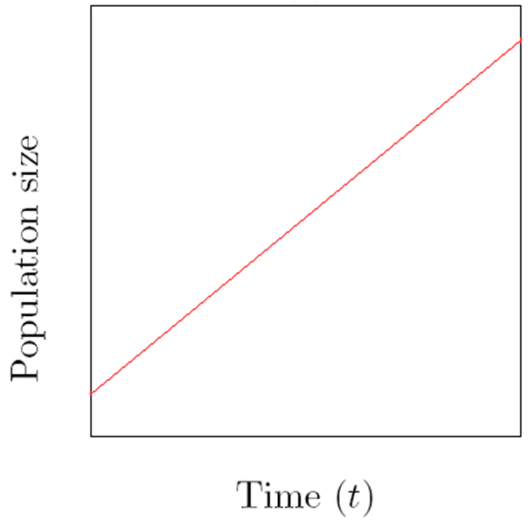
Ordinary Differential Equations (ODEs)

Continuous and Deterministic

Production rate

$$\frac{dB}{dt} = p$$

$$B(t) = B(0) + pt$$



Change in number of B cells per time

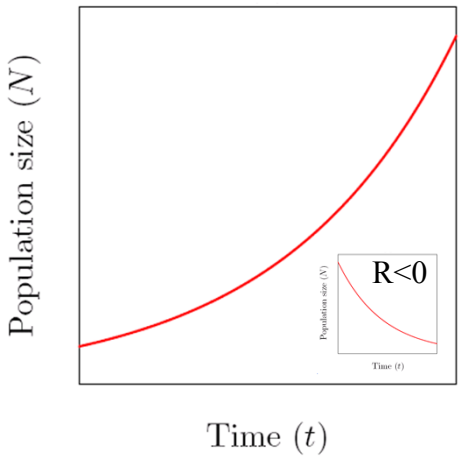
$$\frac{dB}{dt} = \lim_{t \to 0} \frac{B(t + \Delta t) - B(t)}{\Delta t}$$

Most models used in practice not solvable → **simulate**

Exponential growth (and decay)

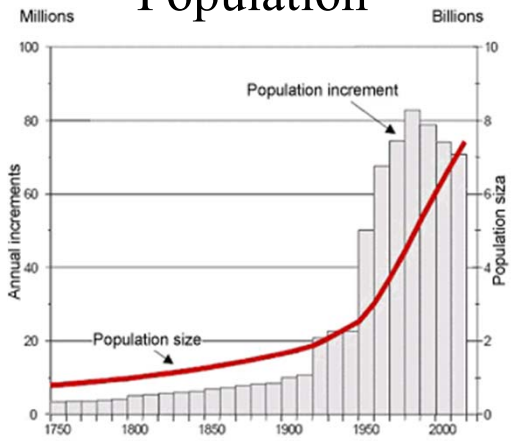
Continuous and Deterministic

$$\frac{dN}{dt} = rN$$



$$N(t) = N(0)e^{rt}$$

Human Population



How long for population to double?

$$2N(0) = N(0)\mathrm{e}^{rt}$$

$$\ln 2 = rt$$

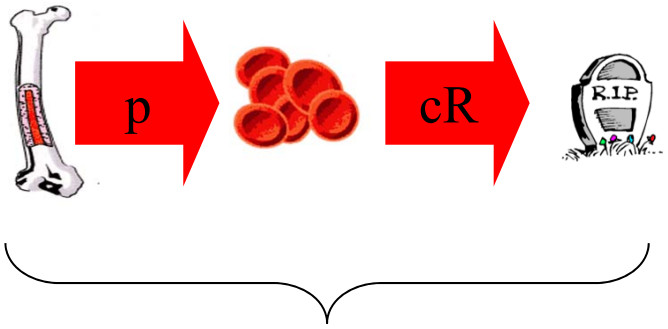
$$t = \ln[2]/r$$

Doubling time: time for population to reach 2x initial value
Half-life: time for population to reach 50% of initial value

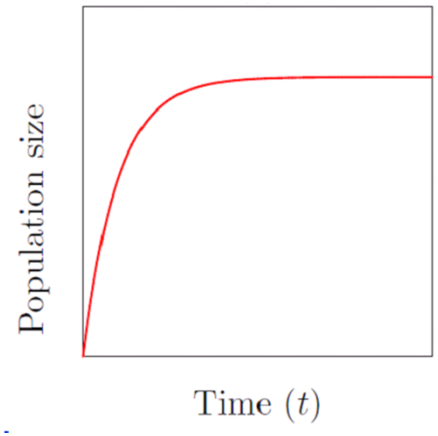
Steady-state

Population sizes remain constant at steady-state

Red Blood Cell production



$$\frac{dR}{dt} = p - cR$$



How many cells at steady-state?

$$0 = p - cR$$

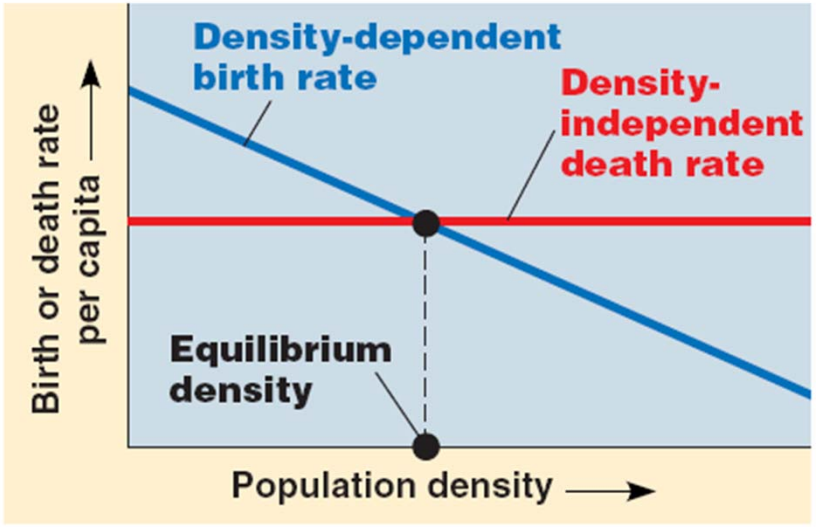
$$R = p/c$$

Solve for steady state by setting derivatives equal to zero

Density dependence

Birth (or death) rate may depend on population size

$$\frac{dN}{dt} = bN \qquad -dN$$



$$N = K\left(1 - \frac{d}{b}\right)$$

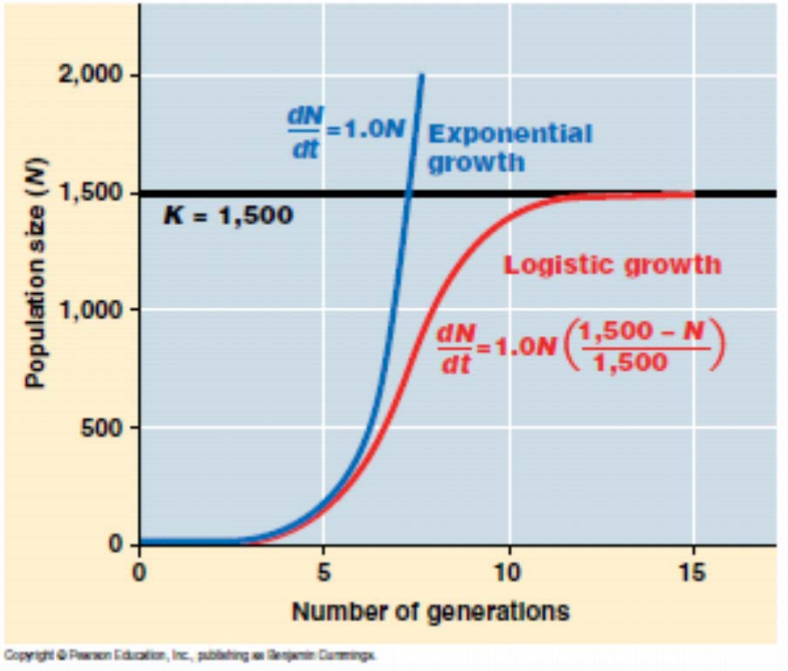
<u>Stable steady-state</u>: small perturbations return to same state

Logistic Model (S-shaped curve)

Includes density-dependent birth and death (r = b - d)

$$\frac{dN}{dt} = rN\left(1-\frac{N}{K}\right)$$

Initial stage of growth is approximately exponential; growth slows as saturation begins, and then stops at maturity.

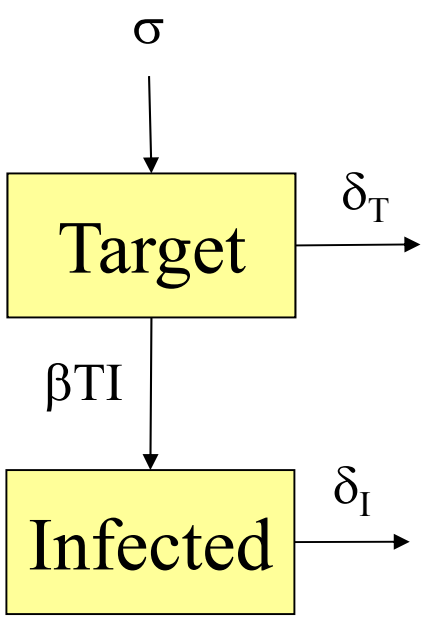


Is this a "model" if can't explain why birth/death rate *r~N/K?*
phenomenological model

Carrying capacity (K): population size that can be sustained indefinitely

Modeling Interactions

Law of mass action (also called the mean-field assumption):
Entities encounter each other according to their relative abundance across space -- the rate of an elementary reaction is proportional to product of concentrations of participating entities



Target cells (T) become infected cells (I)

Target $\frac{dT}{dt} = \sigma - \delta_T T - \beta T I$

Infected $\frac{dI}{dt} = \beta T I - \delta_I I$

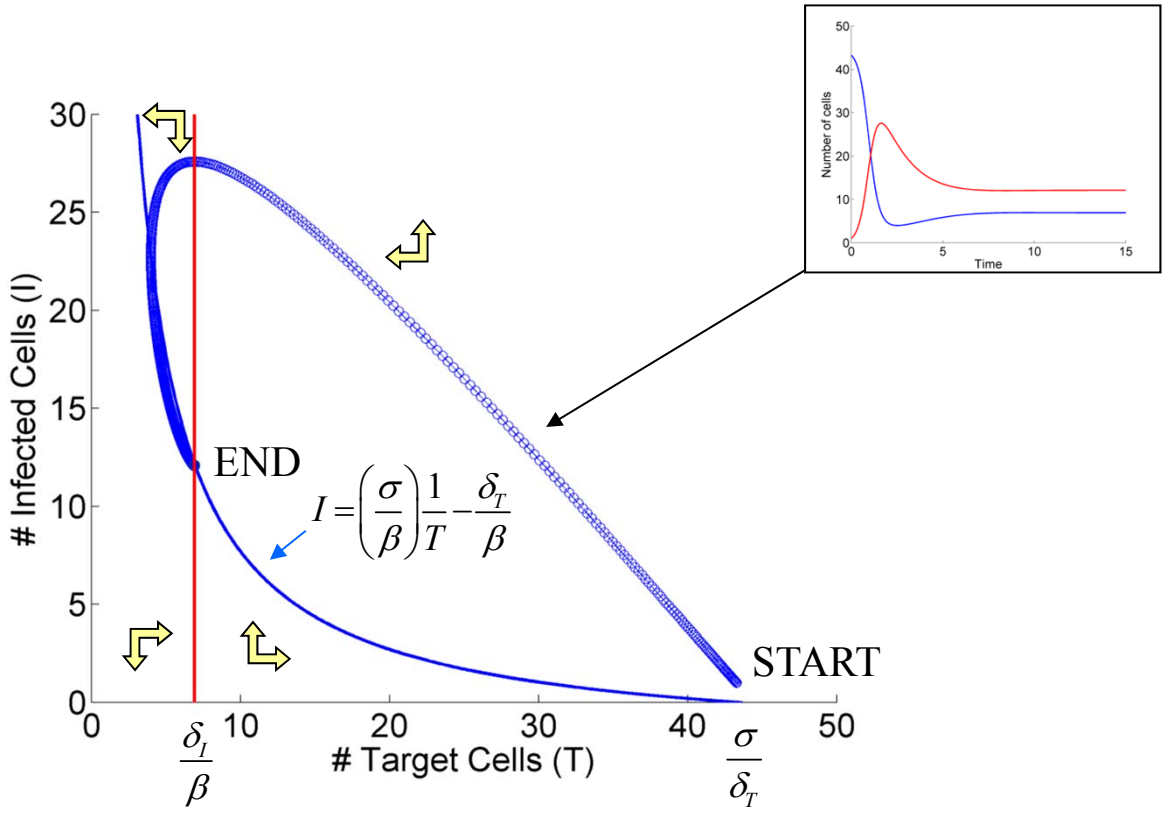
Other approaches are needed to account for spatial structure

Phase Plane Analysis

Nullclines plot where derivatives are zero (cross at steady-state)

Target $\frac{dT}{dt} = \sigma - \delta_T T - \beta T I$

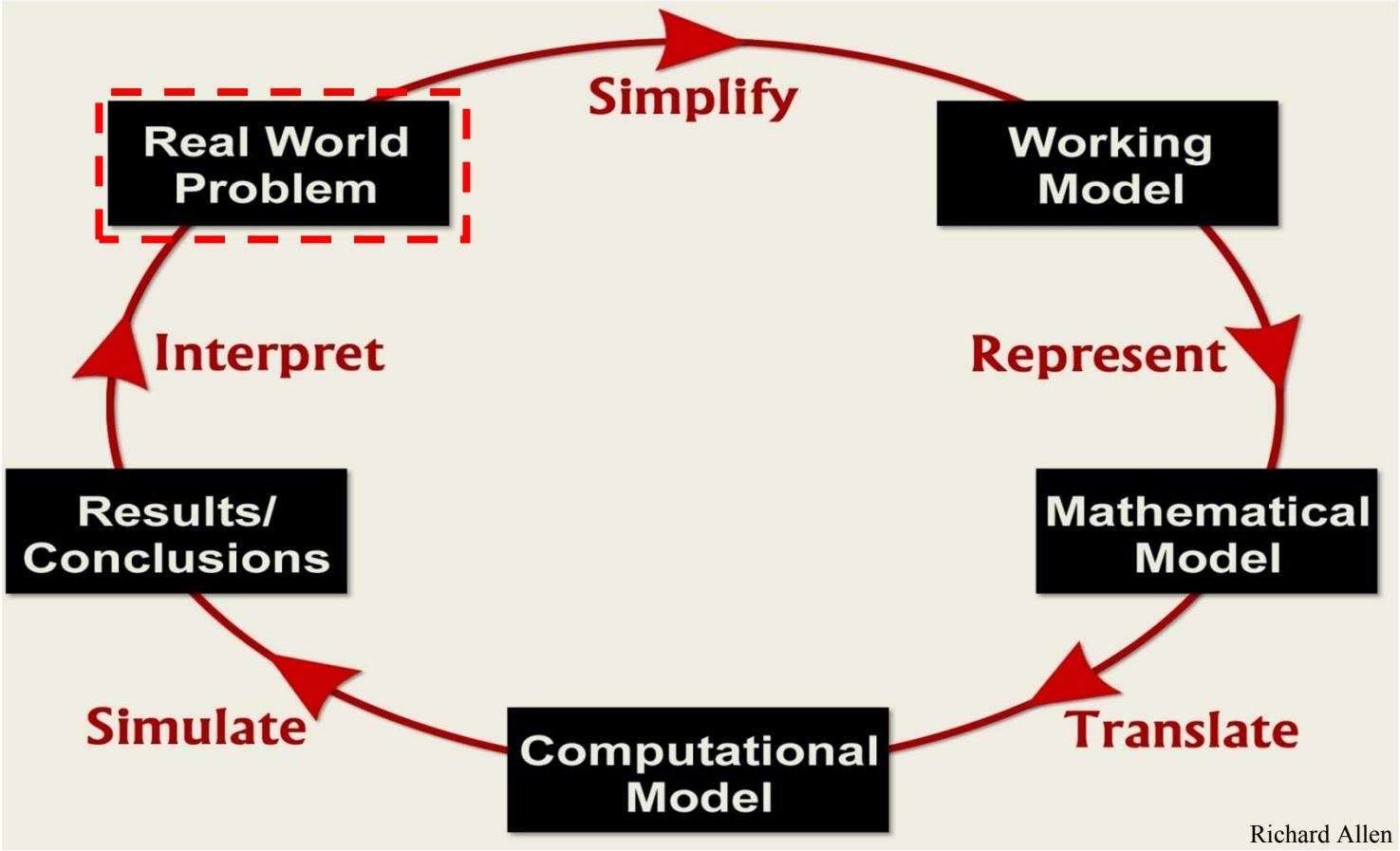
Infected $\frac{dI}{dt} = \beta T I - \delta_I I$



Phase portraits plot typical trajectories in the state space

The Modeling Process

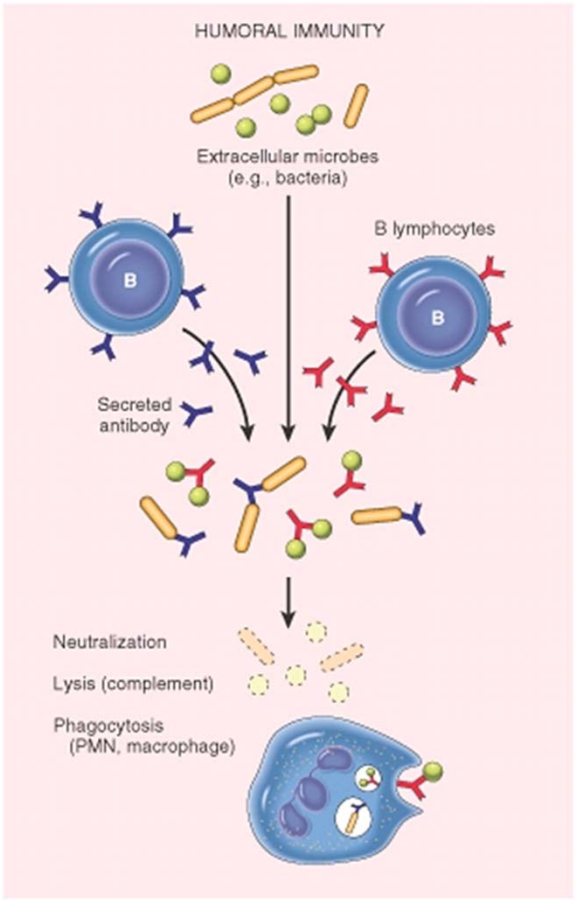
Starts with a specific scientific question



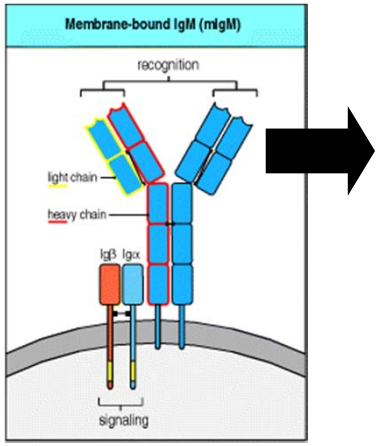
Model should produce predictions that suggest new experiments

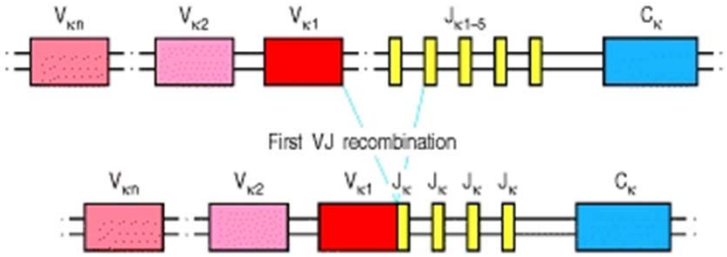
B cells "recognize" antigens thorough antibody receptor

First phase of diversification occurs in bone marrow while cell is maturing



Rearrangement generates diverse receptors:





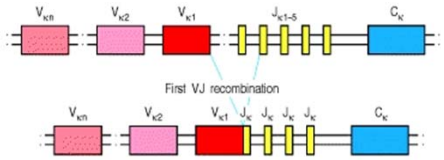
Number of functional gene segments in human immunoglobulin loci

Segment	Light chains		Heavy chain
	κ	λ	H
Variable (V)	40	30	65
Diversity (D)	0	0	27
Joining (J)	5	4	6

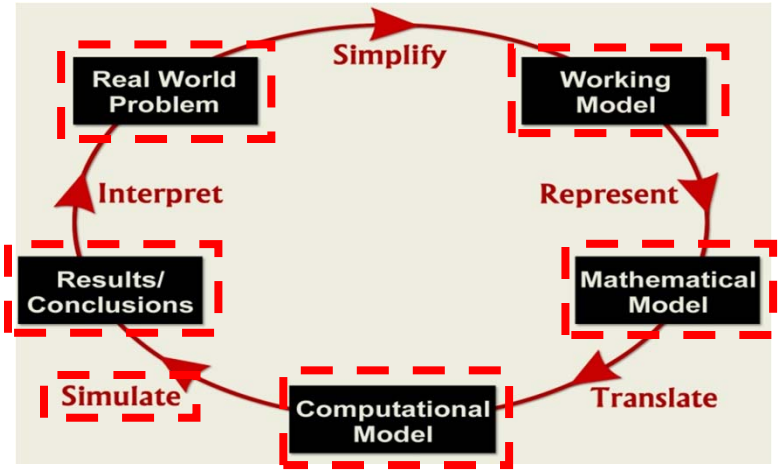
Second phase of diversification (by somatic hypermutation) follows activation

The Modeling Process: V(D)J Recombination

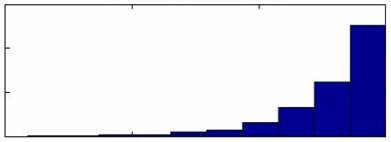
How are VJ segments chosen to generate an Ig light chain?



Hypothesis: VJ chosen randomly with equal probability

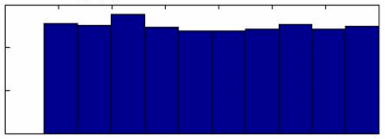


Observed V usage



?

Predicted V usage



$Pr[V_n] = 1/N$; $P[J_m] = 1/M$

randInteger(N) = floor(N * rand()) + 1

Model should produce predictions that suggest new experiments

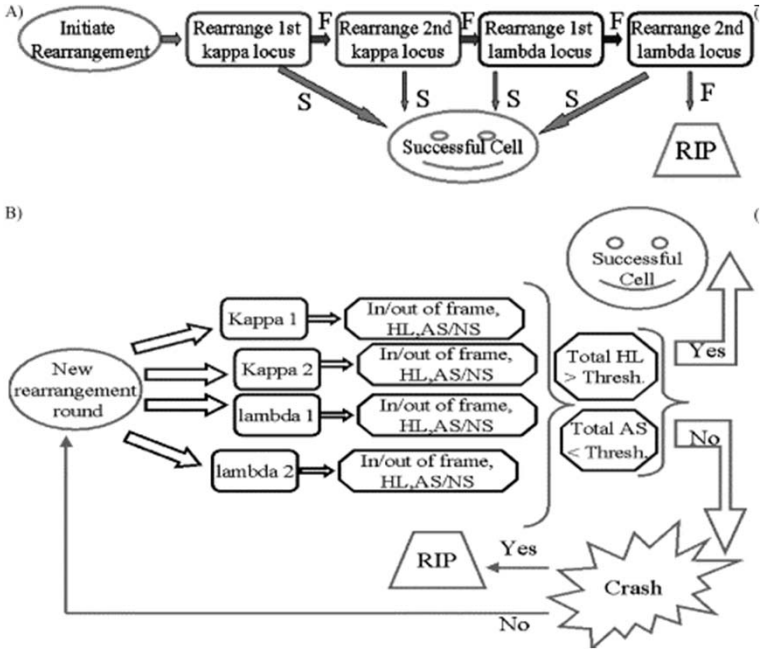
The Modeling Process: V(D)J Recombination

Extend rearrangement model to cover different alleles

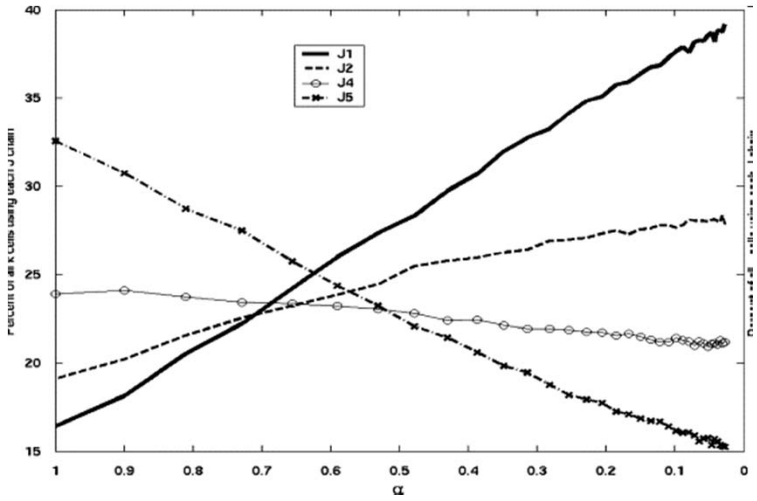
seminars in **IMMUNOLOGY**, Vol. 14, 2002: pp. 169–190
doi:10.1016/S1044–5323(02)00041-6, available online at http://www.idealibrary.com on IDEAL®

Analysis of B cell receptor production and rearrangement Part I. Light chain rearrangement☆

Yoram Louzoun[a,*], *Tzivia Friedman*[a], *Eline Luning Prak*[b], *Sam Litwin*[c] *and Martin Weigert*[a]



A probabilistic model of allelic exclusion fails to explain the status of receptor genes and the receptor phenotype of most B cells… we have revived the purely probabilistic approach in a model that now includes receptor editing and allows for some multi-receptor B cells. **We find that this model can explain the observed properties of B cells when the frequency of self-reactive B cells is high…**



Alpha reflects degree of sequentiality for Jκ rearrrangement.

Revised model of rearrangement suggest new experiments

Things to ask before any modeling study

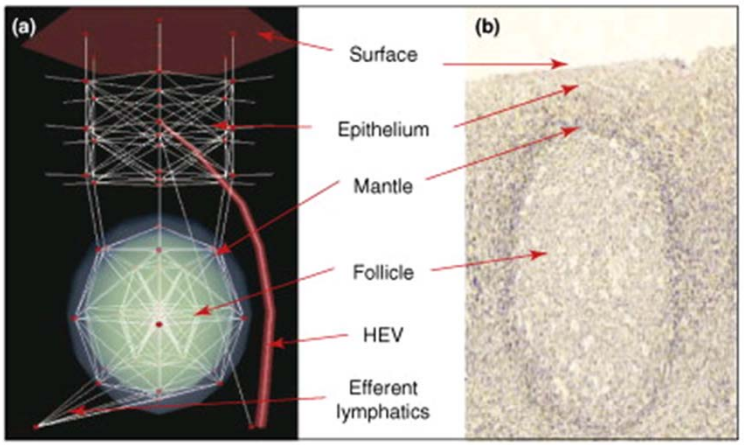
Frank Tobin (2009): Modeling is Powerful BUT Has Far to Go

Bio·IT World.com

1. Why do you want to do modeling?
2. How will you know if you succeed?
3. What will you do with the model once you have it? For what decisions will it be used or what confirmatory experiments will get performed?

Beware motivation: “We want to create a model of process X…”

Forward Modeling



(Thorley-Lawson et al, 2008)

- Detailed mathematical model designed to incorporate a desired level of anatomic or physiologic features
  - Can have arbitrary complexity as desired
  - Parameter values often obtained from published literature
  - Ex: tissue structure formation, cell signaling networks
- Used for simulating realistic experimental data under precisely defined conditions to test hypotheses *in silico*
- Can help design better experiments and reduce animal use
- Generally too complicated for fitting to experimental data

Allows generation of synthetic data sets with prescribed noise characteristics (Monte Carlo simulation) for evaluating parameters obtained by inverse modeling

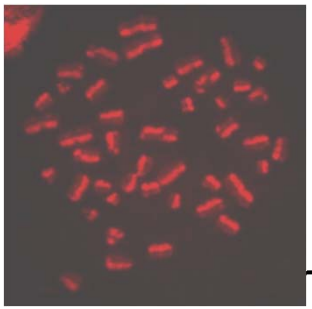
Inverse Model

- A mathematical model designed to fit experimental data so as to explicitly quantify physical or physiological parameters of interest
- Values of model elements are obtained using parameter estimation techniques aimed at providing a “best fit” to the data
- Generally involves an iterative process to minimize the average difference between the model and the data
- Evaluating the quality of an inverse model involves a combination of established mathematical techniques as well as intuition and creative insight

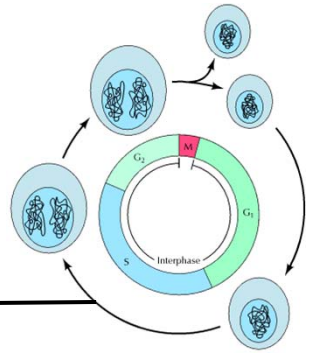
Understanding cell proliferation and death

BrdU (thymidine analog) incorporated into cell DNA during S-phase

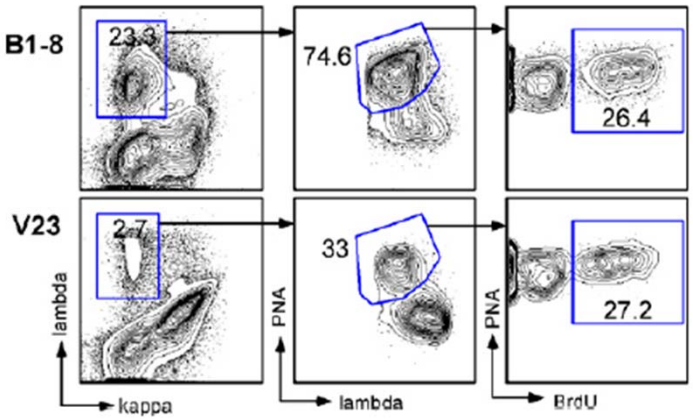
Flow cytometry to quantify antigen-specific germinal center B cells…

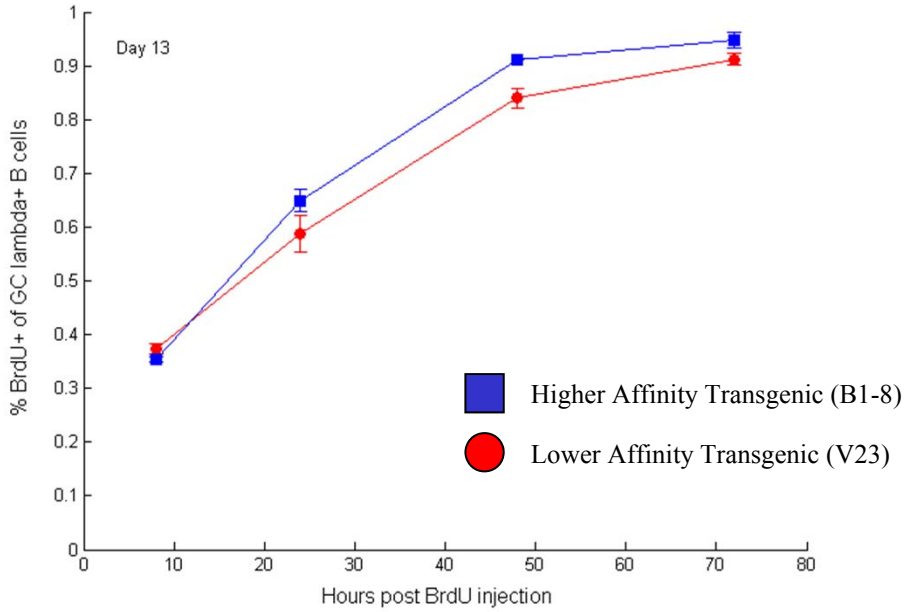


BrdU incorporated during S phase



science.csustan.edu/confocal/Images/SCE/index.SCE.htm





Labeling curves look similar – suggests same proliferation rate?

Understanding cell proliferation and death

At steady-state, rate at which the fraction of BrdU labeled cells increases is indicative of the sum of the per cell proliferation and death rates

Quantification of Cell Turnover Kinetics Using 5-Bromo-2′-deoxyuridine[1]

Sebastian Bonhoeffer,* Hiroshi Mohri,† David Ho,† and Alan S. Perelson[2*‡]

The Journal of Immunology, 2000, 164: 5049–5054.

Rapid Turnover of T Lymphocytes in SIV-Infected Rhesus Macaques

Hiroshi Mohri, Sebastian Bonhoeffer, Simon Monard, Alan S. Perelson, David D. Ho*

www.sciencemag.org • SCIENCE • VOL. 279 • 20 FEBRUARY 1998

International Immunology, Vol. 15, No. 3, pp. 301–312
doi:10.1093/intimm/dxg025, available online at www.intimm.oupjournals.org

Asynchronous differentiation models explain bone marrow labeling kinetics and predict reflux between the pre- and immature B cell pools

Ramit Mehr[1], Gitit Shahaf[1], Alex Sah[2] and Michael Cancro[2]

The Journal of Immunology

Taking Advantage: High-Affinity B Cells in the Germinal Center Have Lower Death Rates, but Similar Rates of Division, Compared to Low-Affinity Cells[1]

Shannon M. Anderson,* Ashraf Khalil,† Mohamed Uduman,‡§ Uri Hershberg,*†§ Yoram Louzoun,¶ Ann M. Haberman,† Steven H. Kleinstein,‡§ and Mark J. Shlomchik[2*†]

Oncogene (2005) 24, 7514–7523
 0950-9232/05 $30.00
www.nature.com/onc

Reduced cell turnover in lymphocytic monkeys infected by human T-lymphotropic virus type 1

Christophe Debacq[1,5], Jean-Michel Héraud[2,5], Becca Asquith[3], Charles Bangham[3], Fabrice Merien[2], Vincent Moules[4], Franck Mortreux[4], Eric Wattel[4], Arsène Burny[1], Richard Kettmann[1], Mirdad Kazanji[2] and Luc Willems*[,1]

Models of BrdU incorporation integral part of many studies

BrdU labeling of CD4+ and CD8+ T lymphocytes

SIV-infected and an uninfected macaque. Data are from Mohri et al., Science (1998)

Rapid Turnover of T Lymphocytes in SIV-Infected Rhesus Macaques

Hiroshi Mohri, Sebastian Bonhoeffer, Simon Monard, Alan S. Perelson, David D. Ho*

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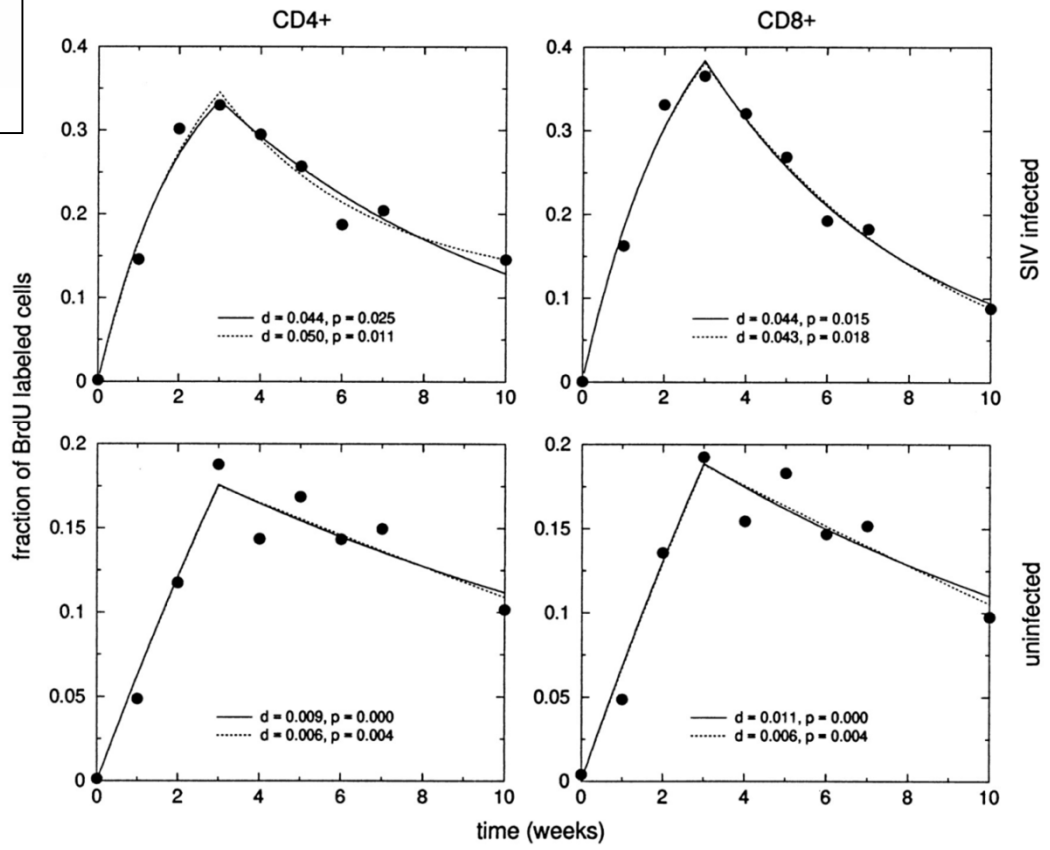
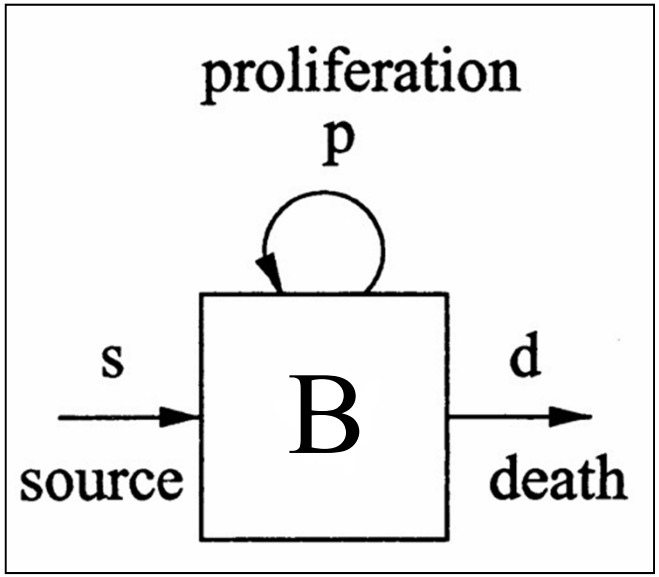


Is there a difference in cell turnover?

Model of BrdU Labeling

Start with a basic model of cell population dynamics…



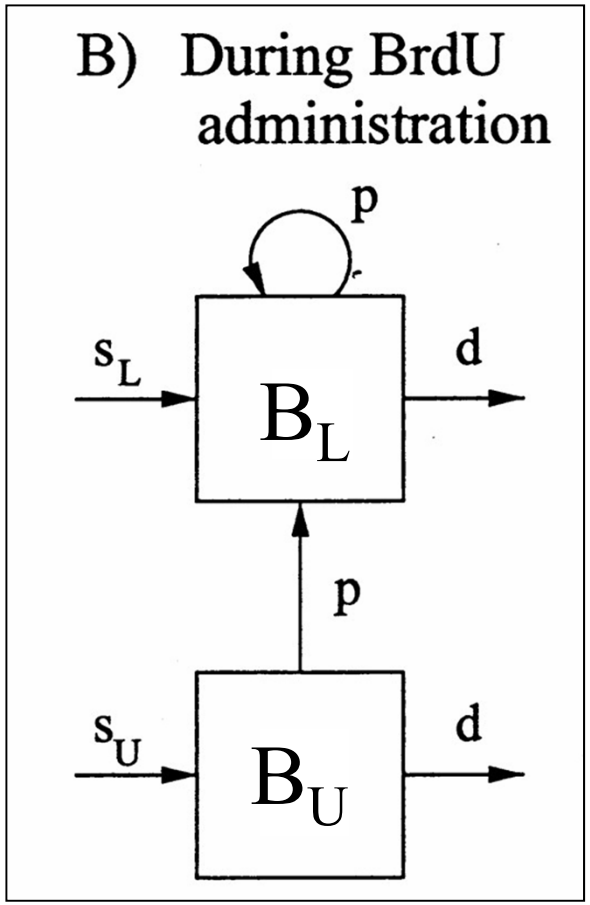
Rate of change in B cell population

$$\frac{dB}{dt} = s + pB - dB$$

Often can often assume population in steady-state (i.e., constant)

Model of BrdU Labeling

Split the B cell population into Labeled (B_L) and Unlabeled (B_U) subsets



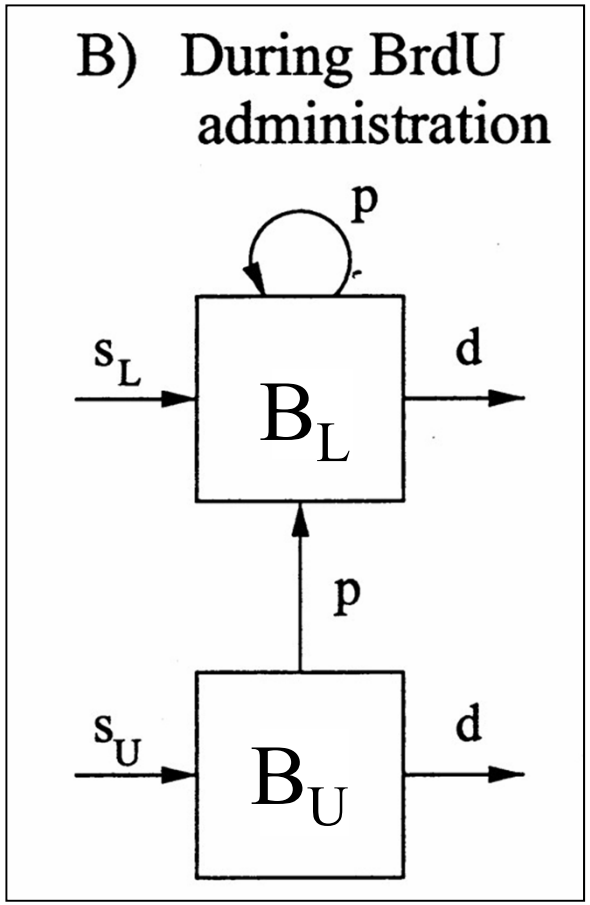
$$\frac{dB_U}{dt} = s_u - pB_U + dB_U$$

$$\frac{dB_L}{dt} = s_l + 2pB_U + pB_L - dB_L$$

Do data contain enough information to estimate parameters?

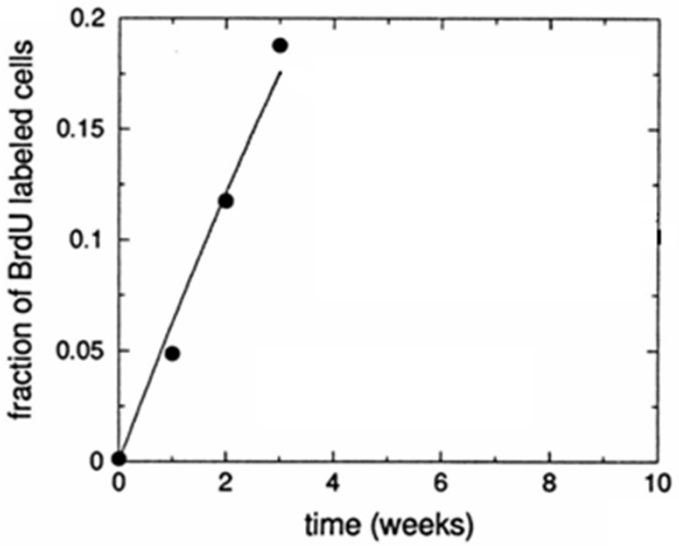
Model of BrdU Labeling

Label is administered continuously over some time-period



$$f_L(t) = A_1(1 - e^{-(d+p)t})$$

$$A_1 = 1 - \frac{s_U}{(s_U + s_L)} \times \frac{(d-p)}{(d+p)}$$



Labeling curve reflects both proliferation AND death

Model Identifiability

A model is identifiable if possible to learn true value of underlying parameter after obtaining enough observations

Identifiable parameters are those which effect the value of the data and can be estimated with some degree of certainty.

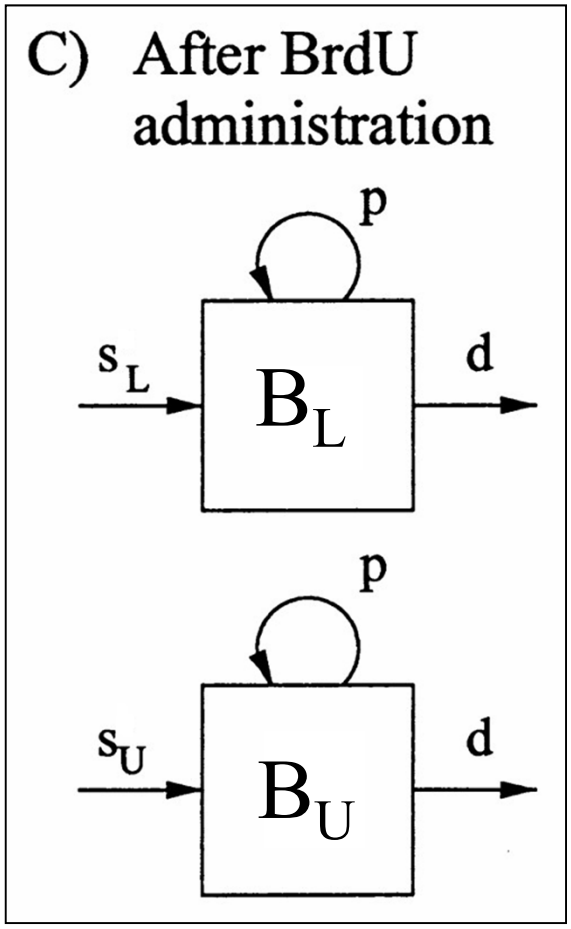
Non-identifiable parameters are those which effect the value of the data but which cannot be estimated accurately

Non-observable parameters are those which don't have an effect on the data.

Cannot estimate both proliferation AND death

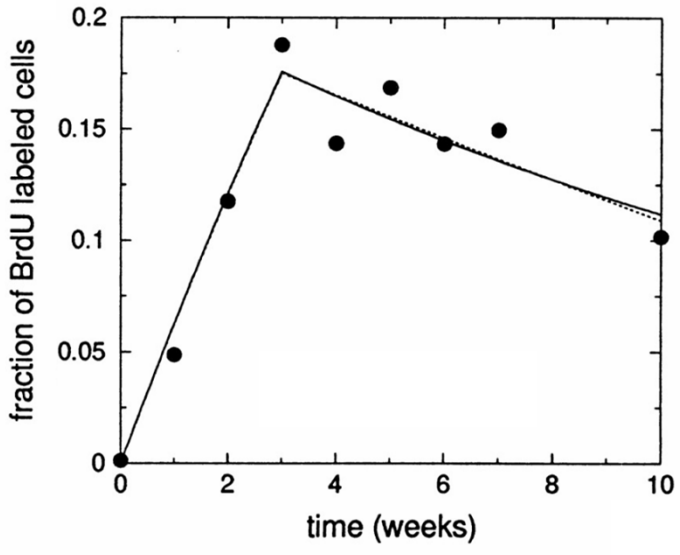
Model of BrdU DE-Labeling

Stop administering label after some time (t_e)



$$f_L(t) = A_2 + A_3 e^{-(d-p)(t-t_e)})$$

$$A_2 = \frac{s_L}{(s_U + s_L)}, A_3 = f_L(t_e) - A_2$$



Now, we can estimate BOTH proliferation AND death

Inverse Model

- A mathematical model designed to fit experimental data so as to explicitly quantify physical or physiological parameters of interest
- Values of model elements are obtained using parameter estimation techniques aimed at providing a “best fit” to the data
- Generally involves an iterative process to minimize the average difference between the model and the data
- Evaluating the quality of an inverse model involves a combination of established mathematical techniques as well as intuition and creative insight

Characteristics of a Good Inverse Model

- Fit is good—model should be able to adequately describe a relatively noise-free data set (of course a poor fit provides some insight also)
- Model parameters are unique
  - Theoretically identifiable for noise-free data
  - Well-determined model parameters in presence of measurement noise
- Values of parameter estimates are consistent with hypothesized physical or physiologic meanings and change appropriately in response to alterations in the actual system