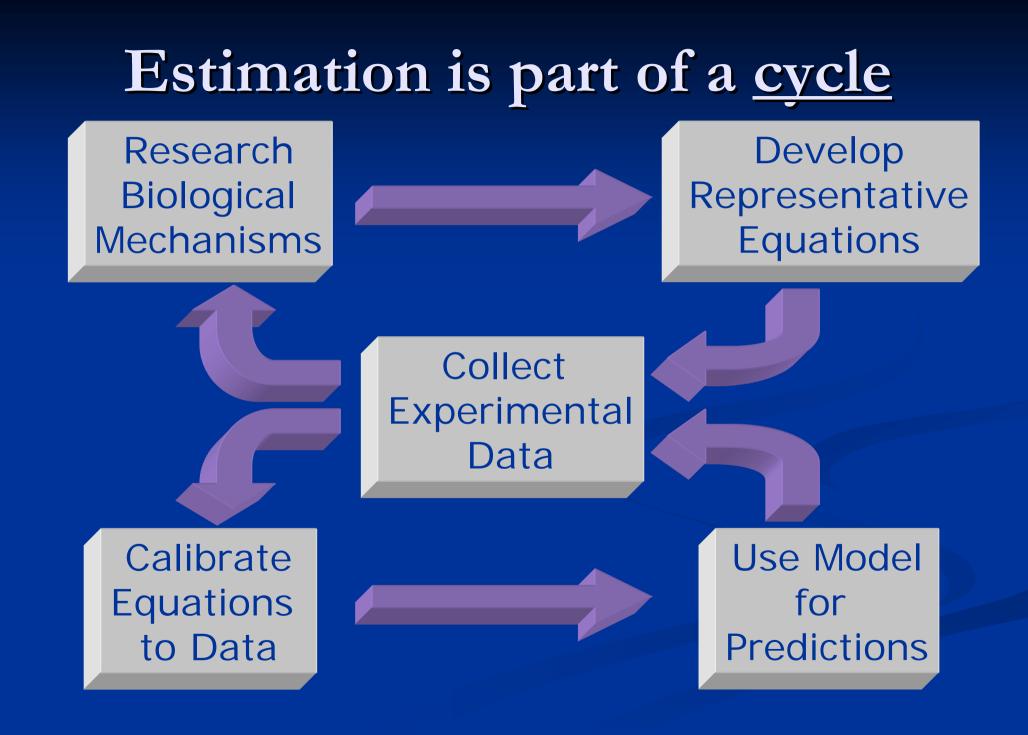
Methods for Inverse Problems In Biology

John Bartels, Immunetrics, Inc.

Problem statement

- Modelers create rules or equations to capture essential biological interactions
 - ODE example: P' = gP * P dP * P * K
- Often employ free parameters for tuning model behavior
- Unknown for many reasons:
 - Unmeasurable, nonphysical, individual variation, etc.
- Inverse problem: given data, find the "right" parameters
- Goals: choose parameter values such that
 - "Fitting is not enough!"
 - We reproduce experimental data well
 - Values are justifiable
 - We understand the error in our estimates



Inputs For Estimation Process

Identify parameters to estimate
 Obtain bounds & initial estimates if possible!

Data

Empirical data (clinic / lab / literature)
e.g. time series for all scenarios of interest
Qualitative heuristics (literature, expert intuition)
e.g. system constraints, parameter constraints
Separate into Training & Validation sets
Don't cheat with validation sets!

Define "best" parameters!

Intuition: choose parameter θ value to maximize "likelihood":
 Probability of predicting data given these parameters

Bayesian statistics gives us formalism

- Need two probabilities
 - "Probability of data" given some parameters
 - Natural for stochastic model
 - Deterministic (e.g. ODE) models add noise
 - Probability of a parameter value
 - Based on a priori knowledge what's biologically plausible?
 - Often no info assume some distribution!

Maximum Likelihood Principle

Likelihood of parameter values given by Bayes' Theorem:

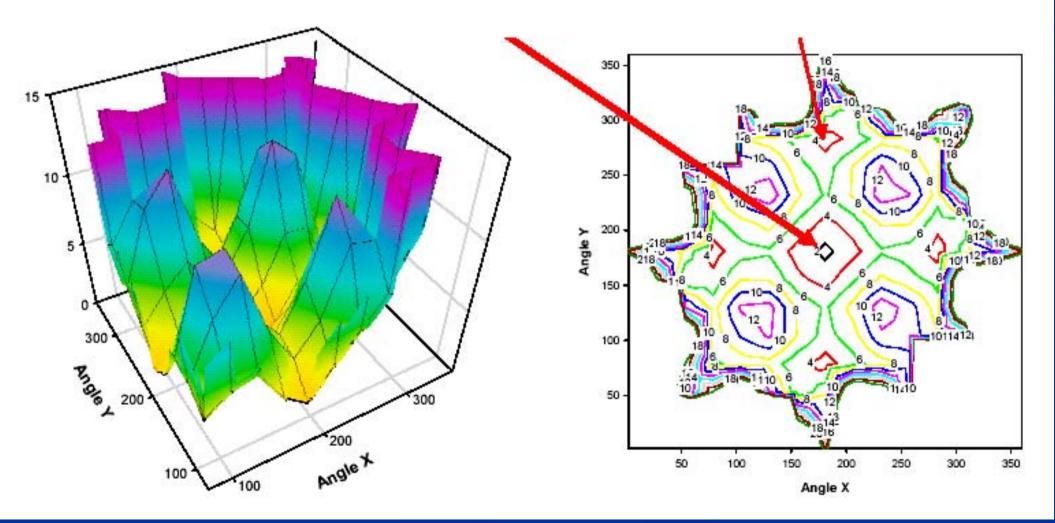
 $P(params \mid data) = \frac{P(data \mid params)P(params)}{P(data)}$

Concrete example - estimate parameter θ from some data:

 $P(\theta == 1.8 | data) = \frac{P(map(1) = 100, map(2) = 95, ... | \theta = 1.8)P(\theta == 1.8)}{P(map(1) == 100, map(2) = 95, ...)}$

- Gives basis for practical methods:
 - Least-squares fitting
 - Monte Carlo (e.g. Markov Chain, etc.)
 - Kalman Filters

Visualizing likelihoods



How hard can it be?

- Nonlinear interactions: easy for linear problems
- High Dimensionality (10's to 1000's)
- Rough Fitness Landscape
 - many comparable "high scoring" solutions
- Large spread in data
- Sparseness of data
 - Many unmeasured system variables!
 - Limited time-points
- Must generalize beyond training scenarios
- Beware of <u>overfitting</u>!

Approach I: Least Squares Fits

If errors in data follow normal dist with mean=0, minimize:

$$Err(\theta) = \sum_{s} \sum_{v} \sum_{t} (obs(s,v,t) - pred(\theta,s,v,t))^{2}$$

Advantages:

- Optimal under *somewhat* realistic assumptions
- Intuitive, symmetric, cheap, differentiable
- Chi-square term for measurement error
- Confidence interval formulas

• How to find the values of θ that minimize the error?

Numerical Optimization For Least Squares

Exhaustive search (simple, slow/intractable)

- Linear programming (only for linear problems)
- Dynamic programming (only for decomposable problems)
- Gradient searches: potential candidate!
 - Recall: derivative ==0 at minimum of a function
 - Gradient of scoring function is direction of steepest change follow it!
 - Problems: Step size choice! Gets stuck!

Common Search Algorithms

Gradient methods (local search)

- Levenberg-Marquardt, Gauss-Newton, etc.
 Hillclimbing
- Stochastic Gradient-like methods (global)
 Simulated Annealing
 Evolutionary / Genetic Algorithms

Simplex methods (e.g. Nelder-Mead)

Practical concerns

Guide the optimizer:

- Exploit domain knowledge: symmetry, conservation, physical limits, etc.
- Weight Important features of curves, etc.

Beware of:

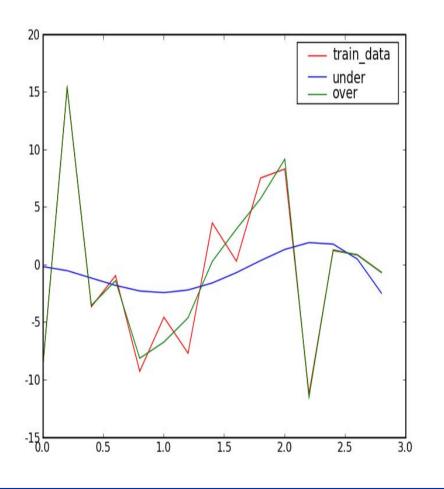
- Non-physical solutions
- Data on vastly different scales
- Effects of noisy data
- Biased training sets

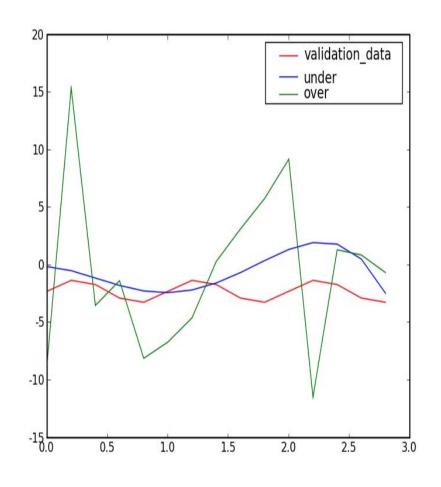
Dangers: Overfitting

Problem:

- Model trains "too well"
- Poor generalization to prediction sets
- Causes: Too many parameters, too little data!
 - Model memorizes noise in input
- Worse fit is sometimes better?

Overfitting Example





Dangers: Identifiability

Question: how reliably can we estimate the parameters?

- Three classes: Unique / Non-unique / Non-identifiable
 - Estimates of non-identifiable parameters are meaningless!
- Consider:
 - $A'(x) = \theta_1 B \theta_2 B = B(\theta_1 \theta_2)$
 - $A'(x) = \theta_1 B \theta_2 C$
- **Complicated by:**
 - Scarce / noisy data
 - Biology's full of feedback loops & compensation

Quantified by: PCA / SVD, correlation matrices

Approach II: Back to Bayes

Best point estimate for 1 parameter is the average value: $\theta^* = \int \theta P(\theta | data) \partial \theta$ min

• For n > 1, same idea: mean of multi-dim function: $\theta_i^* = \int \theta_i P(\theta_i \mid data \,) \partial \theta_i \quad \text{where}$ $P(\theta_i \mid data) = \int \int \int \dots \int P(\theta \mid data) \partial \theta_1, \dots, \partial \theta_{i-1}, \partial \theta_{i+1}, \dots, \partial \theta_n$ $\min_1 \min_2 \min_n$

Two big problems to solve

Bayes: we can get $P(\theta | data)$ if we know $P(data | \theta)$

- Stochastic model: repeat runs
- Deterministic model: add noise to data
 - Know your error sources!
- Priors for parameter values!

Multi-dimensional integrals are hugely expensive!

- Solution: throw a lot of darts to approximate it
- Intuitive method: rejection sampling
- Better, fancier methods based on these ideas
 - Terms: Gibbs Sampling, Markov Chain Monte Carlo, VEGAS

Least-Squares vs. Monte Carlo

Least Squares

- Classic, widely used, lots of libraries
- Assumes normal-dist, independent errors!
- (Rough) Confidence intervals available
- Often faster, good enough
- Monte Carlo
 - Relatively new, fewer libraries
 - Immune to badly distributed error in data
 - Sensitive to assumed priors
 - Still computationally expensive
 - Probably the way of the future (eventually)

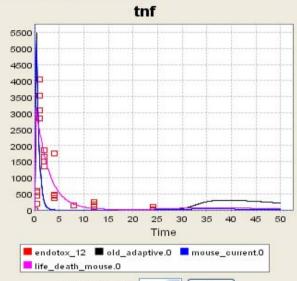
Real world examples

Apply these algorithms to existing model

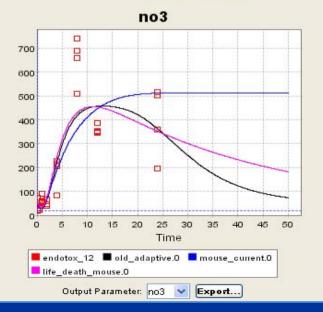
- Training Data: only 4 measured curves curves
- Can we fit the training data well (over all scenarios)?
- Try multiple fits: do they find similar results?
- What about the unmeasured variables?

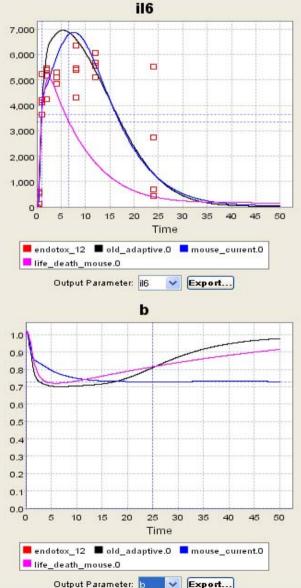
4 Equation / 5 Scenario Fits

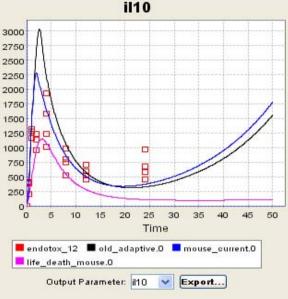
Summunetrics ModelTool

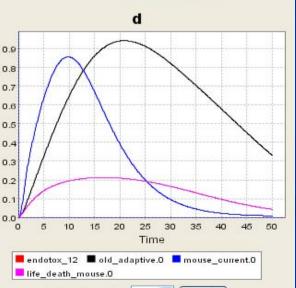










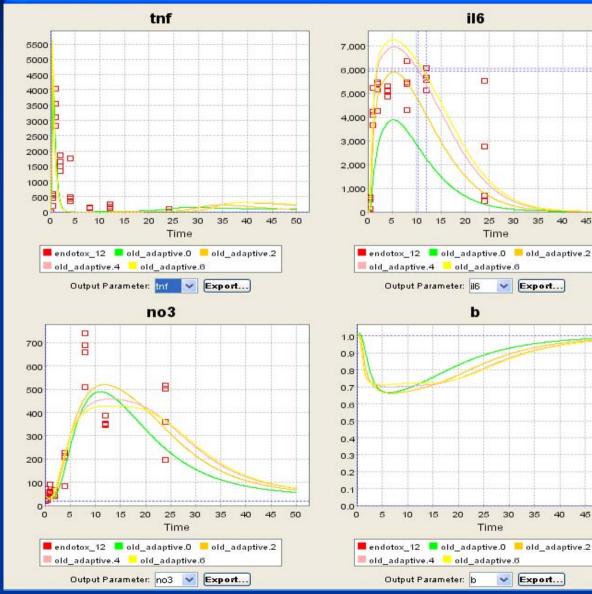


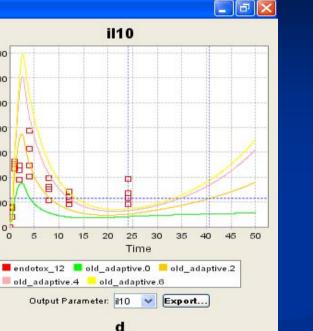


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Without Heuristics: Violates Biology

Immunetrics ModelTool







Results

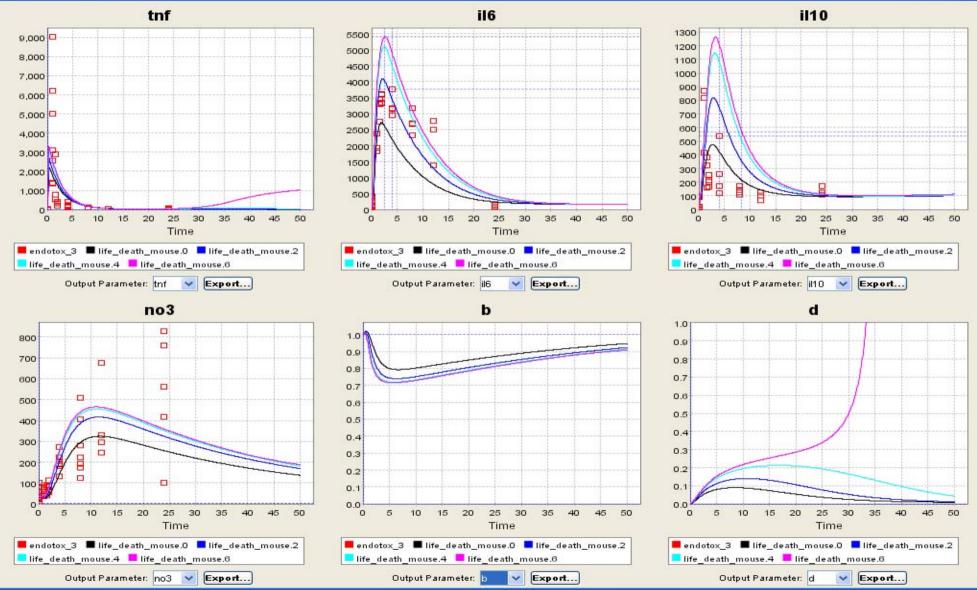
Multiple models that fit, but too under-constrained!

- Models show different behavior on untrained data
- Identifiability: similar fits but
 - Different mechanisms used
 - Very different parameter values
- Assessing models:
 - Biological intuition for simple cases?
 - Without intuition: when is the model right?
 - Good fits for the wrong reasons

Heuristic Fit: Enforces Qualitative Rules

Immunetrics ModelTool

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Fitting Underconstrained Models

- Assess model identifiability
- Consider Model Clouds
- Model & experiment design must influence each other!
- Simplification:
 - Reduce to simplest justifiable model (PCA)
- Knowledge of the model:
 - Imit parameters (and ranges) to search
 - Optimization algorithms with greater awareness of the model's structure
 - Biological heuristics as further constraints

Some References

- Books / Papers:
 - Overview: Schittkowski
 - MC: Tarantola, Geman & Geman,
 - Identifiability: Jaquez
 - Genetic Algorithms: M. Mitchell; D. Goldberg
 - Simulated Annealing: Kirkpatrick
 - General numerics, simple optimization: Numerical Recipes: Press, et al.

Software:

- Matlab (plus add-ons; LS, MC)
- DAKOTA (LS)
- BUGS (MC)
- GNU Scientific Library (LS)
- Lots of open-source (and commercial) code
- Write your own?