Estimating demographic parameters from samples of unmarked individuals

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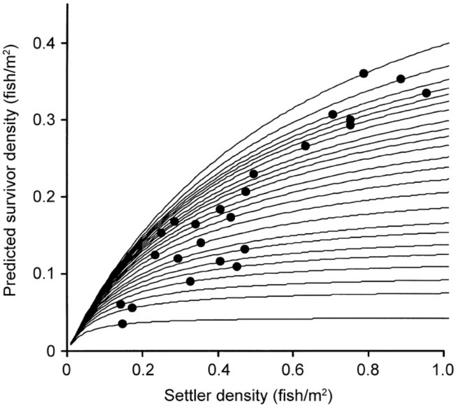
Outline

Cryptic density-dependence



(Wilson & Osenberg 2002, Shima & Osenberg 2003)

- Environmental variation
- + correlated variation in density ...
- = **cryptic density-dependence**
- best possible estimates of demographic parameters?

Data

- Repeated samples of individual animals
- . . . Multiple times, observers, locations
- Presence and size (imperfect)
- Estimate demographic parameters:
  - birth/immigration
  - death/emigration
  - change (growth)
- . . . as a function of size, (population density)

Data

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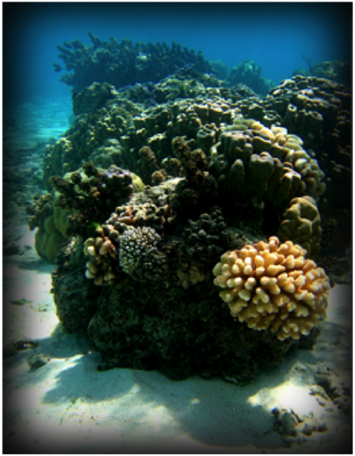
Natural history

photo: Leonard Low, Flickr via `species.wikimedia.org`

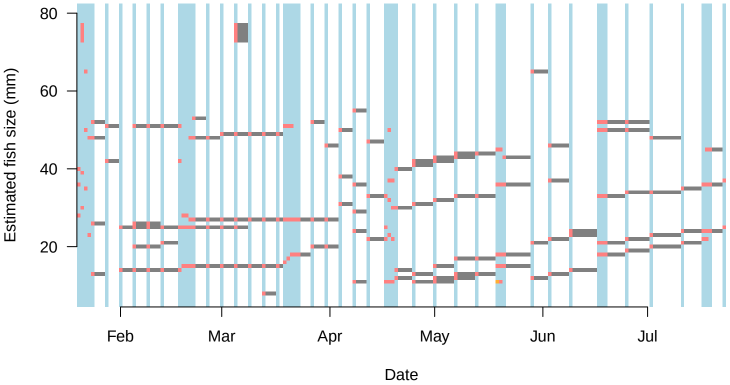
- **Thalassoma hardwicke** (sixbar wrasse)
- **Settlement**: $\approx$ 5–10 mm
- **Growth**: a few mm per month
- **Death**: by predator (competition for refuges)
- **Immigration/emigration**: rare below 40–50 mm

Where they live



Patch reefs, French Polynesia (and throughout the south Pacific)

What they look like to me



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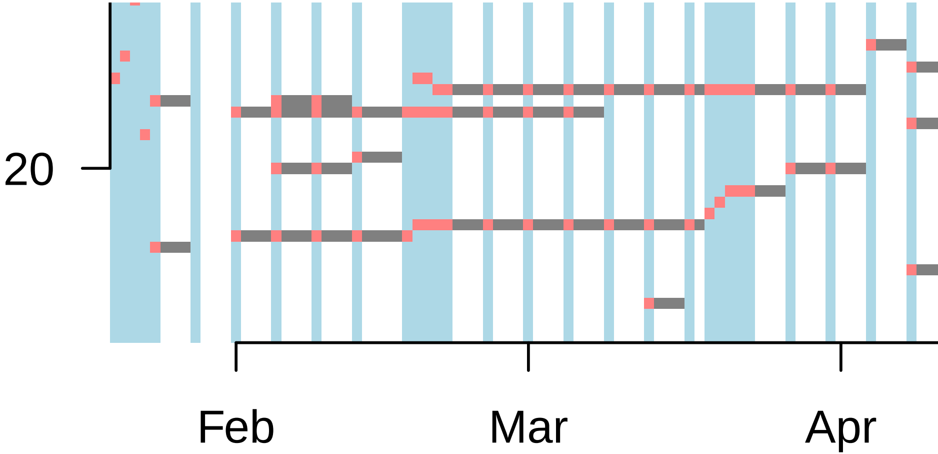

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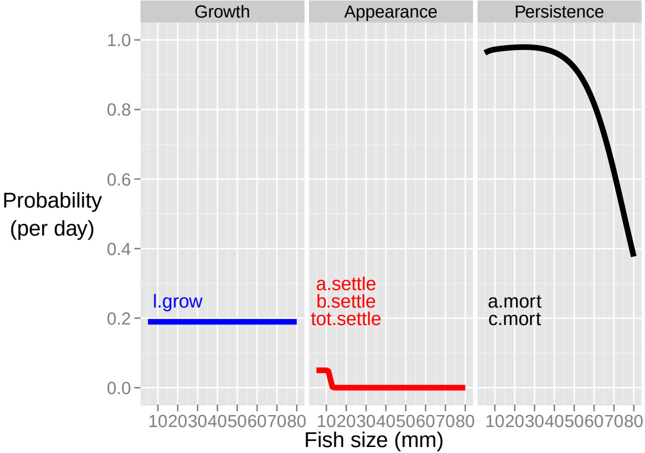
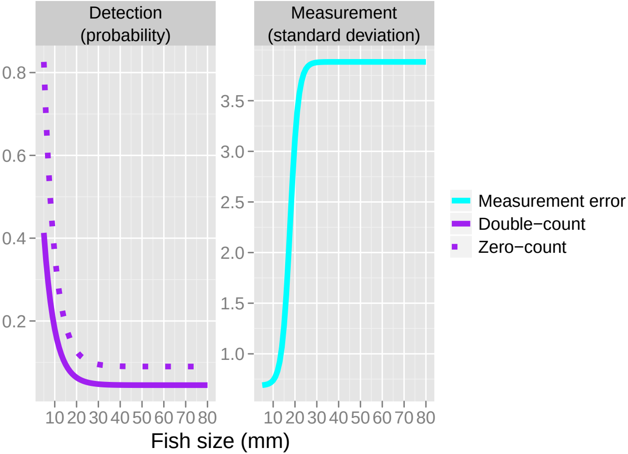
Demographic parameters as f(size)



Observation model

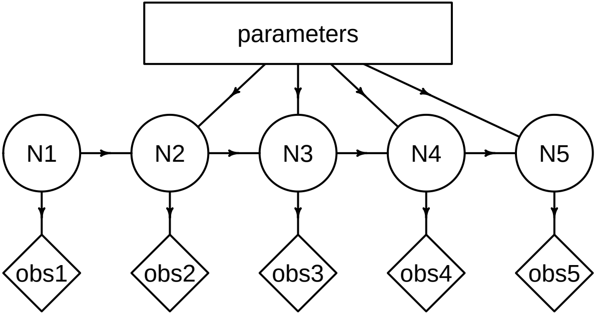


Outline

State-space models

- **Problem**: estimating parameters of systems with un- or imperfectly-observed states?
- Easy if no feedback (measurement error models)
- With feedback (dynamic models), brute force approaches become infeasible . . .

Directed acyclic graph (DAG)



Bayesian statistics, in 30 seconds

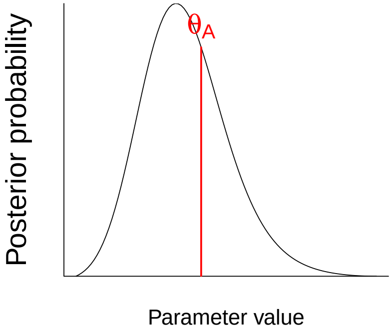
- **computational** (**convenience**) Bayesian statistics

  (forget all that stuff about philosophy of statistics, subjectivity, incorporating prior information ...)
- have a **likelihood**, $L(\boldsymbol{\theta}) = \text{Prob}(\text{data}|\boldsymbol{\theta})$
- want a **posterior probability**, $P_{\text{post}}(\boldsymbol{\theta}) = \text{Prob}(\boldsymbol{\theta}|\text{data})$
- Bayes' rule:

$$P_{\text{post}}(\boldsymbol{\theta}) = \frac{L(\boldsymbol{\theta}) \cdot \text{prior}(\boldsymbol{\theta})}{\iiint L(\boldsymbol{\theta}') \cdot \text{prior}(\boldsymbol{\theta}')\, d\boldsymbol{\theta}'}$$

- may want mean, mode, confidence intervals, ... denominator **very** high-dimensional

Markov chain Monte Carlo



MCMC rule:

$$\text{if } \frac{P(\theta_A)}{P(\theta_B)} = \frac{J(\theta_B \to \theta_A)}{J(\theta_A \to \theta_B)}$$

then stationary distribution = posterior probability (provided chain is irreducible etc.)

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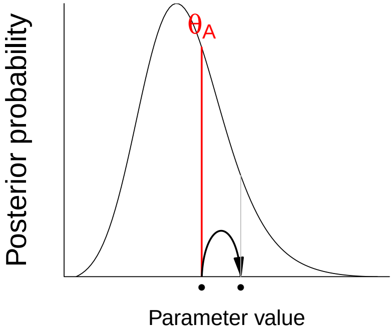

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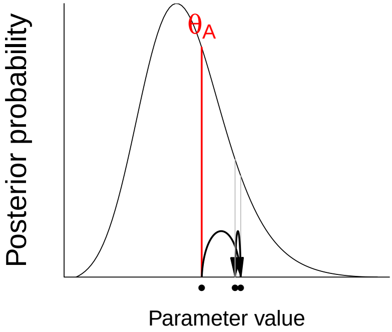

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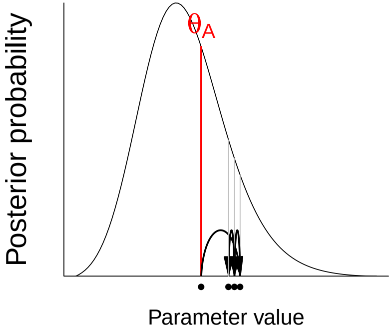

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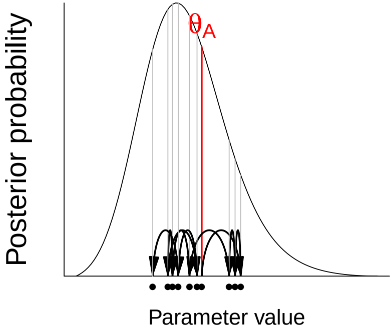

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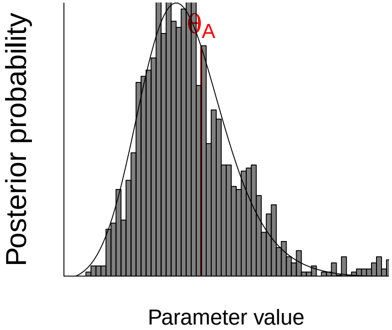

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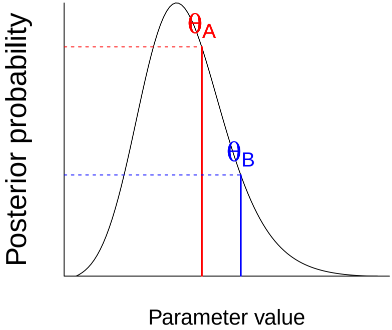

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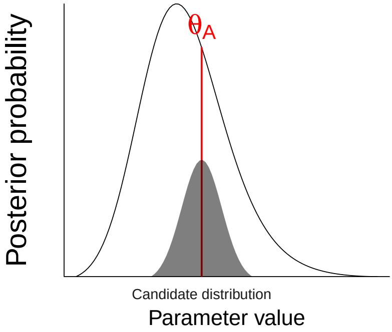
Metropolis-(Hastings) updating



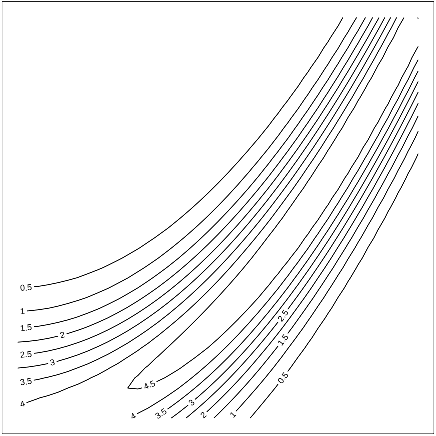
Metropolis rule:

accept B with probability

$$\min\left(1, \frac{P(\boldsymbol{\theta}_B)}{P(\boldsymbol{\theta}_A)}\right)$$

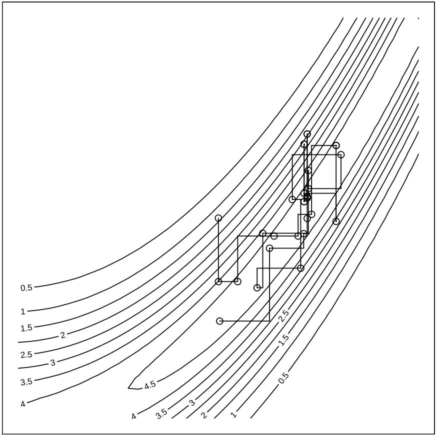
satisfies MCMC rule . . . Don't need to know denominator!

Gibbs sampling



- **Joint** distribution of parameters often difficult
- Condition each element on "known" (i.e. imputed) values of all other elements: $P(a, b, c) = P(a|b, c)P(b, c)$
- **Gibbs sampling**: do this repeatedly for each element, or block of elements

Gibbs sampling



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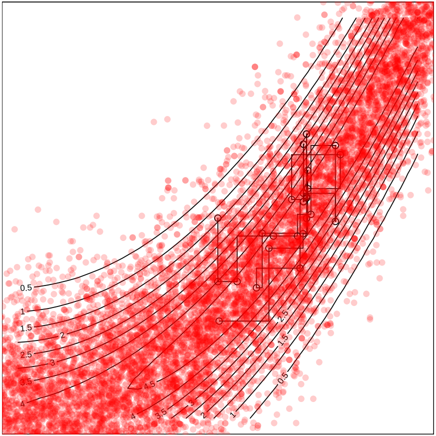

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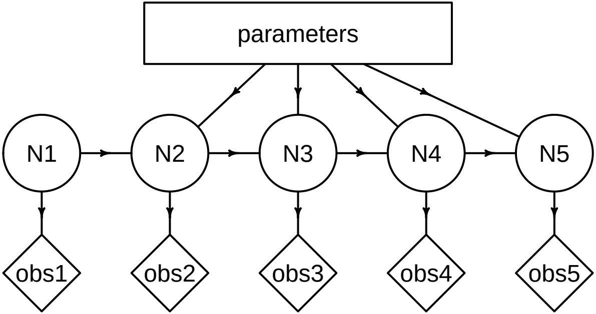
Back to the DAG



Outline

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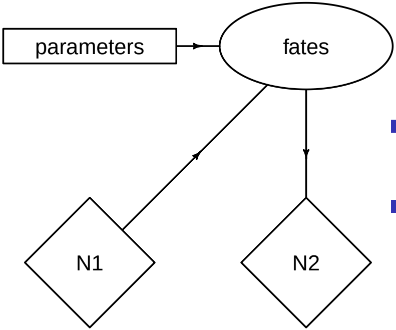
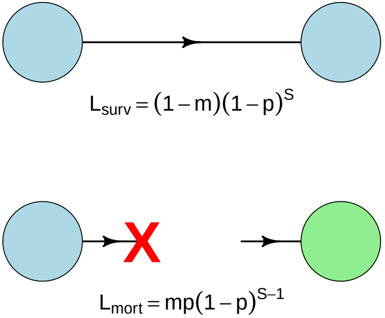
DAG



- Demographic parameters|fates: standard M-H
- Fates|parameters

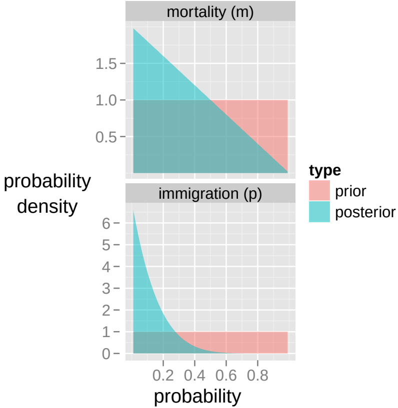
Scenario



One fish of the same size observed on two consecutive days . . .
was it the same individual?

$$P(\text{surv}|m,p) = \frac{(1-m)(1-p)}{1-m-p+2mp}$$

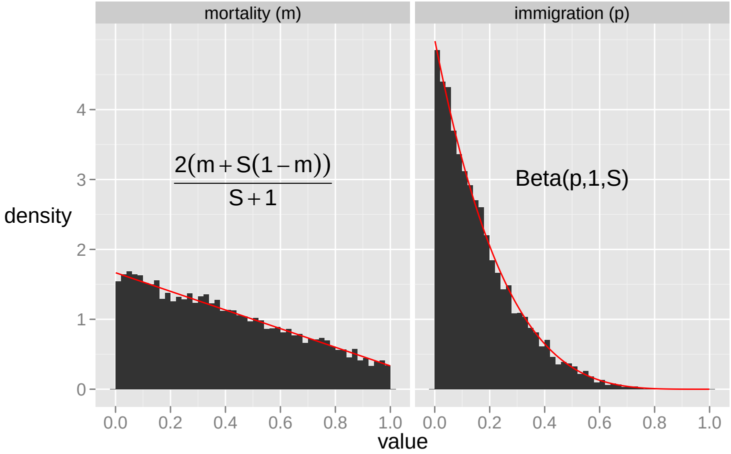
Updating probabilities for parameters



If the fish survived, then our posterior probabilities for the parameters are:

- $m \sim \text{Beta}(1, 2)$ (0 mortalities, 1 survival)
- $p \sim \text{Beta}(1, S + 1)$ (0 immigrations, S non-immigrations)

Trivial example: results



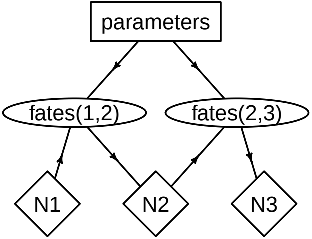
- $P(\text{mortality \& no immigration}) \approx 0.16 = 1/(S+1)$; $P(\text{survival \& immigration}) \approx 0.83 = S/(S+1)$;
- results are simple and make sense; closed form solution is possible but ugly ...
- combination of observations and **non-observation** of other individuals provides information (could fail with non-detection)

Outline

Non-trivial dynamics

- Multiple individuals, measured over multiple days
- Still simple: no density-dependent rates, immigration/emigration of large individuals
- **observations still error-free**

Parameter/fate sampling



- Parameter sampling: M-H updating with simple candidate distributions
- Fate sampling: ???
  - Enumerating possibilities is tedious

    . . .

M-H fate sampling

	6 mm	7 mm	dead
5 mm	$G(5) \cdot (1 - M(5))$	X	$M(5)$
6 mm	$(1 - G(6)) \cdot (1 - M(6))$	$G(6) \cdot (1 - M(6))$	$M(6)$
absent	$I(6)$	$I(7)$	X

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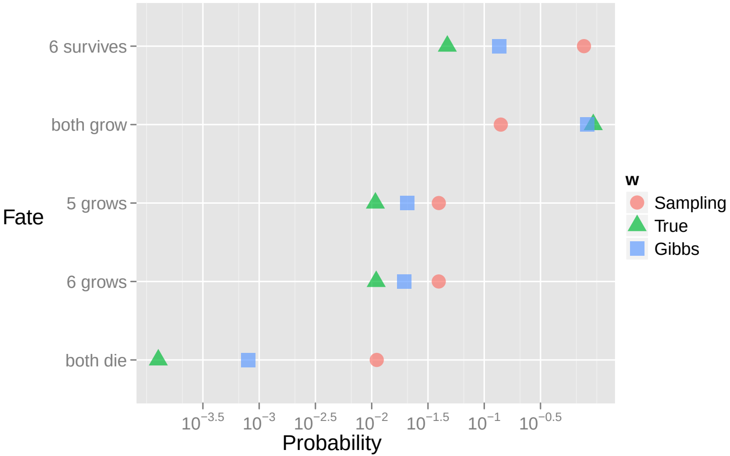
Sampling test



Testbed

- Simulate for 80 days, with a settlement rate (`tot.settle`) of 5% day:
- 29 distinct individuals, size range 5–30, total of 618 fish-days (observations).
- Sample fates only (1000 MCMC steps), fixed demographic parameters

Sampled 1000 unique fates (but only 895 unique likelihoods)

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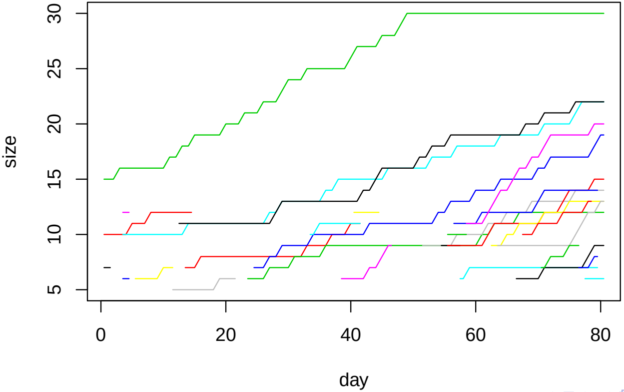
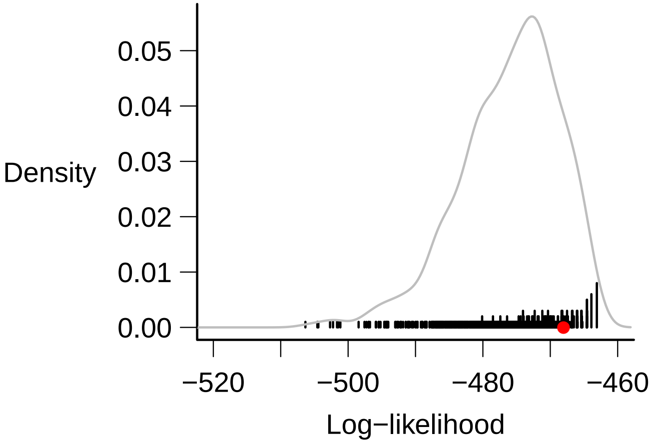
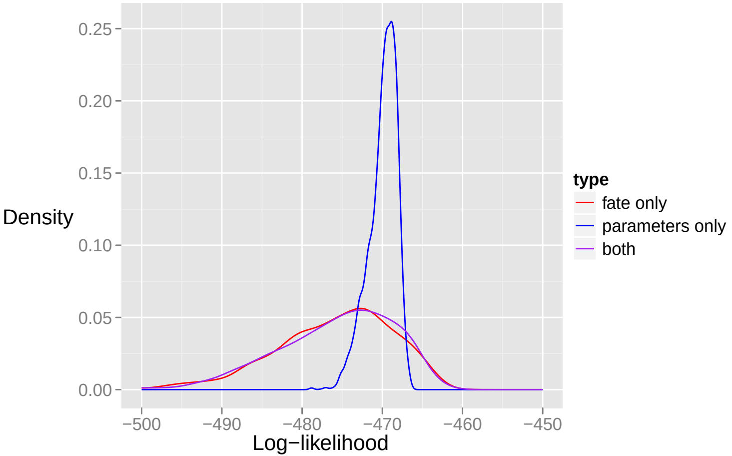
True demography



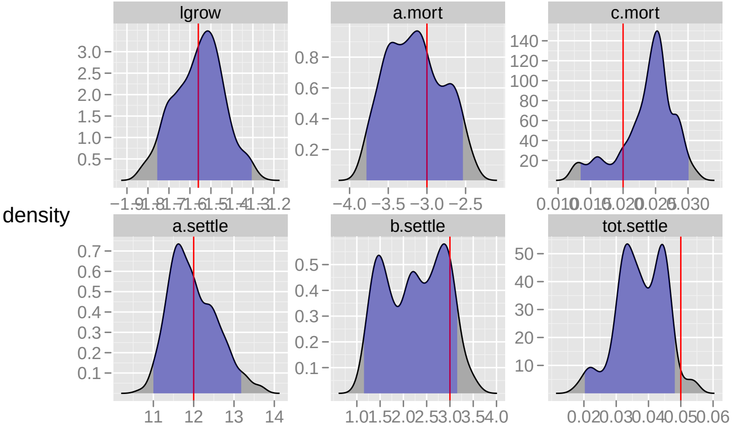
Fate-only results



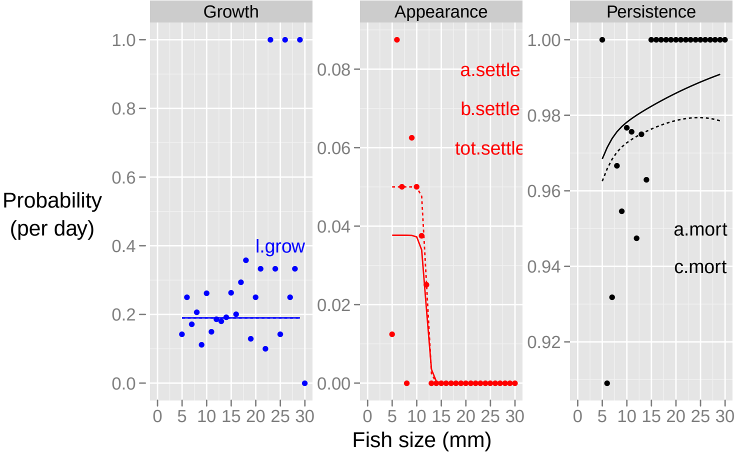
Sampling fates, parameters, both . . .



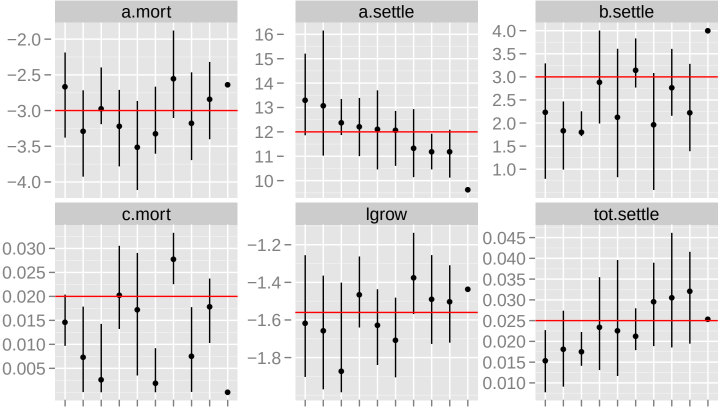
Parameter estimates 1



Parameter estimates 2



Parameter estimates 3



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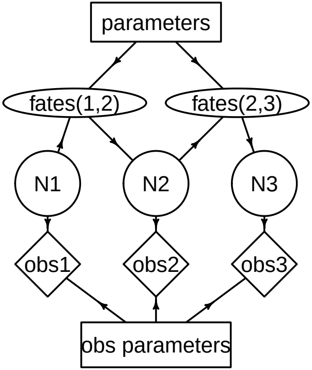
Adding errors



Back to the more typical graph: incorporate information from $N(t-1)$, $N(t+1)$, and current observation

New algorithm

For each individual:

- Pick true state at $N(t)$, from **all** possible states, conditioning on $N(t-1)$
- Pick identity at time $N(t+1)$ from feasible set: update probabilities
- Pick corresponding observation from observed(t): update probabilities
- Calculate likelihood, M-H update

Open questions, caveats

- Will it work ??
- Add complexities:
  - Multiple populations
  - Spatial variation, correlation among parameters
- Simplify/generalize code
- Speed?

Conclusions & musings

- MCMC as powerful technology
- . . . can it be democratized?
- Data limitations shift over time:
  hierarchical models are great for “modern” (high-volume, low-quality) data