Bayesian Data Analysis, class 1a

Andrew Gelman

Introductory examples:
Soccer ratings and Population toxicokinetics

Bayesian data analysis: (1) Modeling

- "Generative models"
  - Data are a realization from a (multivariate) probability distribution
  - Data vector y, probability model $p(y|\theta)$, parameter vector θ
- Prior distributions

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Bayesian data analysis: (2) Inference

- Inference is represented by a matrix of posterior simulations
  - 1000 simulations of 90 parameters: a 1000×90 matrix
- Postprocessing

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Bayesian data analysis: (3) Model checking/improvement

- Do the inferences make sense?
- Are the model's predictions consistent with the data?
- *Not*: Is the model true?
- *Not*: What is Pr (model is true)?
- *Not*: Can we "reject" the model?
- Expanding the model
- Including more data

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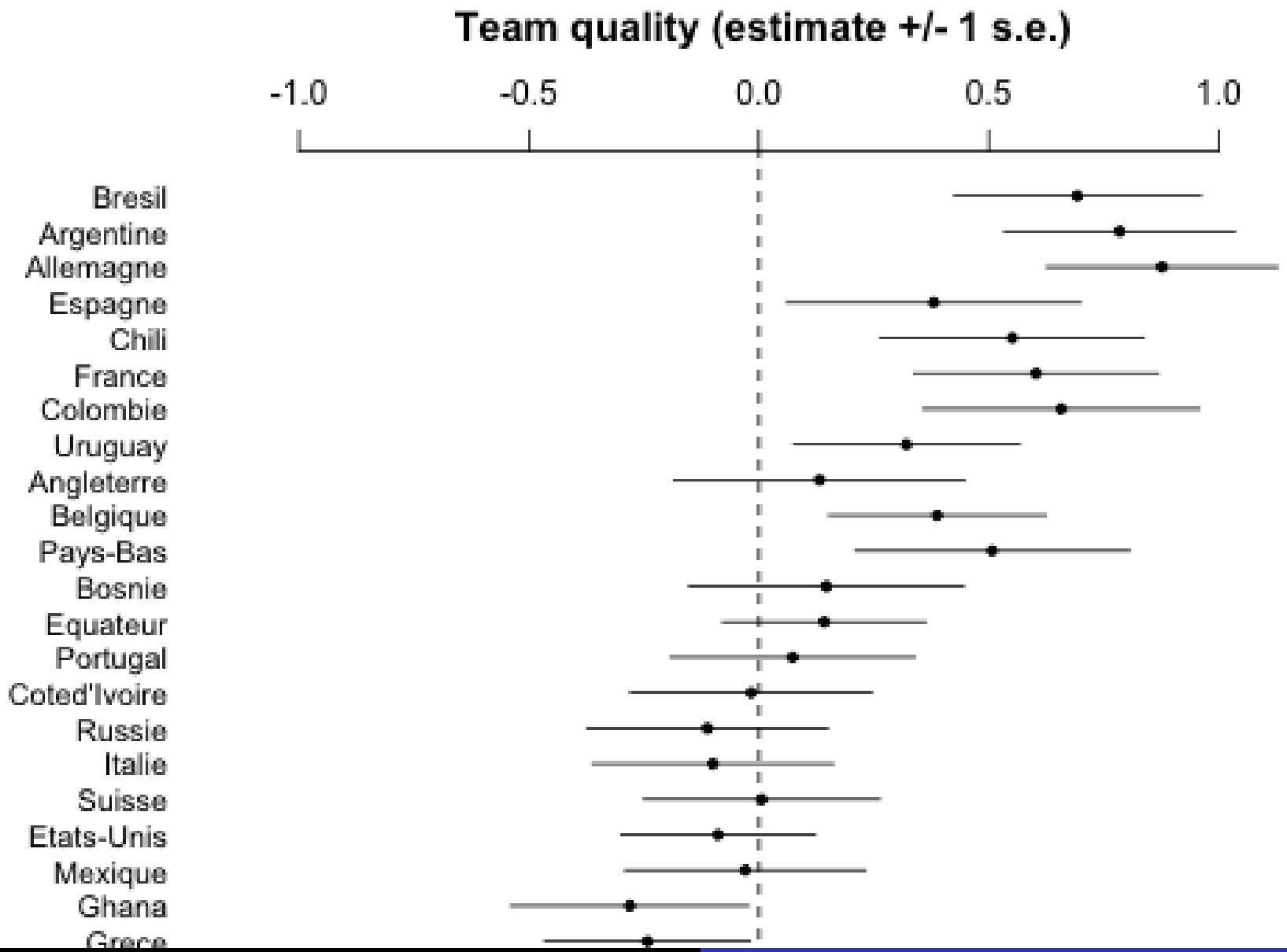
Stan goes to the World Cup



The model

- Fit data on signed square roots:

$$y_{ij} = \sqrt{\text{score differential when team } i \text{ plays team } j}$$

- Model $y_{ij} \sim \text{N}(a_i - a_j, \sigma_y^2)$
- a_i and a_j are "ability parameters"
- σ_y is a scale parameter
- To allow for outliers, use t_7 instead of normal
- Prior info on abilities:

$$a_i \sim \text{N}(\mu + b * \text{prior.score}_i, \sigma_a^2)$$

- We can set $\mu = 0$
- No further prior info in model

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Stan model (part 1)

```
data {
  int nteams;
  int ngames;
  vector[nteams] prior_score;
  int team1[ngames];
  int team2[ngames];
  vector[ngames] score1;
  vector[ngames] score2;
  real df;
}
transformed data {
  vector[ngames] dif;
  vector[ngames] sqrt_dif;
  dif <- score1 - score2;
  for (i in 1:ngames)
    sqrt_dif[i] <- (step(dif[i])-.5)*sqrt(fabs(dif[i]));
}
```

Stan model (part 2)

```
parameters {
  real b;
  real<lower=0> sigma_a;
  real<lower=0> sigma_y;
  vector[nteams] eta_a;
}
transformed parameters {
  vector[nteams] a;
  a <- b*prior_score + sigma_a*eta_a;
}
model {
  eta_a ~ normal(0,1);
  for (i in 1:ngames)
    sqrt_dif[i] ~ student_t(df, a[team1[i]]-a[team2[i]],sigma_y)
}
```

Fitting the model

- Go into R
- Read in the data
- Fit the Stan model
- Check convergence
- Graph the estimated team abilities
- Re-fit without prior information
- Compare to model with prior information

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Checking model fit

- Still inside R
- For each game, plot actual score differential and 95% predictive intervals
  - Not cross-validated but no big deal in this case because n is large
- The predictions don't fit the data!!
- Redoing the predictive intervals
- Re-plot, still a problem!

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I found the bug!

- Still inside R
- Re-fit the model on the original scale
- Display the estimated team abilities
- Updated plot of data with predictive intervals—now it's ok!
- Go back and find the bug in the square-root-scale model
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- Bayesian inference combines prior information and data
- Unresolved questions
- How the model all fits together

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Toxicokinetics of perchloroethylene

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  - Population distribution
- Experimental data: Expose 6 healthy volunteers to PERC for four hours, then measure concentrations in blood and air for 2 weeks
- 4-compartment model, metabolism in liver
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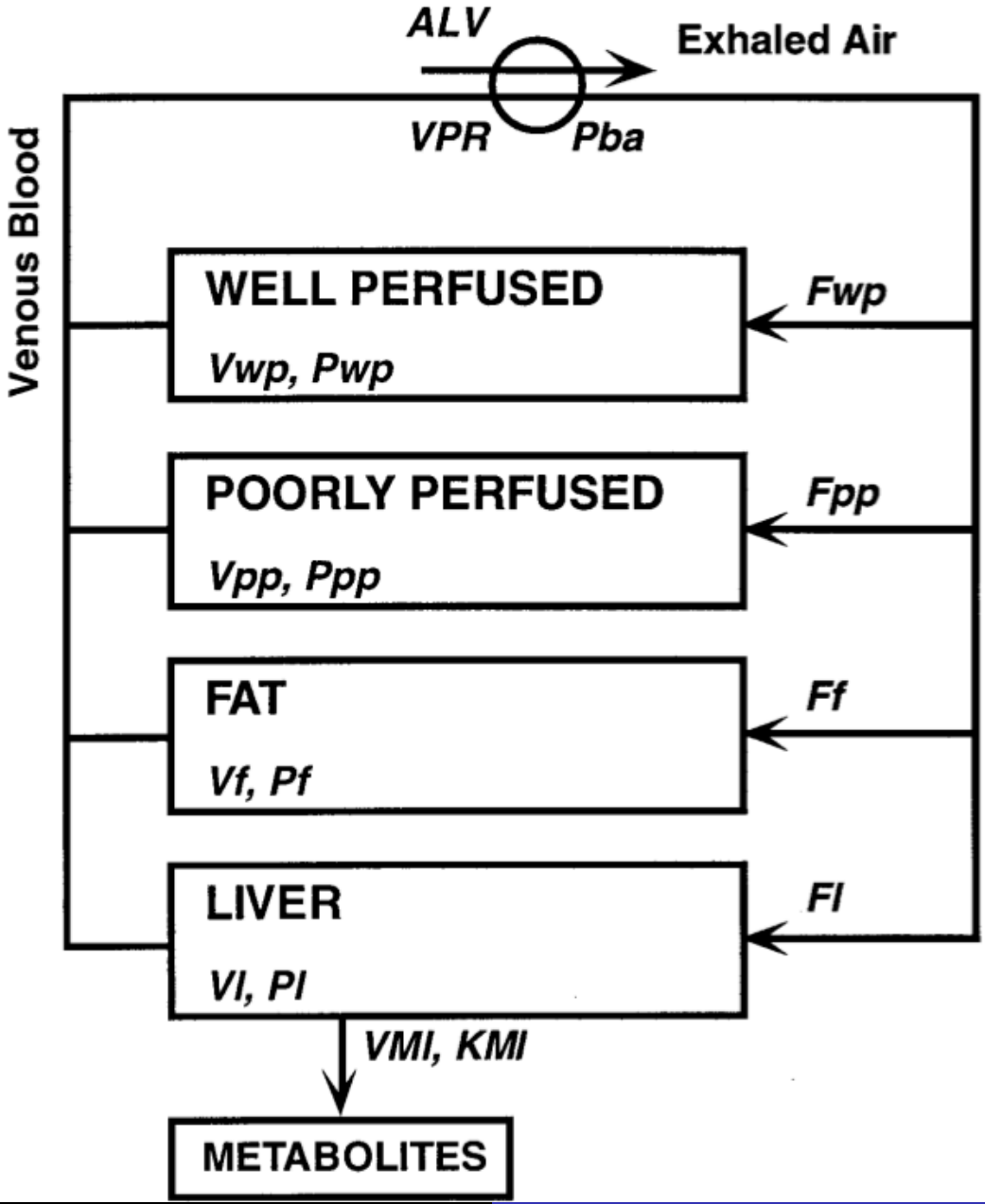
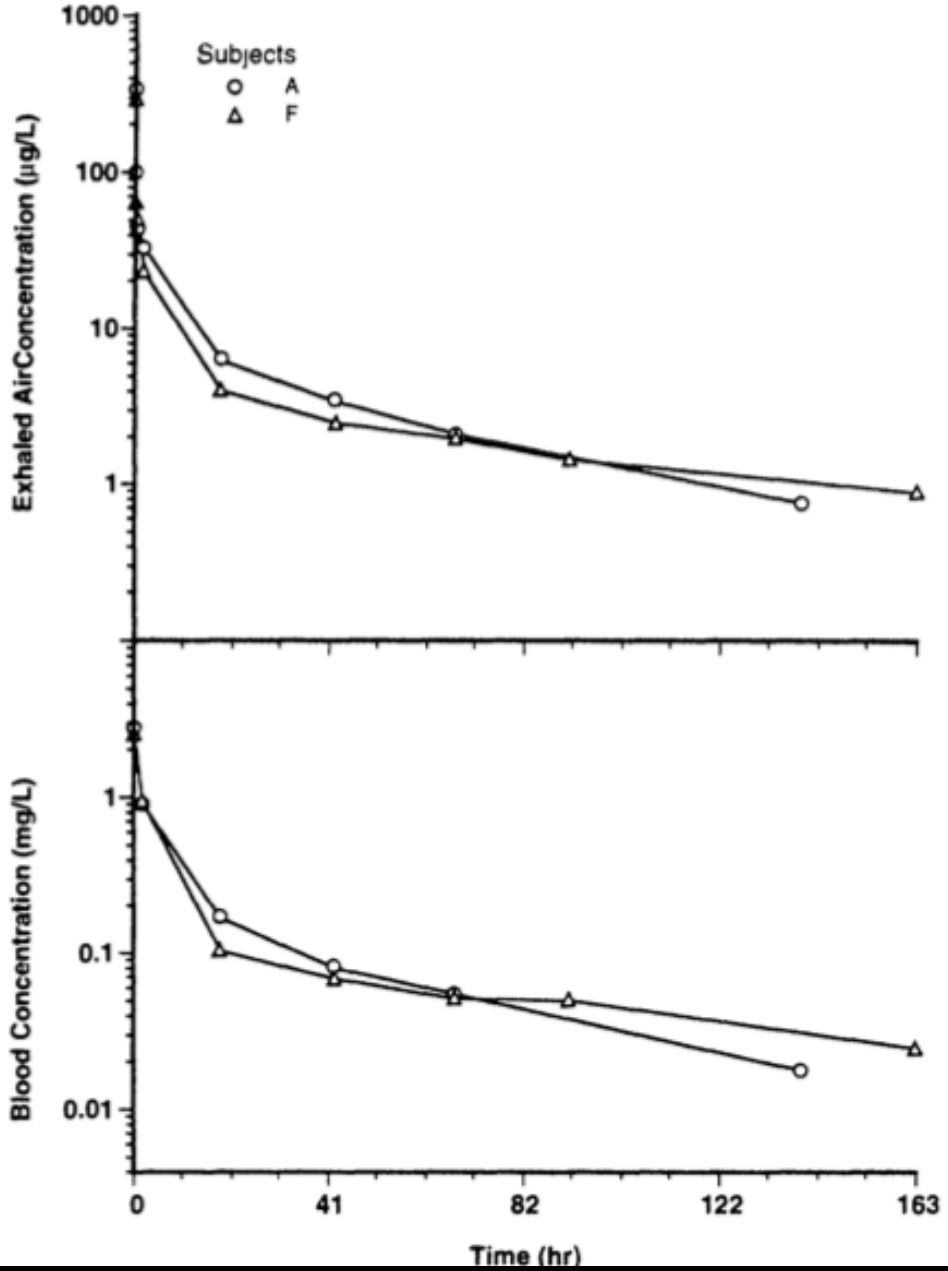


Some data


Subjects
A
F
Exhaled AirConcentration (µg/L)
1000
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10
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Blood Concentration (mg/L)
1
0.1
0.01
0
41
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122
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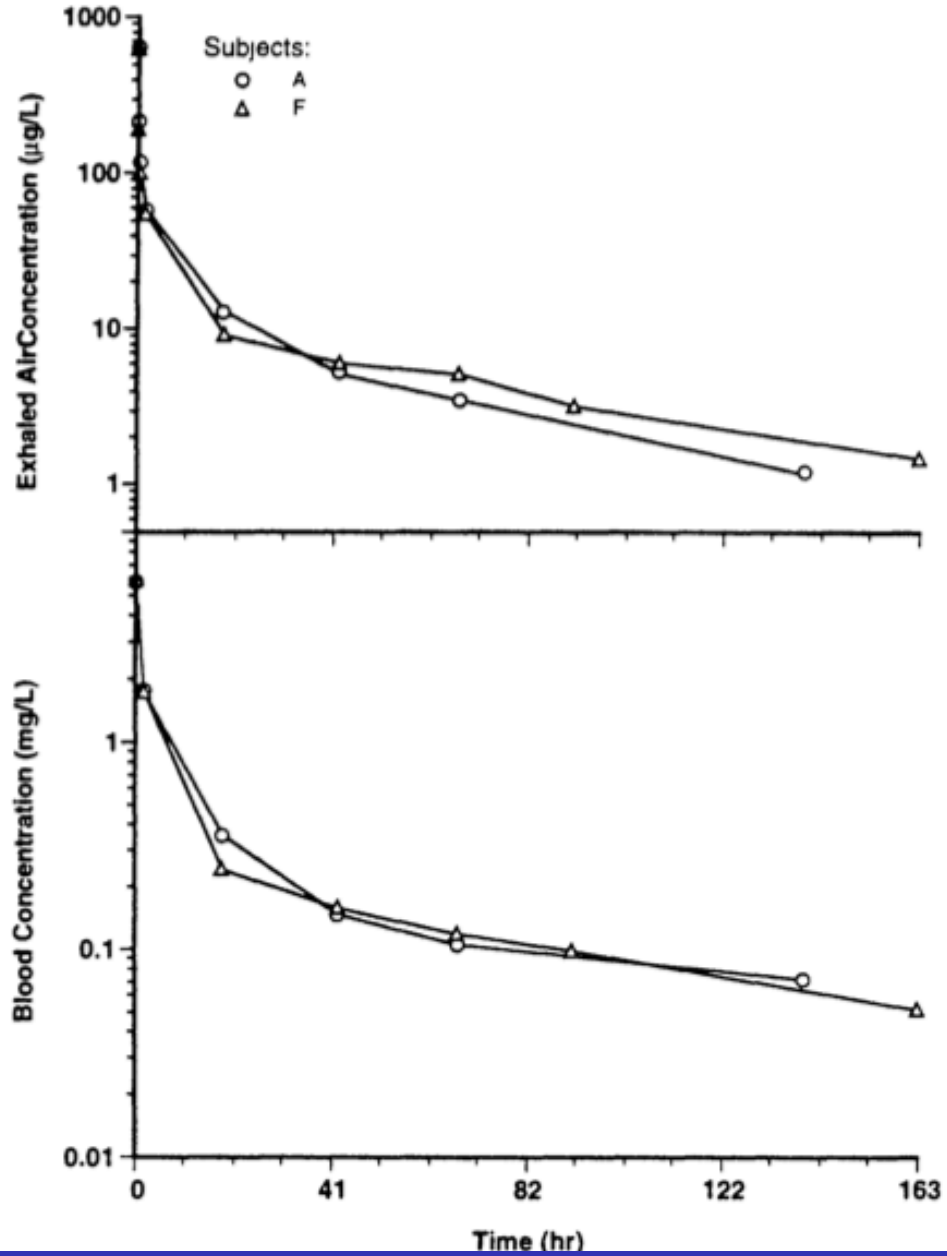
Time (hr)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- Prior distribution for a rate parameter in the metabolism, θ_j for person j
  - $\log \theta_j \sim N(\mu, \tau^2)$
  - $\mu \sim N(\log 16, (\log 10)^2)$
  - $\tau \simeq \log 2$
- Large uncertainty, small variation
- Can learn about μ using data from several people
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Hierarchical prior distributions

Parameter	*Population prior*
Ventilation/perfusion ratio (VPR)	$1.6(\times\div 1.3)$ $\times\div 1.3$
Blood flow, well-perfused tissues (Fwp)	$.47(\times\div 1.17)$ $\times\div 1.17$
Blood flow, poorly perfused tissues (Fpp)	$.20(\times\div 1.22)$ $\times\div 1.22$
Blood flow, fat (Ff)	$.07(\times\div 1.27)$ $\times\div 1.27$
Blood flow, liver (Fl)	$.25(\times\div 1.15)$ $\times\div 1.15$
Volume, well-perfused tissues (Vwp)	$.27(\times\div 1.36)$ $\times\div 1.36$
Volume, poorly perfused tissues (Vpp)	$.55(\times\div 1.17)$ $\times\div 1.17$
Volume, liver (Vl)	$.033(\times\div 1.1)$ $\times\div 1.1$
Partition coeff, blood/air (Pba)	$12(\times\div 1.5)$ $\times\div 1.3$
Partition coeff, well-perfused (Pwp)	$4.8(\times\div 1.5)$ $\times\div 1.3$
Partition coeff, poorly perfused (Ppp)	$1.6(\times\div 1.5)$ $\times\div 1.3$
Partition coeff, fat (Pf)	$125(\times\div 1.5)$ $\times\div 1.3$
Partition coeff, liver (Pl)	$4.8(\times\div 1.5)$ $\times\div 1.3$
Max metabolic rate in liver (VMl)	$.042(\times\div 10)$ $\times\div 2$
K_m in liver (KMl)	$16(\times\div 10)$ $\times\div 1.5$

What we did

- Set up a hierarchical prior distribution with uncertainty and population variation for a 4-compartment model
- Fit the model to data (much computation)
- Checked inferences about parameters to see that they made sense
- Re-ran model under hypothetical low-dose, high-dose exposures

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- Computationally intensive
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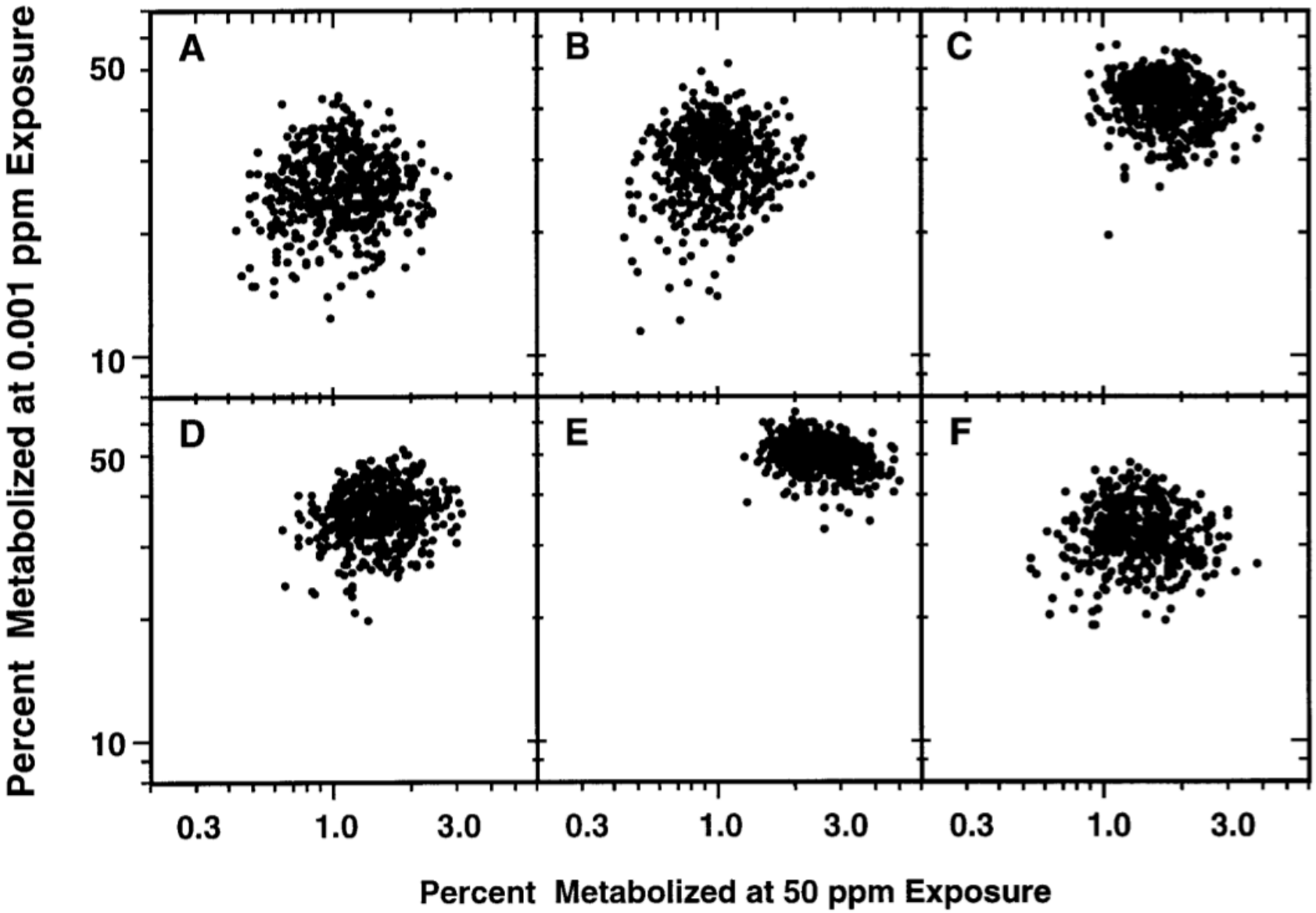
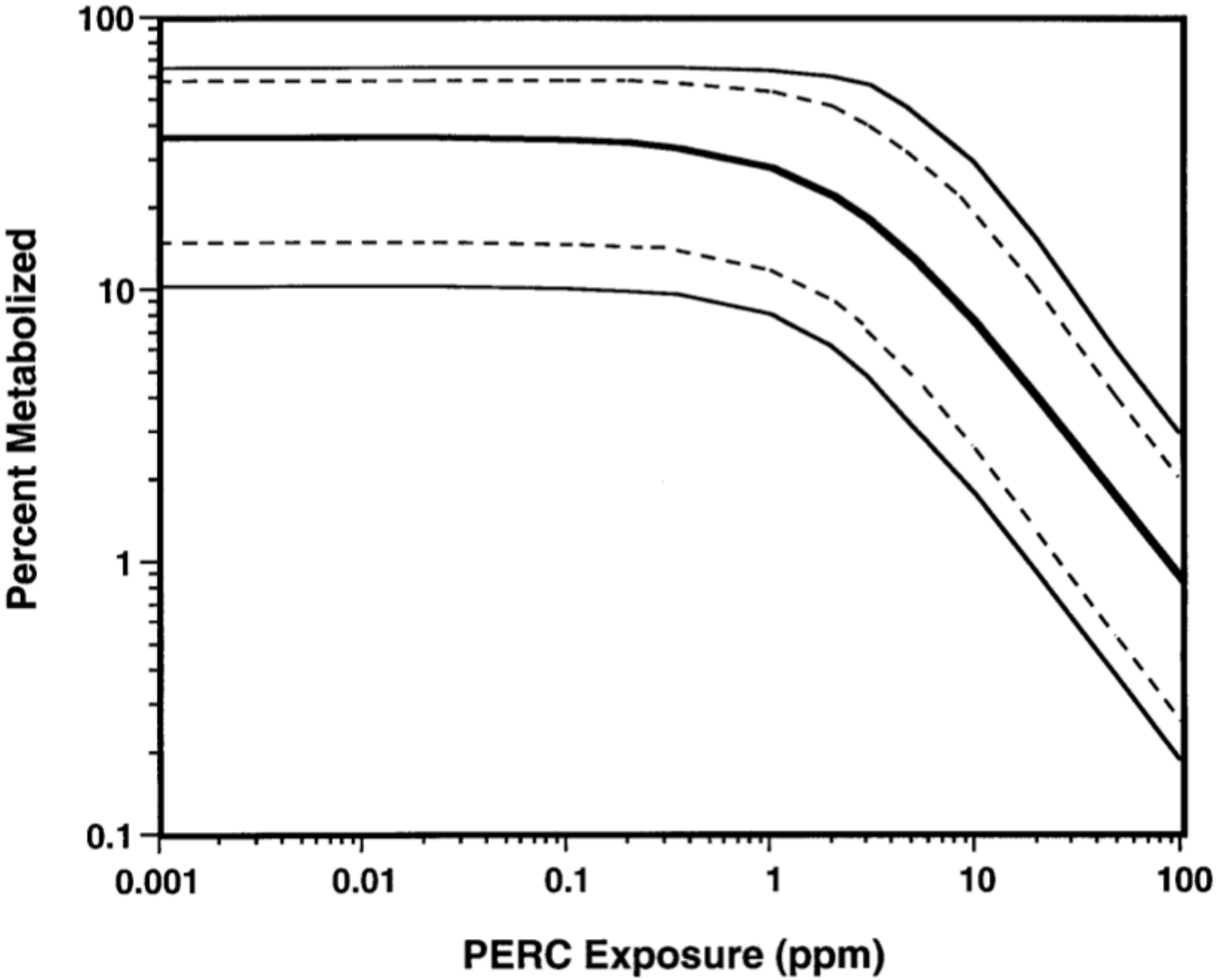
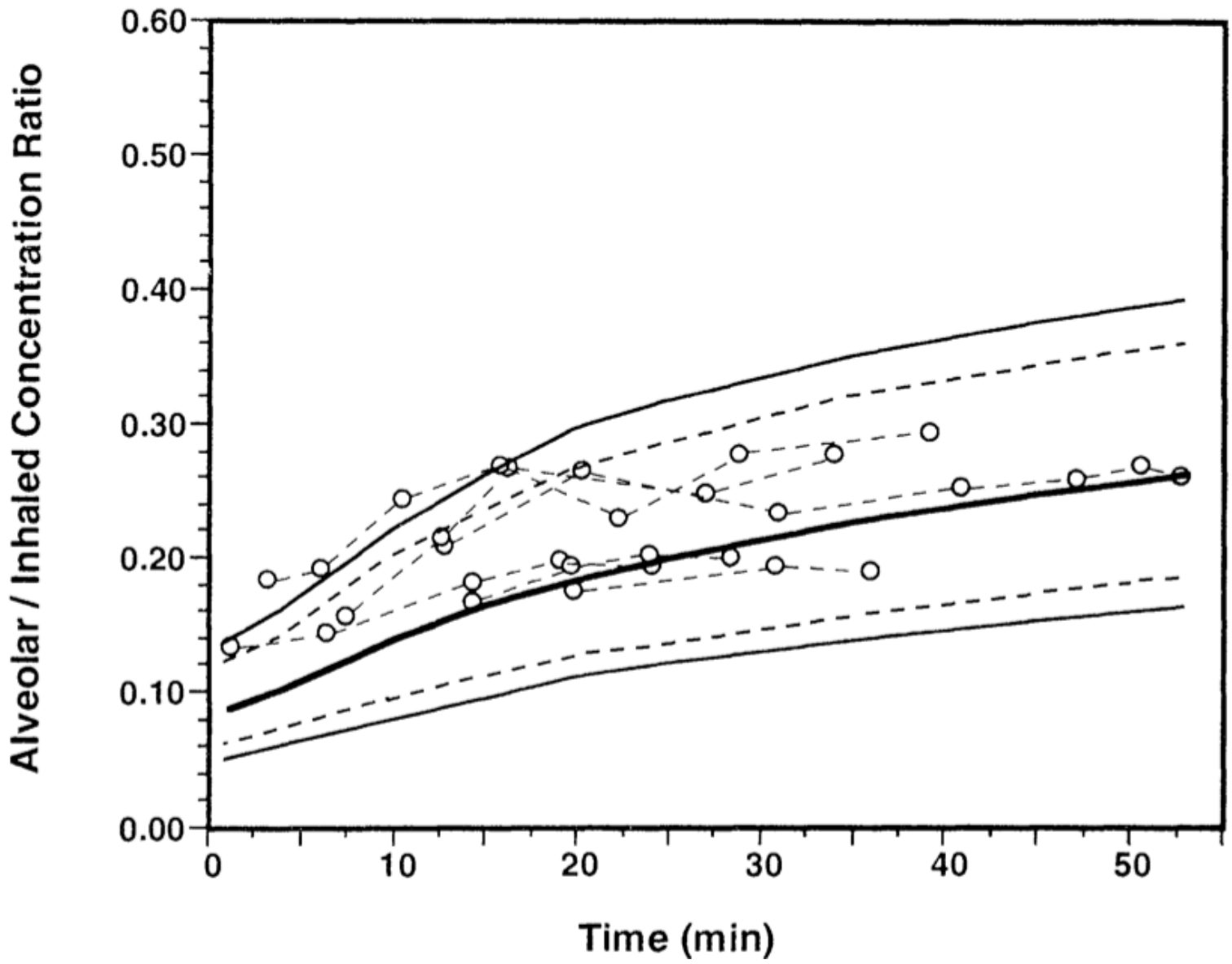
Inference for 6 individuals



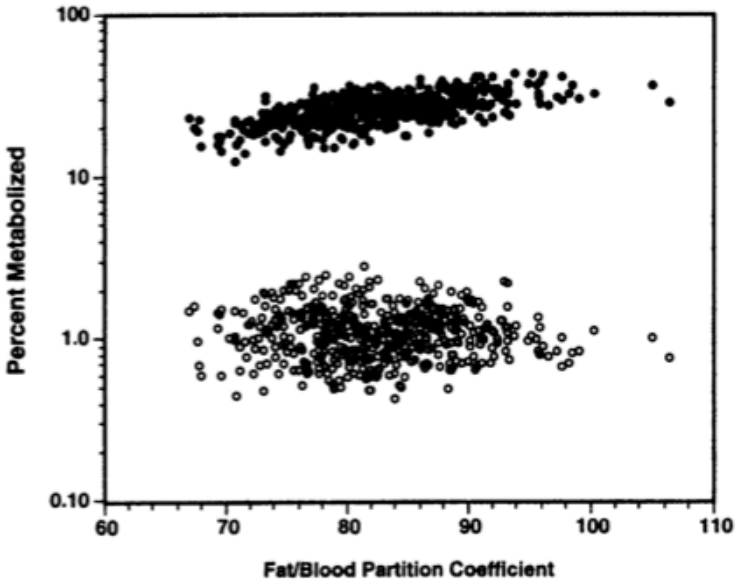
Inference for the population



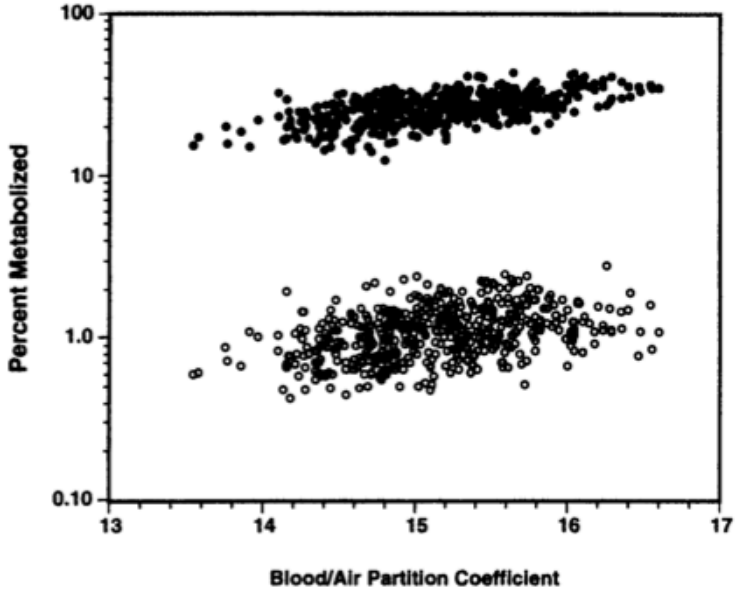
Prediction of data from a new study



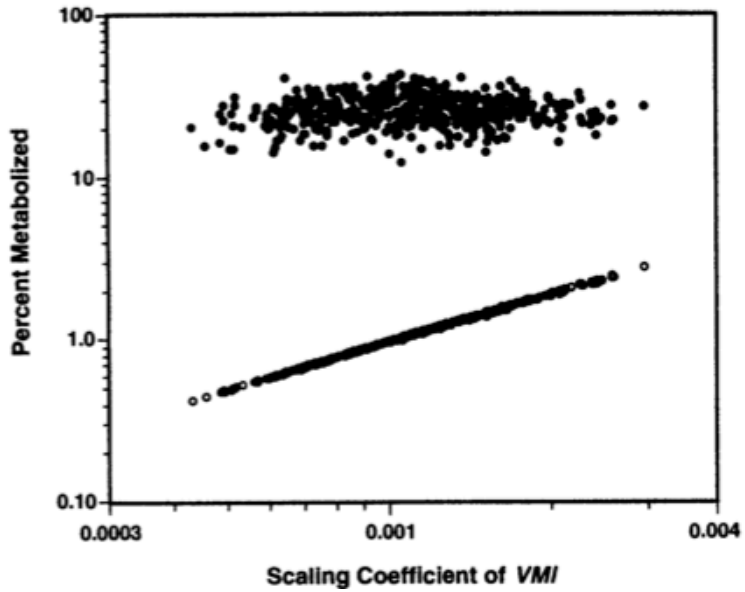
Sensitivity to priors

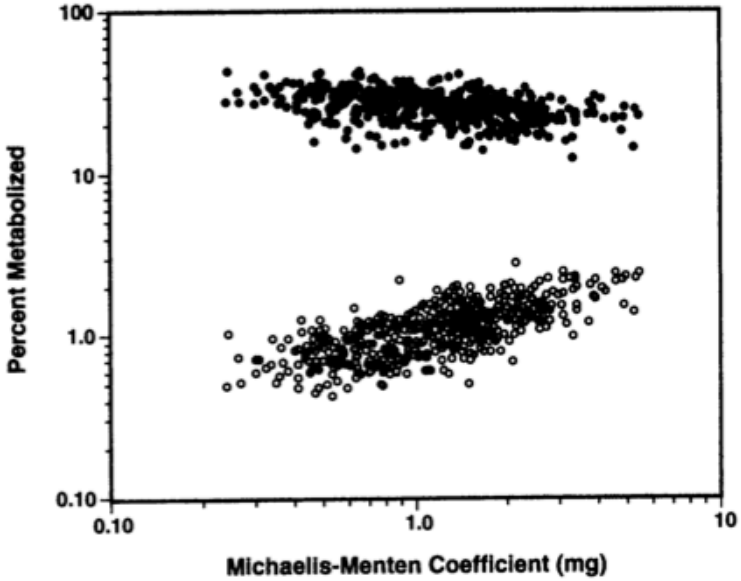


(a)



(b)





Putting it all together

(a) Physiological pharmacokinetic model
(b) Hierarchical population model
(c) Prior information
(d) Experimental data
(e) Bayesian inference
(f) Computation
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- We need all of these!

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- We need physiological parameters (not just curve-fitting of the data) to efficiently combine information across different people

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- We need prior information. Otherwise, our estimates don't make sense (the 8 kg liver)
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- Using Bayesian inference, we can find parameters that are consistent with both prior information and data, if such agreement is possible
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- Old-fashioned differential-equation solver is still sitting inside the model
- Our computers are never fast enough. We want more, more, more!

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- Check inferences about parameters
  - Do they make sense?
  - Are they consistent with prior distributions
- Check fit to data
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- Accounting for uncertainty (especially for decisions)
- Checking model fit
- Using models to combine different sources of information (partial pooling)
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