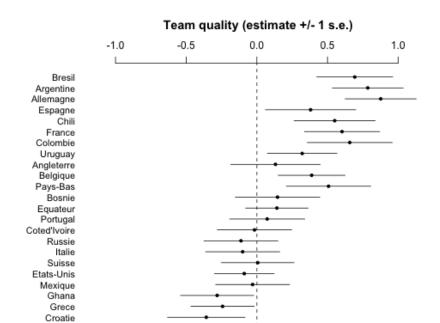
What is Bayesian data analysis? Some examples

Andrew Gelman

17 Feb 2016

Example 1: Stan goes to the World Cup



worldcup2012.txt Bresil 3 Croatie 1 Mexique 1 Cameroun 0 Bresil 0 Mexique 0 Cameroun 0 Croatie 4 Cameroun 1 Bresil 4 Croatie 1 Mexique 3 Espagne 1 Pays-Bas 5 Chili 3 Australie 1 Espagne 0 Chili 2 Australie 2 Pays-Bas 3 Australie 0 Espagne 3 Pays-Bas 2 Chili 0 Colombie 3 Grece 0 Coted'Ivoire 2 Japon 1 Colombie 2 Coted'Ivoire 1 Japon 0 Grece 0 Japon 1 Colombie 4 Grece 2 Coted'Ivoire 1 Uruguay 1 CostaRica 3 Angleterre 1 Italie 2 Uruguay 2 Angleterre 1

Soccerpowerindex.txt Bresil Argentine Allemagne Espagne Chili France Colombie Uruguay Angleterre Belgique Pays-Bas Bosnie Equateur Portugal Coted'Ivoire Russie Italie Suisse Etats-Unis Mexique

The model

Fit data on signed square roots:

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

- Model $y_{ij} \sim N(a_i a_j, \sigma_y^2)$
- a_i and a_j are "ability parameters"
- σ_y is a scale parameter
- ▶ To allow for outliers, use t₇ instead of normal
- Prior info on abilities:

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

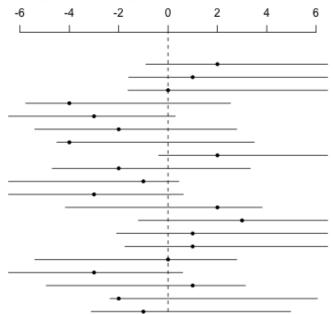
- We can set $\mu = 0$
- No further prior info in model

```
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]));</pre>
}
```

```
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;</pre>
}
model {
  eta_a \tilde{} normal(0,1);
  for (i in 1:ngames)
    sqrt_dif[i] ~ student_t(df, a[team1[i]]-a[team2[i]],sigma_y)
}
```

- 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

Game score differentials compared to 95% predictive interval from model

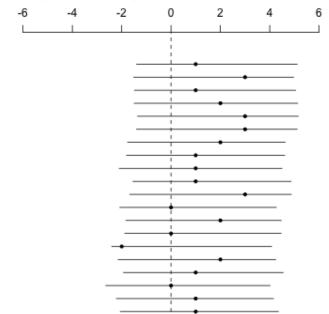


Bresil vs. Croatie Mexique vs. Cameroun Bresil vs. Mexique Cameroun vs. Croatie Cameroun vs. Bresil Croatie vs. Mexique Espagne vs. Pays-Bas Chili vs. Australie Espagne vs. Chili Australie vs. Pays-Bas Australie vs. Espagne Pays-Bas vs. Chili Colombie vs. Grece Coted'Ivoire vs. Japon Colombie vs. Coted'Ivoire Japon vs. Grece Japon vs. Colombie Grece vs. Coted'Ivoire Uruguay vs. CostaRica Anglotorro ve Italio

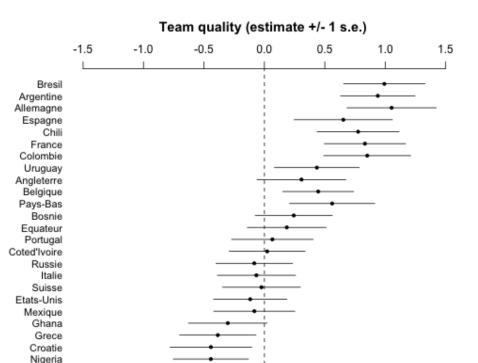
- Still inside R
- For each game, plot actual score differential and 95% predictive intervals
 - Not cross-validated but no big deal in this case because n is large
- The predictions don't fit the data!!
- Redoing the predictive intervals
- Re-plot, still a problem!

- 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
- Re-fit the debugged model

Game score differentials compared to 95% predictive interval from model



Allemagne vs. Algerie Espagne vs. Australie Argentine vs. Iran Chili vs. Australie Bresil vs. Cameroun France vs. Honduras Bresil vs. Croatie Argentine vs. Nigeria Belgique vs. Algerie Pays-Bas vs. Australie Colombie vs. Japon Bresil vs. Mexique France vs. Nigeria Allemagne vs. Ghana Uruguay vs. CostaRica Bosnie vs. Iran Equateur vs. Honduras Angleterre vs. CostaRica Argentine vs. Suisse Allomagno ve Etate-Unie



"Generative models"

- Data are a realization from a (multivariate) probability distribution
- ▶ Data vector y, probability model $p(y|\theta)$, parameter vector θ
- Prior distributions
 - In Bayes inference, the parameter vector θ is a realization from a prior distribution, p(θ|φ)
 - \blacktriangleright Vector of hyperparameters ϕ is specified or itself modeled

- Inference is represented by a matrix of posterior simulations
 - \blacktriangleright 1000 simulations of 90 parameters: a 1000 \times 90 matrix
- Postprocessing
 - Inference for qoi's
 - Decision analysis

- 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

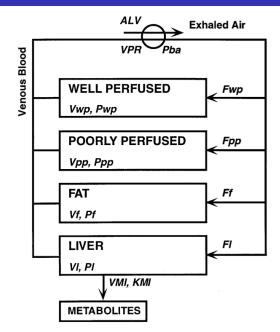
- Central story: 4-compartment model of toxicokinetics of perchloroethylene
- Bayesian inference combines prior information and data
- Unresolved questions
- How the model all fits together

Toxicokinetics of perchloroethylene

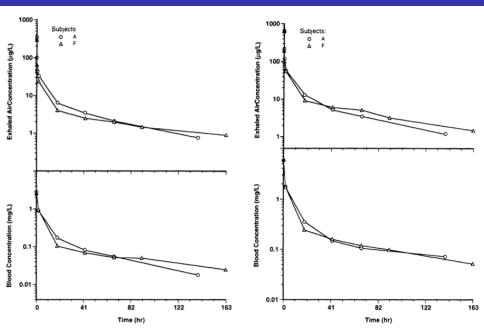
Goal:

- How much PERC is metabolized at low doses
- 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
- Our analysis:
 - Simple data-fitting did not work
 - Use Bayes to combine data and prior info within model

4-compartment model



Some data



- Fitting 4-compartment model directly to data
- Assisted model fit
- 1 or 2-compartment model
- Simulation from prior distribution

Simple statistical ideas that did not work: Fitting 4-compartment model directly to data

- Nonlinear least squares
- Fitting to each person separately:
 - Unstable: approx 30 data points, 15 param
 - "8 kg liver"
- Pooling data and estimating parameters for "the standard man"
 - Not useful for our goal of population inference

Simple statistical ideas that did not work: Assisted model fit

- Set some parameters to fixed values (from the pharmacology literature)
- Estimate the other parameters
- Results:
 - Couldn't fit the data well
 - Difficult to get fixed values for PERC-specific parameters such as equilibrium concentration ratios

Simple statistical ideas that did not work: 1 or 2-compartment model

- Simpler model can be estimated easily and robustly
- Does not fit the data well
 - Most of the PERC leaves in a few hours, but some stays in the body after a week or more
- Not realistic for low-dose extrapolation

Simple statistical ideas that did not work: Simulation from prior distribution

- Get prior information on parameters from pharmacology literature
- Try to fit data within these prior constraints
- Does not fit the data well
- Difficult to get good prior information for PERC-specific parameters such as equilibrium concentration ratios

- 4-compartment model
- ▶ 15 parameters for each person
- Prior information
 - Strong for some parameters (e.g., volume of liver)
 - Weak for others (e.g., Michaelis-Menten coef)
 - Model includes uncertainty and variation
- Posterior simulation: random walk through parameter space
- Inference for parameters and predictions
- Model checking

- Prior distribution for a rate parameter in the metabolism, θ_j for person j
 - $\log \theta_j \sim N(\mu, \tau^2)$
 - $\mu \sim N(\log 16, (\log 10)^2)$
 - $\blacktriangleright \ \tau \approx \log 2$
- Large uncertainty, small variation
- Can learn about μ using data from several people
- Can't do this without a hierarchical model
- Transformations and prior correlations (why transformations are particularly important for Bayesians)

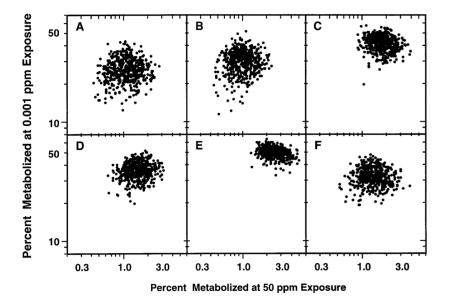
Hierarchical prior distributions

Parameter	Population prior		
Ventilation/perfusion ratio (VPR)	1.6(×÷ 1.3) ×÷ 1.3		
Blood flow, well-	.47(×÷ 1.17)	Partition coeff,	12(×÷ 1.5)
perfused tissues (Fwp)	×÷ 1.17	blood/air (Pba)	×÷ 1.3
Blood flow, poorly	.20(×÷ 1.22)	Partition coeff,	4.8(×÷ 1.5)
perfused tissues (Fpp)	×÷ 1.22	well-perfused (Pwp)	×÷ 1.3
Blood flow,	.07(×÷ 1.27)	Partition coeff,	1.6(×÷ 1.5)
fat (Ff)	×÷ 1.27	poorly perfused (Ppp)	×÷ 1.3
Blood flow,	.25(×÷ 1.15)	Partition coeff,	125(×÷ 1.5)
liver (Fl)	×÷ 1.15	fat (Pf)	×÷ 1.3
Volume, well-	.27(×÷ 1.36)	Partition coeff,	4.8(×÷ 1.5)
perfused tissues (Vwp)	×÷ 1.36	liver (PI)	×÷ 1.3
Volume, poorly	.55(×÷ 1.17)	Max metabolic rate	.042(×÷ 10)
perfused tissues (Vpp)	×÷ 1.17	in liver (VMI)	×÷ 2
Volume,	.033(×÷ 1.1)	K _m	16(×÷ 10)
liver (VI)	×÷ 1.1	in liver (KMI)	×÷ 1.5

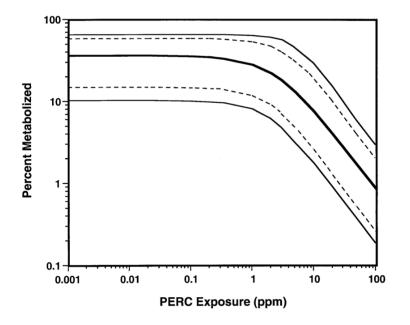
- Set up a hierarchical prior distribution with uncertainty and population variation for a 4-compartment model
- Fit the model to data (much computation)
- Checked inferences about parameters to see that they made sense
- Re-ran model under hypothetical low-dose, high-dose exposures

- Use Gibbs sampler and Metropolis algorithm to take a random walk through parameter space
- Computationally intensive
 - Each step requires evaluation of the numerical differential equation solver
- Check inferences: Do they make sense?
- Re-run the model several times to simulate what would happen under different conditions

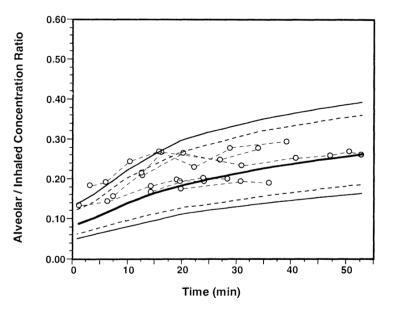
Inference for 6 individuals



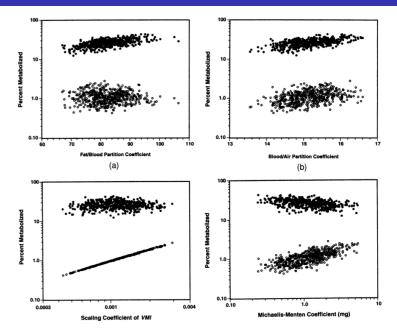
Inference for the population



Prediction of data from a new study



Sensitivity to priors



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

- Without a physiological model, there is no good way to get prior information on the parameters
- We need physiological parameters (not just curve-fitting of the data) to efficiently combine information across different people

- Without a population model, there generally are not enough data to estimate the parameters separately for each individual
- And there is too much variation among bodies (even among healthy young male volunteers) to pool all the data together and estimate common parameters

(c) Prior information(d) Experimental data

- We need prior information. Otherwise, our estimates don't make sense (the 8 kg liver)
- We need experimental data to learn about perchloroethylene in particular

- Using Bayesian inference, we can find parameters that are consistent with both prior information and data, if such agreement is possible
- Automatically includes uncertainty and variability, so inferences can be plugged in directly to risk assessment and decision analysis

- Our models are big. Least squares, maximum likelihood, etc., are not enough
- Old-fashioned differential-equation solver is still sitting inside the model
- Our computers are never fast enough. We want more, more, more!

- Check inferences about parameters
 - Do they make sense?
 - Are they consistent with prior distributions
- Check fit to data
- Check predictions on new data

- Regularization (for example, avoiding estimates on the boundary of parameter space)
- Accounting for uncertainty (especially for decisions)
- Checking model fit
- Using models to combine different sources of information (partial pooling)
- Better dialogue with subject-matter experts (more windows into the model and data)

- Population pharmacokinetic models have many moving parts
- Complexity in one place can make it *easier*, not harder, to add information in other places

- "Bayesian inference" is too narrow; "Bayesian statistics" is too broad
- "Bayes" is a good brand name; "Statistics using conditional probability" is confusing
- Everyone uses Bayesian inference when it is appropriate.
 A Bayesian is a statistician who uses Bayesian inference even when it is inappropriate.

I am a Bayesian.

- Bayes is data + regularization
- Bayes is data + prior information
- Bayes is logical probabilistic reasoning
- Bayes is different things at different times

- Three steps:
 - 1. Setting up a probability model
 - 2. Inference
 - 3. Model checking
- Then go back and improve the model

Example 3: Spell checking

- The typed word "Radom" is actually Random (θ = 1), Radon (θ = 2), or Radom (θ = 3)
- Prior distribution:

Likelihood:

θ	p(heta)				
random	$7.60 imes10^{-5}$				
radon	$6.05 imes10^{-6}$				
radom	$3.12 imes10^{-7}$				
θ	p(``radom'' heta)				
random	0.00193				
radon	0.000143				
radom	0.975				

Prior, likelihood, posterior distributions:

θ	p(heta)	$p(y \theta)$	p(heta)p(y heta)	$p(\theta y)$
random	$7.60 imes10^{-5}$	0.00193	$1.47 imes10^{-7}$	0.325
radon	$6.05 imes10^{-6}$	0.000143	$8.65 imes10^{-10}$	0.002
radom	$3.12 imes10^{-7}$	0.975	$3.04 imes10^{-7}$	0.673

- Decision making
- Model checking
- Model improvement

On Dec 7, 2015, at 11:16 AM, Tom Daula <<u>***@***.com</u>> wrote:

Interesting applied project for your students, or as a warning for decisions under uncertainty / statistical significance. Real money on the line so the length of time and number of entries required to get a winner may be an interesting dataset after this is all done.

http://www.informath.org/Contest1000.htm

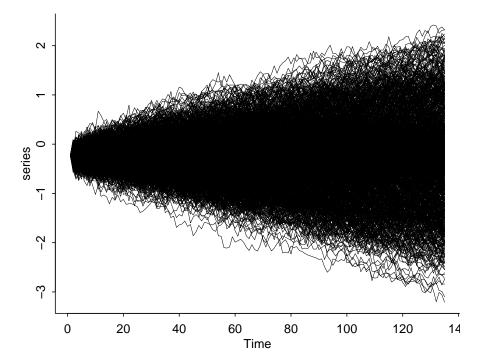
Terms of the Contest

The file Series1000.txt contains 1000 simulated time series. Each series has length 135: the same length as that of the most commonly studied series of global temperatures (which span 1880-2014). The 1000 series were generated as follows. First, 1000 random series were obtained (for more details, see below). Then, some of those series were randomly selected and had a trend added to them. Each added trend was either $1^{\circ}C$ /century or $-1^{\circ}C$ /century. For comparison, a trend of $1^{\circ}C$ /century is greater than the trend that is claimed for global temperatures.

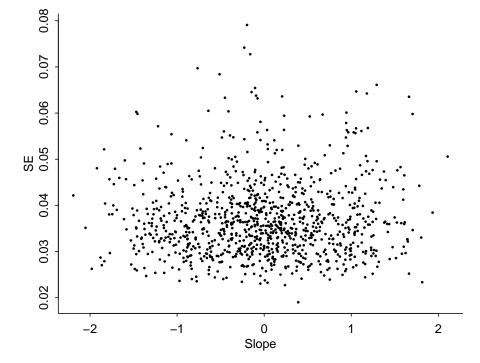
A prize of \$100 000 (one hundred thousand U.S. dollars) will be awarded to the first person who submits an entry that correctly identifies at least 900 series: which series were generated without a trend and which were generated with a trend.

For instructions on how to submit an entry, see the Contest Entry page. Each entry must be accompanied by a payment of \$10; this is being done to inhibit non-serious entries. There is a limit of one entry per person.

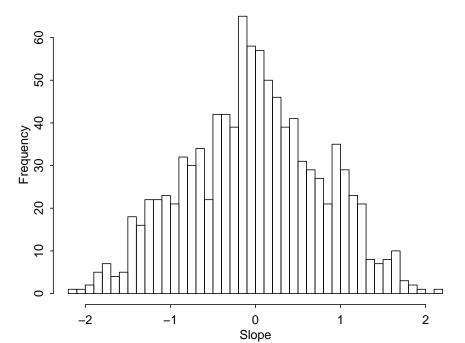
```
series <- matrix(scan("Series1000.txt"), nrow=1000, ncol=135,</pre>
  byrow=TRUE)
T <- 135
N < -1000
pdf("series_1.pdf", height=5, width=6)
par(mar=c(3,3,2,0), tck=-.01, mgp=c(1.5,.5,0))
plot(c(1,T), range(series), bty="l", type="n",
  xlab="Time", ylab="series")
for (n \text{ in } 1:N){
  lines(1:T, series[n,], lwd=.5)
}
dev.off()
```



```
library("arm")
slope <- rep(NA, N)</pre>
se <- rep(NA, N)</pre>
for (n \text{ in } 1:N){
  data <- series[n,]</pre>
  time <- 1:T
  fit <- lm(data ~ time)
  slope[n] <- 100*coef(fit)[2]
  se[n] <- 100*se.coef(fit)[2]</pre>
}
pdf("series_2.pdf", height=5, width=6)
par(mar=c(3,3,2,0), tck=-.01, mgp=c(1.5,.5,0))
plot(slope, se, bty="l", xlab="Slope", ylab="SE", pch=20, cex=.5)
dev.off()
```



Histogram of slope



Program a mixture model in Stan

```
data {
  int K;
  int N;
  real y[N];
  real mu[K];
}
parameters {
  simplex[K] theta;
  real sigma;
}
model {
  real ps[K];
  sigma ~ cauchy(0,2.5);
  mu \sim normal(0,10);
  for (n \text{ in } 1:N) {
    for (k \text{ in } 1:K) {
      ps[k] <- log(theta[k]) + normal_log(y[n], mu[k], sigma);</pre>
    }
    increment_log_prob(log_sum_exp(ps));
  }
```

```
y <- slope
K <- 3
mu <- c(0,-1,1)
mix <- stan("mixture.stan")
print(mix)</pre>
```

>

Inference for Stan model: mixture.
4 chains, each with iter=2000; warmup=1000; thin=1;
post-warmup draws per chain=1000, total post-warmup draws=4000.

	mean	se_mean	sd	2.5%	25%	50%	75%	97.5%	n_{eff}	Rhat
theta[1]	0.54	0	0.02	0.49	0.52	0.54	0.55	0.58	2449	1
theta[2]	0.24	0	0.02	0.21	0.23	0.24	0.25	0.27	2537	1
theta[3]	0.22	0	0.02	0.19	0.21	0.22	0.23	0.26	2444	1
sigma	0.40	0	0.02	0.37	0.39	0.40	0.42	0.45	2078	1

For each series, compute probability of it being in each component

```
generated quantities {
  matrix[N,K] p;
  for (n \text{ in } 1:\mathbb{N})
    vector[K] p_raw;
    for (k in 1:K){
       p_raw[k] <- theta[k]*exp(normal_log(y[n], mu[k], sigma));</pre>
    }
    for (k \text{ in } 1:K){
       p[n,k] <- p_raw[k]/sum(p_raw);</pre>
    }
  }
}
```

Results

[,1] [,2] [,3][1,] 0.09 0.00 0.91[2,] 0.41 0.59 0.00 [3,] 0.93 0.01 0.06 [4,] 0.83 0.17 0.00 [5,] 0.82 0.17 0.00 [6,] 0.95 0.01 0.05 [7,] 0.74 0.00 0.26 [8,] 0.86 0.14 0.00 [9,] 0.11 0.00 0.89 [10.] 0.87 0.00 0.13 [11,] 0.94 0.01 0.06 [12.] 0.29 0.71 0.00 [13.] 0.09 0.91 0.00 [14.] 0.67 0.33 0.00 [15.] 0.93 0.01 0.06 [16.] 0.95 0.01 0.04 [17,] 0.16 0.84 0.00 [18,] 0.95 0.04 0.01 [19,] 0.77 0.23 0.00

Best guess for each series:

1 2 3 559 232 209

• Expected # correct and sd:

854.1 10.3

Probability of getting at least 900 correct:

> pnorm(expected_correct, 899.5, sd_correct)
[1] 5.421277e-06

Ummmmm . . .

> 1/pnorm(expected_correct, 899.5, sd_correct)
[1] 184458.4

Should I play the \$100,000 challenge?

► From the discussion thread: <u>Richard Tol (@RichardTol)</u> says:

November 20, 2015 at 8:31 pm

Why don't you guys just pay £10 to win £100,000? You don't need to accept that the challenge has any bearing on climate change — it has not — but it is a great opportunity to make £99,990.

Expected return on \$10 bet:

$$(5.4\cdot 10^{-6})\cdot 10^5 = \$0.54$$

What would you do?

Different approaches to statistics:

- Traditional likelihood
- Pure nonparametric, robust
- Full Bayes modeling
 - "A chicken is an egg's way of making another egg"