

# BAYESIAN CLINICAL TRIALS: WHY BOTHER?

---

Thomas A. Louis, PhD  
Department of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
[www.biostat.jhsph.edu/~tlouis/](http://www.biostat.jhsph.edu/~tlouis/)  
[tlouis@jhsph.edu](mailto:tlouis@jhsph.edu)

## BAYESIAN ANALYSIS

---

- 1 Design a study (possibly using a Bayesian approach)
  - 2 Specify a (hyper) Prior (possibly using the design information)
  - 3 Collect data and compute a likelihood
  - 4 Bayes' theorem  $\Rightarrow$  Posterior Distribution
  - 5 Do something with it, possibly structured by a loss function
    - $(\dots)^2$ : Posterior Mean
    - $|\dots|$ : Posterior median
    - $0/1 + c \times \text{volume}$ : Tolerance Interval (CI)
    - $0/1$ : Hypothesis Test/Model Choice
- Steps 1-3 should depend on goals
  - Steps 4 & 5 obey the rules of probability
  - Step 4 doesn't know what you are going to do in Step 5

**Evidence, then decisions**

## Bother when you want

---

- Excellent Bayesian performance
- Excellent Frequentist performance
  - use priors and loss functions as tuning parameters
- To strike an effective Variance/Bias trade-off
- Full uncertainty propagation
- To design, conduct and analyze complex studies
- **Sometimes it isn't worth the bother**
- **Sometimes you are (almost) forced into it**

## Design

---

- Everyone is a Bayesian in the design phase
- All evaluations are “preposterior,” integrating over both the data (a frequentist act) and the parameters (a Bayesian act)
  - Rubin (1984), “A Bayesianly justifiable frequentist calculation”
- A frequentist designs to control frequentist risk over a range of parameter values
- A Bayesian designs to control preposterior (Bayes) risk
- Bayesian design is effective  
**for both Bayesian and frequentist goals**

## Bayesian Design to Control Frequentist CI Length

---

- Variance of a single observation:  $\sigma^2$
- L is the maximal total length of the CI length
- For two-sided coverage probability  $(1 - \alpha)$ :

$$n(\sigma, L, \alpha) = 4Z^2 \left( \frac{\sigma}{L} \right)^2$$

- If we don't know  $\sigma^2$ , then CI length is a RV
- Can do a series of “what ifs” or a “worst case”
- Can use a probability distribution (Bayes):  $[\sigma^2 \mid \text{prior}]$
- Can also adapt:  $[\sigma^2 \mid \mathbf{Y}_{\text{available}}, \text{prior}]$

## Frequentist CI Length: The Bayesian approach

---

- Background data or prior elicitation provide,

$$[\sigma^2|\text{data/opinion}] \sim G \{\text{e.g., log-normal}\}$$

$$E(\sigma^2|\text{data/opinion}) = \bar{\sigma}^2$$

$$\text{CoefVar}(\sigma^2|\text{data/opinion}) = \eta$$

- Goals:

$$E_G(\text{CI length}|\text{design}_n) < L$$

$$pr_G(\text{CI length} > L|\text{design}_n) \leq \gamma$$

- Similarly, for testing:

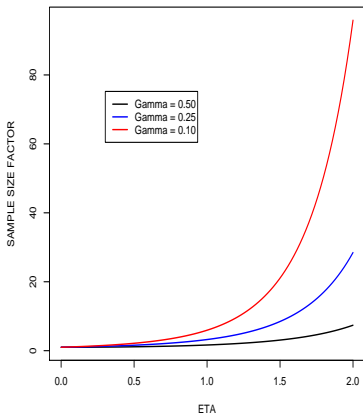
$$pr_G(\text{Power} < 0.84|\text{design}_n) \leq \gamma$$

- More generally,

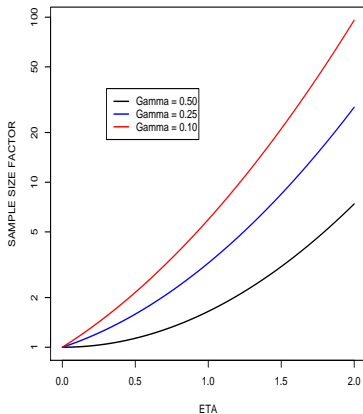
$$pr_G(\text{Bayes risk} > R^*|\text{design}_n) \leq \gamma$$

## CI Length: Sample size factors relative to knowing $\sigma$

SAMPLE SIZE FACTOR FOR A LOG NORMAL VARIANCE



SAMPLE SIZE FACTOR FOR A LOG NORMAL DISTRIBUTED VARIANCE



- Monitor to adjust sample size in the context of accruing information on  $\sigma^2$

## The Basic, Hierarchical Model

---

$$[\boldsymbol{\theta} | \boldsymbol{\eta}] \sim g(\cdot | \boldsymbol{\eta}) \quad \text{Prior}$$

$$[\mathbf{Y} | \boldsymbol{\theta}] \sim f(\mathbf{y} | \boldsymbol{\theta}) \quad \text{Likelihood}$$

$$g(\boldsymbol{\theta} | \mathbf{y}, \boldsymbol{\eta}) = \frac{f(\mathbf{y} | \boldsymbol{\theta})g(\boldsymbol{\theta} | \boldsymbol{\eta})}{f_G(\mathbf{y} | \boldsymbol{\eta})} \quad \text{Posterior}$$

$$f_G(\mathbf{y} | \boldsymbol{\eta}) = \int f(\mathbf{y} | \boldsymbol{\theta})g(\boldsymbol{\theta} | \boldsymbol{\eta})d\boldsymbol{\theta} \quad \text{Marginal}$$

Or, Bayes empirical Bayes via a hyper-prior ( $H$ ),

$$g(\boldsymbol{\theta} | \mathbf{y}) = \int g(\boldsymbol{\theta} | \mathbf{y}, \boldsymbol{\eta})h(\boldsymbol{\eta} | \mathbf{y})d\boldsymbol{\eta}$$



## Compound Sampling, the Objectivity Enabler

### Shrinkage, Variance Reduction, Borrowing Information

---

#### Multiple draws from the prior: Gaussian Case

$$\begin{aligned}\theta_1, \dots, \theta_K & \text{ iid } N(\mu, \tau^2) \\ [Y_k | \theta_k] & \text{ ind } N(\theta_k, \sigma_k^2) \\ [\theta_k | Y_k] & \sim N(\mu + (1 - B_k)(Y_k - \mu), (1 - B_k)\sigma_k^2) \\ B_k & = \frac{\sigma_k^2}{\sigma_k^2 + \tau^2}\end{aligned}$$

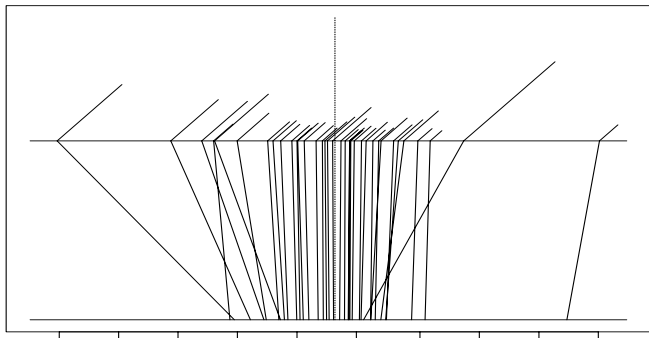
EB when  $\sigma_k^2 \equiv \sigma^2$  (column means with equal n):

$$\begin{aligned}\hat{\mu} & = \mathbf{Y}_\bullet \\ \hat{\tau}^2 & = (\mathbf{S}^2 - \sigma^2)^+ = \sigma^2(\mathbf{F} - 1)^+\end{aligned}$$

## Toxoplasmosis Rates in Guatemala and Honduras

top(MLEs), whiskers(SEs), bottom(Posterior Means)

---



- The relatively high-SE estimates are pulled in more, reducing MSE by striking an effective variance/bias trade-off

## Historical Controls

---

	C	E	Total
Tumor	0	3	3
No Tumor	50	47	97
	50	50	100

- Fisher's exact one-sided  $P = 0.121$
- But, scientists get excited:
  - “The 3 tumors are **Biologically Significant**”
- Statisticians protest:
  - “But, they aren't **Statistically Significant**”

## Include Historical Data

---

- Same species/strain, same Lab, recently
- 0 tumors in 450 control rodents

Pooled Analysis			
	C	E	Total
Tumor	0	3	3
No Tumor	500	47	547
	500	50	550

- Fisher's exact one-sided  $P \doteq .0075$
- **Biological and Statistical significance!**

## Bringing In History

---

- Control rates are drawn from a  $\text{Beta}(\mu, M)$
- Use all of the data to estimate  $\mu$  and  $M$
- Give the historical data weight equivalent to a sample size of  $\hat{M}$  with rate  $\hat{\mu}$
- Female, Fisher F344 Male Rats, 70 historical experiments (Tarone 1982)

Tumor	N	$\hat{M}$	$\hat{\mu}$	$\frac{\hat{M}}{N}$
Lung	1805	513	.022	28.4%
Stromal Polyp	1725	16	.147	0.9%

- Adaptive down-weighting of history

## Design and Analysis for Cluster Randomized Studies

---

### Setting

- Compare two weight loss interventions
- Randomize clinics in pairs, one to A and one to B
- Compute clinic-pair-specific comparisons combine over pairs
- How to design and how to analyze, especially with a small number of clinics?

## The equal sample size, unpaired case

---

- There are  $K$  clusters
- Within-cluster sample sizes are  $n_k \equiv n$
- The  $V(\text{treatment comparison})$ , when computed under the assumption of independence is  $V_{ind}$
- Adjust this by the among-clinic variance component

$$V_{icc} = V_{ind} \times [\mathbf{1 + \rho(n - 1)}] = V_{ind} \times [\mathbf{\text{design effect}}]$$

$$\rho = \tau^2 / \sigma^2 + \tau^2 \text{ (the ICC)}$$

$$\tau^2 = \left( \frac{\rho}{1 - \rho} \right) \sigma^2 \text{ (the among-clinic variance)}$$

$$\sigma^2 = \text{single-observation variance}$$

## Design and Analysis Considerations

---

- In the paired-clinic case, to compute

$$V_{icc} = V(\text{treatment comparison}),$$

need to account for the following variances:

- Individual measurement ( $\sigma^2$ )
  - The trial will provide sufficient information
- Among-clusters: within ( $\tau_w^2$ ) and between ( $\tau_b^2$ ) cluster pairs with ( $\tau^2 = \tau_w^2 + \tau_b^2$ )



## The need for an informative prior

---

- With a small number of clusters, the trial will provide little information on  $\tau^2$  and even less information on  $\gamma = \tau_w^2 / (\tau_w^2 + \tau_b^2)$
- Without informative priors, an “honest” computation of posterior uncertainty (one that integrates over uncertainty in  $\tau^2$  and  $\gamma$ ) will be so large as to be useless
- Therefore, either don't do the study or use informative priors to “bring in” outside information
- Fortunately, other weight loss studies provide credible and informative prior information on  $\tau^2$ , but not so for  $\gamma$ 
  - For  $\gamma$ , we need to rely primarily on expert opinion and sensitivity analysis

## A Bayesian Model

- Use an informative, data-based prior for  $\tau^2$  and a small-mean, small-variance prior for  $\gamma$

$$\tau^2 \sim \text{IG} := \tau_{50}^2 \text{ with } \tau_{95}^2 = 2 \times \tau_{50}^2$$

$$[\gamma \mid \epsilon, M] \sim \text{Beta}(\epsilon, M)$$

$$E(\gamma) = \epsilon, V(\gamma) = \epsilon(1 - \epsilon)/M$$

- Take the “best estimates” of  $(\sigma^2, \rho)$  from other cluster-randomized studies of weight change and obtain  $\sigma^2 \approx (0.34)^2$ , likely  $\hat{\rho}$ : (0.006, 0.010, 0.050)
- $\Rightarrow 10^4 \times \tau^2 = (7.0, 11.7, 60.8)$ ,  
 **$10^4 \tau_{50}^2 = 11.7, 10^4 \tau_{95}^2 = 23.4$**
- Use  $\epsilon \approx 0.10$  and a relatively large  $M = 15$ 
  - The 90<sup>th</sup> percentile is approximately 0.20
  - Conservative in that there is little gain from pairing

## Addressing non-standard and otherwise challenging goals

### Bayesians have a corner on the market

---

- Ranks and Histograms
- Complicated, non-linear models
- Complicated goals like adaptive design
- Regions
  - Bioequivalence & non-Inferiority
  - Inherently bivariate treatment comparisons
  - Adaptive design based on relations among parameters

## Bioequivalence & Non-inferiority

---

- $\Delta$  is the treatment difference
- $(-\Delta_*, \Delta^*)$  is the interval of equivalence  
(determined by clinical/biologic/policy considerations)

**Bio-equivalence:**  $-\Delta_* \leq \Delta \leq \Delta^*$

**Non-inferiority:**  $-\Delta_* \leq \Delta$  (negative  $\Delta$  is inferior)

- Compute relevant posterior probabilities and design so that these will be sufficiently extreme under parameter scenarios of interest
- Can use this formalism to produce desired frequentist properties

## Inherently bivariate treatment comparisons

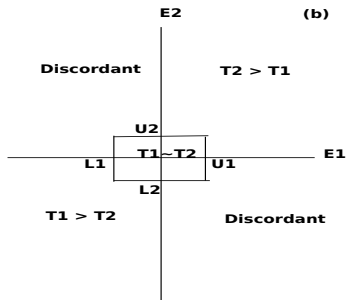
---

- Compare two treatments based on a bivariate outcome
  - Viral load and CD<sub>4</sub>
  - Efficacy and SAE incidence
- Construct  $R^2$  regions of equivalence and advantage
- Inherently  $R^2$  regions can capture clinically important trade-offs
  - But, only generalized rectangles result from combining single-endpoint, univariate regions
- The Bayesian formalism is needed to compute,

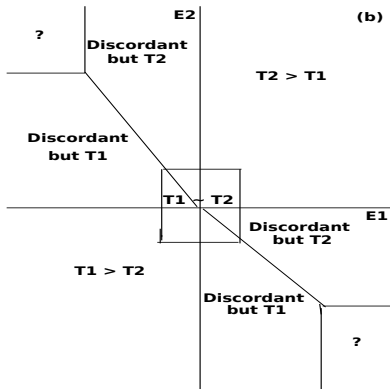
**pr (region | data)**

## Combining endpoint-specific, univariate regions

---



## Inherently $R^2$ Regions



## Adaptive design based on relations among parameters

---

- Single parameter assessments
  - ① if  $pr(\theta > \theta_{safety} > 0 \mid \text{data}) > 0.20$ , stop
  - ② if  $pr(\theta < \theta_{efficacy} < 0 \mid \text{data}) > 0.98$ , stop
  - ③ if  $pr(\text{either 1 or 2 by end of study} \mid \text{data}) > 0.90$ , continue as is, otherwise, either stop for futility or increase accrual/clinics
    - Requires simulating futures, conditional on current information
    - This requires assumptions on accrual, dropouts, cross-overs, ...
- Parameter relations
  - if  $pr(\text{Rel}(\theta_1, \theta_2) > 0 \mid \text{data}) > 0.98$ , stop

**Don't insist on strict frequentist goals**



## Continue or stop a dose

---

- Start with doses  $(d_1, \dots, d_m)$
- $P(d, \theta) = pr(\text{favorable response} \mid d, \theta)$ 
  - If  $P(d, \theta \mid \text{data}) \geq 0.75$ , continue accruing to the dose
  - If  $P(d, \theta \mid \text{data}) < 0.75$ , stop accruing to the dose
- More generally, when allocating to doses, trade-off gaining information on  $\theta$  and doing the best for the next patient

## Allocation on Outcome

---

- Controversial in clinical trials, but can be effective
- Less controversial: Adaptive randomization stratification
- Best approaches use Bayesian structuring for either Bayes or Frequentist goals

## ≈ Louis 1975 Biometrika

---

- Gaussian Responses, treatments  $T_A$  and  $T_B$
- SPRT Stopping based on the likelihood-ratio ( $L_{mn}$ ) after  $m$  responses  $T_A$  and  $n$  on  $T_B$ 
  - Continue if  $0 < A < L_{mn} < B < \infty$
  - No maximum accrual
- For non-anticipating, adaptive allocation rules, frequentist type I and II errors are controlled

## Approximately the Louis (1975) rule

---

- $\pi_{mn} = pr(T_B > T_A \mid \text{data}) = L_{mn}/(1 + L_{mn})$  for a 50/50 prior
  - Can use  $\pi_{00} \neq 0.5$ , but equipoise requires close to 0.5
- Select an imbalance parameter:  $0.5 \leq \phi < 1.0$
- Allocate to keep

$$m/(m+n) \approx \phi\pi_{mn} + (1-\phi)(1-\pi_{mn})$$

## Simulation Results, Treatment A is better

---

$100\phi \rightarrow$	50	55	70
$M_\phi$	78.2	87.6	127.5
$N_\phi$	77.7	71.7	57.2
$M_\phi + N_\phi$	155.9	159.3	184.7
Cost	0	<b>3.4</b>	<b>28.8</b>
Benefit	0	<b>6.0</b>	<b>20.5</b>

- $M_\phi$  and  $N_\phi$  are expected sample sizes
- $\text{Cost} = (M_\phi + N_\phi) - (M_{0.5} + N_{0.5})$
- $\text{Benefit} = N_{0.5} - N_\phi$

## Bayes & Multiplicity

---

- The prior to posterior mapping doesn't "know" about multiple comparisons
- With additive, component-specific losses each comparison is optimized separately with no accounting for the number of comparisons
- However, use of a hyper-prior (or EB) links the components since the posterior "borrows information"
  - Inducing shrinkage as a multiplicity control
- If collective penalties are needed, use a multiplicity-explicit loss function

## The k-ratio, Z test

### RE ANOVA

- $\theta_1, \dots, \theta_K$  iid  $N(\mu, \tau^2)$
  - $[Y_{ik} | \theta_k]$  ind  $N(\theta_k, \sigma^2)$
  - $[\theta_k | Y_{.k}] \sim N\left(\mu + (1 - B)(Y_{.k} - \mu), (1 - B)\frac{\sigma^2}{n}\right)$
- $$F = 1/\hat{B}$$

### Compare columns 1 and 2:

$$Z_{12}^{Bayes} = Z_{12}^{freq} \left\{ \frac{(F-1)^+}{F} \right\}^{\frac{1}{2}} = \left( \frac{\sqrt{n}(Y_{.1} - Y_{.2})}{\hat{\sigma}\sqrt{2}} \right) \left\{ \frac{(F-1)^+}{F} \right\}^{\frac{1}{2}}$$

## Comments

---

- The magnitude of  $F$  adjusts the test statistic
- For large  $K$ , under the global null hypothesis ( $\tau^2 = 0$ ),  
 $\text{pr}[\text{all } Z_{ij} = 0] \geq 0.5$
- The FW rejection rate is much smaller than 0.5
- “Scoping” is important because the number of candidate comparisons influences the value of  $\hat{\mu}$  and  $\hat{B}$  and performance more generally
- Non-additive loss functions can be used
  - e.g.,  $1 + 1 = 2.5$
- These link inferences among components in addition to that induced by shrinkage



## Bayes and Subgroups: HDFP

---

- Randomized between Referred Care (RC) and Stepped Care (SC)
- Outcome: 5-year death rate, overall and in 12 strata
- $Y = 1000 \log[\text{OR}(\text{SC}:\text{RC})]$
- Strata
  - Initial diastolic blood pressure
    - I = 90-104
    - II = 105-114
    - III =  $\geq 115$
  - Race (B/W)
  - Gender (F/M)

## HDFP Results

---

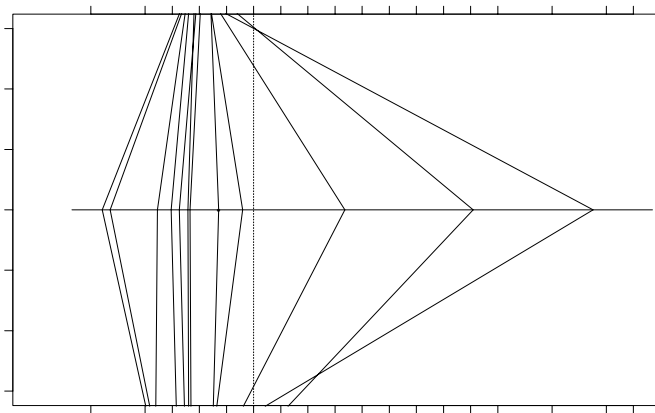
Group		$Y$	$\hat{\theta}$	$1 - B$	$\hat{\sigma}$	PSD
I	BM	-129	-157	54	170	125
	BF	-304	-240	44	206	137
	WM	-242	-220	59	153	117
	WF	-355	-253	39	231	144
II	BM	-274	-213	29	290	155
	BF	-529	-266	23	337	161
	WM	-41	-156	22	349	162
	<b>WF</b>	809	-61	13	479	171
III	BM	-558	-273	23	337	161
	BF	-235	-197	18	389	166
	<b>WM</b>	336	-122	13	483	171
	<b>WF</b>	1251	-103	6	730	178

All posterior means are negative

## HDFP Subgroup Analysis: Ensemble Estimates

$(1 - B)^{\frac{1}{2}}$  on data rather than  $(1 - B)$

---



Top:PMs Middle:MLEs Bottom:Ensemble

## Bayesian Monitoring

---

### CPCRA-TOXO: Prevention of Toxoplasmosis

- Eligibility
  - Either an AIDS defining illness or  $CD4 < 200$
  - A positive titre for *toxoplasma gondii*
- Originally designed with four treatment groups
  - Active & placebo clindamycin, 2:1
  - Active & placebo pyrimethamine, 2:1
- The clindamycin arm was stopped after a few months
- We look at PYRI vs Placebo

## Analysis of the Toxo Trial

---

WE

- Used the Cox model
  - Adjusted for baseline CD4
- Elicited priors from three HIV/AIDS clinicians, one PWA conducting AIDS research and one AIDS epidemiologist
- Monitored the trial after-the-fact
  - The DSMB monitored it during-the-fact
- “Stopped” when the posterior probability of benefit or the posterior probability of harm got sufficiently high
- Used a variety of prior distributions, including an equally-weighted mixture of the five elicited priors

## The Cox Model

---

- Partial likelihood:

$$L(\theta_1, \theta_2) = \prod_{j=1}^d \left( \frac{e^{\theta_1 z_{1j} + \theta_2 z_{2j}}}{\sum_{\nu \in \mathcal{R}_j} e^{\theta_1 z_{1\nu} + \theta_2 z_{2\nu}}} \right)$$

- $d$  is the number of individuals experiencing the endpoint (death or TE)
- $\mathcal{R}_j$  is the  $j^{\text{th}}$  risk set
  - The collection of individuals alive and in the study immediately preceding the  $j^{\text{th}}$  endpoint
- Covariates
  - Treatment group status:  $z_{1j} = 1$  or  $0$  a.a. person  $j$  received pyrimethamine or placebo
  - CD4 cell count at study entry: ( $z_{2j}$ )
- Negative values of  $\theta_1$  indicate a benefit for pyrimethamine

## Prior Distributions

---

- We put a flat prior on the CD4 effect ( $\theta_2$ )
- We elicited priors for the Pymethamine effect ( $\theta_1$ )

## Elicitation

---

- Ask about potential observables
- $P = \text{pr}[\text{event in two years}]$
- $P_0 = \text{best guess for the placebo}$ 
  - mode, median, mean
- Then, distribution of  $P_{pyri} \mid P_0$ 
  - percentiles
  - draw a picture
- Convert to Cox model parameter:

$$\theta_1 = \log(1 - P_0) - \log(1 - P_{pyri})$$



# Elicited Priors

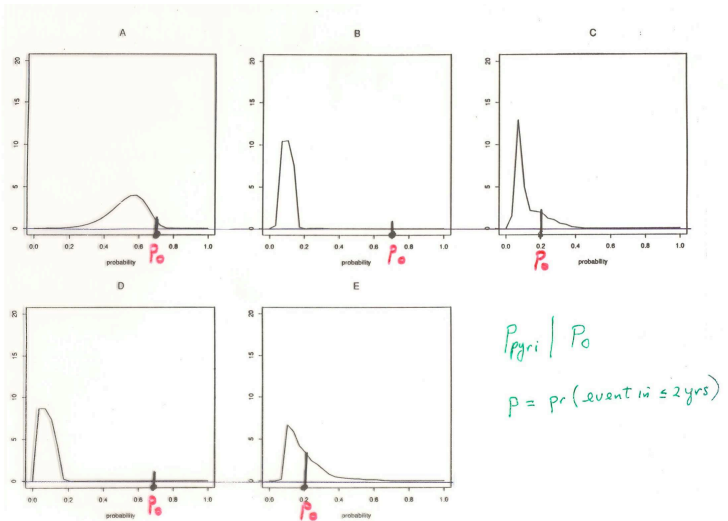


Fig 2: the prior distributions on the probabilities

## Actual TOXO Monitoring

---

- Monitored for file closing dates:  
01/15/91, 07/31/91, and 12/31/91
- At its final meeting the board recommended stopping
- The pyrimethamine group had not shown significantly fewer TE events and the low overall TE rate made a statistically significant difference unlikely to emerge.
- Also, an *increase* in the number of deaths in the pyrimethamine group was noted

## Posteriors for a flat prior

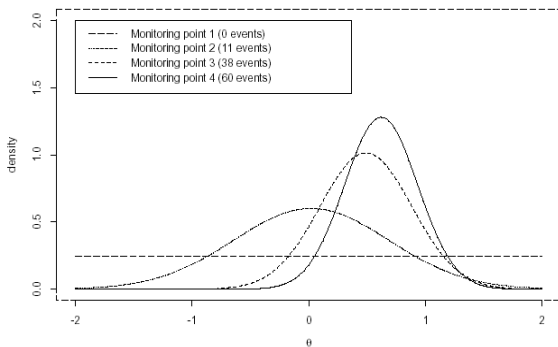
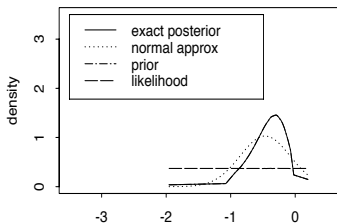
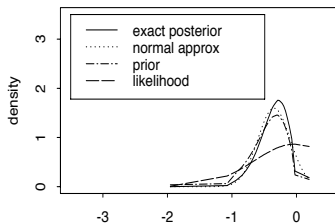


Figure 3: Posterior for the treatment effect under a flat prior, TE trial data.  
Endpoint is TE or death; Covariate is baseline CD4 count

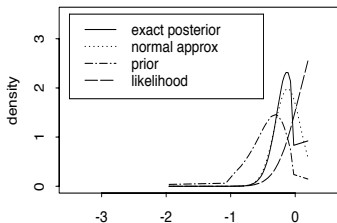
## Various Posterior Distributions



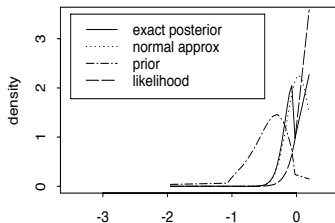
n = 0 events



n = 11 events

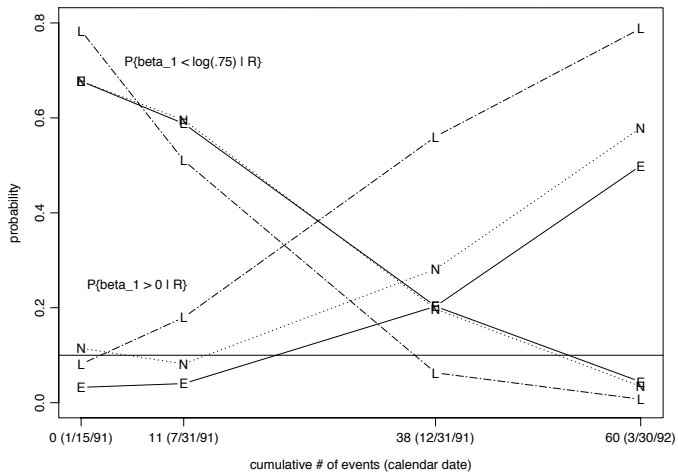


n = 38 events



n = 60 events

## Posterior Probabilities of regions (Bayes can take longer to stop!)



E = exact; N = normal approximation; L = likelihood

## After the Fact Monitoring

---

- The elicited priors bear almost no resemblance to the eventual data
- Our experts believed
  - That TE is common in this patient population
  - That pyrimethamine has a substantial prophylactic effect
- Yet, eventually the data overwhelmed the elicited priors

**Would it have been ethical to wait  
so that these experts were convinced?**

## Summary

---

- There have been many Bayesian successes, but much remains to be done
  - Methodologically
  - Sociologically
- CDRH, its encouragement and guidance have accelerated adoption and innovation
  - *Guidance for the Use of Bayesian Statistics in Medical Device Clinical Trials*
- The CDRH stem cell is seeding metastases to other FDA Centers

## Recommendations

---

- 1 Encourage Bayesian design for frequentist analysis
  - To promote formal assembly of prior information
  - To produce realistic designs in the context of important uncertainties
- 2 Encourage use of the Bayesian formalism to develop all monitoring plans
  - Sample size adjustment, accrual termination, follow-up termination (for efficacy or curtailment)
    - Priors and losses as tuning parameters for frequentist goals
    - Bayesian goals
- 3 Evaluate and introduce fully Bayesian designs and analyses



## Closing

---

- Potential Bayesian benefits are substantial, but validity and effectiveness require expertise and care
- Bayes isn't always worth the bother, but acceptance and benefits burgeon
- The philosophy and formalism are by no means panaceas
- There are no free lunches in statistics

**Happily, there are a broad array of reduced-price meals**

**Many based on Bayesian recipes!**