Bayesian Modeling, Inference, Prediction and Decision-Making

5: Bayesian Model Specification (Section 1)

David Draper (draper@ams.ucsc.edu)

Department of Applied Mathematics and Statistics University of California, Santa Cruz (USA)

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Outline

(1) An axiomatization of statistics (Draper 2011).

(2) Foundations of probability seem (to me) to be secure: (RT Cox, 1946) Principles \rightarrow Axioms \rightarrow Theorem:

- (3) Foundations of inference, prediction and decision-making not yet secure: fixing this would yield a Theory of Applied Statistics, which we do not yet have; two remaining challenges:
 - (a) **Cox's Theorem** doesn't **require** You to **pay attention** to a **basic scientific issue**: how **often** do You get the **right answer**?

(b) Too much ad hockery in model specification: still lacking **Principles** \rightarrow **Axioms** \rightarrow **Theorems**.

(4) A Calibration Principle fixes 3 (a) via Bayesian decision theory.

(5) The Modeling-As-Decision Principle, the Prediction Principle and the Decision-Versus-Inference Principle help with 3 (b).

An Example, to Fix Ideas

Example (Krnjajić, Kottas, Draper [KKD] 2008): *In-home geriatric* assessment (*IHGA*). In an **experiment** conducted in the **1980s** (Hendriksen et al. 1984), **572** elderly people, representative of $\mathcal{P} =$ {all **non-institutionalized elderly people** in **Denmark**}, were randomized, **287** to a **control** (*C*) group (who received **standard health care**) and **285** to a **treatment** (*T*) group (who received **standard care plus IHGA**: a kind of **preventive medicine** in which each person's **medical** and **social needs** were assessed and acted upon **individually**).

One **important outcome** was the **number of hospitalizations** during the **two-year** life of the study:

	Number of Hospitalizations						
Group	0	1		k	n	Mean	SD
Control	<i>n</i> _{C0}	n_{C1}			$n_{C} = 287$	ӯс	s _C
Treatment	n_{T0}	n_{T1}		n _{Tk}	$n_T = 285$	\bar{y}_T	s_T

Let μ_C and μ_T be the **mean hospitalization rates** (per two years) in \mathcal{P} under the *C* and *T* conditions, respectively.

Here are **four statistical questions** that **arose** from **this study**:

The Four Principal Statistical Activities

 Q_1 : Was the mean number of hospitalizations per two years in the IHGA group smaller than that in control by an amount that was large in practical terms? $\left[\frac{\text{description}}{\text{involving}} \left(\frac{\bar{y}_T - \bar{y}_C}{\bar{y}_C} \right) \right]$



 Q_2 : Did IHGA reduce the mean number of hospitalizations per two years by an amount that was large in statistical terms?

inference about $\left(\frac{\mu_T - \mu_C}{\mu_C}\right)$

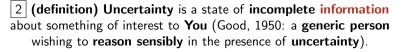
 Q_3 : On the basis of this study, how accurately can You predict the total decrease in hospitalizations over a period of N years if IHGA were implemented throughout Denmark? [prediction]

 Q_4 : On the basis of this study, is the decision to implement IHGA throughout Denmark optimal from a cost-benefit point of view? [decision-making]

These questions **encompass** almost all of the **discipline** of **statistics**: describing a data set D, generalizing outward inferentially from D, predicting new data D^* , and helping people make decisions in the presence of uncertainty (I include sampling/experimental design under decision-making; omitted: data quality assurance (QA), ...).

An Axiomatization of Statistics

1 (definition) Statistics is the study of uncertainty: how to measure it well, and how to make good choices in the face of it.



3 (axiom) (Your uncertainty about) "Something of interest to You" can always be expressed in terms of propositions: true/false statements A, B, \ldots

Examples: You may be uncertain about the truth status of

• A = (a Democrat will be elected U.S. President in 2016), or

• B = (the **in-hospital mortality rate** for patients at **hospital** H admitted in **calendar 2010** with a principal diagnosis of **heart attack** was **between 5% and 25%**).

4 (implication) It follows from 1-3 that statistics concerns Your information (NOT Your beliefs) about A, B, ...

Axiomatization (continued)

5 (axiom) But Your information cannot be assessed in a vacuum: all such assessments must be made relative to (conditional on) Your background assumptions and judgments about how the world works vis à vis A, B, \ldots .

6 (axiom) These assumptions and judgments, which are themselves a form of information, can always be expressed in a set B of propositions (examples below).

7 (definition) Call the "something of interest to You" θ ; in applications θ is often a vector (or matrix, or array) of real numbers, but in principle it could be almost anything (a function, an image of the surface of Mars, a phylogenetic tree, ...).

IHGA example: θ = mean relative decrease $\left(\frac{\mu_T - \mu_C}{\mu_C}\right)$ in hospitalization rate in \mathcal{P} .

8 (axiom) There will typically be an information source (data set) D that You judge to be relevant to decreasing Your uncertainty about θ ; in applications D is often again a vector (or matrix, or array) of real numbers, but in principle it too could be almost anything (a movie, the words in a book, ...).

Axiomatization (continued)

Examples of \mathcal{B} :

• In the IHGA study, based on the experimental design, ${\cal B}$ would include the propositions

(Subjects were representative of [like a random sample from] \mathcal{P}),

(Subjects were randomized into one of two groups, treatment (standard care + IHGA) or control (standard care)).

9 (implication) The presence of *D* creates a dichotomy:

• Your information about θ {internal, external} to D.

(People often talk about a different dichotomy: Your information about θ {before, after} D arrives (prior, posterior), but temporal considerations are actually irrelevant.)

- 10 (implication) It follows from 1-9 that statistics concerns itself principally with five things (omitted: description, data QA, ...):
 - (1) Quantifying Your information about θ internal to D (given \mathcal{B}), and doing so well (this term is not yet defined);

(2) Quantifying Your information about θ external to D (given \mathcal{B}), and doing so well;

(3) Combining these two information sources (and doing so well) to create a summary of Your uncertainty about θ (given \mathcal{B}) that includes all available information You judge to be relevant (this is inference);

and using all Your information about θ (given \mathcal{B}) to make

(4) **Predictions** about **future** data values D^* and

(5) **Decisions** about how to **act sensibly**, even though **Your information** about θ may be **incomplete**.

Foundational question: How should these tasks be accomplished?

This question has **two parts**: **probability** and **statistics**; in my view, the **probability foundations** are **secure**, but the **statistics foundations** still need **attending to**.

Let's look first at the probability foundations.

Theory of Probability: Kolmogorov

From the 1650s (Fermat, Pascal) through the 18th century (Bayes, Laplace) to the period 1860–1930 (Venn, Boole, von Mises), three different approaches for how to think about uncertainty quantification — classical, Bayesian, and frequentist probability were put forward in an intuitive way, but no one ever tried to prove a theorem of the form {given these premises, there's only one sensible way to quantify uncertainty} until Kolmogorov, de Finetti, and RT Cox.

— Kolmogorov (1933): following (and rigorizing) Venn, Boole and von Mises, probability is a function on (possibly some of) the subsets of a sample space Ω of uncertain possibilities, constrained to obey some reasonable axioms; this is excellent, as far as it goes, but many types of uncertainty cannot (uniquely, comfortably) be fit into this framework (examples follow).

Kolmogorov was trying to make precise the intuitive notion of repeatedly choosing a point at random in a Venn diagram and asking how frequently the point falls inside a specified set, i.e., his concept of probability had a repeated-sampling, frequentist character:

Frequentist Probability: Kolmogorov

"The basis for the applicability of the results of the mathematical theory of probability to real 'random phenomena' must depend on some form of the frequency concept of probability, the unavoidable nature of which has been established by von Mises in a spirited manner."

* **Example:** You're about to roll a **pair of dice** and **You regard** this dice-rolling as **fair**, by which You mean that (in Your judgment) all $6^2 = 36$ elemental outcomes in $\Omega = \{(1, 1), (1, 2), \dots, (6, 6)\}$ are equally probable; then the Kolomogorov probability of snake eyes ((1, 1)) exists and is unique (from Your fairness judgment), namely $\frac{1}{36}$; but

* **Example:** You're a **doctor**; a **new patient** presents saying that he may be **HIV positive**; what's the **Kolmogorov probability** that he is?

What's Ω? This patient is not the result of a uniquely-specifiable repeatable "random" process, he's just a guy who walked into Your doctor's office, and — throughout the repetitions of whatever repeatable phenomenon anyone might imagine — his HIV status is not fluctuating "randomly": he's either HIV positive or he's not.

Theory of Probability: de Finetti

The closest You can come to making Kolmogorov's approach work here is to imagine the set Ω of all people {similar to this patient in all relevant ways} and ask how often You'd get an HIV-positive person if You repeatedly chose one person at random from Ω , but to make this operational You have to specify what You mean by "similar to, in all relevant ways," and if You try to do this You'll notice that it's not possible to do so uniquely (in such a way that all other reasonable people would unanimously agree with You).

de Finetti (1937): rigorizing Bayes, probability is a quantification of betting odds about the truth of a proposition, constrained to obey axioms guaranteeing coherence (absence of internal contradictions); this is more general than Kolmogorov — in fact, it's as general as You can get: any statement about sets can be expressed in terms of propositions — but betting odds are not fundamental to science.

de Finetti made **many important contributions** — in particular, his concept of **exchangeability** (more on this later) is **crucial** in **Bayesian modeling** — but **science** is about **information**, not **betting**.

Theory of Probability: RT Cox

 — RT Cox (1946): following Laplace, probability is a quantification of information about the truth of one or more propositions, constrained to obey axioms guaranteeing internal logical consistency; this is both fundamental to science and as general as You can get.

Cox's goal was to identify what **basic rules** p/(A|B) — the **plausibility** (weight of evidence in favor) of (the truth of) A given B — should follow so that p/(A|B) behaves **sensibly**, where A and B are **propositions** with B assumed by You to be true and the truth status of A unknown to You.

He did this by **identifying** a set of **principles** making **operational** the word **"sensible"** (Jaynes, 2003):

• Suppose You're willing to represent degrees of plausibility by real numbers (i.e., pI(A|B) is a function from propositions A and B to \Re);

- You insist that Your reasoning be logically consistent:
- If a plausibility assessment can be arrived at in more than one way, then every possible way must lead to the same value.

Cox's Principles and Axioms

— You always take into account **all of the evidence** You judge to be **relevant** to the **plausibility assessment** under consideration (this is the **Bayesian** version of **objectivity**).

— You always represent equivalent states of information by equivalent plausibility assignments.

From these principles Cox derived a set of axioms:

• The plausibility of a proposition determines the plausibility of the proposition's negation; each decreases as the other increases.

• The plausibility of the conjunction AB = (A and B) of two propositions A, B depends only on the plausibility of B and that of $\{A \text{ given that } B \text{ is true}\}$ (or equivalently the plausibility of A and that of $\{B \text{ given that } A \text{ is true}\}$).

• Suppose *AB* is **equivalent** to *CD*; then if You acquire **new information** *A* and later acquire **further new information** *B*, and **update** all **plausibilities** each time, the **updated plausibilities** will be the **same** as if You had **first acquired new information** *C* and **then acquired further new information** *D*.

Cox's Theorem

From these axioms Cox proved a theorem showing that uncertainty quantification about propositions behaves in one and only one way:

Theorem: If You accept **Cox's axioms**, then to be **logically consistent** You **must** quantify uncertainty as follows:

• Your plausibility operator pl(A|B) — for propositions A and B — can be referred to as Your probability P(A|B) that A is true, given that You regard B as true, and $0 \le P(A|B) \le 1$, with certain truth of A (given B) represented by 1 and certain falsehood by 0.

• (normalization) $P(A|B) + P(\overline{A}|B) = 1$, where $\overline{A} = (\text{not } A)$.

• (the product rule):

 $P(AB|C) = P(A|C) \cdot P(B|AC) = P(B|C) \cdot P(A|BC).$

The proof (see, e.g., Jaynes (2003)) involves deriving two functional equations F[F(x, y), z] = F[x, F(y, z)] and $x S\left[\frac{S(y)}{x}\right] = y S\left[\frac{S(x)}{y}\right]$ that pl(A|B) must satisfy and then solving those equations.

A number of important corollaries arise from Cox's Theorem:

Optimal Reasoning Under Uncertainty

• (the sum rule):

 $P(A \text{ or } B|C) \equiv P(A+B|C) = P(A|C) + P(B|C) - P(AB|C).$

• Extensions of the product and sum rules to an arbitrary finite number of propositions are easy, e.g.,

$$P(A B C|D) = P(A|D) \cdot P(B|AD) \cdot P(C|ABD) \text{ and}$$

$$P(A+B+C|D) = P(A|D) + P(B|D) + P(C|D) - P(AB|D) - P(AC|D) - P(AC|D) - P(BC|D) + P(ABC|D).$$

This framework (obviously) covers optimal reasoning about uncertain quantities θ taking on a finite number of possible values; less obviously, it also handles (equally well) situations in which the set Θ of possible values of θ has infinitely many elements.

- **Example:** You're studying **quality of care** at the **17 Kaiser Permanente (KP) northern California hospitals** in **2003–7**, before the era of **electronic medical records**; during that time there was a **population** \mathcal{P} of N = 8,561 patients at these facilities with a primary admission diagnosis of heart attack. You take a simple random sample of n = 112 of these admissions and record whether or not each patient had an unplanned transfer to the intensive care unit (ICU), observing s = 4 who did; θ is the proportion of such unplanned transfers in all of \mathcal{P} ; here $\Theta = \{\frac{0}{N}, \frac{1}{N}, \dots, \frac{N}{N}\}$, which can be conveniently approximated by $\Theta' = [0, 1]$.

Prior to 2003, the **proportion** of such **unplanned transfers** for heart **attack patients** at **KP** in the **northern California region** was about q = 0.07, so **interest** focuses on P(A|DB), where A is the **proposition** $(\theta \le q)$, D is the **proposition** (s = 4), and B includes (among other things) **details** about the **sampling experiment** (e.g., (n = 112)).

In this setup θ is usually called a (population) parameter, and is not itself the result of any sampling experiment (random or otherwise); for this reason, it's not possible to (directly) quantify uncertainty about θ from the Kolmogorov (set-theoretic) point of view, but it makes perfect sense to do so from the RT Cox (propositional) point of view.

Optimal Reasoning About a Continuous θ

You could now more generally define a function $F_{(\theta|DB)}(q) = P(\theta \le q|DB)$ and call it the cumulative distribution function (CDF) for (not of) $(\theta|DB)$, which is shorthand for

the **CDF** for **Your uncertainty about** θ given D and \mathcal{B} .

If $F_{(\theta|DB)}(q)$ turns out to be **continuous** and **differentiable** in q (I haven't said yet how to **calculate** F), it will be **convenient** to write

$$F_{(\theta|D\mathcal{B})}(b) - F_{(\theta|D\mathcal{B})}(a) = P(a < \theta \le b|D\mathcal{B}) = \int_a^b p_{(\theta|D\mathcal{B})}(q) dq, \quad (1)$$

where the (partial) derivative $p_{(\theta|DB)}(q)$ of $F_{(\theta|DB)}$ with respect to q can be called the density for (not of) (Your uncertainty about) θ given D and B.

In a small abuse of notation it's common to write $F(\theta|DB)$ and $p(\theta|DB)$ instead of $F_{(\theta|DB)}(q)$ and $p_{(\theta|DB)}(q)$ (respectively), letting the argument θ of $F(\cdot|DB)$ and $p(\cdot|DB)$ serve as a reminder of the uncertain quantity in question.

Ontology and Epistemology

<u>NB</u> In the Kolmogorov approach a random variable X is a function from Ω to some outcome space O, and if $O = \Re$ You'll often find it useful to summarize X's behavior through the CDF of X: $F_X(x) = P$ (the set of $\omega \in \Omega$ such that $X(\omega) \le x$), usually written in propositional-style shorthand as $F_X(x) = P(X \le x)$.

In the **RT** Cox approach, there are no random variables; there are uncertain things θ whose uncertainty (when $\Theta = \Re^k$, for integer $1 \le k < \infty$) can usefully be summarized with **CDFs** and densities.

Jaynes (2003) makes a worthwhile distinction: the statements

There is noise in the room.

The room is noisy.

Talking about "the density of θ " would be to confuse ontology and epistemology;

The Mind-Projection Fallacy

Jaynes calls this confusion of {the world} (ontology) with {Your uncertainty about the world} (epistemology) the mind-projection fallacy, and it's clearly a mistake worth avoiding.

Returning to the corollaries of Cox's Theorem,

• Given the set \mathcal{B} , of propositions summarizing Your background assumptions and judgments about how the world works as far as θ , D and future data D^* are concerned:

(a) It's **natural** (and indeed **You must be prepared** in this approach) to specify **two conditional probability distributions**:

- $p(\theta|B)$, to quantify **all information** about θ **external** to D that You judge **relevant**; and
 - $p(D|\theta B)$, to quantify Your predictive uncertainty, given θ , about the data set D before it's arrived.

(b) Given the distributions in (a), the distribution $p(\theta|DB)$ quantifies all relevant information about θ , both internal and external to D, and must be computed via Bayes's Theorem:

Optimal Inference, Prediction and Decision

$$p(\theta|D\mathcal{B}) = c \, p(\theta|\mathcal{B}) \, p(D|\theta\mathcal{B}) \,, \qquad \text{(inference)} \qquad (2)$$

where c > 0 is a normalizing constant chosen so that the left-hand side of (2) integrates (or sums) over Θ to 1;

(c) Your predictive distribution $p(D^*|DB)$ for future data D^* given the observed data set D must be expressible as follows:

$$p(D^*|D\mathcal{B}) = \int_{\Theta} p(D^*|\theta D\mathcal{B}) p(\theta|D\mathcal{B}) d\theta;$$

often there's **no information** about D^* contained in D if θ is known, in which case this expression **simplifies** to

$$p(D^*|D\mathcal{B}) = \int_{\Theta} p(D^*|\theta\mathcal{B}) p(\theta|D\mathcal{B}) d\theta; \qquad \text{(prediction)} \qquad (3)$$

(d) to make a sensible **decision** about which **action** *a* You should take in the face of Your **uncertainty** about θ , You **must be prepared to specify**

(i) the set \mathcal{A} of **feasible actions** among which You're **choosing**, and

Bayesian Reasoning

(ii) a utility function $U(a, \theta)$, taking values on \Re and quantifying Your judgments about the rewards (monetary or otherwise) that would ensue if You chose action *a* and the unknown actually took the value θ — without loss of generality You can take large values of $U(a, \theta)$ to be better than small values;

then the **optimal decision** is to choose the action a^* that **maximizes** the **expectation** of $U(a, \theta)$ over $p(\theta|DB)$:

$$a^* = \operatorname*{argmax}_{a \in \mathcal{A}} E_{(\theta | D \mathcal{B})} U(a, \theta) = \operatorname*{argmax}_{a \in \mathcal{A}} \int_{\Theta} U(a, \theta) \, p(\theta | D \mathcal{B}) \, d\theta \,. \tag{4}$$

The equation solving the **inference problem** is **traditionally** attributed to **Bayes (1764)**, although it's just an **application** of the **product rule** (page 14), which was **already in use** by **(James) Bernoulli** and **de Moivre** around **1715**, and **Laplace** made **much better use** of this equation from **1774** to **1827** than Bayes did in **1764**; nevertheless the **Laplace/Cox propositional approach** is typically referred to as **Bayesian reasoning**.

Logical Consistency \rightarrow Bayesian Reasoning Justified

Cox's Theorem is equivalent to the assertion

If You wish to quantify Your uncertainty about an unknown θ (and make predictions and decisions in the presence of that uncertainty) in a logically internally consistent manner (as specified through Cox's axioms), on the basis of data D and background assumptions/judgments \mathcal{B} , then You can achieve this goal with Bayesian reasoning, by specifying $p(\theta|\mathcal{B})$, $p(D|\theta \mathcal{B})$, and $\{\mathcal{A}, U(a, \theta)\}$ and using equations (2-4).

This assertion has not rendered Bayesian analyses ubiquitous, although the value of Bayesian reasoning has become increasingly clear to an increasingly large number of people in the last 20 years, now that advances in computing have made the routine use of equations (2-4) feasible.

Advantages include a unified probabilistic framework: e.g., in my earlier ICU example, Kolmogorov's non-Bayesian approach does not permit direct probability statements about a population parameter,

but **Cox's Theorem permits You** to make such statements (summarizing **all relevant available information**) in a natural way.

The Specification Burden

It's worth noting, however, that there really is a theorem here, of the form $A \rightarrow B$, from which $\overline{B} \rightarrow \overline{A}$; this comes close to the assertion

If You employ non-Bayesian reasoning then You're open to the possibility of logical inconsistency,

and indeed there have been some **embarrassing moments** in **non-Bayesian inference** over the past **100 years** (e.g., **negative estimates** for quantities that are **constrained** to be **non-negative**).

Challenges: These **corollaries** to **Cox's theorem** solve problems (3–5) above (page 8) — they leave **no ambiguity** about how to draw **inferences**, and make **predictions** and **decisions**, in the presence of **uncertainty** — but problems (1) and (2) are still **unaddressed**: to **implement** this **logically-consistent approach** in a given application, You have to **specify**

p(θ|B), usually called Your prior information about θ (given B; this is better understood as a summary of all relevant information about θ external to D, rather than by appeal to any temporal (before-after) considerations);

The Specification Burden (continued)

- p(D|θ B), often referred to as Your sampling distribution for D given θ (and B; this is better understood as Your conditional predictive distribution for D given θ, before D has been observed, rather than by appeal to other data sets that might have been observed); and
 - the action space A and the utility function U(a, θ) for decision-making purposes.

The results of implementing this approach are

- p(θ|D B), often referred to as Your posterior distribution for θ given D (and B; as above, this is better understood as the totality of Your current information about θ, again without appeal to temporal considerations);
- Your posterior predictive distribution $p(D^*|DB)$ for future data D^* given the observed data set D; and
 - the optimal decision a^* given all available information (and \mathcal{B}).

To summarize: Inference and prediction require You to specify $p(\theta|B)$ and $p(D|\theta|B)$; decision-making requires You to specify the same

two **ingredients** plus A and $U(a, \theta)$; how should this be done in a **sensible** way?

Cox's Theorem and its corollaries provide no constraints on the specification process, apart from the requirement that all probability distributions be proper (integrate or sum to 1).

In my view, in seeking answers to these specification questions, as a profession we're approximately where the discipline of statistics was in arriving at an optimal theory of probability before Cox's work: many people have made ad-hoc suggestions (some of them good), but little formal progress has been made.

Developing (1) principles, (2) axioms and (3) theorems about optimal specification could be regarded as creating a Theory of Applied Statistics, which we need but do not yet have.

 $p(\theta|\mathcal{B}), p(D|\theta \mathcal{B}) \text{ and } \{\mathcal{A}, U(a, \theta)\}$ are all **important**; I'll **focus** here on the **problem** of **specifying** $\{p(\theta|\mathcal{B}), p(D|\theta \mathcal{B})\}$ — call such a **specification** a **model** M for **Your uncertainty** about θ (I'll have one **brief comment** about **decision theory** at the end).

What I Mean By Optimal Model Specification

How should M be specified? Where is the progression

 $\textbf{Principles} \rightarrow \textbf{Axioms} \rightarrow \textbf{Theorems}$

to guide You, the way Cox's Theorem settled the foundational questions for probability?

In my view this is the **central unsolved foundational problem** in **statistical inference** and **prediction**.

Making progress on this problem requires defining the phrase "optimal model specification;" for this purpose the following two-step argument is helpful:

• All **Bayesian reasoning** under **uncertainty** is based on $P(A|B) = \frac{P(A|B)}{P(B)}$ for **true/false propositions** A and B, and this is **undefined** if B is **false**; therefore

Rule 1: You should **try hard not to condition on propositions** (a) that You **know to be false** and (b) that **MAY be false**.

This motivates the following

Getting From the Context and Design to the Model

Definition: In model specification, optimal = {to come as close as possible to the goal of conditioning only on propositions rendered true by the context of the study and the design of the data-gathering process}.

This seems hard to achieve; for example, in the IHGA case study, visualizing the data set before it arrives, it would look like the table shell presented back on page 3:

	Number of Hospitalizations						
Group	0	1		k	n	Mean	SD
Control	n _{C0}	n _{C1}		n _{Ck}	$n_{C} = 287$	ӯc	s C
Treatment	n_{T0}	n_{T1}		n_{Tk}	$n_T = 285$	Īγτ	ST

The problem context and design make this table shell something You can condition on, and the lack of previous trials with IHGA (this was the first time it was implemented anywhere) implies that You can also condition on a diffuse choice for $p(\theta|B)$ (with 572 observations, it won't matter much how this diffuseness is specified), but context and design don't seem to have anything to say about the predictive (sampling) distribution $p(D|\theta B)$.

The Calibration Principle

This is where a **good set of principles** starts to **help**: as a small **contribution** to **closing the gap** between **ad-hoc practice** and **lack of theory**, I'll focus in the rest of this **talk** on **four principles** worth considering, the **first** of which is the

Calibration Principle: In model specification, You should pay attention to how often You get the right answer, by creating situations in which You know what the right answer is and seeing how often Your methods recover known truth.

The reasoning behind the Calibration Principle is as follows:

(axiom) You want to help positively advance the course of science, and repeatedly getting the wrong answer runs counter to this desire.

(remark) There's nothing in the Bayesian paradigm to prevent You from making one or both of the following mistakes — (a) choosing $p(D|\theta B)$ badly; (b) inserting {strong information about θ external to D} into the modeling process that turns out after the fact to have been (badly) out of step with reality — and repeatedly doing this violates the axiom above.

Reasoning Behind the Calibration Principle

(remark) Paying attention to calibration is a natural activity from the frequentist point of view, but a desire to be well-calibrated can be given an entirely Bayesian justification via decision theory:

Taking a broader perspective over Your career, not just within any single attempt to solve an inferential/predictive problem in collaboration with other investigators, Your desire to take part positively in the progress of science can be quantified in a utility function that incorporates a bonus for being well-calibrated, and in this context (Draper, 2011) calibration-monitoring emerges as a natural and inevitable Bayesian activity.

This seems to be a **new idea**: **logical consistency** justifies **Bayesian uncertainty assessment** but **does not provide guidance** on **model specification**; if You accept the **Calibration Principle**, some of this guidance is provided, via **Bayesian decision theory**, through a desire on Your part to **pay attention to how often You get the right answer**, which is a **central scientific activity**.

But the Calibration Principle is not enough: in problems of realistic complexity You'll generally notice that (a) You're uncertain about θ

but (b) You're also uncertain about how to quantify Your uncertainty about θ , i.e., You have model uncertainty.

Cox's Theorem says that You can draw **logically-consistent inferences** about an **unknown** θ , given **data** D and **background information** \mathcal{B} , by **specifying** $M = \{p(\theta|M\mathcal{B}), p(D|\theta M\mathcal{B})\}$, but **item (b)** in the previous paragraph implies that there will typically be **more than one such plausible** M; what should You **do** about this?

It would be nice to be able to solve the inference problem by using Bayes's Theorem to compute $p(\theta | D \mathcal{M}_{all} \mathcal{B})$, where \mathcal{M}_{all} is the set of all possible models, but this is not feasible: just as Kolmogorov had to resort to σ -fields because the set of all subsets of an Ω with uncountably many elements is too big to meaningfully assign probabilities to all of the subsets, with a finite data set D, \mathcal{M}_{all} is too big for D to permit meaningful plausibility assessment of all the models in \mathcal{M}_{all} .

Having adopted the **Calibration Principle**, it **makes sense** to talk about an **underlying data-generating model** M_{DG} , which is **unknown to You** (more on this below).

An Ensemble \mathcal{M} of Models

Not being able to compute $p(\theta | D \mathcal{M}_{all} \mathcal{B})$, in practice the best You can do is to compute $p(\theta | D \mathcal{MB})$, where \mathcal{M} is an ensemble of models (finite or countably or uncountably infinite) chosen "well" by You, where "well" can and should be brought into focus by the Calibration Principle (and some of the other Principles to be introduced later): evidently what You want, among other things, is for \mathcal{M} to contain one or more models that are identical (or at least close) to M_{DG} .

Suppose initially, for the sake of discussion, that You've identified such an ensemble (I'll present some ideas for how to do this later) and that it turns out to be finite: $\mathcal{M} = (M_1, \ldots, M_k)$ for $2 \le k < \infty$; what next?

Are You **supposed** to try to **choose** one of these **models** (the **model selection problem**) and **discard** the rest, or **combine** them in some way (if so, **how**?), or **what**?

Solving the model uncertainty problem. People used to "solve" the problem of what to do about model uncertainty by ignoring it: it was common, at least through the mid-1990s, to

Dealing With Model Uncertainty

(a) use the data *D* to conduct a search among possible models, settling on a single (apparently) "best" model *M*^{*} arising from the search, and then

(b) draw inferences about θ pretending that M^* "=" M_{DG} .

This of course can lead to **quite bad calibration**, almost always in the **direction** of **pretending You know more than You actually do**, so that, e.g., Your **nominal 90% posterior predictive intervals** for **data values not used in the modeling process** would typically include **substantially fewer than 90%** of the actual **observations**.

The M^* approach "solves" the problem of how to specify \mathcal{M} by setting $\mathcal{M} = \{M^*\}$; I'll continue to postpone for the moment how You might do a better job of arriving at \mathcal{M} .

Having chosen \mathcal{M} in some way, how can You assess Your uncertainty across the models in \mathcal{M} , and appropriately propagate this through to Your uncertainty about θ , in a well-calibrated way?

I'm aware of three approaches to improved assessment and propagation of model uncertainty: BMA, BNP, CCV.

BMA, BNP

• Bayesian model averaging (BMA): If interest focuses on something that has the same meaning across all the models in \mathcal{M} — for example, a set of future data values D^* to be predicted — calculation reveals (e.g., Leamer, 1978) that

$$p(D^*|D\mathcal{MB}) = \int_{\mathcal{M}} p(D^*|D\mathcal{MB}) p(\mathcal{M}|D\mathcal{MB}) \, d\mathcal{M} \,, \qquad (5)$$

which is **eminently reasonable**: equation (5) tells You to form a **weighted average** of Your conditional predictive distributions $p(D^*|DMB)$, given particular models $M \in \mathcal{M}$, weighted by those models' posterior probabilities p(M|DMB).

This approach typically provides (substantially) better calibration than that obtained by the M^* method.

• Bayesian nonparametric (BNP) modeling: The BMA integral in (5) can be thought of as an approximation to the (unattainable?) ideal of averaging over all worthwhile models; a better approximation to this ideal can often be achieved with Bayesian nonparametric modeling, which dates back to de Finetti (1937). Continuing the Kaiser example on page 15, suppose You also observe (for each of the n = 112 randomly-sampled patients from the population \mathcal{P} of N = 8,561 heart-attack patients) a real-valued conceptually-continuous quality-of-care score y_i , and (following de Finetti) You're thinking about Your predictive distribution $p(y_1 \dots y_n | \mathcal{B})$ for these scores before any data have arrived.

de Finetti pointed out that, if You have no covariate information about the patients, Your predictive distribution $p(y_1 \dots y_n | B)$ should remain the same under arbitrary permutation of the order in which the patients are listed, and he coined the term exchangeability to describe this state of uncertainty.

He (and later **Diaconis/Freedman**) went on to **prove** that, if Your judgment of **exchangeability** extends from $(y_1 \ldots y_n)$ to $(y_1 \ldots y_N)$ (as it certainly **should** here, given the **random sampling**) and $N \gg n$ (as is **true** here), then all **logically-internally-consistent predictive distributions** can **approximately** be expressed **hierarchically** as follows:

Bayesian Nonparametric (BNP) Modeling

letting F stand for the empirical CDF of the population values $(y_1 \ldots y_N)$, the hierarchical model is (for $i = 1, \ldots, n$)

$$\left\{ egin{array}{cc} (F|\mathcal{B}) &\sim & p(F|\mathcal{B}) \ (y_i|F|\mathcal{B}) &\stackrel{ ext{IID}}{\sim} & F \end{array}
ight\} \,.$$

This requires placing a scientifically-appropriate prior distribution p(F|B) on the set \mathcal{F} of all CDFs on \Re , which de Finetti didn't know how to do in 1937; thanks to work by Freedman, Ferguson, Lavine, Escobar/West, and others, two methods for doing this sensibly — Pólya trees and Dirichlet-process (DP) priors — are now in routine use: this — placing distributions on function spaces — is Bayesian nonparametric (BNP) modeling.

IHGA Example, Revisited: Once again visualizing the **IHGA data** set before it arrives, here's the table shell one more time:

	Number of Hospitalizations						
Group	0	1		k	n	Mean	SD
Control	<i>n</i> _{C0}	n_{C1}		n _{Ck}	$n_{C} = 287$	ӯc	s _C
Treatment	<i>n</i> _{T0}	n_{T1}	•••	n_{Tk}	$n_T = 285$	\bar{y}_T	s _T

BNP Case Study

Letting (as before) μ_C and μ_T be the mean hospitalization rates (per two years) in the population \mathcal{P} (of all elderly non-institutionalized people in Denmark in the early 1980s) under the *C* and *T* conditions, respectively, the inferential quantity of main interest is still $\theta = \frac{\mu_T - \mu_C}{\mu_C}$ (or this could be redefined without loss as $\theta = \frac{\mu_T}{\mu_C}$); how can You draw valid and accurate inferences about θ while coping with Your uncertainty about the population *C* and *T* CDFs — call them *F*_C and *F*_T, respectively — of numbers of hospitalizations per person (per two years)?

One approach: Bayesian qualitative-quantitative inference (Draper 2011): exchangeability implies a multinomial sampling distribution on the qualitative outcome variable with category labels 0, 1, ..., and this permits optimal model specification here (this approach treats the hospitalization outcome categorically but permits quantitative inference about θ).

Another approach: Bayesian nonparametric modeling — it turns out that DP priors put all their mass on discrete distributions, so one BNP model for this data set would involve placing parallel DPs priors on F_C and F_T ; see KKD (2008) for details on the results. To serve as the **basis** of the M^* (cheating) approach (in which You look at the data for inspiration on which models to fit), here's a table of the actual data values:

	Number of Hospitalizations										
Group	0	1	2	3	4	5	6	7	n	Mean	SD
Control	138	77	46	12	8	4	0	2	287	0.944	1.24
Treatment	147	83	37	13	3	1	1	0	285	0.768	1.01

Evidently (description) IHGA lowered the mean hospitalization rate (for these elderly Danish people, at least) by (0.944 - 0.768) = 0.176, which is a $\{100 \left(\frac{0.768 - 0.944}{0.944}\right) \doteq\}$ 19% reduction from the control level, a difference that's large in clinical terms, but (inference) how strong is the evidence for a positive effect in $\mathcal{P} = \{\text{all people similar to those in the experiment}\}$?

It's **natural** to think **initially** of **parallel Poisson**(λ_C) and Poisson(λ_T) modeling (M_1), but there's **substantial over-dispersion**: the *C* and *T* **variance-to-mean ratios** are $\frac{1.24^2}{0.944} \doteq 1.63$ and $\frac{1.01^2}{0.768} \doteq 1.33$.

Bayesian Parametric Modeling

Unfortunately we have **no covariates** to help **explain** the **extra-Poisson variability**, and there's **little information external** to the **data set** about the **treatment effect**; this latter **state of knowledge** is expressed in **prior distributions** on **parameters** by making them **diffuse** (i.e., ensuring they have **large variability** to express **substantial uncertainty**).

In this situation You could fit parallel Negative Binomial models (M_2) , but a parametric choice that more readily generalizes is obtained by letting $(x_i, y_i) = (C/T \text{ status, outcome})$ — so that $x_i = 1$ if **Treatment**, 0 if **Control** and y_i = the **number of hospitalizations** — for person i = 1, ..., n and considering the random-effects Poisson regression model (M_3) :

$$\begin{array}{lll} (y_i | \lambda_i \ M_3 \ \mathcal{B}) & \stackrel{\text{indep}}{\sim} & \text{Poisson}(\lambda_i) \\ & \log(\lambda_i) & = & \gamma_0 + \gamma_1 x_i + \epsilon_i \\ (\epsilon_i | \sigma_{\epsilon}^2 \ M_3 \ \mathcal{B}) & \stackrel{\text{ID}}{\sim} & \mathcal{N}(0, \sigma_{\epsilon}^2) \\ (\gamma_0 \ \gamma_1 \ \sigma_{\epsilon}^2 | \mathcal{M}_3 \ \mathcal{B}) & \sim & \text{diffuse.} \end{array}$$

$$(6)$$

In this model the unknown of main policy interest is

BNP Example

 $\theta = \frac{\text{population } \bar{\tau}}{\text{population } \bar{c}} = e^{\gamma_1}$; the other parameters can be collected in a vector $\eta = (\gamma_0, \sigma_{\epsilon}^2)$; and the random effects ϵ_i can be thought of as proxying for the combined main effect $\sum_{j=2}^{J} \gamma_j (x_{ij} - \bar{x}_j)$ of all the unobserved relevant covariates (age, baseline health status, ...).

The first line of (6) makes good scientific sense (the y_i are counts of relatively rare events), but the Gaussian assumption for the random effects is conventional and not driven by the science; a potentially better model (M_4) is obtained by putting a prior distribution on the CDF of the ϵ_i that's centered at the $N(0, \sigma_{\epsilon}^2)$ distribution but that expresses substantial prior uncertainty about the Gaussian assumption:

 $\begin{array}{lll} (y_i | \lambda_i \ M_4 \ \mathcal{B}) & \stackrel{\text{indep}}{\sim} & \text{Poisson}(\lambda_i) \\ & \log(\lambda_i) & = & \gamma_0 + \gamma_1 x_i + \epsilon_i \\ (\epsilon_i | F \ M_4 \ \mathcal{B}) & \stackrel{\text{IID}}{\sim} & F \\ (F | \alpha \ \sigma_\epsilon^2 \ M_4 \ \mathcal{B}) & \sim & DP(\alpha, F_0), \ F_0 = N(0, \sigma_\epsilon^2) \\ (\gamma_0 \ \gamma_1 \ \sigma_\epsilon^2 | M_4 \ \mathcal{B}) & \sim & \text{diffuse; } (\alpha | M_4) \sim \text{small positive.} \end{array}$

Dirichlet-Process Mixture Modeling

Many Bayesian prior distributions $p(\theta|M_j B)$ have two user-friendly inputs: a quantity θ_0 that acts like a prior estimate of the unknown θ , and a number n_0 that behaves like a prior sample size (i.e., a measure of how tightly the prior is concentrated around θ_0); DP priors are no exception to this pattern.

In equation (7), $DP(\alpha, F_0)$ is a Dirichlet-process prior on F with prior estimate $F_0 = N(0, \sigma_{\epsilon}^2)$ and a quantity (α) that behaves something like a prior sample size; this is referred to as Dirichlet-process mixture modeling, because (7) is a mixture model — each person in the study has her/his own λ , drawn from F_C (control) or F_T (treatment) — in which uncertainty about F_C and F_T is quantified via a DP.

NB Bayesian model averaging (BMA) with a finite set of models can be regarded as a crude approximation to what Bayesian nonparametric (BNP) modeling is trying to do, namely average over Your uncertainty in model space to provide an honest representation of Your overall uncertainty that doesn't condition on things You don't know are true.

Cross-Validation

• Calibration cross-validation (CCV): The way the IHGA example unfolded looks a lot like the *M*^{*} approach I condemned previously: I used the entire data set to suggest which models to consider.

This has the (strong) potential to underestimate uncertainty; Bayesians (like everybody else) need to be able to look at the data to suggest alternative models, but all of us need to do so in a way that's well-calibrated.

Cross-validation — partitioning the data (e.g., exchangeably) into subsets used for different tasks (modeling, validation, ...) can help.

— The M^* approach is an example of what might be called **1CV** (one-fold cross-validation): You use the entire data set D both to model and to see how good the model is (this is clearly inadequate).

— 2CV (two-fold cross-validation) is frequently used: You (a) partition the data into modeling (M) and validation (V) subsets, (b) use M to explore a variety of models until You've found a "good" one M*, and (c) see how well M* validates in V (a useful Bayesian way to do this is to use the data in M

Calibration Cross-Validation (CCV)

to construct **posterior predictive distributions** for **all of the data values** in V and see how the **latter compare** with the **former**).

2CV is a lot better than **1CV**, but what do You do (as frequently happens) if *M*^{*} doesn't validate well in V?

- CCV (calibration cross-validation): going out one more term in the Taylor series (so to speak),
 - (a) partition the data into modeling (M), validation (V) and calibration (C) subsets,
 - (b) use M to explore a variety of models until You've found one or more plausible candidates $\mathcal{M} = \{M_1, \dots, M_m\}$,

(c) see **how well** the models in \mathcal{M} **validate** in V,

(d) if **none of** them do, **iterate (b) and (c)** until You do get **good validation**, and

(e) fit the best model in \mathcal{M} (or, better, use BMA) on the data in M + V, and report both (i) inferential conclusions based on this fit and (ii) the quality of predictive calibration of Your model/ensemble) in C.

CCV (continued)

The goal with this method is both

(1) a good answer, to the main scientific question, that has paid a reasonable price for model uncertainty (the inferential answer is based only on M + V, making Your uncertainty bands wider) and

(2) an indication of how well calibrated {the iterative fitting process yielding the answer in (1)} is in C (a good proxy for future data).

You can use **decision theory** (Draper, 2011) to decide **how much data** to put in each of M, V and C: the **more important calibration** is to You, the **more data** You want to put in C, but **only up to a point**, because getting a **good answer** to the **scientific question** is also **important** to You.

This is related to the machine-learning practice (e.g., Hastie, Tibshirani, Friedman [HTF] 2009) of Train/Validation/Test partitioning, with one improvement (decision theory provides an optimal way to choose the data subset sizes); I don't agree with HTF that this can only be done with large data sets: it's even more important to do it with small and medium-size data sets (You just need to work with multiple (M, V, C) partitions and average).

Modeling Algorithm

CCV provides a way to **pay** the **right price** for **hunting around in the data** for **good models**, motivating the following **modeling algorithm**:

- (a) Start at a model M_0 (how choose?); set the current model $M_{\text{current}} \leftarrow M_0$ and the current model ensemble $\mathcal{M}_{\text{current}} \leftarrow \{M_0\}$.
- (b) If $M_{current}$ is good enough to stop (how decide?), return $\mathcal{M}_{current}$; else
- (c) Generate a new candidate model M_{new} (how choose?) and set $\mathcal{M}_{\text{current}} \leftarrow \mathcal{M}_{\text{current}} \cup M_{\text{new}}.$
- (d) If M_{new} is better than M_{current} (how decide?), set $M_{\text{current}} \leftarrow M_{\text{new}}$.
- (e) Go to (b).

For human analysts the choice in (a) is not hard, although it might not be easy to automate in full generality; for humans the choice in (c) demands creativity, and as a profession, at present, we have no principled way to automate it; here I want to focus on the questions in (b) and (d):

 Q_1 : Is M_1 better than M_2 ? Q_2 : Is M_1 good enough?

The Modeling-As-Decision Principle

These questions **sound fundamental** but **are not**: better **for what purpose**? Good enough **for what purpose**? This **implies** (see, e.g., Bernardo and Smith, 1995; Draper, 1996; Key et al., 1999) a

Modeling-As-Decision Principle: Making clear the purpose to which the modeling will be put transforms model specification into a decision problem, which should be solved by maximizing expected utility with a utility function tailored to the specific problem under study.

Some examples of this may be found (e.g., Draper and Fouskakis, 2008: variable selection in generalized linear models under cost constraints), but this is hard work; there's a powerful desire for generic model-comparison methods whose utility structure may provide a decent approximation to problem-specific utility elicitation.

Two such methods are Bayes factors and log scores.

• **Bayes factors.** It looks **natural** to **compare models** on the basis of their **posterior probabilities**; from **Bayes's Theorem** in **odds form**,

$$\frac{p(M_2|D\mathcal{B})}{p(M_1|D\mathcal{B})} = \left[\frac{p(M_2|\mathcal{B})}{p(M_1|\mathcal{B})}\right] \cdot \left[\frac{p(D|M_2\mathcal{B})}{p(D|M_1\mathcal{B})}\right];$$
(8)

the **first term** on the right is just the **prior odds** in favor of M_2 over M_1 , and the **second term** on the right is called the **Bayes factor**, so in words equation (8) says

$$\begin{pmatrix} \text{posterior} \\ \text{odds} \\ \text{for } M_2 \\ \text{over } M_1 \end{pmatrix} = \begin{pmatrix} \text{prior odds} \\ \text{for } M_2 \\ \text{over } M_1 \end{pmatrix} \cdot \begin{pmatrix} \text{Bayes factor} \\ \text{for } M_2 \\ \text{over } M_1 \end{pmatrix}. \quad (9)$$

(Bayes factors seem to have first been considered by Turing and Good (\sim 1941), as part of the effort to break the German Enigma codes.)

Odds *o* are related to **probabilities** *p* via $o = \frac{p}{1-p}$ and $p = \frac{o}{1+o}$; these are **monotone increasing transformations**, so the **decision rules** {choose M_2 over M_1 if the **posterior odds** for M_2 are greater} and {choose M_2 over M_1 if $p(M_2|DB) > p(M_1|DB)$ } are **equivalent**.

Decision-Theoretic Basis for Bayes Factors

This approach does have a **decision-theoretic basis**, but it's rather **odd**: if You pretend that the **only possible data-generating mechanisms** are $\mathcal{M} = \{M_1, \ldots, M_m\}$ for finite *m*, and You pretend that one of the models in \mathcal{M} must be the **true data-generating mechanism** M_{DG} , and You pretend that the **utility function**

$$U(M, M_{DG}) = \left\{ \begin{array}{ll} 1 & \text{if } M = M_{DG} \\ 0 & \text{otherwise} \end{array} \right\}$$
(10)

reflects Your real-world values, then it's decision-theoretically optimal to choose the model in \mathcal{M} with the highest posterior probability (i.e., that choice maximizes expected utility).

If it's scientifically appropriate to take the prior model probabilities $p(M_j|B)$ to be equal, this rule reduces to choosing the model with the highest Bayes factor in favor of it; this can be found by (a) computing the Bayes factor in favor of M_2 over M_1 ,

$$BF(M_2 \text{ over } M_1 | D \mathcal{B}) = \frac{p(D|M_2 \mathcal{B})}{p(D|M_1 \mathcal{B})}, \tag{11}$$

favoring M_2 if $BF(M_2 \text{ over } M_1|DB) > 1$, i.e., if $p(D|M_2B) > p(D|M_1B)$, and calling the **better model** M^* ; (b) **computing the Bayes factor** in favor of M^* over M_3 , calling the **better model** M^* ; and so on up through M_m .

Notice that there's something else a bit funny about this: $p(D|M_j B)$ is the prior (not posterior) predictive distribution for the data set Dunder model M_j , so the Bayes factor rule tells You to choose the model that does the best job of predicting the data before any data arrives.

Let's look at the general problem of parametric model comparison, in which model M_j has its own parameter vector γ_j (of length k_j), where $\gamma_j = (\theta, \eta_j)$, and is specified by

$$M_{j}: \left\{ \begin{array}{c} (\gamma_{j}|M_{j}\mathcal{B}) \sim p(\gamma_{j}|M_{j}\mathcal{B}) \\ (D|\gamma_{j}M_{j}\mathcal{B}) \sim p(D|\gamma_{j}M_{j}\mathcal{B}) \end{array} \right\}.$$
(12)

Here the quantity $p(D|M_j B)$ that **defines the Bayes factor** is

Integrated Likelihoods

$$p(D|M_j \mathcal{B}) = \int p(D|\gamma_j M_j \mathcal{B}) p(\gamma_j|M_j \mathcal{B}) d\gamma_j; \qquad (13)$$

this is called an **integrated likelihood** (or **marginal likelihood**) because it tells You to take a **weighted average** of the **sampling distribution/likelihood** $p(D|\gamma_j M_j B)$, but **NB** weighted by the **prior** for γ_j in model M_j ; as noted above, this may seem **surprising**, but it's **correct**, and it can lead to **trouble**, as follows.

The first trouble is **technical**: the **integral** in (13) can be **difficult to compute**, and may not even be easy to **approximate**.

The second thing to **notice** is that (13) can be **rewritten** as

$$p(D|M_j \mathcal{B}) = E_{(\gamma_j|M_j \mathcal{B})} p(D|\gamma_j M_j \mathcal{B}).$$
(14)

In other words the **integrated likelihood** is the **expectation** of the **sampling distribution** over the **prior** for γ_j in model M_j (evaluated at the **observed data set** D).

A few additional words about prior distributions on parameters:

A distribution (density) for a real-valued parameter θ that summarizes the information

 $\{\theta \text{ is highly likely to be near } \theta_0\}$

will have most of its mass concentrated near θ_0 , whereas the information

{**not much is known** about θ }

would correspond to a **density** that's rather **flat** (or **diffuse**) across a broad range of θ values; thus when the **scientific context** offers **little information** about γ_j **external** to the data set D, this translates into a **diffuse prior** on γ_j , and this spells **trouble** for **Bayes factors**:

 $p(D|M_j \mathcal{B}) = E_{(\gamma_j|M_j \mathcal{B})} p(D|\gamma_j M_j \mathcal{B}).$

You can see that if the **available information** implies that $p(\gamma_j | M_j B)$ should be **diffuse**, the **expectation** defining the **integrated likelihood** can be **highly unstable** with respect to **small details** in how the **diffuseness is specified**.

Example: Integer-valued data set $D = (y_1 \dots y_n)$; $\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$;

Instability of Bayes Factors (continued)

 $M_1 =$ **Geometric**(θ_1) likelihood with a **Beta**(α_1, β_1) prior on θ_1 ;

 $M_2 =$ **Poisson**(θ_2) likelihood with a **Gamma**(α_2, β_2) prior on θ_2 .

The **Bayes factor** in favor of M_1 over M_2 turns out to be

$$\frac{\Gamma(\alpha_1+\beta_1)\Gamma(n+\alpha_1)\Gamma(n\bar{y}+\beta_1)\Gamma(\alpha_2)(n+\beta_2)^{n\bar{y}+\alpha_2}\left(\prod_{i=1}^n y_i!\right)}{\Gamma(\alpha_1)\Gamma(\beta_1)\Gamma(n+n\bar{y}+\alpha_1+\beta_1)\Gamma(n\bar{y}+\alpha_2)\beta_2^{\alpha_2}}.$$
 (15)

With standard diffuse priors — take $(\alpha_1, \beta_1) = (1, 1)$ and $(\alpha_2, \beta_2) = (\epsilon, \epsilon)$ for some $\epsilon > 0$ — the **Bayes factor** reduces to

$$\frac{\Gamma(n+1)\,\Gamma(n\bar{y}+1)\,\Gamma(\epsilon)\,(n+\epsilon)^{n\bar{y}+\epsilon}\,\left(\prod_{i=1}^{n}\,y_{i}!\right)}{\Gamma(n+n\bar{y}+2)\,\Gamma(n\bar{y}+\epsilon)\,\epsilon^{\epsilon}}.$$
(16)

This goes to $+\infty$ as $\epsilon \downarrow 0$, i.e., You can make the evidence in **favor** of the **Geometric model** over the **Poisson** as **large** as You want, **no matter what the data says**, as a function of a quantity near 0 that **scientifically** You have **no basis** to specify.

If instead You fix and bound (α_2, β_2) away from 0 and let $(\alpha_1, \beta_1) \downarrow 0$, You can completely reverse this and make the evidence in favor of the Poisson model over the Geometric as large as You want (for any y).

Approximating Integrated Likelihoods

The bottom line is that, when scientific context suggests diffuse priors on the parameter vectors in the models being compared, the integrated likelihood values that are at the heart of Bayes factors can be hideously sensitive to small arbitrary details in how the diffuseness is specified.

This has been well-known for quite awhile now, and it's given rise to an amazing amount of fumbling around, as people who like Bayes factors have tried to find a way to fix the problem: at this point the list of attempts includes {partial, intrinsic, fractional} Bayes factors, well-calibrated priors, conventional priors, intrinsic priors, expected posterior priors, ... (e.g., Pericchi 2004), and all of them exhibit a level of ad-hockery that's otherwise absent from the Bayesian paradigm.

Approximating integrated likelihoods. The goal is

$$p(D|M_j \mathcal{B}) = \int p(D|\gamma_j M_j \mathcal{B}) p(\gamma_j|M_j \mathcal{B}) d\gamma_j; \qquad (17)$$

maybe there's an **analytic approximation** to this that will suggest how to **avoid trouble**.

Laplace Approximation

Laplace (1785) already faced this problem 225 years ago, and he offered a solution that's often useful, which people now call a Laplace approximation in his honor (it's an example of what's also known in the applied mathematics literature as a saddle-point approximation).

Noticing that the **integrand** $P^*(\gamma_j) \equiv p(D|\gamma_j M_j B) p(\gamma_j|M_j B)$ in $p(D|M_j B)$ is an **un-normalized version** of the **posterior distribution** $p(\gamma_j|D M_j B)$, and appealing to a **Bayesian version** of the **Central Limit**

Theorem — which says that with a lot of data, such a posterior distribution should be close to Gaussian, centered at the posterior mode $\hat{\gamma}_j$ — You can see that (with a large sample size *n*) log $P^*(\gamma_j)$ should be close to quadratic around that mode; the Laplace idea is to take a Taylor expansion of log $P^*(\gamma_j)$ around $\hat{\gamma}_j$ and retain only the terms out to second order; the result is

$$\log p(D|M_j \mathcal{B}) = \log p(D|\hat{\gamma}_j M_j \mathcal{B}) + \log p(\hat{\gamma}_j | M_j \mathcal{B}) + \frac{k_j}{2} \log 2\pi - \frac{1}{2} \log |\hat{l}_j| + O\left(\frac{1}{n}\right); \quad (18)$$

here $\hat{\gamma}_j$ is the maximum likelihood estimate of the parameter vector γ_j under model M_j and \hat{l}_j is the observed information matrix under M_j .

Notice that the **prior** on γ_j in model M_j enters into this **approximation** through log $p(\hat{\gamma}_j | M_j B)$, and this is a term that **won't go away with more data**: as *n* increases this term is O(1).

Using a **less precise Taylor expansion**, Schwarz (1978) obtained a **different approximation** that's the **basis** of what has come to be **known** as the **Bayesian information criterion (BIC)**:

$$\log p(y|M_j \mathcal{B}) = \log p(y|\hat{\gamma}_j M_j \mathcal{B}) - \frac{k_j}{2} \log n + O(1).$$
(19)

People often work with a multiple of this for model comparison:

$$BIC(M_j|D\mathcal{B}) = -2\log p(D|\hat{\gamma}_j M_j \mathcal{B}) + k_j \log n$$
(20)

(the -2 multiplier comes from deviance considerations); multiplying by -2 induces a search (with this approach) for models with small BIC.

This model-comparison method makes an explicit trade-off between model complexity (which goes up with k_j at a log *n* rate) — and model lack of fit (through the $-2 \log p(D|\hat{\gamma}_j M_j B)$ term).

BIC and the Unit-Information Prior

BIC is called an information criterion because it resembles AIC (Akaike, 1974). which was derived using information-theoretic reasoning:

$$AIC(M_j|D\mathcal{B}) = -2\log p(D|\hat{\gamma}_j M_j \mathcal{B}) + 2k_j.$$
(21)

AIC penalizes model complexity at a linear rate in k_j and so can have different behavior than BIC, especially with moderate to large n (BIC tends to choose simpler models; more on this later).

It's possible to work out what **implied prior BIC is using**, from the point of view of the **Laplace approximation**; the result is

$$(\gamma_j | M_j \mathcal{B}) \sim N_{k_j}(\hat{\gamma}_j, n \hat{l}_j^{-1}).$$
 (22)

In the literature this is called a unit-information prior, because in large samples it corresponds to the prior being equivalent to 1 new observation yielding the same sufficient statistics as the observed data.

This prior is data-determined, but this effect is close to negligible even with only moderate n.

Bayes Factors; Log Scores

The BIC approximation to Bayes factors has the extremely desirable property that it's free of the hideous instability of integrated likelihoods with respect to tiny details, in how diffuse priors are specified, that do not arise directly from the science of the problem; in my view, if You're going to use Bayes factors to choose among models, You're well advised to use a method like BIC that protects You from Yourself in mis-specifying those tiny details.

I said back on page 45 that there are two generic utility-based model-comparison methods: Bayes factors and log scores.

• Log scores are based on the

Prediction Principle: Good models make good predictions, and bad models make bad predictions; that's one scientifically important way You know a model is good or bad.

This suggests developing a **generic utility structure** based on **predictive accuracy**: consider first a **setting** in which $D = y = (y_1 \dots y_n)$ for real-valued y_i and the **models** to be **compared** are (as before)

$$M_{j}: \left\{ \begin{array}{c} (\gamma_{j}|M_{j}\mathcal{B}) \sim p(\gamma_{j}|M_{j}\mathcal{B}) \\ (y|\gamma_{j}M_{j}\mathcal{B}) \sim p(y|\gamma_{j}M_{j}\mathcal{B}) \end{array} \right\}.$$
(23)

When comparing a (future) data value y^* with the predictive distribution $p(\cdot|y M_j B)$ for it under M_j , it's been shown that (under reasonable optimality criteria) all optimal scores measuring the discrepancy between y^* and $p(\cdot|y M_j B)$ are linear functions of $\log p(y^*|y M_j B)$ (the log of the height of the predictive distribution at the observed value y^*).

Using this **fact**, perhaps the most **natural-looking** form for a **composite measure** of **predictive accuracy** of M_j is a **cross-validated** version of the resulting **log score**,

$$LS_{CV}(M_j|y \mathcal{B}) = \frac{1}{n} \sum_{i=1}^n \log p(y_i|y_{-i} M_j \mathcal{B}), \qquad (24)$$

in which y_{-i} is the y vector with observation i omitted.

Somewhat **surprisingly**, Draper and Krnjajić (2010) have shown that a **full-sample log score** that **omits** the **leave-one-out idea**,

Full-Sample Log Score

$$LS_{FS}(M_j|y \mathcal{B}) = \frac{1}{n} \sum_{i=1}^n \log p(y_i|y M_j \mathcal{B}), \qquad (25)$$

made **operational** with the **rule** {favor M_2 over M_1 if $LS_{FS}(M_2|y B) > LS_{FS}(M_1|y B)$ }, can have **better small-sample model discrimination ability** than LS_{CV} (in addition to being **faster** to **approximate** in a **stable** way).

If, in the spirit of calibration, You're prepared to think about an underlying data-generating model M_{DG} , LS_{FS} also has a nice interpretation as an approximation to the Kullback-Leibler divergence between M_{DG} and $p(\cdot|y M_j B)$, in which M_{DG} is approximated by the empirical CDF:

$$\begin{aligned} \mathsf{KL}[p(\cdot|y\ M_j\ \mathcal{B})||M_{DG}] &= \mathsf{E}_{M_{DG}}\log M_{DG} - \mathsf{E}_{M_{DG}}\log p(\cdot|y\ M_j\ \mathcal{B}) \\ &\doteq \mathsf{E}_{M_{DG}}\log M_{DG} - \mathsf{LS}_{FS}(M_j|y\ \mathcal{B}); \end{aligned} (26)$$

the first term on the right side of (26) is constant in $p(\cdot|y|M_j|B)$, so minimizing $KL[p(\cdot|y|M_j|B||M_{DG})]$ is approximately the same as maximizing LS_{FS} .

Bayes Factors/BIC Versus Log Scores

What follows is a **sketch** of **recent results** (Draper, 2011) based on **simulation experiments** with **realistic sample sizes**; in my view **standard asymptotic calculations** — **choosing between** the **models** in $\mathcal{M} = \{M_1, M_2\}$ as $n \to \infty$ with \mathcal{M} **remaining fixed** — are **essentially irrelevant** in **calibration studies**, for **two reasons**:

(1) With increasing *n*, You'll want \mathcal{M} to grow to satisfy Your desire to do a better job of capturing real-world complexities, and

(2) Data usually accumulate over time, and with increasing n it becomes more likely that the real-world process You're modeling is not stationary.

• Versions of Bayes factors that behave sensibly with diffuse priors on the model parameters (e.g., intrinsic Bayes factors: Berger and Pericchi, 1996, and more recent cousins) tend to have model discrimination performance similar to that of BIC in calibration (repeated-sampling with known M_{DG}) environments; I'll show results for BIC here.

Example: Consider assessing the performance of a drug, for lowering

Clinical Trial to Quantify Improvement

systolic blood pressure (SBP) in hypertensive patients, in a phase–II clinical trial, and suppose that a Gaussian sampling distribution for the outcome variable is reasonable (possibly after transformation).

Two frequent designs in settings of this type have as their goals quantifying improvement and establishing bio-equivalence.

• (quantifying improvement) Here You want to estimate the mean decline in blood pressure under this drug, and it would be natural to choose a repeated-measures (pre-post) experiment, in which SBP values are obtained for each patient, both before and after taking the drug for a sufficiently long period of time for its effect to become apparent.

Let θ stand for the **mean difference** $(SBP_{before} - SBP_{after})$ in the **population** of **patients** to which it's **appropriate** to **generalize** from the **patients** in Your **trial**, and let $D = y = (y_1 \dots y_n)$. where y_i is the **observed difference** $(SBP_{before} - SBP_{after})$ for **patient** i $(i = 1, \dots, n)$.

The real-world purpose of this experiment is to decide whether to take the drug forward to phase III; under the weight of 20th-century

Decision, Not Inference

inertia (in which decision-making was strongly — and incorrectly subordinated to inference), Your first impulse might be to treat this as an inferential problem about θ , but it's not;

it's a decision problem that involves θ .

This is an **example** of the

• Decision-Versus-Inference Principle: We should all get out of the habit of using inferential methods to make decisions: their implicit utility structure is often far from optimal.

The action space here is $\mathcal{A} = (a_1, a_2) = (\text{don't take the drug forward to phase III, do take it forward), and a sensible utility function <math>U(a_j, \theta)$ should be continuous and monotonically increasing in θ over a broad range of positive θ values (the bigger the SBP decline for hypertensive patients who start at (say) 160 mmHg, the better, up to a drop of about 40 mmHg, beyond which the drug starts inducing fainting spells).

However, to facilitate a comparison between BIC and log scores, here I'll compare two models M_1 and M_2 that dichotomize the θ range,

Models For Quantifying Improvement

but not at 0: despite a century of textbook claims to the contrary, there's nothing special about $\theta = 0$ in this setting, and in fact You know scientifically that θ is not exactly 0 (because the outcome variable in this experiment is conceptually continuous).

 $\label{eq:hardware} \begin{array}{l} \mbox{What matters here is whether } \theta > \Delta, \mbox{ where } \Delta \mbox{ is a} \\ \mbox{practical significance improvement threshold} \mbox{ below which the drug is} \\ \mbox{not worth advancing into phase III (for example, any drug that did not lower SBP for severely hypertensive patients — those whose \\ \mbox{pre-drug values average 160 mmHg or more — by at least 15 mmHg} \\ \mbox{would not deserve further attention}. \end{array}$

With little information about θ external to this experimental data set, what counts in this situation is the comparison of the following two models:

$$M_{1}: \left\{ \begin{array}{cc} (\theta|\mathcal{B}) & \sim & \text{diffuse for } \theta \leq \Delta \\ (y_{i}|\theta|\mathcal{B}) & \stackrel{\text{IID}}{\sim} & N(\theta, \sigma^{2}) \end{array} \right\} \text{ and } (27)$$
$$M_{2}: \left\{ \begin{array}{cc} (\theta|\mathcal{B}) & \sim & \text{diffuse for } \theta > \Delta \\ (y_{i}|\theta|\mathcal{B}) & \stackrel{\text{IID}}{\sim} & N(\theta, \sigma^{2}) \end{array} \right\}, (28)$$

Quantifying Improvement: Model Comparison Methods

in which for simplicity I'll take σ^2 to be known (the results are similar with σ^2 learned from the data).

This gives rise to **three model-selection methods** that can be **compared calibratively**:

• Full-sample log scores: choose M_2 if $LS_{FS}(M_2|y B) > LS_{FS}(M_1|y B)$.

• Posterior probability: let

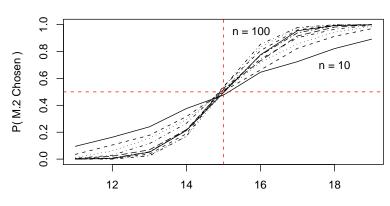
 $M^* = \{(\theta|\mathcal{B}) \sim \text{diffuse on } \Re, (y_i|\theta|\mathcal{B}) \stackrel{\text{ILD}}{\sim} N(\theta, \sigma^2)\} \text{ and choose } M_2 \text{ if } p(\theta > \Delta|y|M^*|\mathcal{B}) > 0.5.$

• BIC: choose M_2 if $BIC(M_2|y \mathcal{B}) < BIC(M_1|y \mathcal{B})$.

Simulation experiment details, based on the SBP drug trial: $\Delta = 15$; $\sigma = 10$; $n = 10, 20, \ldots, 100$; data-generating $\theta_{DG} = 11, 12, \ldots, 19$; $\alpha = 0.05$; 1,000 simulation replications; Monte-Carlo approximations of the predictive ordinates in LS_{FS} based on 10,000 posterior draws.

The **figures** below give **Monte-Carlo estimates** of the **probability that** M_2 **is chosen**.

LS_{FS} Results: Quantifying Improvement



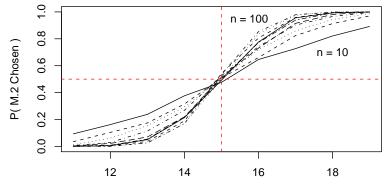
Data-Generating Theta

LS.FS

This exhibits all the monotonicities that it should, and correctly yields 0.5 for all *n* with $\theta_{DG} = 15$.

Posterior Probability Results: Quantifying Improvement

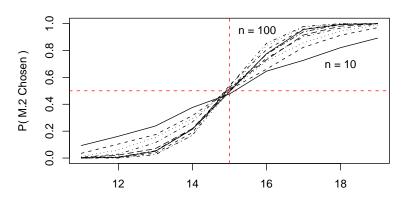
Posterior Probability



Data-Generating Theta

Even though the LS_{FS} and posterior-probability methods are quite different, their information-processing in discriminating between M_1 and M_2 is identical to within ± 0.003 (well within simulation noise with 1,000 replications).

BIC Results: Quantifying Improvement



Data-Generating Theta

BIC

Here **BIC** and the **posterior-probability approach** are **algebraically identical**, making the **model-discrimination performance** of **all three approaches** the **same** in **this problem**.

Establishing Bio-Equivalence

• (establishing bio-equivalence) In this case there's a previous hypertension drug *B* (call the new drug *A*) and You're wondering if the mean effects of the two drugs are close enough to regard them as bio-equivalent.

A good design here would again have a repeated-measures character, in which each patient's SBP is measured four times: before and after taking drug *A*, and before and after taking drug *B* (allowing enough time to elapse between taking the two drugs for the effects of the first drug to disappear).

Let $\boldsymbol{\theta}$ stand for the mean difference

 $[(SBP_{before,A} - SBP_{after,A}) - (SBP_{before,B} - SBP_{after,B})]$ (29)

in the **population** of **patients** to which it's **appropriate** to **generalize** from the **patients in Your trial**, and let y_i be the **corresponding difference** for patient i (i = 1, ..., n).

Again in this setting there's nothing special about $\theta = 0$, and as before You know scientifically that θ is not exactly 0;

Bio-Equivalence Modeling

what matters here is whether $|\theta| \le \lambda$, where $\lambda > 0$ is a practical significance bio-equivalence threshold (e.g., 5 mmHg).

Assuming as before a Gaussian sampling story and little information about θ external to this experimental data set, what counts here is a comparison of

$$M_{3}: \left\{ \begin{array}{l} (\theta|\mathcal{B}) & \sim & \text{diffuse for } |\theta| \leq \lambda \\ (y_{i}|\theta|\mathcal{B}) & \stackrel{\text{IID}}{\sim} & N(\theta, \sigma^{2}) \end{array} \right\} \text{ and } (30)$$
$$M_{4}: \left\{ \begin{array}{l} (\theta|\mathcal{B}) & \sim & \text{diffuse for } |\theta| > \lambda \\ (y_{i}|\theta|\mathcal{B}) & \stackrel{\text{IID}}{\sim} & N(\theta, \sigma^{2}) \end{array} \right\}, (31)$$

in which σ^2 is again taken for **simplicity** to be **known**.

A natural alternative to BIC and LS_{FS} here is again based on posterior probabilities: as before, let $M^* = \{(\theta|\mathcal{B}) \sim \text{diffuse on } \Re, (y_i|\theta \mathcal{B}) \stackrel{\text{ID}}{\sim} N(\theta, \sigma^2)\}$, but this time favor M_4 over M_3 if $p(|\theta| > \lambda|y M^* \mathcal{B}) > 0.5$.

As before, a careful real-world choice between M_3 and M_4 in this case would be based on a utility function that quantified the

Bio-Equivalence Model Comparison

costs and benefits of

{claiming the two drugs were bio-equivalent when they were, concluding that they were bio-equivalent when they were not, deciding that they were not bio-equivalent when they were, judging that they were not bio-equivalent when they were not},

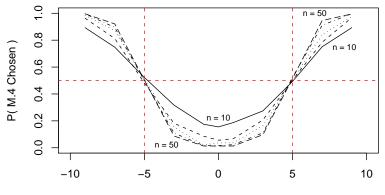
but here I'll again simply compare the calibrative performance of LS_{FS} , posterior probabilities, and BIC.

Simulation experiment details, based on the SBP drug trial: $\lambda = 5$; $\sigma = 10$; n = 10, 20, ..., 100; data-generating $\theta_{DG} = \{-9, -7, -5, -3, -1, 0, 1, 3, 5, 7, 9\}$; $\alpha = 0.05$; 1,000 simulation replications, M = 10,000 Monte-Carlo draws for LS_{FS} .

NB It has previously been established that when making the (unrealistic) sharp-null comparison $\theta = 0$ versus $\theta \neq 0$ in the context of $(y_i | \theta B) \stackrel{\text{IID}}{\sim} N(\theta, \sigma^2)$, as $n \to \infty LS_{FS}$ selects the $\theta \neq 0$ model with probability $\to 1$ even when $\theta_{DG} = 0$; this "inconsistency of log scores at the null model" has been used by some people as a reason to dismiss log scores as a model-comparison method.

LS_{FS} Results: Bio-Equivalence

LS.FS

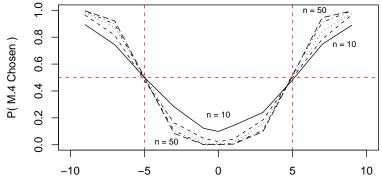


Data-Generating Theta

In this more realistic setting, comparing $|\theta| \leq \lambda$ versus $|\theta| > \lambda$ with $\lambda > 0$, LS_{FS} has the correct large-sample behavior, both when $|\theta_{DG}| \leq \lambda$ and when $|\theta_{DG}| > \lambda$.

Posterior Probability Results: Bio-Equivalence

Posterior Probability

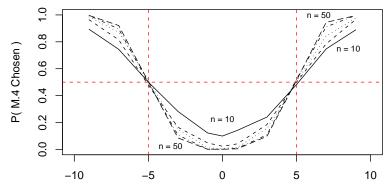


Data-Generating Theta

The qualitative behavior of the LS_{FS} and posterior-probability methods is identical, although there are some numerical differences (highlighted later).

BIC Results: Bio-Equivalence

BIC

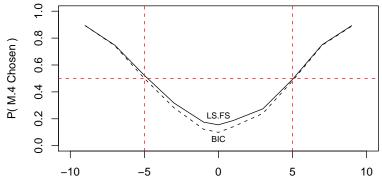


Data-Generating Theta

In the quantifying-improvement case, the BIC and posterior-probability methods were algebraically identical; here they nearly coincide (differences of ± 0.001 with 1,000 simulation repetitions).

LS_{FS} Versus BIC Results: Bio-Equivalence

LS.FS Versus BIC (n = 10)

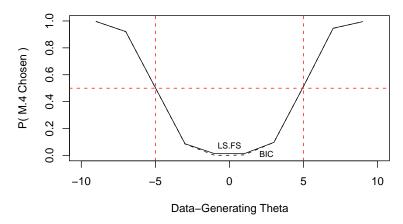


Data-Generating Theta

If You call choosing M_4 : $|\theta| > \lambda$ when $|\theta_{DG}| \le \lambda$ a false-positive error and choosing M_3 : $|\theta| \le \lambda$ when $|\theta_{DG}| > \lambda$ a false-negative mistake, with n = 10 there's a trade-off: LS_{FS} has more false positives and BIC has more false negatives.

LS_{FS} Versus BIC Results: Bio-Equivalence

LS.FS Versus BIC (n = 50)



By the time You reach n = 50 in this problem, LS_{FS} and BIC are essentially equivalent.

The Decision-Versus-Inference Principle, Revisited

In the context of the quantifying-improvement example, the real-world purpose of the experiment was to decide whether or not to take the drug forward to phase III.

Suppose that You tried to solve this decision problem with a popular inferential tool: frequentist hypothesis-testing of $H_0: \theta \le \Delta$ versus $H_A: \theta > \Delta$ at significance level α .

Decision-theoretically this is **already wrong**; as **noted** back on **page 61**, the **utility function** should **actually** be **continuous** in θ rather than **artificially dichotomizing** Θ into $(-\infty, \Delta]$ and (Δ, ∞) .

Even if You temporarily buy into this incorrect dichotomization, to solve the problem properly You'd have to quantify the real-world consequences of each of the cells in this table specifying $U(a, \theta)$ (here $u_{ii} > 0$):

	Truth	
Action	$\theta \leq \Delta$	$\theta > \Delta$
$a_1 \; (stop)$	<i>u</i> ₁₁	$-u_{12}$
a ₂ (phase III)	$-u_{21}$	U ₂₂

Decision-Theory (Not Inference) For Decision Problems

	Truth	
<u>Action</u>	$\theta \leq \Delta$	$\theta > \Delta$
a_1 (stop)	<i>u</i> ₁₁	$-u_{12}$
a ₂ (phase III)	$-u_{21}$	U ₂₂

- *u*₁₁ is the gain from correctly not taking the drug forward to phase III (this is clearly 0);
- u_{12} is the loss from incorrectly failing to take the drug forward to phase III;
- *u*₂₁ is the loss from incorrectly taking the drug forward to phase III;
- *u*₂₂ is the gain from correctly taking the drug forward to phase III.

The **optimal Bayesian decision** turns out to be: **choose** *a*₂ (go **forward to phase III**) iff

$$P(\theta > \Delta | y \mathcal{B}) \ge \frac{u_{21}}{u_{12} + u_{21} + u_{22}} = u^*.$$
(32)

The frequentist (hypothesis-testing) inferential approach is equivalent to this only if

Optimal Decision-Making in Phase-II Trials

$$\alpha = 1 - u^* = \frac{u_{12} + u_{22}}{u_{12} + u_{21} + u_{22}}.$$
(33)

The implicit trade-off between false positives and false negatives in BIC and LS_{FS} — and the built-in trade-off in level- α hypothesis-testing for any given α — may be close to optimal or not, according to the real-world values of $\{u_{12}, u_{21}, u_{22}\}$.

In phase-II clinical trials or micro-array experiments, when You're screening many drugs or genes for those that may lead to an effective treatment and — from the drug company's point of view — a false-negative error (of failing to move forward with a drug or gene that's actually worth further investigation) can be much more costly than a false-positive mistake, this corresponds to $u_{12} \gg u_{21}$ and leads in the hypothesis-testing approach in phase-II trials to a willingness to use (much) larger α values than the conventional 0.01 or 0.05, something that good frequentist biostatisticians have long known intuitively.

(In work I've done with a Swiss pharmaceutical company, this approach led to α values on the order of 0.45, which is close to the implicit trade-off in BIC and $LS_{FS.}$)

For People Who Like to Test Sharp-Null Hypotheses

An extreme example of the false-positive/false-negative differences between LS_{FS} and BIC in this setting may be obtained, albeit unwisely, by letting $\lambda \downarrow 0$.

This is **unwise** here (and is **often unwise**) because it **amounts**, in **frequentist language**, to **testing** the **sharp-null hypothesis** $H_0: \theta = 0$ against the **alternative** $H_A: \theta \neq 0$.

It's necessary to distinguish between problems in which there is or is not a structural singleton in the (continuous) set Θ of possible values of θ : settings where it's scientifically important to distinguish between $\theta = \theta_0$ and $\theta \neq \theta_0$ — an example would be discriminating between {these two genes are on different chromosomes (the strength θ of their genetic linkage is $\theta_0 = 0$)} and {these two genes are on the same chromosome ($\theta > 0$)}.

Sharp-null testing without structural singletons is always unwise because

(a) You already know from scientific context, when the outcome variable is continuous, that H_0 is false, and (relatedly)

Testing Sharp-Null Hypotheses (continued)

(b) it's silly from a measurement point of view: with a (conditionally) IID $N(\theta, \sigma^2)$ sample of size *n*, your measuring instrument \bar{y} is only accurate to resolution $\frac{\sigma}{\sqrt{n}} > 0$; claiming to be able to discriminate between $\theta = 0$ and $\theta \neq 0$ — with realistic values of *n* — is like someone with a scale that's only accurate to the nearest ounce telling You that Your wedding ring has 1 gram (0.035 ounce) less gold in it than the jeweler claims it does.

Nevertheless, for people who like to test sharp-null hypotheses, here are some results: here I'm comparing the models (i = 1, ..., n)

$$M_{5}: \left\{ \begin{array}{cc} (\sigma^{2}|\mathcal{B}) & \sim & \text{diffuse on } (0, \text{large}) \\ (y_{i}|\sigma^{2}|\mathcal{B}) & \stackrel{\text{IID}}{\sim} & \mathcal{N}(0, \sigma^{2}) \end{array} \right\} \text{ and } (34)$$

$$M_{6:} \left\{ \begin{array}{cc} (\theta \, \sigma^{2} | \mathcal{B}) & \sim & \text{diffuse on } (-\text{large}, \text{large}) \times (0, \text{large}) \\ (y_{i} | \theta \, \sigma^{2} \, \mathcal{B}) & \stackrel{\text{ID}}{\sim} & N(\theta, \sigma^{2}) \end{array} \right\}, \quad (35)$$

In this case a natural Bayesian competitor to BIC and LS_{FS} would be to construct the central $100(1 - \alpha)$ % posterior interval for θ under M_6 and choose M_6 if this interval doesn't contain **0**.

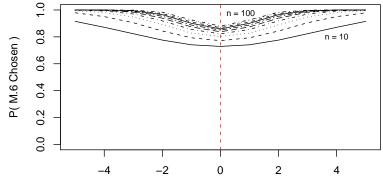
Testing Sharp-Null Hypotheses (continued)

Simulation experiment details: data-generating $\sigma_{DG} = 10$; n = 10, 20, ..., 100; data-generating $\theta_{DG} = \{0, 1, ..., 5\}$; **1,000** simulation replications, M = 100,000 Monte-Carlo draws for LS_{FS} ; the figures below give Monte-Carlo estimates of the probability that M_6 is chosen.

As before, let's call **choosing** M_6 : $\theta \neq 0$ when $\theta_{DG} = 0$ a **false-positive** error and **choosing** M_5 : $\theta = 0$ when $\theta_{DG} \neq 0$ a **false-negative** mistake.

LS_{FS} Results: Sharp-Null Testing



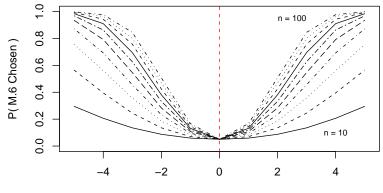


Data-Generating Theta

In the limit as $\lambda \downarrow 0$, the *LS_{FS}* approach makes hardly any false-negative errors but quite a lot of false-positive mistakes.

Interval ($\alpha = 0.05$) Results: Sharp-Null Testing

Posterior Interval (alpha = 0.05)

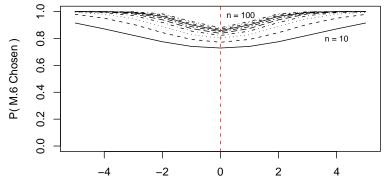


Data–Generating Theta

The behavior of the posterior interval approach is of course quite different: it makes many false-negative errors because its rate of false-positive mistakes is fixed at 0.05.

Interval (α Modified to LS_{FS} Behavior) Results

Posterior Interval (alpha Modified to LS.FS Behavior)

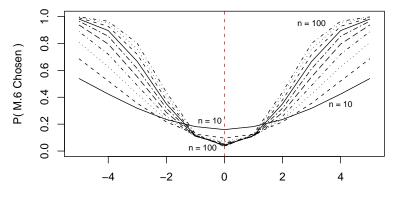


Data–Generating Theta

When the **interval method** is **modified** so that α **matches** the LS_{FS} **behavior** at $\theta_{DG} = 0$ (letting α **vary** with n), the **two approaches** have **identical model-discrimination ability**.

BIC Results: Sharp-Null Testing

BIC

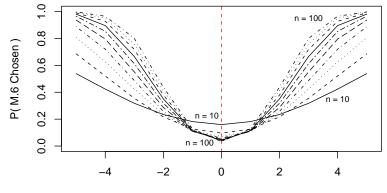


Data–Generating Theta

BIC's behavior is **quite different** from that of LS_{FS} and **fixed**- α **posterior intervals**: its **false-positive rate decreases** as *n* grows, but it **suffers a high false-negative rate** to **achieve** this **goal**.

Interval (α Modified to BIC Behavior) Results

Posterior Interval (alpha Modified to BIC Behavior)



Data–Generating Theta

When the **interval method** is **modified** so that α **matches** the **BIC behavior** at $\theta_{DG} = 0$ (again letting α **vary** with n), the **two approaches** have **identical model-discrimination ability**.

LS_{FS} Versus BIC: Geometric Versus Poisson

As another **model-comparison example**, suppose You have an **integer-valued** data set $D = y = (y_1 \dots y_n)$ and You wish to **compare**

$$M_7 = \mathbf{Geometric}(heta_1)$$
 sampling distribution with a $\mathbf{Beta}(lpha_1,eta_1)$ prior on $heta_1$, and

 $M_8 = \text{Poisson}(\theta_2)$ sampling distribution with a Gamma(α_2, β_2) prior on θ_2 .

 LS_{FS} and **BIC** both have **closed-form expressions** in this **situation**: with $s = \sum_{i=1} y_i$ and $\hat{\theta}_1 = \frac{\alpha_1 + n}{\alpha_1 + \beta_1 + s + n}$,

$$LS_{FS}(M_7|y \mathcal{B}) = \log \Gamma(\alpha_1 + n + \beta_1 + s) + \log \Gamma(\alpha_1 + n + 1) - \log \Gamma(\alpha_1 + n) - \log \Gamma(\beta_1 + s)$$
(36)
$$+ \frac{1}{n} \sum_{i=1}^{n} [\log \Gamma(\beta_1 + s + y_i) - \log \Gamma(\alpha_1 + n + \beta_1 + s + y_i + 1)],$$
$$BIC(M_7|y \mathcal{B}) = -2[n \log \hat{\theta}_1 + s \log(1 - \hat{\theta}_1)] + \log n,$$
(37)

Geometric Versus Poisson (continued)

$$LS_{FS}(M_8|y B) = (\alpha_2 + s) \log(\beta_2 + n) - \log \Gamma(\alpha_2 + s) -(\alpha_2 + s) \log(\beta_2 + n + 1)$$
(38)
$$+ \frac{1}{n} \sum_{i=1}^{n} [\log \Gamma(\alpha_2 + s + y_i) - y_i \log(\beta_2 + n + 1) -\log \Gamma(y_i + 1)], \text{ and} BIC(M_8|y B) = -2[s \log \hat{\theta}_2 - n \hat{\theta}_2 - \sum_{i=1}^{n} \log(y_i!)] + \log n,$$
(39)
where $\hat{\theta}_2 = \frac{\alpha_2 + s}{\beta_2 + n}.$

Simulation details: $n = \{10, 20, 40, 80\}, \alpha_1 = \beta_1 = \alpha_2 = \beta_2 = 0.01,$ 1,000 simulation replications; it turns out that with $(\theta_1)_{DG} = 0.5$ (Geometric) and $(\theta_2)_{DG} = 1.0$ (Poisson), both data-generating distributions are monotonically decreasing and not easy to tell apart by eye.

Let's call choosing M_8 (Poisson) when M_{DG} = Geometric a false-Poisson error and choosing M_7 (Geometric) when M_{DG} = Poisson a false-Geometric mistake.

Geometric Versus Poisson (continued)

The table below records the Monte-Carlo probability that the Poisson model was chosen.

M.DG = Poisson	M.DG = Geometric
n LS.FS BIC	n LS.FS BIC
10 0.8967 0.8661	10 0.4857 0.4341
20 0.9185 0.8906	20 0.3152 0.2671
40 0.9515 0.9363	40 0.1537 0.1314
80 0.9846 0.9813	80 0.0464 0.0407

Both methods make more false-Poisson errors than false-Geometric mistakes; the results reveal once again that neither BIC nor LS_{FS} uniformly dominates — each has a different pattern of false-Poisson and false-Geometric errors (LS_{FS} correctly identifies the Poisson more often than BIC does, but as a result BIC gets the Geometric right more often than LS_{FS}).

• Log scores are entirely free from the diffuse-prior problems bedeviling Bayes factors:

$$LS_{FS}(M_j|y \mathcal{B}) = \frac{1}{n} \sum_{i=1}^n \log p(y_i|y M_j \mathcal{B}),$$

in which

$$p(y_i|y M_j \mathcal{B}) = \int p(y_i|\gamma_j M_j \mathcal{B}) p(\gamma_j|y M_j \mathcal{B}) d\gamma_j \qquad (40)$$
$$= E_{(\gamma_j|y M_j \mathcal{B})} p(y_i|\gamma_j M_j \mathcal{B});$$

this expectation is over the posterior (not the prior) distribution for the parameter vector γ_j in model M_j , and is therefore completely stable with respect to small variations in how prior diffuseness (if scientifically called for) is specified, even with only moderate n.

• Following the Modeling-As-Decision Principle, the decision-theoretic justification for Bayes factors involves not only the Bayes factors themselves but also the prior model probabilities, which can be hard to specify in a scientifically-meaningful way: under the Bayes-factor (possibly unrealistic) 0/1 utility structure,

Properties of LS_{FS} (continued)

You're supposed to choose the model with the highest posterior probability, not the one with the biggest Bayes factor.

By contrast, **specification** of **prior model probabilities** doesn't arise with **log scores**, which have a **direct decision-theoretic justification** based on the **Prediction Principle**.

• It may seem that log scores have no penalty for unnecessary model complexity, but this is not true: for example, if one of Your models carries around a lot of unnecessary parameters, this will needlessly inflate its predictive variances, making the heights of its predictive densities go down, thereby lowering its log score.

• It may also seem that the behavioral rule based on posterior Bayes factors (Aitkin 1991) is the same as the rule based on LS_{FS} , which favors model M_j over $M_{i'}$ if

$$n LS_{FS}(M_j|y, \mathcal{B}) > n LS_{FS}(M_{j'}|y, \mathcal{B}).$$
(41)

But this is **not true either**: for example, in the **common situation** in which the **data set** D consists of **observations** y_i that are **conditionally IID** from $p(y_i|\eta_j, M_j, B)$ under M_j ,

$$nLS_{FS}(M_j|y,\mathcal{B}) = \log \prod_{i=1}^n \left[\int p(y_i|\eta_j, M_j, \mathcal{B}) p(\eta_j|y, M_j, \mathcal{B}) d\eta_j \right], \quad (42)$$

and this is not the same as

$$\log \int \left[\prod_{i=1}^{n} p(y_i|\eta_j, M_j, \mathcal{B})\right] p(\eta_j|y, M_j, \mathcal{B}) \, d\eta_j = \bar{L}_j^{PBF}$$
(43)

because the product and integral operators do not commute.

• Some take-away messages:

— In the bio-equivalence example, even when You (unwisely) let $\lambda \downarrow 0$, thereby testing a sharp-null hypothesis, the asymptotic behavior of log scores is irrelevant; what counts is the behavior of log scores and Bayes factors with Your sample size and the models being compared, and for any given *n* it's not possible to say that the false-positive/false-negative trade-off built into Bayes factors is universally better for all applied problems than the false-positive/false-negative trade-off built into log scores,

or vice versa — You have to think it through in each problem.

For instance, the tendency of log scores to choose the "bigger" model in a nested-model comparison is exactly the right qualitative behavior in the following two examples (and many more such examples exist):

— Variable selection in searching through many compounds or genes to find successful treatments: here a false-positive mistake (taking an ineffective compound or gene forward to the next level of investigation) costs the drug company C, but a false-negative error (failing to move forward with a successful treatment, in a highly-competitive market) costs k C with k = 10-100.

- In a two-arm clinical-trial setting, consider the random-effects Poisson regression model

$$\begin{array}{lll} (y_i|\lambda_i,\mathcal{B}) & \stackrel{\text{indep}}{\sim} & \text{Poisson}(\lambda_i) \\ \log \lambda_i & = & \beta_0 + \beta_1 x_i + e_i \\ (e_i|\sigma_e^2,\mathcal{B}) & \stackrel{\text{IID}}{\sim} & \mathcal{N}(0,\sigma_e^2), \quad (\beta_0,\beta_1,\sigma_e^2) \sim \text{diffuse}, \end{array}$$

$$(44)$$

where the y_i are counts of a relatively rare event and x_i is 1 for the treatment group and 0 for control; You would consider fitting this model instead of its fixed-effects counterpart, obtained by setting $\sigma_e^2 = 0$, to describe unexplainable heterogeneity (Poisson over-dispersion).

In this setting, Bayes factors will make the mistake of {telling You that $\sigma_e^2 = 0$ when it's not} more often than log scores, and log scores will make the error of {telling You that $\sigma_e^2 > 0$ when it's actually 0} more often than Bayes factors, but the former mistake is much worse than the latter, because You will underpropagate uncertainty about the fixed effect β_1 , which is the whole point of the investigation.

• All through this discussion it's vital to keep in mind that

the gold standard for false-positive/false-negative behavior is provided neither by Bayes factors nor by log scores but instead by Bayesian decision theory in Your problem.

• Asymptotic conclusions are often misleading: while it's true that

Old Theorem: $P_{\theta_{DG}=0}(LS_{FS} \text{ chooses } \theta = 0) \rightarrow 0 \text{ as } n \rightarrow \infty$,

it's also true that

 $\begin{array}{c|c|c|c|c|c|c|} \hline \textbf{New Theorem} & (\text{Draper, 2011}): \text{ for any } \lambda > 0, \\ \hline P_{|\theta_{DG}| \leq \lambda}(LS_{FS} \text{ chooses } |\theta| \leq \lambda) \to 1 \text{ as } n \to \infty, \end{array}$

and the second theorem would seem to call the relevance of the first theorem into question.

• As a profession, we need to strengthen the progression

 $\textbf{Principles} \rightarrow \textbf{Axioms} \rightarrow \textbf{Theorems}$

in optimal model specification; the Calibration Principle, the Modeling-As-Decision Principle, the Prediction Principle and the Decision-Versus-Inference Principle seem helpful in moving toward this goal. What about Q_2 : Is M_1 good enough?

As discussed previously, by the Modeling-As-Decision Principle a full judgment of adequacy requires real-world input ("To what purpose will the model be put?"), so it's not possible to propose generic methodology to answer Q_2 (apart from maximizing expected utility, with a utility function that's appropriately tailored to the problem at hand), but the somewhat related question

 $\overline{Q_{2'}}$: **Could** the **data have arisen** from **model** M_j ?

can be **answered in a general way** by **simulating** from M_j **many times**, developing a **distribution** of (e.g.) LS_{FS} values, and seeing how **unusual** the **actual data set's log score** is in **this distribution**.

This is **related** to the **posterior predictive model-checking** method of Gelman et al. (1996), which **produces** a *P*-value.

However, **this sort of thing** needs to be **done carefully** (Draper 1996), or the result will be **poor calibration**; indeed, Bayarri and Berger (2000) and Robins et al. (2000) have **demonstrated** that the

Is M_1 Good Enough? (continued)

Gelman et al. procedure may be (sharply) conservative: You may get P = 0.4 from Gelman et al. (indicating that Your model is fine) when a well-calibrated version of their idea would have P = 0.04 (indicating that it's not fine).

Using a modification of an idea suggested by Robins et al., Draper and Krnjajić (2010) have developed a simulation-based method for accurately calibrating the log-score scale (I'd be happy to send You the paper).

How should You judge how unusual the actual data set's log score is in the simulation distribution?

In all of Bayesian inference, prediction and decision-making, except for calibration concerns, there's no need for *P*-values, but — since this is a calibrative question — it's no surprise that tail areas (or something else equally ad-hoc, such as the ratio of the attained height to the maximum height of the simulation distribution) arise.

I don't see how to avoid this ad-hockery except by directly answering Q_2 with decision theory (instead of answering $Q_{2'}$ with a tail area).



• I've offered an axiomatization of inferential, predictive and decision-theoretic statistics based on information, not belief, and RT Cox's (1946) notion of probability as a measure of the weight of evidence in favor of the truth of a true-false proposition whose truth status is uncertain for You.

• Cox's Theorem lays out a progression from

 $\textbf{Principles} \rightarrow \textbf{Axioms} \rightarrow \textbf{Theorem}$

to prove that Bayesian reasoning is justified under natural logical consistency assumptions; for me this secures the foundations of applied probability.

• But Cox's Theorem does not go far enough for statistical work in science, in two ways related to model specification:

— Nothing in its consequences requires You to pay attention to how often You get the right answer, which is a basic scientific concern, and

— it doesn't offer any advice on how to specify the required ingredients: with θ as the unknown of principal interest, \mathcal{B} as Your relevant background assumptions and judgments, and an information source (data set) D relevant to decreasing Your uncertainty about θ , the ingredients are

* $\{p(\theta|\mathcal{B}), p(D|\theta|\mathcal{B})\}$ for inference and prediction, and

* in addition $\{\mathcal{A}, U(a, \theta)\}$ for decision, where \mathcal{A} is Your set of available actions and $U(a, \theta)$ is Your utility function (mapping from actions *a* and unknown θ to real-valued consequences).

• To secure the foundations of statistics, work is needed laying out the logical progression

 $\textbf{Principles} \rightarrow \textbf{Axioms} \rightarrow \textbf{Theorems}$

for model specification; progress in this area is part of the Theory of Applied Statistics.

• A Calibration Principle helps address the first of the two deficiencies above:

Calibration Principle: In model specification, You should pay attention to how often You get the right answer, by creating situations in which You know what the right answer is and seeing how often Your methods recover known truth.

Interest in calibration can be seen to be natural in Bayesian work by thinking decision-theoretically, with a utility function that rewards both quality of scientific conclusions and good calibration of the modeling process yielding those conclusions.

 In problems of realistic complexity You'll generally notice that (a) You're uncertain about θ but (b) You're also uncertain about how to quantify Your uncertainty about θ, i.e., You have model uncertainty.

• This acknowledgment of Your model uncertainty implies a willingness by You to consider two or more models in an ensemble $\mathcal{M} = \{M_1, M_2, ...\}$, which gives rise immediately to two questions:

 Q_1 : Is M_1 better than M_2 ? Q_2 : Is M_1 good enough?

• These questions sound fundamental but are not: better for what purpose? Good enough for what purpose? To address the second of the two deficiencies above (lack of guidance from Cox's Theorem on model specification), this implies a

Modeling-As-Decision Principle: Making clear the purpose to which the modeling will be put transforms model specification into a decision problem, solvable by maximizing expected utility with a utility function tailored to the specific problem under study.

This solves the model-specification problem but is hard work; there's a powerful desire for generic model-comparison methods whose utility structure may provide a decent approximation to problem-specific utility elicitation.

Two such methods are **Bayes factors** (whose **utility justification** is **less than compelling**) and **log scores**, which are based on the

Prediction Principle: Good models make good predictions, and bad models make bad predictions; that's one scientifically important way You know a model is good or bad.

• I'm aware of three approaches to improved assessment and propagation of model uncertainty: Bayesian model averaging (BMA), Bayesian nonparametric (BNP) modeling, and calibration (3-fold) cross-validation (CCV).

• CCV provides a way to pay the right price for hunting around in the data for good models, motivating the following modeling algorithm:

- (a) Start at a model M_0 (how choose?); set the current model $M_{\text{current}} \leftarrow M_0$ and the current model ensemble $\mathcal{M}_{\text{current}} \leftarrow \{M_0\}$.
- (b) If $M_{current}$ is good enough to stop (how decide?), return $\mathcal{M}_{current}$; else
- (c) Generate a new candidate model M_{new} (how choose?) and set $\mathcal{M}_{\text{current}} \leftarrow \mathcal{M}_{\text{current}} \cup M_{\text{new}}.$
- (d) If M_{new} is better than M_{current} (how decide?), set $M_{\text{current}} \leftarrow M_{\text{new}}$.
- (e) Go to (b).
- For the choice in (a), there's usually a default off-the-shelf initial model based on the structure of the data set *D* and the scientific context.

• In manual model search the choice in (c) is typically based on the results of a variety of diagnostics, with the new model suggested by deficiencies revealed in this way; at present, we have no better way to automate this choice in many cases than choosing M_{new} at random (I offer no new ideas on this topic today).

• In comparing M_1 with M_2 (the choice in (d)), consider a calibrative scenario in which the the data-generating model M_{DG} is one or the other of $\mathcal{M} = \{M_1, M_2\}$ (apart from parameter estimation), and call {choosing M_2 when $M_{DG} = M_1$ } a false positive and {choosing M_1 when $M_{DG} = M_2$ } a false negative; then

— The **right way** to do this, following the **Modeling-As-Decision Principle**, is to build a **utility function** by **quantifying** the **real-world consequences** of

{choosing M_1 when $M_{DG} = M_1$, choosing M_1 when $M_{DG} = M_2$, choosing M_2 when $M_{DG} = M_1$, choosing M_2 when $M_{DG} = M_2$ }

and maximize expected utility.

— If instead You contemplate using Bayes factors/BIC or log scores, it is not the case that one of these two methods uniformly dominates the other in calibrative performance; in some settings they behave the same, in others (for Your sample size) they will have a different balance of false positives and false negatives; it's a good idea to investigate this before settling on one method or the other.

• See Draper and Krnjajić (2010) for a **method** for **answering the question** $Q_{2'}$: Could the data have arisen from model M_j ? in a well-calibrated way.

• CCV provides an approach to finding a good ensemble \mathcal{M} of models, and gives You a decent opportunity both to arrive at good answers to Your main scientific questions and to evaluate the calibration of the iterative modeling process that led You to Your answers.

• Decision-Versus-Inference Principle: We should all get out of the habit of using inferential methods to make decisions: their implicit utility structure is often far from optimal.

Another Unsolved Foundational Problem

• One more unsolved foundational problem: how can good decisions be arrived at when "You" is a collective of individuals, all with their own utility functions that imply partial cooperation and partial competition?

Example: Allocation of finite resources by two or more people who have agreed to band together in some sense (i.e., politics, at the level of family or nation or ...).

An instance of this: Defining and funding good quality of health care — the actors in the drama include

{patient, doctor, hospital, state and local regulatory bodies, federal regulatory system};

all are in **partial agreement** and **partial disagreement** on how (and how many) **resources** should be **allocated** to the **problem** of addressing **this patient's immediate health needs**.

(But that's for **another day**, as is the topic of **Bayesian computing** with **large data sets**.)