Second-order Probabilism: Expressive Power and Accuracy

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Abstract.

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1 Introduction

As rational agents, we form beliefs about a variety of propositions on the basis of the evidence available to us. But believing a proposition is not an all-or-nothing affair; it is a matter of degrees. We are uncertain, to a greater or lesser extent, about the truth of many propositions since the evidence we possess about them is often fallible. To represent this uncertainty, it is natural to use a probability measure that assigns to each proposition a value between 0 and 1 (also called a degree of belief or credence). This approach—known as *precise probabilism*— models an agent's state of uncertainty (or credal state) with a single probability measure: each proposition is assigned one probability value (a sharp degree of belief). The problem is that a sharp probability measure is not expressive enough to distinguish between intuitively different states of uncertainty rational agents may find themselves in (§2). To avoid this problem, a *set* of probability measures, rather than a single one, can be used to represent the uncertainty of a rational agent. This approach is known as *imprecise probabilism*. It outperforms precise probabilism in some respects, but also runs into problems of its own (§3).

To make progress, this paper argues that the uncertainty of a rational agent is to be represented neither by a single probability measure nor a set of measures. Rather, it is to be represented by a higher-order probability measure, more specifically, a probability distribution over parameter values intepreted as probabilities. Call this view *higher-order probabilism*. We show that higher-order probabilism addresses all the problems and philosophical puzzles that plague both precise and imprecise probabilism (§4 and §5).

Moreover, Bayesian probabilistic programming already provides a fairly reliable implementation framework of this approach.

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2 Precise probabilism

Precise probabilism (PP) holds that a rational agent's uncertainty about a proposition is to be represented as a single, precise probability measure. Bayesian updating regulates how the prior probability measure should change in light of new evidence that the agent learns. The updating can be iterated multiple times for multiple pieces of evidence considered successively. This is an elegant and simple theory with many powerful applications. Unfortunately, representing our uncertainty about a proposition in terms of a single, precise probability measure runs into a number of difficulties.

Precise probabilism fails to capture an important dimension of how our fallible beliefs reflect the evidence we have (or have not) obtained. A couple of stylized examples featuring coin tosses should make the point clear.

> **No evidence v. fair coin** You are about to toss a coin, but have no evidence about its bias. You are completely ignorant. Compare this to the situation in which you know, based on overwhelming evidence, that the coin is fair.

On precise probabilism, both scenarios are represented by assigning a probability of .5 to the outcome *heads*. If you are completely ignorant, the principle of insufficient evidence suggests that you assign .5 to both outcomes. Similarly, if you know for sure the coin is fair, assigning .5 seems the best way to quantify the uncertainty about the outcome. The agent's evidence in the two scenarios is quite different, but precise probabilities fail to capture this difference.

> **Learning from ignorance** You toss a coin with unknown bias. You toss it 10 times and observe *heads* 5 times. Suppose you toss it further and observe 50

heads in 100 tosses.

Since the coin initially had unknown bias, you should presumably assign a probability of .5 to both outcomes if you stick with precise probabilism. After the 10 tosses, you again assess the probability to be .5. You must have learned something, but whatever that is, it is not modeled by precise probabilities. When you toss the coin 100 times and observe 50 heads, you learn something new as well. But your precise probability assessment will again be .5.

These examples suggest that precise probabilism is not appropriately responsive to evidence. Representing an agent's uncertainty by a precise probability measure can fail to track what an agent has learned from new evidence. Precise probabilism assigns the same probability in situations in which one's evidence is quite different: when no evidence is available about a coin's bias; when there is little evidence that the coin is fair (say, after only 10 tosses); and when there is strong evidence that the coin is fair (say, after 100 tosses). In fact, analogous problems also arise for evidence that the coin is not fair. Suppose the rational agent starts with a weak belief that the coin is .6 biased towards heads. They can strengthen that belief by tossing the coin repeatedly and observing, say, 60 heads in 100 tosses. But this improvement in their evidence is not mirrored in the .6 probability they are supposed to assign to *heads*.[1]

These problems generalize beyond cases of coin tossing. It is one thing not to know much about whether a proposition is true, for example, whether an individual is guilty of a crime. It is another thing to have strong evidence that favors a hypothesis and equally strong evidence that favors its negation, for example, strong evidence favoring the guilt hypothesis and equally strong evidence favoring the hypothesis of innocence. Despite this difference, precise probabilism would reccomend that a probability of .5 be assigned to both hypotheses in either case. Here, too, precise probabilities fail to be appropriately responsive to the evidence.

In addition, evidence can accumulate in a way that does not require changing our initial probability assignments. Suppose that, at first, one's overall evidence favors A over B. So the probability assigned to A should be greater than that assigned to B. Next, the agent acquires new evidence. The total quantity of evidence has increased, but suppose this larger body of evidence overall still favors A over B. So no change in the probabilities seems required. Still, something has changed about the agent's state of uncertainty towards A and B: the quantity of evidence on which the agent can make their assessment whether A is more probable than B has become larger. And yet, this change in the quantity of overall evidence is not reflected in the precise probabilities assigned to the propositions A and B.[2]

3 Imprecise probabilism

What if we give up the assumption that probability assignments should be precise? Imprecise probabilism (IP) holds that a rational agent's credal stance towards a hypothesis is to be represented by a *set of probability measures*, typically called a representor $\mathbb{P}$, rather than a single measure P. The representor should include all and only those probability measures which

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[1]Here is another problem for precise probabilism. Imagine a rational agent who does not know the bias of the coin. For precise probabilism, this state of uncertainty should be represented by a .5 probability assignment to the *heads*. Next, the agent learns that the bias towards heads, whatever the bias is, has been slightly increased, say by .001. The addition of this new information is called *sweetening* in the philosophical literature. This sweetening should now make the agent bet on heads: if the probability of *heads* was initially .5, it must be ever so slightly above .5 after sweetening. But, intuitively, the new information should leave the agent equally undecided about betting on heads or tails. After sweetening, the agent still does not know much about the actual bias of the coin.

[2]Following Keynes, the distinction here is between the *balance* of the evidence—whether the evidence available tips in favor a proposition or another—and the *weight* of the evidence—the overall quantity of evidence. **ADD REFRENCE TO KEYNES**

are compatible with the evidence (more on this point later).[3] It is easy to see that modeling an agent's credal state by sets of probability measures avoids some of the shortcomings of precise probabilism. For instance, if an agent knows that the coin is fair, their credal state would be represented by the singleton set {P}, where P is a probability measure that assigns .5 to *heads*. If, on the other hand, the agent knows nothing about the coin's bias, their credal state would be represented by the set of all probabilistic measures, since none of them is excluded by the available evidence. Note that the set of probability measures does not represent admissible options that the agent could legitimately pick from. Rather, the agent's credal state is essentially imprecise and should be represented by means of the entire set of probability measures.

So far so good. But, just as precise probabilism fails to be appropriately evidence-responsive in certain scenarios, imprecise probabilism runs in similar difficulties in other scenarios.

> **Even v. uneven bias:** You have two coins and you know, for sure, that the probability of getting heads is .4, if you toss one coin, and .6, if you toss the other coin. But you do not know which is which. You pick one of the two at random and toss it. Contrast this with an uneven case. You have four coins and you know that three of them have bias .4 and one of them has bias .6. You pick a coin at random and plan to toss it. You should be three times more confident that the probability of getting heads is .4. rather than .6.

The first situation can be easily represented by imprecise probabilism. The representor would contain two probability measures, one that assigns .4. and the other that assigns .6 to the hypothesis 'this coin lands heads'. But imprecise probabilism cannot represent the second situation. Since the probability measures in the set are all compatible with the agent's evidence, no probability measure can be assigned a greater (higher-order) probability than any other.[4]

These examples show that imprecise probabilism is not expressive enough to model the scenario of uneven bias. Defenders of imprecise probabilism could concede this point but prefer their account for reasons of simplicity. They could also point out that imprecise probabilism models scenarios that precise probabilism cannot model, for example, a state of complete lack of evidence. In this respect, imprecise probabilism outperforms precise probabilism in expressive power, but also retains theoretical simplicity. Unfortunately, it is questionable whether imprecise probabilism outperforms precise probabilism *all things considered*. In fact, imprecise probabilism suffers from a number of shortcomings that do not affect precise probabilism.

The first shortcoming has not received extensive discussion in the literature, but it is fundamental. Recall that, for imprecise probabilism, an agent's state of uncertainty is represented by those probability measures that are *compatible* with the agent's evidence. The question is, how should the notion of compatibility be understood here? Perhaps we can think of compatibility as the fact that the agent's evidence is consistent with the probability measure in question.

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[3] For the development of imprecise probabilism, see Keynes (1921); Levi (1974); Gärdenfors & Sahlin (1982); Kaplan (1968); Joyce (2005); Fraassen (2006); Sturgeon (2008); Walley (1991). Bradley (2019) is a good source of further references. Imprecise probabilism shares some similarities with what we might call **interval probabilism** (Kyburg, 1961; Kyburg Jr & Teng, 2001). On interval probabilism, precise probabilities are replaced by intervals of probabilities. On imprecise probabilism, instead, precise probabilities are replaced by sets of probabilities. This makes imprecise probabilism more general, since the probabilities of a proposition in the representor set do not have to form a closed interval.

[4] Other scenarios can be constructed in which imprecise probabilism fails to capture distinctive intuitions about evidence and uncertainty; see, for example, (Rinard, 2013). Suppose you know of two urns, GREEN and MYSTERY. You are certain GREEN contains only green marbles, but have no information about MYSTERY. A marble will be drawn at random from each. You should be certain that the marble drawn from GREEN will be green (G), and you should be more confident about this than about the proposition that the marble from MYSTERY will be green (M). In line with how lack of information is to be represented on IP, for each $r \in [0, 1]$ your representor contains a P with $P(M) = r$. But then, it also contains one with $P(M) = 1$. This means that it is not the case that for any probability measure P in your representor, $P(G) > P(M)$, that is, it is not the case that RA is more confident of G than of M. This is highly counter-intuitive.

But mere consistency wouldn't get the agent very far in excluding probability measures, as too many probability measures are strictly speaking still consistent with most observations and data. Admittedly, there will be clear-cut cases: if you see the outcome of a coin toss to be heads, you reject the measure with $P(H) = 0$, and similarly for tails. Another class of cases might arise while randomly drawing objects from a finite set where the true frequencies or objective chances are already known, because the finite set has been inspected. But such clear-cut cases aside, what else? In the end, evidence will often be consistent with almost any probability measure.[5]

A second, well-known problem for imprecise probabilism is belief inertia. Precise probabilism offers an elegant model of learning from evidence: Bayesian updating. Imprecise probabilism, at least *prima facie*, offers an equally elegant model of learning from evidence, richer and more nuanced. It is a natural extension of the classical Bayesian approach that uses precise probabilities. When faced with new evidence E between time t_0 and t_1, the representor set should be updated point-wise, running the standard Bayesian updating on each probability measure in the representor:

$$\mathbb{P}_{t_1} = \{ P_{t_1} | \exists P_{t_0} \in \mathbb{P}_{t_0} \ \forall H \ \left[P_{t_1}(H) = P_{t_0}(H|E) \right] \}.$$

The hope is that, if we start with a range of probabilities that is not extremely wide, point-wise learning will behave appropriately. For instance, if we start with a prior probability of *heads* equal to .4 or .6, then those measures should be updated to something closer to .5 once we learn that a given coin has already been tossed ten times with the observed number of heads equal 5 (call this evidence E). This would mean that if the initial range of values was $[.4, .6]$ the posterior range of values should be narrower.

Unfortunately, this narrowing of the range of values becomes impossible whenever the starting point is complete lack of knowledge, as imprecise probabilism runs into the problem of belief inertia (Levi, 1980). This problem arises in situations in which no amount of evidence could lead the agent to change their belief state, according to a given modeling strategy. Consider a situation in which you start tossing a coin knowing nothing about its bias. The range of possibilities is $[0, 1]$. After a few tosses, if you observed at least one tail and one heads, you can exclude the measures assigning 0 or 1 to *heads*. But what else have you learned? If you are to update your representor set point-wise, you will end up with the same representor set. For any sequence of outcomes that you can obtain and any probability value in $[0, 1]$, there will exist a probability measure (conditional on the oucomes) that assigns that probability to *heads*. Consequently, the edges of your resulting interval will remain the same. In the end, it is not clear how you are supposed to learn anything if you start from complete ignorance.[6]

Some downplay the problem of belief inertia. After all, if you started with knowing truly nothing, then it is right to conclude that you will never learn anything. Joyce (2010) writes:

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[5] Probability measures can be inconsistent with evidential constraints that agents believe to be true. Mathematically, non-trivial evidential constraints are easy to model (Bradley, 2012). They can take the form, for example, of the *evidence of chances* $\{P(X) = x\}$ or $P(X) \in [x, y]$, or *structural constraints* such as "X and Y are independent" or "X is more likely than Y." These constraints are something that an agent can come to accept outright, but only if offered such information by an expert whom the agent completely defers to. But, besides these idealized cases, it is unclear how an agent could come to accept such structural constraints upon observation. There will usually be some degree of uncertainty about the acceptability of these constraints.

[6] Here's another example of inertia, coming from Rinard (2013). Either all the marbles in the urn are green (H_1), or exactly one tenth of the marbles are green (H_2). Suppose your initial credence about these two hypothesis is complete uncertainty with interval. Next, suppose you learn that a marble drawn at random from the urn is green (E). After using this evidence to condition each probability measure in your representor (which initially contains all possible probability measures over the relevant space) on this evidence, you end up with the same spread of values for H_1 that you had before learning E. This holds no matter how many marbles are sampled from the urn and found to be green. This is counterintuitive: if you continue drawing green marbles, even if you started with complete uncertainty, you should become more inclided towards the hypothesis that all marbles are green.

> You cannot learn anything in cases of pronounced ignorance simply because a prerequisite for learning is to have prior views about how potential data should alter your beliefs (p. 291)

The upshot is that vacuous priors should not be used and that imprecise probabilism gives the right results when the priors are non-vacuous. Another strategy is to say that, in a state of complete ignorance, a special updating rule should be deployed.[7]

Finally, imprecise probabilism faces a third, deeper problem that does not arise for precise probabilism. As it turns out, it is impossible to define proper scoring rules for measuring the accuracy of a representor. Workable *scoring rules* exist for measuring the accuracy of a single, precise probability measure, such as the Brier score. These rules measure the distance between a rational agent's probability measure and the actual value. A requirement of scoring rules is that they be *proper*: any rational agent will expect their own probability measure to be more accurate than any other. After all, if an agent thought a different probability measure was more accurate, they should switch to it. Proper scoring rules are then used to formulate accuracy-based arguments for precise probabilism. These arguments show (roughly) that, if your precise measure follows the axioms of probability theory, no other non-probabilistic measure is going to be more accurate than yours whatever the facts are. Can the same be done for imprecise probabilism? It cannot. Impossibility theorems demonstrate that no proper scoring rules are available for representor sets. So, as many have noted, the prospects for an accuracy-based argument for imprecise probabilism look dim (Campbell-Moore, 2020; Mayo-Wilson & Wheeler, 2016; Schoenfield, 2017; Seidenfeld, Schervish, & Kadane, 2012). Moreover, as shown by Schoenfield (2017), if an accuracy measure satisfies certain plausible formal constraints, it will never strictly recommend an imprecise stance, as for any imprecise stance there will be a precise one with at least the same accuracy.

4 Higher-order probabilism

Let us take stock. Imprecise probabilism is more expressive than precise probabilism. It can model the difference between a state in which there is no evidence about a proposition (or its negation) and a state in which the evidence for and against a proposition is in equipoise. But imprecise probabilism has its own expressive limitations, for example, it cannot model the case of uneven bias. In addition, imprecise probabilism faces difficulties that do not affect precise probabilism: the notion of compatibility between a probability measure and the evidence is too permissive; belief inertia makes it impossible for a rational agent to learn via Bayesian updating; and no proper scoring rules exist for imprecise probabilism. In this section, we show that higher-order probabilism overcomes the expressive limitations of imprecise probabilism without falling prey to any such difficulties.

Proponents of imprecise probabilism already hinted at the need of relying on higher order-probabilities. For instance, Bradley compares the measures in a representor to committee members, each voting on a particular issue, say the true chance or bias of a coin. As they acquire more evidence, the committee members will often converge on a chance hypothesis.

> …the committee members are "bunching up". Whatever measure you put over the set of probability functions—whatever "second order probability" you use—the "mass" of this measure gets more and more concentrated around the true chance hypothesis. (Bradley, 2012, p. 157)

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[7]Elkin (2017) suggests the rule of *credal set replacement* that recommends that upon receiving evidence the agent should drop measures rendered implausible, and add all non-extreme plausible probability measures. This, however, is tricky. One needs a separate account of what makes a distribution plausible from a principled account of why one should use a separate special update rule when starting with complete ignorance.

[Margin note: add reference. Joyce, J. M. (2010). A Defence of Imprecise Credences in Inference and Decision Making, *Philosophical Perspectives* 24, pp. 281–323.]

[Margin note: Rafal to develop a response to this point.]

But such bunching up cannot be modeled by imprecise probabilism alone: a probability distribution over chance hypotheses is needed.[8] That one should use higher-order probabilities has also been suggested by critics of imprecise probabilism. For example, Carr (2020) argues that sometimes evidence requires uncertainty about what credences to have. Carr, however, does not articulate this suggestion more fully; does not develop it formally; and does not explain how her approach would fare against the difficulties affecting precise and imprecise probabilism. We now set out to do precisely that.

The central idea of higher-order probabilism is this: a rational agent's uncertainty is not single-dimensional and thus cannot be mapped onto a one-dimensional scale like the real line. Uncertainty is best modeled by the shape of a probability distribution over multiple probability measures. Stated more formally, a rational agent's state of uncertainty (or credal stance) towards a proposition X is not represented by a single probability value $P(X)$ between 0 and 1, but by a probability (density) distribution $f_{P(X)}$, where the first-order probability measure $P(X)$ is treated as a random variable. Crucially, this representation is completely general. Unlike the examples used so far, the proposition X is not restricted to chance hypotheses or the bias of a coin. The probability distribution $f_{P(X)}$ assigns a second-order probability to each of the first-order probabilities $P(X)$.

How should these second-order probabilities be understood? It is helpful to think of higher-order probabilism as a generalization of imprecise probabilism. Imprecisers already admit that some probability measures are compatible and others incompatible with the agent's evidence at some point. Compatibility is a coarse notion; it is an all-or-nothing affair. But, as seen earlier, evidence can hardly exclude a probability measure in a definitive manner except in clear-cut cases. Just as it is often a matter of degrees whether evidence supports a proposition, the notion of compatibility between evidence and probability measures can itself be a matter of degrees. On this picture, the evidence justifies different values of first-order probability to various degrees. So, second-order probabilities express the extent to which the first-order probabilities are supported by the evidence.

This higher-order approach at the technical level is by no means novel. Bayesian probabilistic programming languages embrace the well-known idea that parameters can be stacked and depend on each other (Bingham et al., 2021). But, while the technical machinery has been around for a while, it has not been deployed by philosophers to model a rational agent's uncertainty or credal state. Because of its greater expressive power, higher-order probabilism can represent uncertainty in a more fine-grained manner, as illustrated in Figure 1. In particular, the uneven coin scenario in which the two biases of the coin are not equally likely—which imprecise probabilism cannot model—can be easily modeled within high-order probabilism by assigning different probabilities to the two biases.

An agent's uncertainty could—perhaps, should—sometimes be represented by a sigle probability value. Higher-order probabilism does not prohibit that. For example, there may well be cases in which an agent's uncertainty is aptly represented by the expectation.[9] But this need not always be the case. If the probability distribution is not sufficiently concentrated around a single value, a one-point summary will fail to do justice to the nuances of the agent's credal state.[10] For example, consider again the scenario in which the agent knows that the bias of the

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[8]In a similar vein, Joyce (2005), in a paper defending imprecise probabilism, explicates the notion of weight of evidence using a probability distribution over chance hypotheses. Oddly, representor sets play no central role in Joyce's account of the weight of evidence.

[9]The expectation is usually defined as $\int_0^1 x f(x)\, dx$. In the context of our approach here, x is the first-order probability of a given proposition, and f is the density representing the agent's uncertainty about x.

[10]This approach lines up with common practice in Bayesian statistics, where the primary role of uncertainty representation is assigned to the whole distribution. Summaries such as the mean, mode standard deviation, mean absolute deviation, or highest posterior density intervals are only succinct ways for representing the uncertainty of a given scenario.
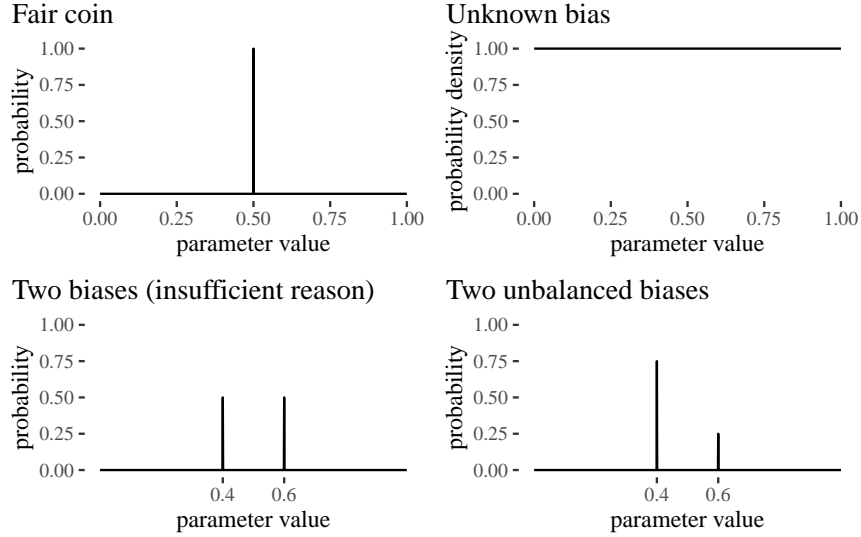
Figure 1: Examples of higher-order distributions for a few scenarios problematic for both precise and imprecise probabilism.

coin is either .4 or .6 but the former is three times more likely. Representing the agent's credal state with the expectation $P(X) = .75 \times .4 + .25 \times .6 = .45$ would fail to capture the agent's different epistemic attitudes towards the two biases. The agent believes the two biases have different probabilities, but is also certain the bias is *not* .45.

Besides its greater expressive power in modelling uncertainty, higher-order probabilism does not fall prey to belief inertia or the impossibility of proper scoring rules. Consider a situation in which you have no idea about the bias of a coin. You start with a uniform distribution over $[0, 1]$ as your prior. Observing any non-zero number of heads will exclude 0 and observing any non-zero number of tails will exclude 1 from the basis of the posterior. The posterior distribution will become more centered as the observations come in. This result is a straightforward application of Bayesian updating. Instead of plugging sharp probability values into the formula for Bayes's theorem , the factors to be mutiplied in the theorem will be probability densities (or ratios of densities as needed). Figure 2 illustrates—starting with a uniform prior distribution—how the posterior (beta) distribution changes after successive observations of heads, heads again, and then tails.[11]

The impossibility of defining proper scoring rules was another weakness of imprecise probabilism. This is a significant shortcoming, especially because proper scores do exist for precise probabilism. Fortunately, one can show that there exist proper scoring rules for higher-order probabilism. These rules can then be used to formulate accuracy-based arguments. In addition, recall the point made by Schoenfield (2017): an accuracy measure will not usually recommend an imprecise stance. This argument fails against imprecise probabilism: there are

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[11]Assuming independence and constant probability for all the observations, learning is modeled the Bayesian way. You start with some prior density p over the parameter values. If you start with complete lack of information, p should be uniform. Then, you observe the data D which is the number of successes s in a certain number of observations n. For each particular possible value θ of the parameter, the probability of D conditional on θ follows the binomial distribution. The probability of D is obtained by integration. That is:

$$p(\theta|D) = \frac{p(D|\theta)p(\theta)}{p(D)}$$
$$= \frac{\theta^s(1-\theta)^{(n-s)}p(\theta)}{\int (\theta')^s(1-\theta')^{(n-s)}p(\theta')\, d\theta'}.$$

Figure 2: As observations of heads, heads and tails come in, extreme parameter values drop out of the picture and the posterior is shaped by the evidence.

cases in which accuracy considerations recommend an imprecise stance (that is, a multi-modal distribution) over a precise one. We will defend these claims in the next section. The argument, however, will be more formal and a bit rough going. The section can be skipped upon first reading without losing track of the main line of the argument.

5 Proper scoring for higher-order probabilism

As already noted, one challenge for the imprecisers is providing a proper scoring rule that would be a counterpart of, say, the Brier score for the precise case. A crucial and well acknowledged characteristic for such a scoring rule is known as *strict propriety*.[12]

This challenge becomes particularly pronounced in the context of imprecise probabilism, where meeting the requirement of strict propriety proves elusive. However, this paragraph aims to illustrate that higher-order probabilism can indeed offer a scoring rule that satisfies this crucial characteristic.

The primary objective is to devise a scoring rule capable of assessing the accuracy of probability distributions while ensuring its propriety. The scoring rule we propose is based on well-known measures of divergence between probability distributions, building on existing work on this topic (Hersbach (2000), Pettigrew (2012), Gneiting & Raftery (2007)). A key modification to this framework involves abandoning the assumption that only two possible outcomes (truth and false) exist.

Subsequently, we demonstrate that holding such an assumption leads to improper results, justifying its exclusion from our proposed framework.

Our method incorporates Kullback-Leibler Divergence between probability distributions. For computational ease, we will use a grid approximation instead of continous distributions, as in practice we are unable to work with infinite precision. To this end, x will denote the finite vector of discrete states under consideration (by default, we will use equally spaced values between 0 and 1 here).

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[12]When an inaccuracy measure is strictly proper each probability distribution anticipates itself to be the least inaccurate.

Kullback-Leibler Divergence measure:

$$D_{\mathrm{KL}}(p \,||\, q) = \sum_x p(x) \log \left(\frac{p(x)}{q(x)} \right)$$

which is a standard information-theoretic measure of divergence of q from p from the perspective of p.[13]

To convert this measure into the measure of *(in)accuracy*, we need to define relations between probability distributions and possible worlds. Let the outcome under consideration in w be $V(w)$ (in a very simple case you might take there to be two possible oucomes, 0 and 1, the range of V is simply the vector of possible states, x). The KL-inaccuracy of a distribution p with respect to w is defined, as follows:

$$I_{\mathrm{KL}}(p, w) = D_{\mathrm{KL}}(f(w)||p)$$

where P is the cumulative probability corresponding to the probability distribution p, and

$$f(x) = \begin{cases} 1 & \text{if } x = V(w) \\ 0 & \text{o /w.} \end{cases}$$

That is, it is the KL-divergence of p from the "true" probability distribution which assigns probability 1 to the outcome $V(w)$ and probability 0 to any other outcome,[14] as seen from the perspective of w, the "ground truth" here, conceptually.

At the beginning, we mentioned that the crucial characteristic of a scoring rule that we go after is strict-propriety. Further discussion will be based on an example, however, we have included the proof of strict propriety of the KLD as an inaccuracy measure in the appendix. In a nutshell, the argument demonstrates that for a second-order discretized probability mass p over a parameter space $[0, 1]$, with the actual probability denoted as θ, the Kullback-Leibler divergence of p from the indicator distribution of θ (which assigns 1 to θ and 0 to all other parameter values in the parameter space) is expressed as $\mathcal{J}^2_{D_{\mathrm{KL}}}$.[15] This serves as a demonstration of the strict propriety of the inaccuracy measure: each p anticipates itself to be the least inaccurate distribution.[16]

A final notion that we need is *expected inaccuracy*. We will use expected accuracy to measure the distance to every possible true hypothesis (considering every world) in order to give a more comprehensive accuracy measure. This also signifies a departure from the framework mentioned at the beginning of this section. It is defined using the discretized vector x of outcomes.

$$\mathbb{E}_{\mathtt{discretized}} I(p, q) = \sum I(p, w) q(w),$$

M: From the footnote the scoring rule seems to -log p(theta). how does this connect with the divergence measures from before?

M: Why need expected inaccuracy? Is it needed to show (im)propriety?

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[13] In the continuous case, the measure is in the form of differential KL divergence.

[14] If you prefer to think in continuous terms, you'd need to use Delta-Dirac distributions here.

[15] The argument generalizes to parameter spaces that correspond to probabilities of multiple propositions which are Cartesian products of parameter spaces explicitly used in the argument in this section.

[16] The argument has four key moves:

1. the inaccuracy of p w.r.t. to parameter θ is just $-\log_2 p(\theta)$,

2. the expected inaccuracy of p from the perspective of p is the entropy of p, $H(p)$,

3. the inaccuracy of q from the perspective of p is the cross-entropy $H(p, q)$,

4. and it is an established result that cross-entropy is strictly larger than entropy as soon as $p \neq q$.

where $I(p, w)$ is an inaccuracy score of distribution p relative to the possible world w, whethere in the form of KL-divergence or different. In practice, instead of working with w and saying things like $V(w) = x$, we will be working with scalars and finite vectors, and simply say that the outcome is x.

Let's now compare, and show on an example the difference between our approach, which uses KL-divergence and the classical approach represented by CRPS[17]. We will start by providing a definition of another inaccuracy measure, Cramer-Von-Mises.

The Cramer-Von-Mises measure of which we will be using a discretized version:[18]

$$D_{\mathrm{CM}}(p, q) = \sum_x |P(x) - Q(x)|^2$$

Similarly, as in the case of KL-divergence, we can define the inaccuracy of p with respect to w as follows:

$$I_{\mathrm{CRPS}}(p, w) = \sum |\mathrm{P}(x) - \mathbf{1}(x \geq V(w))|^2$$

where P is the cumulative probability corresponding to the probability distribution p, and

$$\mathbf{1}(x \geq V(w)) = \begin{cases} 1 & \text{if } x \geq V(w) \\ 0 & \text{o /w.} \end{cases}$$

Cramer-Von-Mises can also be used to define the expected inaccuracy, analogously to the case of KL-divergence. However, let's represent a case where there are only two possible outcomes, tails and heads, *and you take the distributions* expected values as the probabilities they assign to those outcomes, you might think a seemingly simpler notion of expected inaccuracy is preferrable:

$$\mathbb{E}_{\mathtt{binary}}(p, q) = I(p, \text{heads}) \mathbb{E}q(\text{heads}) + I(p, \text{tails}) \mathbb{E}q(\text{tails}).$$

We will start by reflecting on this binary approach, as its a part of the original framework, but we will soon see that it runs into difficulties. To fix ideas, consider a variation of a scenario by Schoenfield (2017). A rational agent is invited to engage in a bet by an opponent who has a representative bag of coins coming from a factory where the distribution of bias among the coins produced, the true generative process, is known. It is a mixture of two normal distributions centered at .3 and at .5, both with standard deviation of .05. The opponent randomly selects one of these coins and flips it. The rational agent knows all the details of this set-up.

What credal state should the rational agent form in response? Consider three out of many possible options: first, a *faithful bimodal* distribution centered at .3 and .5; second, a *unimodal* distribution centered at .4; third, a *wide bimodal* distribution centered at .2 and .6. The three options are depicted in Figure 3. All of them have expected values at .4 rounded to four digits.

Denote these distributions as b, c, w correspondingly. Now consider what happens if we think of expected inaccuracy of these distributions assuming there are only two possible true outcomes, conceptualized as either heads (H) or tails (T). Whatever our inaccuracy measure, we will have six inaccuracy scores of the form $I(\text{distribution}, \text{outcome})$, where outcome is one of two omniscient distributions that give all weight to either heads or tails. In the calculation of expected values, these will need to be multiplied by the probability of H and the probability

---

[17]Note that there are no readily computable solutions to the integral used in the definition of CRPS, although it can sometimes be evaluated in closed form (Gneiting & Raftery, 2007, p. 366).

[18]In the continuous case, this measure is defined as the area under the squared Euclidean distances between the corresponding cumulative density functions That is, $D_{CM}(p, q) = \int_0^1 |P(x) - Q(x)|^2 \, dx$. Looking at cumulative densities ensures that all densities are considered on the same scale.

of T. However, none of these distributions assigns such a probability. They all assign probabilities to different values of coin bias, but not to different *outcomes* directly. Suppose we do what seems to be the natural way to go and obtain such probabilities by taking expected values of the form $\mathbb{E}_{\text{distribution}}(H) = \sum(x * \text{distribution}(x))$, where x are the values on the discretized grid (as in our example these expectations are pretty much the same, we can simply take distribution(H) to be .4):

Bimodal, with modes at .3 and .5

Centered around .4
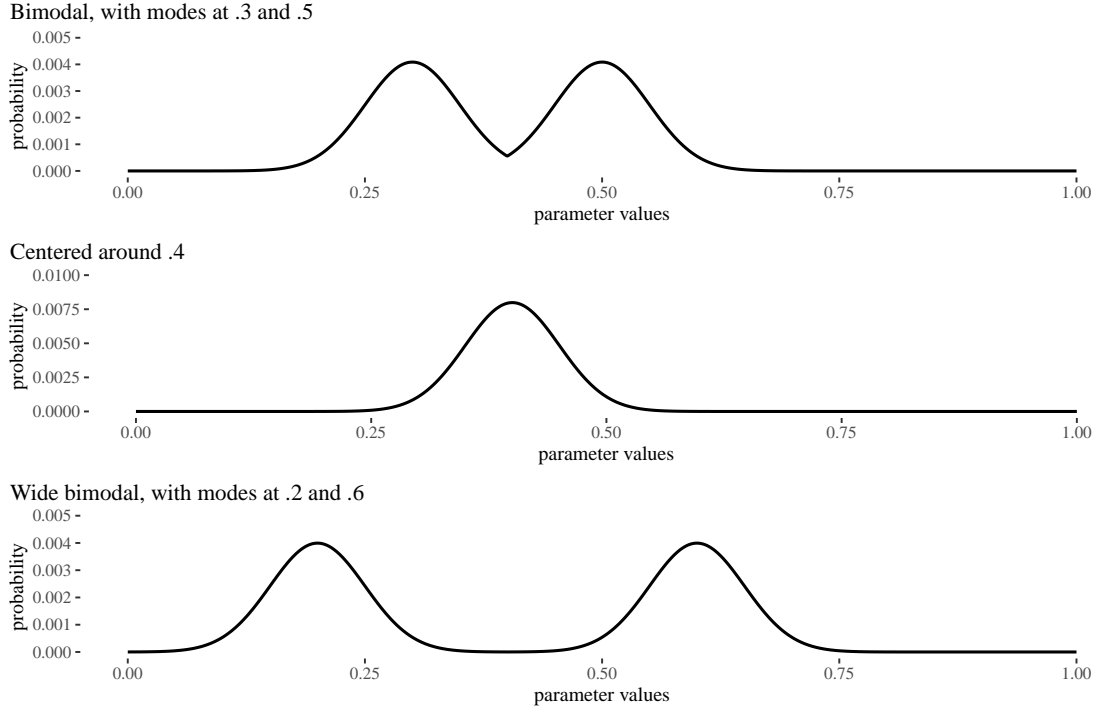

Wide bimodal, with modes at .2 and .6

Figure 3: Three distributions in a vague EMS scenario. The distributions are built from normal distributions with standard deviation .05, the bimodal ones are joint in the middle. All of them have expected values $\approx .4$.

Table 1 displays the accuracy scores assigned by CRPS assuming the true outcome is *heads* (CRPS1) and assuming the true outcome is *tails* (CRPS0), and analogously for the KL divergence. Then, we obtain the expected inaccuracies by averaging the two scores by using the point probability of heads set to .4. These result in ExpCRPS and ExpKL respectively, note that since the probability of heads is the same on all the distributions, those are expected values from the perspective of each of the measures; changing the perspective in this example doesn't change the expected inaccuracy.

distribution	CRPS1	CRPS0	KLD1	KLD0	ExpCRPS	ExpKLD
bimodal	534.7305	334.9305	80.06971	33.90347	414.8505	52.36997
centered	571.2192	371.4192	110.84220	53.13440	451.3392	76.21752
wide bimodal	485.4052	285.6177	54.13433	19.50965	365.5340	33.35974

Table 1: CPRS and KLD inaccuracies of the three distributions to the TRUE and FALSE omniscient functions, with expected inaccuracies.

As it turns out, the expected CRPS score recommends the wide bimodal distribution as the most accurate (or least inaccurate). The KL divergence from the omniscient measure makes

the same reccomendation.[19] This is counterintuitive, because the faithful bimodal seems the one most appropriately evidence-responsive. The unimodal distribution, while centering on the expected value, gets the chances wrong, and the wide bimodal has its guesses too close to the truth values and too far from the known chances. But there is a further problem. While the wide bimodal distribution expects itself to be the least inaccurate, the other distributions also expect the wide bimodal to be the least inaccurate. This indicates that in this setting the CRPS score and the KL divergence are not proper scores, as they allow for cases of some distributions recommending other distributions as less accurate, whatever the true state of the world turns out to be.

What are we to make of this result? Note that the three distributions share the same expected value $.4$. The latter is then used in the calculations of the expected inaccuracies for both CRPS and KL with the assumption there are two possible outcomes with respect to which expected inaccuracy calculations are to be made. This approach, however, runs against the spirit of our enterprise. If expected values are often not good representations of a rational agent's uncertainty, it should not be surprising that relying on them fails to deliver plausible expected accuracy scores. By reducing each of the distributions' stance towards heads to a single point value $.4$, we've effectively washed out key information. So the question is, how can we adequately account for the complexity of a rational agent's credal state in formulating a proper accuracy score?

Here is our proposal. Rather than measuring inaccuracy in relation to "true states of the world" conceptualized as two omniscient credences that peak at either 0 or 1 and averaging using expected values of the distributions, we should instead utilize a set of n potential true probability hypotheses (ideally, going continuous, but we're working with a discrete grid of $n = 1000$ possible coin baises in this paper). We then compute all the inaccuracies with respect to each of these n values represented by "omniscient" distributions (or true chance hypotheses) and determine the expected inaccuracy scores using the entire distributions rather than relying solely on the expected values of the distributions.

For the three distributions under consideration, the accuracy scores calculated using CRPS and KL divergence with respect to omniscient distributions corresponding to various values of x are given by Figure 4. The expected inaccuracies of the distributions from their perspective are given by Table 2. The results now match our common sense: each distribution recommends itself. So, once we pay attention to the whole range of possiblities, the CRPS score and KL divergence are now proper scores.

M: what is a formal statement of this accuracy measure / scoring rule?

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[19]This indicates that the choice of the evaluation metric is not the cause of the recommendation.
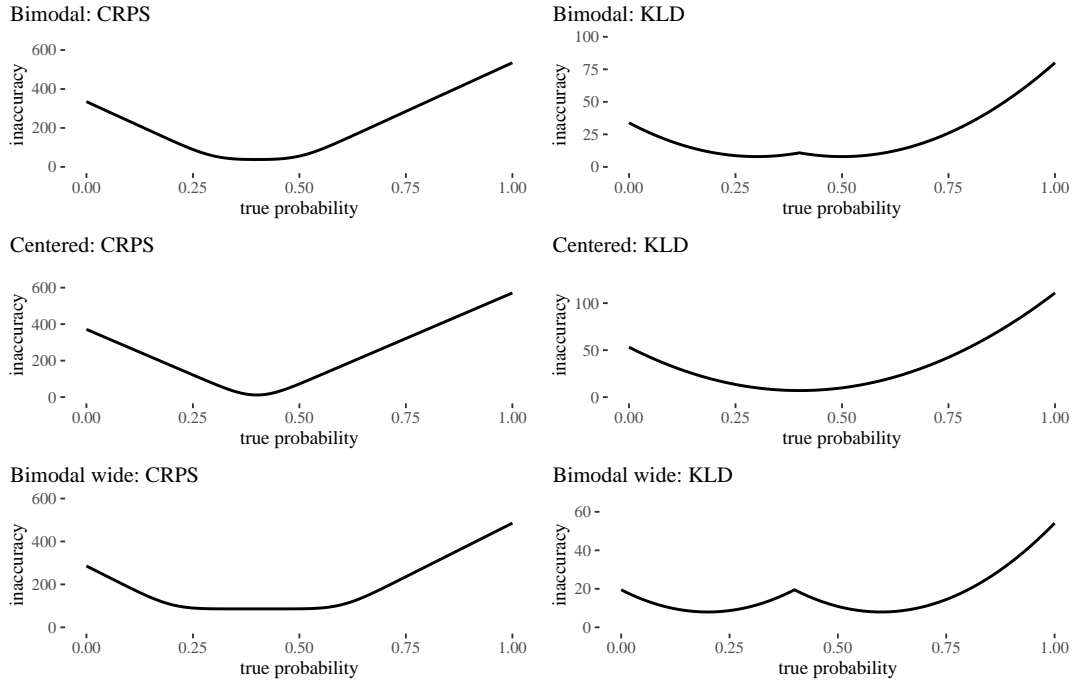
Figure 4: CLPSR and KL divergence based inaccuracies vs (omniscient functions corresponding to) n true probability hypotheses for the three distributions discussed in this section.

	CPRS			KLD		
	bimodal	centered	wide bimodal	bimodal	centered	wide bimodal
bimodal	64.670	78.145	88.380	8.577	10.655	11.336
centered	41.657	28.181	85.911	9.239	7.690	15.627
wide bimodal	137.699	171.719	113.989	11.541	19.231	8.689

Table 2: Expected inaccuracies of the three distributions from their own perspectives. Each row corresponds to a perspective.

One important difference transpires between using CRPS and KLD. Notice how for chance hypotheses between the actual peaks the inaccuracy remains flat. This seems to be an artifice of choosing a squared distance metric. If instead we go with a more principled, information-theory-inspired KL divergence, inaccuracy in fact jumps a bit for values in between the peaks for the bimodal distributions, which seems intuitive and desirable. This seems to be a reason to prefer a KL-based accuracy measure.

One question remains: how does the framework capture the idea that it is the bimodal distribution that seems more adequate than the others? One way to interpret that is by looking at inaccuracy concerning chance hypotheses given by the testimonial evidence. In this case, these are H_3, where the true chance is 0.3, and H_5, where the true chance is 0.5. You can find the specific inaccuracies for them in Table 3. To make sure that this favorable outcome isn't due to not using pointed credences, we can redo the calculations using the pointed version. In the pointed version, all the focus is on 0.4, or the weight is evenly divided between 0.3 and 0.5, or between 0.2 and 0.6. As anticipated, when we consider inaccuracy, both of these setups recommend the bimodal version (Table 4).

	CRPS		KLD	
	H3	H5	H3	H5
bimodal	55.475	55.378	7.935	7.935
centered	72.281	72.090	9.836	9.825
wide bimodal	86.230	86.223	10.871	10.882

Table 3: CRPS and KLD inaccuracies of the three distributions with respect to the two hypotheses. On both inaccuracy measures the bimodal distribution dominates the other two.

	CRPS		KLD	
	H3	H5	H3	H5
pointed bimodal	49.75	49.75	1.00	1.00
pointed centered	100.00	100.00	16.61	16.61
pointed wide bimodal	99.75	99.75	16.61	16.61

Table 4: CRPS and KLD inacurracies of the three-pointed distributions with respect to the two hypotheses.

6 Evidence aggregation: the simple case

As we have seen, higher-order probabilism outperforms both precise and imprecise probabilism, at the descriptive as well as the normative level. From a descriptive standpoint, higher-order probabilism can model scenarios that cannot be modeled by the other versions of probabilism. From a normative standpoint, accuracy maximization may sometimes recommend that a rational agent represent their credal state with a distribution over probability values rather than a precise probability measure (more on this soon).[20] In this and the next section, we examine the question of how multiple items of evidence should be aggregated and evaluated toghether. This question raises difficulties for both precise and imprecise probabilism. We show how higher-order probabilism can handle them.

Rational agents are often tasked with aggregating pieces of evidence and assessing their value relative to a hypothesis. A popular measure of the value of the evidece is the likelihood ratio. This ratio is relative to a pair of competing hypotheses, say H and its negation $\neg H$ (though the two hypotheses need not be one the negation of the other). Relative to these hypotheses, the likelihood ratio of a single piece of evidence E is the probability of E given H divided by the probability of E given $\neg H$, or in short, $\frac{P(E|H)}{P(E|\neg H)}$. Degrees of evidential value (or support, strength) can be expressed as follows:

the higher $\frac{P(E|H)}{P(E|\neg H)}$ (if greater than one), the more strongly E supports H.

The value of the evidence increases whenever $P(E|H)$ increases or whenever $P(E|\neg H)$ decreases. The higher $P(E|H)$, the better the evidence at tracking H (a true positive); the lower $P(E|\neg H)$, the better the evidence at avoiding $\neg H$ (a true negative). If the probability of E is the same given hypothesis H as given its negation, that is, the likelihood ratio equals one, the evidence would have no value for H.

Likelihood ratios can also be used for assessing the value of multiple pieces of evidence in the aggregate, again relative to a pair of hypotheses of interest. In the simplest case (for

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[20]Having read van Fraasen's "Laws and Symmetry", you might also worry that going higher order somehow leads to a contradiction; we will address this concern later on.

add ref to vFraasen in fn; perhaps extend the discussion a bit

where do we show that accuracy recommends a distribution over probability measures? This bit seems missing.

more complex cases, see the next section), multiple items of evidence all bear on the same hypothesis. Then, to obtain their combined evidential value, it is enough to multiply their individual likelihood ratios.

$$\frac{P(E_1 \wedge E_1 \dots E_k | H)}{P(E_1 \wedge E_2 \dots E_k | \neg H)} = \frac{P(E_1 | H)}{P(E_1 | \neg H)} \times \frac{P(E_2 | H)}{P(E_2 | \neg H)} \times \dots \times \frac{P(E_k | H)}{P(E_k | \neg H)}$$

The equality holds provided $E_1, E_2, \dots, E_k$ are probabilistically independent conditional on hypothesis H and its negation. Think, for example, at several diagnostic tests performed by independent laboratories or independent witnesses in a trial testifying about the same issue.

For the precise probabilist, filling in the precise probabilities in the formula above gives an assessment of the value of aggregate evidence. But, as we will now see, this approach risks over- or under-estimating the value of the evidence. (We will focus on likelihood ratios, but the claim we defend can be generalized to other measures of evidential value and posterior probabilites.[21]) To see what the problem is, it is worth working through a specific example.

In a murder case, the police recover two items of trace evidence, both against the defendant. First, hair found at the crime scene matches the defendant's hair; call this evidence 'hair.' Second, the fur of the defendant's dog matches the fur found in a carpet wrapped around one of the bodies; call this evidence 'fur.'[22] The two matches favor the hypothesis that the defendant (and the defendant's dog) must be the source of the crime traces; call this hypothesis 'source'. If the two matches are independent lines of evidence (conditional on the source hypothesis), their likelihood ratios can be multiplied:[23]

$$\frac{P(\text{fur} \wedge \text{hair} | \text{source})}{P(\text{fur} \wedge \text{hair} | \neg \text{source})} = \frac{P(\text{fur} | \text{source})}{P(\text{fur} | \neg \text{source})} \times \frac{P(\text{hair} | \text{source})}{P(\text{hair} | \neg \text{source})}$$

So far so good. But how do we fill in the precise probabilies? The numerators can be equated to one: if the defendant is a contributor, the laboratory will declare a match for sure. This is a simplication, but it will do for our purposes. To fill in the denominators, a trial expert will provide the match probabilities. They express the likelihood that, by coincidence, a random person (or a random dog) who is not a contributor would still match. The match probabilities are approximated by counting of many matches are found in a representative sample of the human population (or the canine population). Suppose the matching hair type occurs 0.0253 times in a reference database, and the matching dog fur type occurs 0.0256 times in a reference database.[24] These frequencies can fill in the match probabilities. Putting everything together:

$$\frac{P(\text{dog} | \text{source})}{P(\text{dog} | \neg \text{source})} \times \frac{P(\text{hair} | \text{source})}{P(\text{hair} | \neg \text{source})} = \frac{1}{0.0252613} \times \frac{1}{0.025641} = 1543.862069$$

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[21] On different measures of degrees of evidential value (or support, confirmation), see **CITE FITELSON**. Posterior probabilities can be obtained from the likelihood ratios via the prior probabilities. The posterior odds are obtained by multiplying the likelihood ratio by the prior odds, as follows:

$$\frac{P(H | E_1 \wedge E_2 \dots E_k)}{P(\neg H | E_1 \wedge E_1 \dots E_k)} = \frac{P(E_1 \wedge E_1 \dots E_k | H)}{P(E_1 \wedge E_2 \dots E_k | \neg H)} \times \frac{P(H)}{P(\neg H)}$$

We will focus on likelihood ratios for ease of exposition.

[22] The hair evidence and the dog fur evidence are stylized after two items of evidence in the notorious 1981 Wayne Williams case (Deadman, 1984b, 1984a).

[23] Strictly speaking, it is possible for A and B to be independent conditional on H, but not conditional on $\neg H$. Here, we require both independencies to hold.

[24] Probabilities have been slightly but not unrealistically modified to be closer to each other in order to make a conceptual point: the same first-order probabilities, even when they sound precise, may come with different degrees of second-order uncertainty (more on this soon). The original probabilities were 1/100 for the dog fur, and 29/1148 for Wayne Williams' hair.

The resulting ratio is a large number. Taken at face value, the match evidence, combined, strongly favor the source hypothesis. Bad news for the defendant.

This is the story about evidence aggregation (in the simple case) told by the precise probabilist. But this story misses something crucial. As it happens, the match probability for the hair evidence is based on 29 matches found in a sample database of size 1148, while the match probability for the dog evidence is based on finding two matches in a smaller database of size 78. The relative frequencies are about .025 in both cases, but the two samples differ in size. The smaller the sample, the greater the uncertainty about the match probabilities. So simply reporting the exact the numbers 0.0253 and 0.0256 makes it seem as though the evidential value of the matches is the same, but actually it is not.

Here is another way to bring the problem into sharper focus. Suppose the match probabilities associated with two matches are set to .02. They are based on the following relative frequencies: two matches occur in a dog fur database and two matches occur in a human hair database, where both databases are very smal, say of size 10. Suppose, as before, both the defedant's hair and defendant's dog match the traces at the crime scene. By mutiplying the individual $1/.02$ likelihood ratios associated with the two matches, their evidential value against the defendant would seem overwhelming: $1/.02 \times 1/.02 = 2500$. But, since the match probabilities are based on frequencies resulting from such small databases, the evidential value of the two matches should be close to worthless. And yet, whether the samples are small or extremely large, or anything in between, a precise likelihood ratio would count the two matches as having the same evidential value. Since their evidential value, intuitively, should be quite different in the different cases, precise probabilism will overestimate or underestimate the value of the evidence in one case or another.

Can imprecise probabilism do better? The probability measures in the representor set are those compatible with the evidence. The problem is that almost any random match probability will be compatible with any sample data—with any number of matches found in a reference database. This point should be familiar from the earlier discussion. Think by analogy to coin tossing: even a coin that has a .99 bias toward tails could come up heads on every toss. This series of outcomes is unlikely, but possible. Similarly, a hair type that has a match probability extremely small could still be found several times in a sample population. So, it is not clear how to proceed if one takes seriously the binary notion of compatibility. Imprecise probabilism is too permissive because almost any match probability will be compatible with the data.

Another option is to rely on reasonable ranges of matches probabilities. Suppose these ranges are (.015,.037) (.002, .103), for hair and fur evidence respectively.[25] The range is wider for dog fur match evidence than hair match evidence. This is as it should be: the uncertainty about the the dog fur match probability is greater since the sample database was assumed to be smaller. To assess the joint uncertainty, it is enough to focus on what happens at the edges of the two intervals. Reasoning with representor members at the edges of the intervals will yield the most extreme probability measure the impreciser is going to be committed to, the worst-case and best-case scenarios. We end up with a new range for the joint match probabilties, (.00003, .003811).[26] The corresponding likelihood ratios could be as high as 3.3333333×10^4 or as low as 262.3983207. The two matches, then, could be much stronger evidence or much weaker

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[25]These are 99% credible intervals starting with uniform priors. A 99% credible interval is the narrowest interval to which the expert thinks the true parameter belongs with probability .99. For a discussion of what credible intervals are, how they differ from confidence intervals, and why confidence intervals should not be used, see Kruschke (2015).

[26]Redoing the calculations using the upper bounds of the two intervals, .037 and .103, yields the following:

$$P(\text{dog} \wedge \text{hair}|\neg\text{source}) = .037 \times .103 = .003811.$$

This number is around 5.88 times greater than the original estimate. Given this number, the two matchs are much weaker evidence for the source hypothesis than previously thought. The calculation for the lower bounds,

evidence than previously thought.

What are we to conclude? Using plausible ranges for the match probabilities leaves the impression that any value in the interval is just as good as any other. Perhpas we should just pick the middle value as representative of the interval? But relying on the entire interval or the middle value will misrepresent the evidence. To see why, consider Figure 5 (upper part). It depicts the probability distribution of different match probabilities given the sample data—the actual number of matches found in the sample database. As expected, some random match probabilities are more likely than others. Recall that, by hypothesis, 29 matches were found in the sample database of human hair of size 1148, and 2 matches were found in the sample database of dog fur of size 78. Since the sizes of the two databases are different, the distributions have different spreads: the smaller the database the greater the spread, the greater the uncertainty about the match probability. In light of this, now consider Figure 5 (lower part). It depicts the probability distribtion for the joint match probability associated with both items of match evidence, hair and fur evidence. Interestingly, the distribution for the joint evidence is not symmetric. So the most likely value of the joint match probability (and the bulk of the distribution, really) does not lie in the middle between the edges. Therefore, only relying on the edges—or taking central values as representative of the interval—can lead to overestimating or underestimating the probabilities at play.[27]

All in all, precise and imprecise probabilims—as well as the interval approach, a variation of imprecise probabilism—do not fare well in modelling how the value of evidence in the aggregate should be assessed. The alternative, we think, is easily available: the evaluation of multiple items of evidence should take into account higher-order uncertainty (as illustrated in Figure 5). Whenever probability distributions for the probabilities of interest are available (and they should be available for match evidence and many forms of scientific evidence whose reliability has been studied), those distributions should be reported for assessing the value of the evidence. This approach avoids hiding actual aleatory uncertainties under the carpet. It also allows for a more balanced assessment of the evidence, whereas using point values or intervals may exaggerate or underestimate the value of the evidence.

Marcello (first point): Can we have a formula of how the two matchs are combined in the higher-order approach. In precise probabilism, you multiply the individual LRs, in higher-order probabilism, what do we do formally? The next section then generalize this simple cases to all complex cases with dependencies between items of evidence and hypotheses.

A final clarification is in order. The problem we are highlighting is not confined to match evidence. Say an eyewitness testifies against the defendant: they saw the defendant near the crime scene at the relevant time. To assess the value of this testimony, one should know something analogous to the match probability: if the defendant was not there, how probable is it that the witness would still say the defendant was there? Or suppose a medical test for a dis-

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.015 and .002, yields the following:

$$P(\text{dog} \wedge \text{hair}|\neg\text{source}) = .015 \times .002 = .00003$$

This number is around 0.46 times lower than the original estimate. Given this number, the two matchs are much stronger evidence for the source hypothesis than previously thought.

[27]An additional problem is worth mentioning. The calculations for the joint interval assume that because the worst- or best-case probability for one event is x and the worst- or best-case probability for another independent event is y, the worst- or best-case probability for their conjunction is xy. But this conclusion does not follow if the margin of error (credible interval) is fixed. Just because the probability of an extreme value x for one variable X is .01, and so it is for the value y of another independent variable Y, it does not follow that the probability that those two independent variables take values x and y simultaneously is the same. In general, it is impossible to calculate the credible interval for the joint distribution based solely on the individual credible intervals corresponding to the individual events.

ease turns out positive. Here again, to asses the evidential value of the positive test, one should know how probable it is that the test would still turn out positive even when a patient is actually negative. And so on. These false positive probabilities are usually derived from sample-based frequencies in surveys or experiments: how often witness misidentify people; how often tests misdiagnose; etc. So, higher-order uncertainty about false positive probabilities is widespread. In addition, the problem we are highlighting is not confined to sample size, alghouth it can be effectively illustrated this way. Probabilities can be subject to uncertainty for other reasons, for example, when they are derived from a probability model for which there is little support, or when the sample size is large but unrepresentative. How to assess higher order uncertainty is difficult. We provide no method for doing that. Our point, rather, is that higher-order uncertainty should not be overlooked when evaluating the value of the evidence, especially when multiple items of evidence are pieced together.

Marcello (another point): as transpired in our discussion on Jan 25, we could get two different liklihood ratios using precise probabilism or usign highere order probabilism. Precise probabilism method: just work with the mean values of the match probabilities (and thus LRs) for the individual pieces of evidence and then aggregate (say by multiplyign match probabilities or LRs). Higher order probabilism method: work first with the individual distributions, then take the distribution for the joint evidence, and finally take that mean of that distribution (which gives the joint match probability and thus the joint LR). If this is right, this would mean that precise probabilism method and higher order probabilism method can give us two different posterior probabilities for the same proposition (give that the LRs are different but the priors are the same, right?). Could these posterior probabilities be radically different, say 0.9 versus 0.1 in some cases? If so, is there an argument that the precise probabilism method can be accuracy dominated?
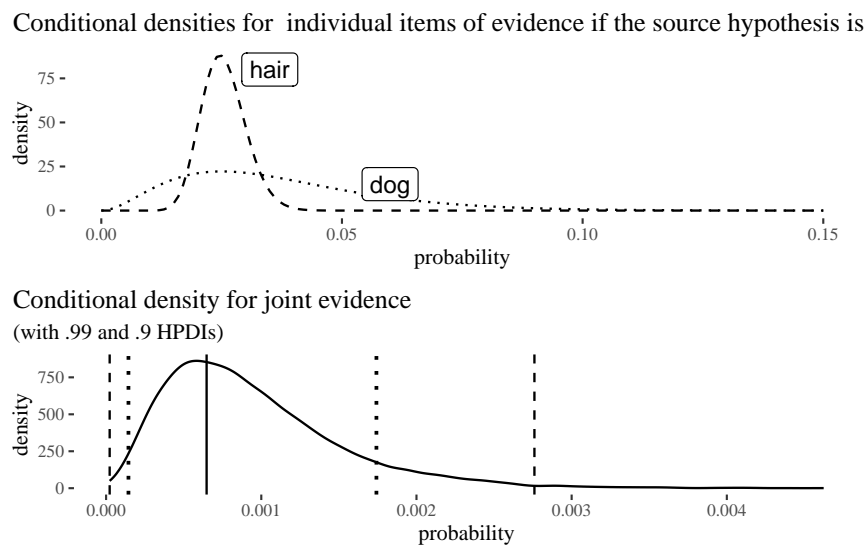

Figure 5: Beta densities for individual items of evidence and the resulting joint density with .99 and .9 highest posterior density intervals, assuming the sample sizes as discussed and independence, with uniform priors.

7 Evidence aggregation: the complex case

We have looked at a simple case of evidence aggregation: the pieces of evidence were about the same hypothesis and probabilistically independent. But different pieces of evidence can bear on different hypotheses and probabilistically depend one another. Think, for example, of

two witnesses testifying in a trial about two related issues, say the defendant's whereabouts and the defendant's motive. In these more complex cases, precise probabilism handles evidence aggregation with the help of Bayesian networks. The grahical part of a Bayesian nextwork consists of nodes and arrows. Arrows between nodes visually represents relationships of probabilistic dependency between different hypotheses and items of evidence, each correspoding to a node in the network. The numerical part of a Bayesian network consists of probability tables in which precise prior probabilities (for nodes without incoming arrows) or conditional probabilities (for nodes with incoming arrows) are entered. Equipped with these input probabilities, the network can run the calculations about the output probabilities of interest.[28] We might be interested, for example, in the probability of a hypothesis given several items of evidence, while keeping track of dependencies between them. In the standard formulation, Bayesian networks run on precise probabilities, but can be extended to handle imprecise and higher order-probabilities. This is the topic of this section.

As an illustration, let us start with a Bayesian network developed by Fenton & Neil (2018). The network in Figure 6 represents the key items of evidence in the infamous British case R. v. Clark (EWCA Crim 54, 2000). Sally Clark, mother of two sons, witnessed her first son die in 1996 soon after birth. Her second son died in similar circumstances a few years later in 1998. These two consecutive deaths raised suspicion. One hypothesis is that Sally murdered her children. An alternative is that both children died of Sudden Infant Death Syndrome (SIDS). At trial, however, the pediatrician Roy Meadow testified that the probability that a child from a family like the Clark's would die of SIDS was quite low, 1 in 8,543. Assuming probabilistic independence between the two events, the probability of both children dying of SIDS becomes extremely low. It equals the product of the two probabilities, approximately 1 in 73 million. Based on this low probability and signs of bruising on the bodies, Sally Clark was convicted of murder. The conviction was reversed on appeal thanks to new evidence, specifically, signs of a potentially lethal disease found in one of the bodies.

Much has been written about Sally Clark by philosophers and statisticians. The discussion has often focused on whether Meadow was allowed to assume, as he did, that the two SIDS death would be independent events. The assumption of independence delivered the low probability of 1 in 73 million by multiplying 1 in 8,543 by itself. Another, much discussed point was this: even if it was unlikely that two consecutive SIDS deaths would occur, it does not follow it was likely that Sally murdered her children.[29] A Bayesian network helps to avoid these mistakes. It also help to view the case holistically. The two consecutive deaths were an important piece of evidence, but other evidence was also important, including signs of bruising and signs of a lethal disease as they were discovered during the appeal process.

Unfortunately, Bayesian networks, in their standard formulation, inherit the shortcomings of precise probabilism. The the choice of the input probabilities should be precise, and it is often unclear where the values come from or whether they are justified. Consider, foir example, the probability that a death by SIDS would occur. How sure are we that this probability equals, exactly, 1 in 8,543? The figure Meadow used is a sample-based frequency. How big was that sample? How representative? Other input probabilities need to be entered in the network to carry out the calculations, for example, the probability that a mother would kill her son, or the probability that signs of brusing would be found given the hypothesis that Sally was trying to murder her child, and so on. There will be uncertainty about these probabilites, since they are based on sample frequencies or expert elicitation.

The standard response to these concerns is to invoke *sensitivity analysis*: a range of plausi-

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[28]The calculations can quickly get out of hand, so softwares exist to perform the calculations automatically.

[29]One could reason that, since 1 in 73 million is a low probability, the alternative explanation, that Sally murdered her children, should be likely. But that a mother would do such a thing is also unlikely, perhaps even less likely than 1 in 73 million.

ble values is tested. Say we are interested in the output probability that Sally is guilty. The network is updated by the known facts—the items of evidence—following standard Bayesian conditionalization. The input probabilities in the network are then assigned a range of possible values to see how they impact the output probability about Sally's guilt. Sensitivity analysys is another variation of the interval approach we considered earlier. But, as already discussed, the interval approach and thus sensitivity analysis ignore the shape of the underlying distributions. They do not distinguish between probability measures (or point estimates) in terms of their plausibility, but some will be more plausible than others. Moreover, if the sensitivity analysis is guided by extreme values, these might play an undeservedly strong role.

These concerns can be addressed, at least in part, by recourse to higher-order probabilities. In a precise Bayesian network, each node is associated with a probability table determined by a finite list of numbers (precise probabilities). But suppose that, instead of precise numbers, we have densities over parameter values for the numbers in the probability tables.[30] An example for the Sally Clark case is represented in Figure 7.
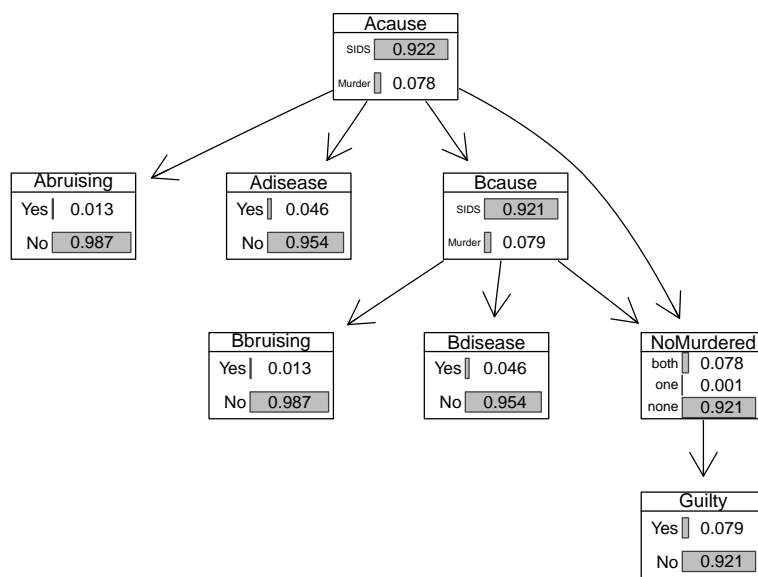

Figure 6: Bayesian network for the Sally Clark case, with marginal prior probabilities.

Using the probabilistic program, we can investigate the impact of different items of evidence on Sally Clark's probability of guilt (Figure 7). The starting point is the prior density for the Guilt node (first graph). Next, the network is updated with evidence showing signs of bruising on both children (second graph). Next, the assumption that both children lack signs of potentially lethal disease is added (third graph). Finally, we consider the state of the evidence at the time of the appellate case: signs of bruising existed on both children, but signs of lethal disease were discovered only on the first child. Interestingly, in the strongest scenario against Sally Clark (third graph), the median of the posterior distribution is above .95, but the uncertainty around that median is still too wide to warrant a conviction.[31] This underscores the fact that relying on point estimates can lead to overconfidence. Paying attention to the higher-order uncertainty about the first-order probability can make a difference to trial decisions.

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[30]The densities of interests can then be approximated by (1) sampling parameter values from the specified distributions, (2) plugging them into the construction of the BN, and (3) evaluating the probability of interest in that precise BN. The list of the probabilities thus obtained will approximate the density of interest. In what follows we will work with sample sizes of 10k.

[31]The lower limit of the 89% Highest Posterior Density Intervals (HPDI) is at .83.

Figure 7: An illustration of a probabilistic program for the Sally Clark case.

Figure 8: Impact of incoming evidence in the Sally Clark case.

One question that arises is how this approach relates to the standard method of using likelihood ratios to report the value of the evidence. On this approach, the conditional probabilities that are used in the likelihood ratio calculations are estimated and come in a package with an uncertainty about them. Accordingly, these uncertainties propagate: to estimate the likelihood ratio while keeping track of the uncertainty involved, we can sample probabilities from the selected distributions appropriate for the conditional probabilities needed for the calculations, then divide the corresponding samples, obtaining a sample of likelihood ratios, thus approximating the density capturing the recommended uncertainty about the likelihood ratio. Uncertainty about likelihood ratio is just propagated uncertainty about the involved conditional probabilities. For instance, we can use this tool to gauge our uncertainty about the likelihood ratios corresponding to the signs of bruising in son A and the presence of the symptoms of a potentially lethal disease in son A (Figure 9).

The reader might also be eager to point out that some of the techinques we mentioned are already available to the impreciser. For instance, one can use uniform sampling with Bayesian networks to approximate the impreciser's epistemic commitments given their assumptions . This doesn't mathematically differ from relying on probabilistic programs with the restriction that some variables corresponding to probabilities are sampled from distributions that are uniform over a set of values determined by the imprecisor's representor. However, this only shows that a computational implementation of the impreciser's perspective is not out of reach—which is to be expected. A critical survey of an approach along these lines uses roughly this computational approach to argue that in complex reasoning situations, if the imprecisor's stance is taken, ''the imprecision of inferences increases rapidly as new premises are added to an argument''. This is in line with our criticism.

LR: Abruising

median =3.89, 89%HPDI = 0.4−19

LR: Adisease

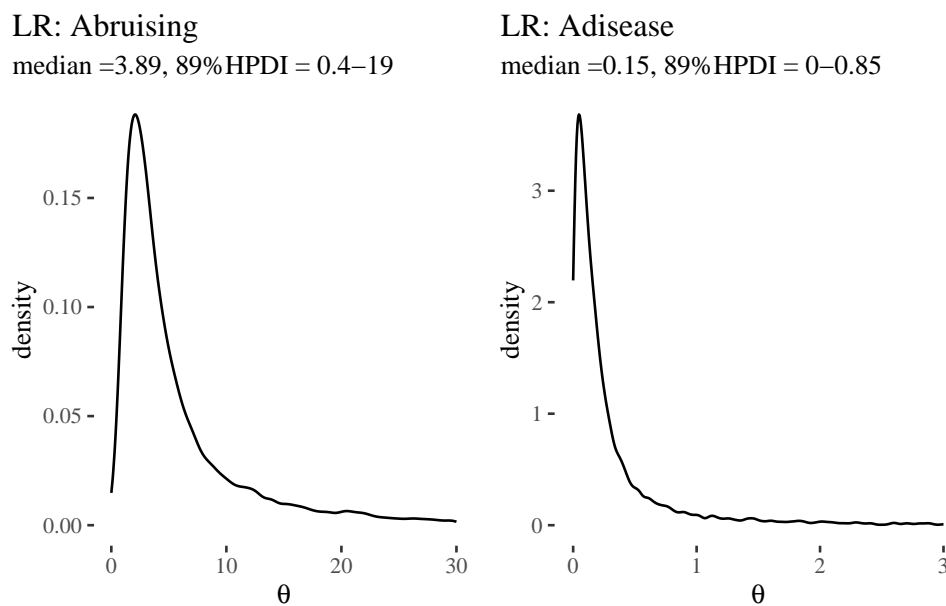median =0.15, 89%HPDI = 0−0.85

Figure 9: Likelihood ratios forbruising and signs of disease in child A in the Sally Clark case.

8 Conclusion

Our approach is similar to standard hierarchical models in the most general sense: there is a meaningful dependence structure and distributions over parameter values that we are working with.

A more fitting term, however, for the representation tool we propose should be used here

is *probabilistic programs*. We do not claim any originality in devising this tool: it's an already existing tool. What we argue for, though, is its ability for being usefully deployed in the context of evidence evaluation and integration with other assumptions and hypotheses. Mathematically, we do not propose anything radically new—we just put together some of the items from the standard Bayesian toolkit. The novelty is rather in our arguing that that these tools are under-appreciated in formal epistemology and in the legal scholarship and should be properly used to incorporate second-order uncertainties in evidence evaluation and incorporation.

Some might dislike the idea of going higher-order for a numbere of reasons, for exmaple, unnecessary complexity. This is a line taken by Bradley, who refuses to go higher-order for the following reason:

> Why is sets of probabilities the right level to stop the regress at? Why not sets of sets? Why not second-order probabilities? Why not single probability functions? This is something of a pragmatic choice. The further we allow this regress to continue, the harder it is to deal with these belief representing objects. So let's not go further than we need. 131-132

We have shown that given the difficulties of precise and imprecise probabilism, we are not going further than we need in using higher-order probabilities. The pragmatic concerns one might have are unclear: parameter uncertainty, approximations and other computational methods are alrady embedded in Bayesian statistical practice and good computational already exist.[32]

Another concern is the lack of a clear semantics. While a more elaborate account is beyond the scope of this paper, the answer should gesture at a modification of the framework of probabilistic frames (Dorst, 2022b, 2022a). Start with a set of possible worlds W. Suppose you consider a class of probability distributions D, a finite list of atomic sentences $q_1, \ldots, q_2$ corresponding to subsets of W, and a selection of true probability hypotheses C (think of the latter as omniscient distributions, $C \subseteq D$, but in principle this restriction can be dropped if need be). Each possible world $w \in W$ and a proposition $p \subseteq W$ come with their true probability distribution, $C_{w,p} \in D$ corresponding to the true probability of p in w, and the distribution that the expert assigns to p in w, $P_{w,p} \in D$. Then, various propositions involving distributions can be seen as sets of possible worlds, for instance, the proposition that the expert assigns d to p is the set of worlds w such that $P_{w,p} = d$.[33]

Appendix: the strict propriety of I_{kl}

The fact that I_{KL} is strictly proper as applied to second-order probabilities is not very surprising. However, in the existing literature, the proof is not usually explicitly given, and some of the pieces are not present in philosophical literature. So we tried to include the whole chain of thought, warning that some of these results are already known and all we did was making the proofs more presentable, and pointing out new elements in the reasoning. Let us start with a definition of concavity.

Definition 1 (concavity). *A function f is convex over an interval (a, b) just in case for all*

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[32] Also, you can insist that instead of going higher order we could just take our sample space to be the cartesian product of the original sample space and parameter space, or use parameters having certain values as potential states of a bayesian network. If you prefer not to call such approaches first-order, I don't mind, as long as you effectively end up assigning probabilities to certain probabilities, the representation means I discussed in this paper should be in principle available to you.

[33] There is at least one important difference between this approach and that developed by Dorst. His framework is untyped, which allows for an enlightening discussion of the principle of reflection and alternatives to it. In this paper I prefer to keep this complexity apart and use an explicitly typed set-up.

$x_1, x_2 \in (a, b)$ *and* $0 \leq \lambda \leq 1$ *we have:*

$$f(\lambda x_1 + (1 - \lambda)x_2) \leq \lambda f(x_1) + (1 - \lambda)f(x_2)$$

A function f is concave just in case:

$$f(\lambda x_1 + (1 - \lambda)x_2) \geq \lambda f(x_1) + (1 - \lambda)f(x_2)$$

A function f is strictly concave just in case the equality holds only if either $\lambda = 0$ or $\lambda = 1$.

For us it is important that if a function is twice differentiable on an interval, then it is (strictly) concave just in case its second derivative is non-positive (negative). In particular, as $(\log_2(x))'' = -\frac{1}{x^2 ln(2)}$, $\log_2$ is strictly concave over its domain.[34]

Lemma 1 (Jensen's inequality). *If f is concave, and g is any function of a random variable, $\mathbb{E}(f(g(x))) \leq f(\mathbb{E}(g(x)))$. If f is strictly concave, the equality holds only if $g(x) = \mathbb{E}g(x)$, that is, if $g(x)$ is constant everywhere.*

Proof. For the base case consider a two-point mass probability function. Then,

$$p_1 f(g(x_1)) + p_2 f(g(x_2)) \leq f(p_1 g(x_1) + p_2 g(x_2))$$

follows directly from the definition of concativity, if we take $\lambda = p_1$, $(1 - \lambda) = p_2$, and substitute $g(x_1)$ and $g(x + 2)$ for x_1 and x_2.

Now, suppose that $p_1 f(g(x_1)) + p_2 f(g(x_2)) = f(p_1 g(x_1) + p_2 g(x_2))$ and that f is strictly concave. That means either $(p_1 = 1 \wedge p_2 = 0)$, or $(p_1 = 0 \wedge p_2 = 1)$. Then either x always takes value x_1, in the former case, or always takes value x_2, in the latter case. $\mathbb{E}g(x) = p_1 g(x_1) + p_2 g(x_2)$, which equals $g(x_1)$ in the former case and $g(x_2)$ in the latter.

Now suppose Jensen's inequality and the consequence of strict contativity holds for $k - 1$ mass points. Write $p'_i = \frac{p_i}{1 - p_k}$ for $i = 1, 2, \dots, k - 1$. We now reason:

$$\sum_{i=1}^{k} p_i f(g(x_i)) = p_k f(g(x_k)) + (1 - p_k) \sum_{i=1}^{k-1} p'_i f(g(x_i))$$

$$\leq p_k f(g(x_k)) + (1 - p_k) f\left(\sum_{i=1}^{k=i} p'_i g(x_i)\right) \quad \text{by the induction hypothesis}$$

$$\leq f\left(p_k(g(x_k)) + (1 - p_k) \sum_{i=1}^{k-1} p'_i g(x_i)\right) \quad \text{by the base case}$$

$$= f\left(\sum_{i}^{k} p_i g(x_i)\right)$$

Notice also that at the induction hypothesis application stage we know that the equality holds only if $p_k = 1 \vee p + k = 0$. In the former case $g(x)$ always takes value $x_k = \mathbb{E}g(x)$. In the latter case, p_k can be safely ignored and $\sum_{i=1}^{k} p_i g(x_i) = \sum_{i=1}^{k-1} p' g(x_i)$ and by the induction hypothesis we already know that $\mathbb{E}g(x) = g(x)$.

$\square$

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[34]I line with the rest of the paper, we'll work with log base 2. We could equally well use any other basis.

In particular, the claim holds if we take $g(x)$ to be $\frac{q(x)}{p(x)}$ (were both p and q are probability mass functions), and f to be $\log_2$. Then, given that A is the support set of p, we have:

$$\sum_{x \in A} p(x) \log_2 \frac{q(x)}{p(x)} \le \log_2 \sum_{x \in A} p(x) \frac{q(x)}{p(x)}$$

Moreover, the equality holds only if $\frac{q(x)}{p(x)}$ is constant, that is, only if p and q are the same pmfs. Let's use this in the proof of the following lemma.

Lemma 2 (Information inequality). *For two probability mass functions p, q, $D_{\mathrm{KL}}(p, q) \ge 0$ with equality iff $p = q$.*

Proof. Let A be the support set of p, and let q be a probability mass function whose support is B.

$$
\begin{aligned}
-D_{\mathrm{KL}}(p, q) &= -\sum_{x \in A} p(x) \log_2 \frac{p(x)}{q(x)} && \text{(by definition)} \\
&= \sum_{x \in A} p(x) - (\log_2 p(x) - \log_2 q(x)) \\
&= \sum_{x \in A} p(x) \left(\log_2 q(x) - \log_2 p(x) \right) \\
&= \sum_{x \in A} p(x) \log_2 \frac{q(x)}{p(x)} \\
&\le \log_2 \sum_{x \in A} p(x) \frac{q(x)}{p(x)} && \text{by Jensen's inequality} \\
&\text{(and the equality holds only if } p = q\text{)} \\
&= \log_2 \sum_{x \in A} q(x) \\
&\le \log_2 \sum_{x \in B} q(x) \\
&= log(1) = 0
\end{aligned}
$$

$\square$

Observe now that D_{KL} can be decomposed in terms of cross-entropy and entropy.

Lemma 3 (decomposition). $D_{\mathrm{KL}} = H(p, q) - H(p)$.

Proof.

$$
\begin{aligned}
D_{\mathrm{KL}}(p, q) &= \sum_{p_i} \left(\log_2 p_i - \log_2 q_i \right) \\
&= -\sum_{p_i} \left(\log_2 q_i - \log_2 p_i \right) \\
&= -\sum_{p_i} \log_2 q_i - \sum_{p_i} -\log_2 p_i \\
&\quad \underbrace{- -\sum_{p_i} \log_2 q_i}_{H(p,q)} \underbrace{- -\sum_{p_i} \log_2 p_i}_{H(p)}
\end{aligned}
$$

$\square$

With information inequality this easily entails Gibbs' inequality:

Lemma 4 (Gibbs' inequality). $H(p, q) \geq H(p)$ *with identity only if* $p = q$.

We are done with our theoretical set-up, which is already common knowledge, except presented in an orderly manner in one place. Now we present our argument for the cliam that the above entails the propriety of I_{KL}. First, let's systematize the notation. Consider a discretization of the parameter space $[0, 1]$ into n equally spaced values $\theta_1, \ldots, \theta_n$. For each i the "true" second-order distribution if the true parameter indeed is θ_i—we'll call it the indicator of θ_i—which is defined by

$$Ind^k(\theta_i) = \begin{cases} 1 & \text{if } \theta_i = \theta_k \\ 0 & \text{otherwise} \end{cases}$$

We will write Ind_i^k instead of $Ind^k(\theta_i)$.

Now consider a probability distribution p over this parameter space, assigning probabilities $p_1, \ldots, p_n$ to $\theta_1, \ldots, \theta_n$ respectively. It is to be evaluated in terms of inaccuracy from the perspective of a given 'true' value θ_k. The inaccuracy of p if θ_k is the 'true' value, is the divergence between Ind^k and p.

$$I_{KL}(p, \theta_k) = D_{\text{KL}}(Ind^k || p)$$
$$= \sum_{i=1}^{n} Ind_i^k \left(\log_2 Ind_i^k - \log_2 p_i \right)$$

Note now that for $j \neq k$ we have $Ind_j^k = 0$ and so $Ind_j^k \left(\log_2 Ind_j^k - \log_2 p_j \right) = 0$. Therefore we continue:

$$= Ind_k^k \left(\log_2 Ind_k^k - \log_2 p_k \right)$$

Further, $Ind_k^k = 1$ and therefore $\log_2 Ind_k^k = 0$, so we simplify:

$$= -\log_2 p_k$$

Now, let's think about expected values. First, what is the inaccuracy of p as expected by p, $\mathbb{E}I_{\text{DK}}(p, p)$?

$$\mathbb{E}I_{\text{DK}}(p, p) = \sum_{i=1}^{n} p_i I_{\text{DK}}(p, \theta_k)$$
$$= \sum_{i=1}^{n} p_i - \log_2 p_k$$
$$= -\sum_{i=1}^{n} p_i \log_2 p_k = H(p)$$

Analogously, the inaccuracy of q as expected from the perspective of p is:

$$\mathbb{E}I_{\text{DK}}(p, q) = \sum_{i=1}^{n} p_i \left(-\log_2 q_i \right)$$
$$= -\sum_{i=1}^{n} p_i \log_2 q_i = H(p, q)$$

But that means, by Gibbs' inequality, that $\mathbb{E}I_{\text{DK}}(p, q) \geq \mathbb{E}I_{\text{DK}}(p, p)$ unless $p = q$, which completes the proof.

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