

## Palavras do Editor

Como muitos já sabem, nesse ano comemora-se o 250<sup>o</sup> aniversário da publicação póstuma do ensaio de Thomas Bayes sobre o problema da probabilidade inversa no *Philosophical Transactions of the Royal Society of London*. E nós, como uma sociedade Bayesiana, não poderíamos deixar esse acontecimento passar despercebido. Entretanto, não vou escrever muito sobre esse fato. Não farei isso pois tive o privilégio de receber belíssimas contribuições sobre esse tema, apresentadas a seguir.

A primeira delas foi de um ilustre pesquisador: o professor “Jay” Kadane, da *Carnegie-Mellon University*, um dos convidados da última edição do EBEB. O professor Kadane é um dos grandes defensores da abordagem bayesiana subjetivista, tendo publicado mais de 270 artigos e contribuído com as mais diversas áreas do conhecimento, como direito, econometria, medicina, ciência política, sociologia, ciência da computação, arqueologia, ciências ambientais, entre outras. Em seu artigo, ele lembra as principais proposições da publicação do Rev. Thomas Bayes em uma linguagem mais atual e resume um pouco da história decorrente.

Outra belíssima contribuição dessa edição é a da jornalista e escritora Sharon Bertsch McGrayne, autora de diversos livros relacionados a descobertas científicas. Dentre outros, ela publicou os livros *The Theory That Would Not Die: How Bayes’ Rule Cracked the Enigma Code, Hunted Down Russian Submarines, and Emerged Triumphant from Two Centuries of Controversy*, lançado pela Yale University Press em 2011, e *Nobel Prize Women in Science: Their Lives, Struggles and Momentous Dis-*

*coveries*, pela Joseph Henry Press em 2001. Esse último ganhou uma versão em português pela Marco Zero Editora. Em seu texto, ela fala um pouco das implicações do Teorema de Bayes nos dias atuais.

A terceira mas não menos importante contribuição é do professor Frank Lad (*University of Canterbury*, Nova Zelândia), que também esteve presente no último EBEB. Frank Lad também é um entusiasta da abordagem bayesiana subjetivista, sendo fortemente influenciado pelos trabalhos de Bruno de Finetti. No artigo, Frank faz uma crítica as abordagens utilizadas no estudo de causalidade baseadas em redes bayesianas, apresenta uma aplicação em genética e propõe uma solução.

Como de costume, a seção Eventos no final do boletim apresenta uma lista de encontros científicos que ocorrerão no próximo semestre. Além dessa, no início do boletim teremos uma seção especial com as primeiras notícias do próximo EBEB, que ocorrerá no início do próximo ano. Essa edição conta também com um relato da professora Cibele Maria Russo Noveli (ICMC-USP) sobre o evento *BAYES 2013*, ocorrido em maio na Holanda.

Aproveito para agradecer a todos que me ajudaram com essa edição. Além das pessoas que contribuíram com seus textos, agradeço também aos professores Carlos A. B. Pereira, Sérgio Wechsler (IME-USP), Adriano Polpo e Márcio Diniz (DEs-UFSCar) que revisaram os manuscritos e auxiliaram na comunicação com alguns pesquisadores internacionais.

Espero que, assim como eu, divirtam-se com essa edição. Boa leitura!

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## Expediente:

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## EBEB 2014 - XII Encontro Brasileiro de Estatística Bayesiana

Atibaia – Brasil, 10 a 14 de março de 2014. ([www.ime.usp.br/isbra/ebeb/](http://www.ime.usp.br/isbra/ebeb/))

Caros leitores, é com satisfação que fazemos o anúncio do EBEB 2014.

O evento será realizado no Hotel Fazenda Hípica Atibaia ([www.hotelfazendaatibaia.com.br](http://www.hotelfazendaatibaia.com.br)), no interior do estado de São Paulo. O local é muito agradável e similar ao do EBEB 2012.

O evento ocorrerá de 10 a 14 de março de 2014, na semana após ao carnaval. Lembrando que 2014

é uma ano de grandes evento no Brasil, ocorrendo primeiro o EBEB e posteriormente a Copa do Mundo de Futebol!

Estamos trabalhando bastante para termos um grande evento e em breve divulgaremos mais detalhes. Todas as informações sobre o evento serão divulgados em sua página web.

Nos vemos em Atibaia!

## BAYES 2013

Cibele Maria Russo Noveli  
(ICMC - USP)

De 21 a 23 de maio de 2013 aconteceu na *Erasmus University Rotterdam*, Holanda, o workshop *BAYES 2013*. A quarta edição do evento reuniu cerca de 80 participantes, com o objetivo de apresentar estudos bayesianos aplicados no ambiente clínico e não clínico e introduzir aos participantes os primeiros passos de histórias de sucesso utilizando o pensamento bayesiano. A ideia inicial do encontro é propagar o pensamento e as práticas bayesianas na indústria farmacêutica e, de forma mais importante, enfatizar as vantagens da modelagem bayesiana em áreas de ciência e negócios, bem como apresentar técnicas alternativas aos estatísticos dentro do mundo (bio)farmacêutico.

Aplicações práticas do pensamento bayesiano na investigação farmacêutica vinham sendo introduzidas lentamente, devido aos desafios computacionais, carência de educação estatística bayesiana na comunidade bioestatística e relutância das autoridades reguladoras sobre a utilização da abordagem. No entanto, desenvolvimentos recentes no cenário pré-clínico e baseado no paradigma conhecido como “*model based drug development*” indicam o crescente interesse e valor agregado de aplicações bayesianas.

O comitê organizador foi composto por Em-

manuel Lesaffre (*Erasmus Medical Center Rotterdam*, Holanda) e Eline van Gent (*Erasmus Medical Center Rotterdam*, Holanda) em conjunto com a Adolphe Quetelet Society (*IBS-Belgian Region*). O comitê científico foi composto por Emmanuel Lesaffre, Brad Carlin (*University of Minnesota*, EUA), Gianluca Baio (*University College London*, Reino Unido), Julien Cornebise (*DeepMind Technologies*, Reino Unido), Muriel Boulton (*Grünenthal*, Alemanha), Christel Faes (*Hasselt University*, Bélgica), Bruno Boulanger (*Arlenda*, Bélgica), Tom Jacobs (*Janssen*, Bélgica), Astrid Jullion (*Arlenda*, Bélgica), Philippe Lambert (*University of Liège*, Bélgica) e Sophie Vanbelle (*University of Maastrich*, Holanda). O evento contou com os palestrantes convidados Emmanuel Lesaffre, Gianluca Baio, Pierre Lebrun (*University of Liège*, Bélgica), Veronika Rockova (*Erasmus Medical Center Rotterdam*, Holanda), Nicky Best (*University College London*, Reino Unido), Alexina Mason (*University College London*, Reino Unido) e David Ohlssen (*Novartis*, EUA) e ainda com 20 comunicações orais. Como programação adicional foi oferecido o curso “*Bayesian statistics*” por Emmanuel Lesaffre, baseado em seu livro publicado recentemente em coautoria com A. B. Lawson (Lesaffre, E. and Lawson, A. B. *Bayesian Biostatistics*. Wiley, 2012).

A quinta edição do BAYES está prevista para acontecer em 2014 em Londres, Reino Unido.

## Bayes at 250

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In 1763, Rev. Richard Price, a friend of Rev. Thomas Bayes, submitted Bayes’ posthumous paper “An Essay Toward Solving a Problem in the Doctrine of Chances” to the Royal Society. How much of this essay is due to Bayes and how much to Price is still debated. Certainly Price was a formidable figure. Bayes’ Theorem, the germ of which can be found in the paper, is now understood to be a simple, almost trivial application of the definition of conditional probability.

Bayes’ paper is hard for modern readers to appreciate. For example, where we write integrals, Bayes writes about areas under curves. However, in modern notation, the heart of the matter is his propositions 8, 9 and 10, as follows:

**Proposition 8** Suppose  $x$  has a uniform distribution and suppose  $n$  independent Bernoulli trials with probability  $x$  of success. Then, for fixed  $0 \leq x_1 < x < x_2$ ,  $P\{x_1 < x < x_2 \text{ and } p \text{ successes in } n \text{ trials}\} =$

$$(1) \quad \int_{x_1}^{x_2} \binom{n}{p} x^p (1-x)^{n-p} dx.$$

**Proposition 9** Let  $0 \leq x_1 < x_2 \leq 1$ . Then

$$(2) \quad P\{x_1 < x < x_2 | p \text{ successes in } n \text{ trials}\} = \frac{\int_{x_1}^{x_2} \binom{n}{p} x^p (1-x)^{n-p} dx}{\int_0^1 \binom{n}{p} x^p (1-x)^{n-p} dx}.$$

**Proposition 10:** Let  $x$  be the probability of an event  $R$ . Then  $\{x_1 < x < x_2 | R \text{ has occurred } p \text{ times in } n \text{ trials}\}$  has probability given in (2).

Bayes (I conjecture) had two sources of discomfort about his results. Mathematically, the incomplete beta function was not well understood at the time, and he explored some ways of approximating it. Philosophically, he seems to have been concerned about the assumption of a uniform prior, and added a further “scholium” to justify it. This assumption, later called “Bayes’ Postulate,” has been the source of continual controversy since. (In philosophy, the same idea is called “the principle of insufficient reason.”) The notion, roughly, is that if I “know nothing,” my prior should be uniform.

A simple example can illustrate why this is problematic. Suppose I flip a coin twice, and “know nothing” about its probability of heads. I could code the events in the usual way,  $\{(HH), (HT), (TH), (TT)\}$  as four events, which by the principle I should regard as equally likely, i.e. probability  $1/4$ . But suppose instead I code the events according to the number of heads: 0, 1, and 2, and take them to be equally likely. What makes the former correct and the latter incorrect? What principle underlies the choice of a coding of the outcomes to which I am supposed to have a uniform distribution?

Apparently independently, Laplace used Bayes’ Theorem in conjunction with flat priors, a usage that became popular in the 19<sup>th</sup> century. Called “inverse probability” because it permits the reversal of the event being conditioned upon with the event whose probability is stated, this became the dominant method in statistical inference.

In the early 20<sup>th</sup> century, Fisher, and later Neyman and Pearson, laid the foundation for sampling theory, an alternative approach that purported to be objective. Thus Fisher, for example, recognized Bayes’ Theorem as valid, but would use it only when the prior distribution had an empirical basis.

The work of Jeffreys is an attempt to use the sampling distribution itself as a source of enlightenment about what prior “should” be used. In this he is followed by various proposals of reference priors, etc., and the current vogue of “objective” rationale for the use of particular prior distributions.

The modern subjectivist Bayesian movement, associated with deFinetti, Savage, Lindley and DeGroot, takes probability to be a statement of personal belief. In this view there is no single prior distribution a statistician is obliged to use, just as there is no single sampling distribution or likelihood one must use on a particular applied problem.

So Happy Birthday to Bayes’ paper! We are all beneficiaries of Bayes, and also of Price, Laplace, Fisher, Neyman, Pearson, Jeffreys, deFinetti, Savage, DeGroot and Lindley. What we learn from each of them, and how we shape our intellectual inheritance into a useable and practical viewpoint to address applied problems, is an issue worthy of our continued attention.

Some references discussing Bayes’ paper:

**Dale, A.I.** (1991). *A History of Inverse Probability, from Thomas Bayes to Karl Pearson*, Springer-Verlag, New York.

**Bayes, T.** (1958). “An essay towards solving a problem in the doctrine of chances,” *Biometrika*, **45**, 293–315, (with a biographical note by G.A. Barnard).

**Pearson, K.** (1921–1933, 1978). *The History of Statistics in the 17<sup>th</sup> and 18<sup>th</sup> Centuries against the Changing Background of Intellectual, Scientific and Religious Thought*, (edited by E.S. Pearson), MacMillan Publishing Co., New York.

# Bayesian Revolution

Sharon Bertsch McGrayne

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*This year, we are celebrating the 250<sup>th</sup> anniversary of the day when Thomas Bayes' paper about his theory was read aloud to members of the Royal Society in London.*

*The anniversary celebration is particularly exciting because for much of the 20<sup>th</sup> century, Bayes was too déclassé to be mentioned, much less lauded.*

*In the excitement over giving the Rev. Bayes' his due, however, I hope we can remember to mention his friend Richard Price. Because without Price, we wouldn't be celebrating Bayes' discovery at all.*

*The Rev. Bayes, a wealthy minister and amateur mathematician in early 18<sup>th</sup> century England, filed his discovery away in a notebook and died in 1761 without publishing it. It was his younger friend – another minister and amateur mathematician Richard Price – who went through the dead man's papers, spent two years correcting and editing it, and sent it to the secretary of the Royal Society on November 10, 1763. A month later on December 23, 1763, it was read aloud at the Royal Society. The following year, it was published in the *Philosophical Transactions*, then a journal for the British gentry. From there, it sank rapidly from view.*

*Today, given Price's extensive reworking of Bayes' work, he would be listed as co-author of the paper and we'd be calling Bayes' rule the Bayes-Price rule.*

*In fact, without Price, we'd be calling Bayes' rule "Laplace's rule", because it was the great French mathematician Pierre-Simon who developed the general form of Bayes' theory employed today.*

*Price is worthy of study in his own right. He became a British supporter of both the American and the French revolutions, a friend of almost every American founding father you can think of, and a founder of the insurance industry.*

In the early years of this century, the reputation of Bayes' rule flipped almost overnight from controversial to chic – and did so for highly pragmatic reasons.

When I first started writing Bayes' story ten years ago, I was thrilled to search for the word "Bayesian" on the web and find 100,000 websites. This summer, I did it again and got 12.3 million.

For much of the 20<sup>th</sup> century, Bayes was so taboo that its name could not be mentioned in public. For example, when I started my project almost ten years ago and asked a statistics professor about Bayes' rule, the man erupted in rage.

During the 2008 election, though, pollster Nate Silver correctly forecast not only the winner in 49 out of 50 states but also the outcome of 35 U.S. Senate races – and announced that he used Bayes' rule. Last year, the chairman of President Obama's Council of Economic Advisers could volunteer to *The New York Times* that he'd read my book and that Bayes is "important in decision making – how tightly should you hold on to your view and how much should you update your view based on the new information that's coming in. We intuitively use Bayes's rule every day." And I recently sat next to a physician at dinner while he told me how he used Bayesian search theory to find his wife's lost cell phone.

So why this sea change in attitude about a very fundamental scientific issue: how we analyze information, evaluate data, and make rational data-based decisions even when we don't know everything there is to know about a problem?

First, it seems to have become trendy, a political shorthand for data-based decision-making as opposed to ideologically-driven decision-making.

More important, Bayes has swept through almost every aspect of our technological, computerized world. It's in our spam filters. It's embedded in Microsoft and Google and in Google's driverless car. It searches the internet for the web pages we want, clarifies our MRI's<sup>1</sup> and PET<sup>2</sup> scans, and sharpens the images from drones flying overhead. It's used on Wall Street and in genetics, artificial intelligence, astronomy, and physics, machine translation of foreign languages, and increasingly, in evaluating the probability of evidence to be submitted in trials. The list goes on and on.

To understand this explosion of interest in Bayes we have to go back to the beginning with Thomas Bayes and – I would add – with Richard Price (see sidebar). We'll see two patterns emerge: first, Bayes became an extreme example of the gap between academia and the real world. And second, military super-secrecy during the Second World War and the Cold War affected Bayes profoundly.

Bayes' rule, of course, is named for the Reverend Thomas Bayes, a Presbyterian minister and amateur mathematician who lived near London in the early 1700s. We know little about him. However, we do know that he discovered his theorem during the 1740s in the midst of an inflammatory religious controversy over whether scientists and others could use evidence about the natural world to make rational conclusions about God the creator, what they called The Cause.

<sup>1</sup>Magnetic Resonance Imaging

<sup>2</sup>Positron Emission Tomography

We don't know that Bayes wanted to prove the existence of God the Cause. But we do know that Bayes tried to deal with the problem of cause and effect mathematically. In so doing, he produced his simple one-line theorem that allows us to start with an initial half-baked idea – Bayes actually used the word “guess” and suggested assigning it 50-50 odds. But then Bayes committed us mathematically to modifying that initial idea with objective new information and even – horror of horrors – to changing our minds.

But Bayes didn't believe in his theorem enough to publish it. He filed it away in a notebook and died 10 or 15 years later. Going through Bayes' papers, his young friend Richard Price, – another Presbyterian minister-mathematician – decided that the theorem could help prove the existence of God the Cause. Price (see sidebar) spent 2 years off and on editing Bayes' theorem and got it published in a journal that, unfortunately, few mathematicians read.

A few years later, a young professional French mathematician, Pierre Simon Laplace – best known today for the Laplace transform – discovered the rule in 1774 independently of Bayes and called it the probability of causes. Laplace mathematized every science known to his era and over the course of 40 years gave what we call Bayes' rule its modern form. Then he actually used it to produce big numbers and ways to calculate them in the days before computers. Until about 50 years ago, Laplace was credited with what we now call Bayes' rule.

During 1700s and early 1800s, improved instrumentation and algebraic techniques as well as international scientific expeditions produced an explosion of precise and trustworthy objective data about the natural world. By the mid-1800s, up-to-date statisticians had so much reliable data that they could reject the uncertainties of Bayes' rule and judge the probability of something according to how frequently it occurred. They become known as frequentists and were the great opponents of Bayes' rule right up until the end of the 20th century. The professor who erupted over the telephone at me was obviously a frequentist.

For them, modern science required both objectivity and precise answers. Bayes, on the other hand, dealt with initial subjective guesses and ended up – not with precise answers – but with probabilities. By 1920, most scientists thought Bayes “smacked of astrology, of alchemy.”

To me, the surprising thing was that all the time that theorists and philosophers denounced Bayes' rule as subjective, people who had to deal with real-world emergencies, who had to make one-time decisions based on incomplete information, kept right on using Bayes' rule. Simply put, Bayes helped them make do with what they had. For example, Bayes rule helped free Dreyfus from a French prison during the 1890s. It helped artillery officers in France, Russia, and the U.S. aim their fire and test their ammunition and cannons during two World Wars; helped the Bell telephone system survive the financial panic of 1907; and helped the U.S. insurance industry start workers' compensation insurance almost overnight.

As far as sophisticated statisticians were concerned, however, Bayes was virtually taboo by the time the Second World War began in 1939. Fortunately, Alan Mathison Turing was not a statistician. He was a mathematician and besides fathering the modern computer, computer science, software, artificial intelligence, the Turing machine, the Turing test – he would father the modern Bayesian revival. Turing's story is also told at some length in *The Theory That Would Not Die*, so here I will say only that Turing developed Bayesian methods to decode the Enigma messages sent from German headquarters to the U-boats that were sinking unarmed freighters shipping food and supplies to Britain. Bayesian methods were also used to build the Colossi computers that broke the code used by the Berlin Supreme Command.

After the peace, Bayes' wartime successes in code-breaking and operations' research were classified, however. Bayes emerged from the Second World War even more suspect than before, and for 30 or 40 years during the Cold War a small group of maybe a 100 or more believers struggled for acceptance. During this period, many Bayesians concentrated on theory in order to make Bayes a respectable branch of mathematics. And Bayes itself survived in various niche specialties outside the statistical mainstream, for example, in insurance, paternity, law, and business schools. Again, these are stories told in *The Theory That Would Not Die*.

During the Cold War – when the military continued to use Bayes but kept it secret and when civilian Bayesians were under attack – there were very few public acknowledgments of Bayes' power. For example, one of the first nuclear power plant safety studies in the United States used Bayesian analysis in 1974 to predict the kind of accident that actually happened at Three Mile Island. The safety report, however, hid the big bad word Bayes in the appendix of volume III. The only extensive public Bayesian application determined the authorship of the Federalist Papers, newspaper essays written to convince New Yorkers to approve the American Constitution in 1787 and 1788.

By the late 1980s, industrial automation, the military, and medical diagnostics were using ultrasound machines, PET scans, MRIs, electron micrographs, telescopes, military aircraft and infrared sensors to produce blurry images that needed sharpening. People wanted to know what the original object in the picture looked like – which of course was ideal for Bayes and Laplace's probability of causes. However, with computers churning out masses of unknowns, Laplace's method using integration of functions was too complicated to be practical. Bayesians did not yet realize that the key to making Bayes useful in the workplace would be computational ease, not more polished theory.

In 1989, Adrian F. M. Smith and Alan Gelfand finally put the pieces together: Bayes, Gibbs sampling, Monte Carlo, chains, and iterations. They wrote their watershed synthesis – now called MCMC for Markov

Chain Monte Carlo – very fast, but also very carefully. In 12 pages, they used the word “Bayes” only 5 times. “There was always some concern about using the b-word,” Gelfand told me, “a natural defensiveness on the part of Bayesians in terms of rocking the boat. ... We were always an oppressed minority, trying to get some recognition. And even if we thought we were doing things the right way, we were only a small component of the statistical community and we didn’t have much outreach into the scientific community.”

The next decade passed in a frenzy of activity as Bayesians and others used MCMC, new powerful workstations, and off-the-shelf computer software to finally – after two and a half centuries – calculate complex realistic problems. Statistics became a combination of applied mathematics and applied computing. Statisticians became the keepers of the scientific method helping scientists understand what they can reasonably conclude from their data. And outsiders from computer science, physics, and artificial intelligence refreshed and broadened Bayes. In the excitement, it was adopted almost overnight.

The Bayesian revolution was a modern paradigm shift for a very pragmatic age. It happened overnight – not because people changed their minds about Bayes as a philosophy of science – but because suddenly Bayes worked.

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## Reassessing causal networks: rejection and reconstruction

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### 1 Introduction

Over its long history, Bayes’ Theorem has sometimes been said to represent a computational form for determining the probabilities of several possible causes of a specified effect. Moreover, during the last twenty years there has been a proliferation of statistical work devoted to causal analysis via Bayesian networks. Seminal works in the field are due to Pearl (1988, 2000 and 2009) and Jensen (1996, 2001) though a large host of leading statisticians have participated in these developments. Notable among recognised research is the article of Greenland, Robins and Pearl (1999).

Despite their evident popularity and the widespread use of several computational packages devoted to applications of the concepts, I have been an outspoken critic of these developments of “causal modeling.” In April, 1997 I presented a critical review of specific arguments in Jensen’s (1996) *Introduction to Bayesian Networks* at the Centre Ettore Majorana for the Peaceful Uses of Science in Erice, Sicily. Professor Jensen was an active participant in the discussions at this meeting of the International School of Mathematics “G. Stampacchia”. The presentation was published under the title “Assessing the foundations of Bayesian networks: a challenge to the principles and the practice” (Lad, 1999), and is meant to be read in conjunction with Jensen’s book. During the course of the lively discussions I was challenged with an applied problem that was presented as a paradigmatic example of causal modeling in genetics which typifies structures that have been proposed and which purportedly requires such concepts for its fruitful analysis.

In this present contribution to further discussion I plan firstly to offer a summary statement of the bold claims that are fully substantiated in my published critique. Then I shall expand more extensively on the challenge problem that was proposed at Erice. I contend that a coherent analysis of this problem can be made within the framework of de Finetti’s subjective construction of probability, and that the concept of causal relations is completely irrelevant to the analysis. Indeed, some principles such as (conditional) independence conditions that have been proposed as fundamental to the analysis of the problem via a causal network are both misleading as presented, and irrelevant to a coherent analysis.

I should identify my perspective on matters of probability as that of an operational subjectivist, in the tradition championed by Bruno de Finetti (1974, 1975). All probabilities and, more generally, previsions (expectations) are recognised as the assertions of someone (you, perhaps, or someone else whose opinions you would like to analyse); and the constraints on their combination are those imposed by the condition of their coherency. Operationally, one’s previsions are defined by one’s willingness to price the value of a risky transaction whose outcome depends on the quantities in question. This viewpoint bears explicit mention because of its non-congruity with the supposition of many network constructors ... that their network probabilities somehow represent structural features of nature that can be discovered. In this context, they typically think of statistical analysis engaging the practice of determining a sound network representation of this structure. A detailed

exposition of the operational subjective viewpoint and its computational application appears in the text of Lad (1996). Some numerical applications of the fundamental theorem of prevision, which governs most every statistical problem, appear in the article of Lad, Dickey, and Rahman (1992). I shall rely on the reader's familiarity with some details of this perspective as I develop my argument here. Primary among these are the construction of a realm matrix for a vector of logically dependent quantities, and the recognition of the linearity of coherent prevision assertions. If you are unfamiliar with this terminology, you may appreciate its relevant detail when we study the genetical problem in Section 3.

## 2 Critique of Bayesian networks: a precis

Again, I invite you to read the full text of the critique presented in the article I've mentioned. Both to intrigue you to such an endeavor and to prepare you for analysis of the problem in genetics that will follow, I present here merely nine summary statements of the critique. The anagram DAG to which they refer is a label for a "directed a-cyclic graph", touted as an underlying feature of causal modeling.

1. The notion of "cause" is observationally meaningless. The modern origins of this understanding come from the works of David Hume, especially his *Enquiry concerning Human Understanding* (1748, 1988 edition, Section VII, Part 2, pp 113-118).
2. The "directions" proposed in DAGs are both misleading and groundless. I discuss this in the context of Jensen's simple DAG for "icy roads."
3. The axiomatic assertion of conditional independence at "causal nodes" in a DAG is misplaced. What might be appropriate in a problem such as the icy roads example is conditional exchangeability.
4. The notion of independence itself is commonly misconstrued by proponents of causality, as in Jensen's example of the "wet grass" DAG.
5. Common constructions of "causal diagrams" routinely ignore relevant arrows when they are inconvenient, as in the example of the "burglar or earthquake alarm".
6. The metaphysical concept of causation is the source of the problems with the application of DAGs.
7. Claims to the "completeness" of serial, converging, and diverging connections for characterising information structures are erroneous.
8. Supposedly "problematic" directed graphs with feedback cycles can be analysed routinely using de Finetti's fundamental theorem of prevision.
9. As opposed to the nomenclature of "directed a-cyclic graphs" used by network theorists, I conclude that the information structures that are really relevant to the problems they propose would be better recognised and analysed as "non-directed, non-cyclic, and a-causal graphs."

Foundational difficulties with the principles underlying the proclaimed practice of the network theorists are fairly deep. I believe that everything substantive they have to offer for consideration is subsumed in the fundamental theorem of prevision, and grounded properly in the operational subjective foundation of coherent probability. As a matter of producing efficient computation, their achievements are laudable. As a matter of sensible thinking about real problems of inference, their prescriptions leave something to be desired. Let us now proceed to the problem with which I was challenged.

## 3 An Example from Genetics

In the discussion at Erice, the following example was proposed to display a problem purportedly portraying an obvious situation of a recognisably causal relationship. Consider a hereditary disease carried through a dominant gene denoted by  $A$ , with the recessive gene denoted by  $a$ . If carried by an individual, however, the disease may or may not exhibit itself symptomatically during the person's lifetime. We wonder whether a specific person (called hereafter "the child") carries the disease genetically. That is, we wonder whether this person is constituted with the gene pair  $AA$  or  $Aa$  as opposed to  $aa$ . Numerically, we define the quantity  $G_C = 0, 1$ , or  $2$  to denote the child's genetic makeup as  $aa, aA$ , or  $AA$ , respectively. We are also uncertain about the genetic makeup of the father and mother, denoted by  $G_F$  and  $G_M$ , whose numerical values are defined in the same way. A medical test is available which yields a value of  $T = 1$ , corresponding to a positive signal that the child carries the disease, or  $T = 0$  corresponding to a negative signal. The test is not perfect, however, allowing both true and false positive, and true and false negative results.

Such a situation is proposed to be describable by a DAG of the form displayed in Figure 1.

The genetic makeup of the parents is said to cause, probabilistically, the genetic makeup of the child. Several relevant probabilities are accorded widely agreed upon values prescribed by the theory of genetics. These include assertions such as

$$P[G_C = 0|(G_F, G_M = 0, 0)] = 1 \quad \text{and} \quad P[G_C = 0|(G_F, G_M = 0, 1)] = \frac{1}{2}.$$

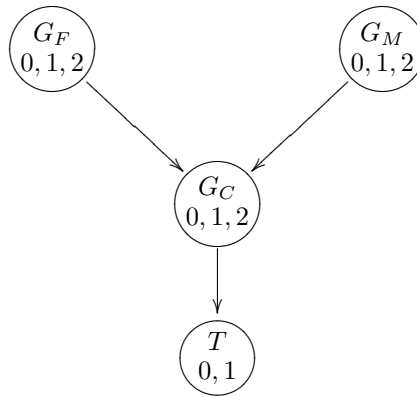


Figure 1: The DAG for genotypes  $(G_F, G_M, G_C)$  and the test result,  $T$ .

In the former case the conditioning event specifies that both parents have a pair of recessive genes, making it certain that the child's pair of genes are both recessive as well. In the latter case the condition is that the female parent's gene pair is doubly recessive, while the male's pair is mixed, dominant *and* recessive. In such a case, either of the male parent paired genes may join with a gene from the female's pair, which are both recessive. The probability that the resulting offspring's gene pair is doubly recessive then equals  $\frac{1}{2}$ , while the probability the resulting gene pair is mixed dominant and recessive also equals  $\frac{1}{2}$ . Following is an exhaustive list of such conditional probabilities specified by genetic theory, enumerating all conditional probabilities of the form  $P(G_C = z | (G_F, G_M) = (x, y))$  for  $(x, y, z) \in \{0, 1, 2\}^3$ :

**Table 1. Conditional Probabilities Induced by Genetic Theory**

$P[G_C = 0   (G_F, G_M) = (0, 0)] = 1$	$P[G_C = 1   (G_F, G_M) = (0, 0)] = 0$	$P[G_C = 2   (G_F, G_M) = (0, 0)] = 0$
$P[G_C = 0   (G_F, G_M) = (0, 1)] = \frac{1}{2}$	$P[G_C = 1   (G_F, G_M) = (0, 1)] = \frac{1}{2}$	$P[G_C = 2   (G_F, G_M) = (0, 1)] = 0$
$P[G_C = 0   (G_F, G_M) = (0, 2)] = 0$	$P[G_C = 1   (G_F, G_M) = (0, 2)] = 1$	$P[G_C = 2   (G_F, G_M) = (0, 2)] = 0$
$P[G_C = 0   (G_F, G_M) = (1, 0)] = \frac{1}{2}$	$P[G_C = 1   (G_F, G_M) = (1, 0)] = \frac{1}{2}$	$P[G_C = 2   (G_F, G_M) = (1, 0)] = 0$
$P[G_C = 0   (G_F, G_M) = (1, 1)] = \frac{1}{4}$	$P[G_C = 1   (G_F, G_M) = (1, 1)] = \frac{1}{2}$	$P[G_C = 2   (G_F, G_M) = (1, 1)] = \frac{1}{4}$
$P[G_C = 0   (G_F, G_M) = (1, 2)] = 0$	$P[G_C = 1   (G_F, G_M) = (1, 2)] = \frac{1}{2}$	$P[G_C = 2   (G_F, G_M) = (1, 2)] = \frac{1}{2}$
$P[G_C = 0   (G_F, G_M) = (2, 0)] = 0$	$P[G_C = 1   (G_F, G_M) = (2, 0)] = 1$	$P[G_C = 2   (G_F, G_M) = (2, 0)] = 0$
$P[G_C = 0   (G_F, G_M) = (2, 1)] = 0$	$P[G_C = 1   (G_F, G_M) = (2, 1)] = \frac{1}{2}$	$P[G_C = 2   (G_F, G_M) = (2, 1)] = \frac{1}{2}$
$P[G_C = 0   (G_F, G_M) = (2, 2)] = 0$	$P[G_C = 1   (G_F, G_M) = (2, 2)] = 0$	$P[G_C = 2   (G_F, G_M) = (2, 2)] = 1$

Finally, the genetic makeup of the child is said to cause, probabilistically, the outcome of the test through specifiable probabilities of the form  $P(T | G_C = 0)$  and  $P(T | G_C > 0)$ . What else could cause the result of the test?

According to causal network theorists, the "causal structure" embedded in the DAG shown in Figure 1 is supposed to imply that the quantities  $G_F$  and  $G_M$  are independent, because they are identified as the exclusive causes of  $G_C$ . In the context of a DAG such as that shown in Figure 1, Jensen says (2001, p.7) "If nothing is known about  $G_C$  (the nodal quantity) except what may be inferred from knowledge of its parents  $G_F$  and  $G_M$  then the parents are independent: evidence on one of them has no influence on the certainty of the others. Knowledge of one possible cause of an event does not tell us anything about other possible causes." A second causal construct that is said to be seen in the DAG, is that the value of  $G_C$ , whatever it may be, is supposed to cause, probabilistically, the outcome of the test variable  $T$ , no matter whether  $T = 0$  or  $T = 1$ . On the face of it, nothing could be simpler to proponents of probabilistic causality in network structures.

My concerns are firstly that the claim to a causal relation of  $G_C$  to  $T$  is vacuous, since it cannot be denied on the basis of any conceivable empirical observation! The only *observable* relations between the values of  $T$  and the event that  $(G_C > 0)$  are exhausted by the possibilities composing the cartesian product:  $(0, 0)$ ,  $(0, 1)$ ,  $(1, 0)$ , and  $(1, 1)$ . Secondly, the supposed independence of  $G_F$  and  $G_M$  induced by their proclaimed causal relation to  $G_C$  (which is an axiom of the causality proponents' causal modeling) is not at all merited by a considered scientific assessment of the situation. In the context that we are only learning about the incidence of the dominant gene in the population gene pool, even in an individual via testing, the incidence of genetic makeup regarding this gene in the population is unknown. For the disease does not necessarily exhibit itself in an individual symptomatically when its gene is carried. Much more reasonable would be a judgment of exchangeability regarding the values of  $G_F$  and  $G_M$ . This is an assessed symmetry structure that allows for extraction of information about any members of an exchangeable group from observations of the others.

The remainder of this Section will show how the operational subjective characterisation of logical relations among the quantities concerned, along with the conditional probabilities motivated by knowledge of genetics, provides a complete representation of what is known and what is not known in this problem. As we shall see,



the conditional probability assertions merited by our experience with the test observation  $T$  have nothing to do with claims of causality.

### 3.1 The realm matrix for the genetic composition of $(G_F, G_M, G_C)$

We begin by producing the *realm matrix* of all the quantities that shall be relevant to our analysis. This matrix is presented in divided sections that shall be considered in sequential stages of the discussion. The first section of three rows lists as columns the 15 possibilities for the observable triple  $(G_F, G_M, G_C)^T$ . This realm matrix of dimension  $3 \times 15$  exhibits the “logical dependence” among the three quantities. Quantities are said to be logically dependent if and only if the realm of possibilities for the vector of their values is a *proper* subset of the cartesian product of the realms for each component. In the case we address here, the realm for each quantity denoting a genetic-makeup is the set  $\{1, 2, 3\}$ . The three quantities we are considering would be “logically independent” only if the column vectors of their possible measurement values specified a realm matrix of dimension  $3 \times 27$ , whose columns would be the elements of  $\{0, 1, 2\}^3$ . It is apparent that this condition does *not* hold in our problem, since the columns  $(0, 0, 1)^T$  and  $(0, 0, 2)^T$  do not appear in the matrix, for examples. These triples would represent impossible occurrences. If both parents were to have genotype  $aa$ , identified by  $G_F = G_M = 0$ , it would be impossible that the child has either genotype  $aA$  or  $AA$ , identified by  $G_C = 1$  or  $G_C = 2$ . Similarly, although  $(1, 0, 0)^T$  and  $(1, 0, 1)^T$  *do appear* as columns 2 and 3 of the realm matrix, no column of the form  $(1, 0, 2)^T$  appears, since it also would represent a situation that is impossible genetically. In contrast, the complexity of the logical relation here is identifiable through the presence of *all three vectors* of the form  $(1, 1, 0)^T$ ,  $(1, 1, 1)^T$ , and  $(1, 1, 2)^T$ , which appear as columns 7, 8, and 9 of the realm matrix.

Realm Matrix for all quantities assessed in the problem

$$\mathbf{R} \begin{pmatrix} G_F \\ G_M \\ G_C \\ \text{*****} \\ (\mathbf{G}_3 = 0, 1, 0) - \frac{1}{2}(\mathbf{G}_2 = 0, 1) \\ (\mathbf{G}_3 = 1, 0, 0) - \frac{1}{2}(\mathbf{G}_2 = 1, 0) \\ (\mathbf{G}_3 = 1, 1, 0) - \frac{1}{4}(\mathbf{G}_2 = 1, 1) \\ (\mathbf{G}_3 = 1, 1, 1) - \frac{1}{4}(\mathbf{G}_2 = 1, 1) \\ (\mathbf{G}_3 = 1, 2, 1) - \frac{1}{2}(\mathbf{G}_2 = 1, 2) \\ (\mathbf{G}_3 = 2, 1, 1) - \frac{1}{2}(\mathbf{G}_2 = 2, 1) \\ (\mathbf{G}_3 = 1, 1, 2) - \frac{1}{4}(\mathbf{G}_2 = 1, 1) \\ \text{*****} \\ (\mathbf{G}_2 = 0, 1) - (\mathbf{G}_2 = 1, 0) \\ (\mathbf{G}_2 = 0, 2) - (\mathbf{G}_2 = 2, 0) \\ (\mathbf{G}_2 = 1, 2) - (\mathbf{G}_2 = 2, 1) \\ \text{*****} \\ \text{Column Number} \end{pmatrix} = \begin{pmatrix} 0 & 1 & 1 & 2 & 0 & 0 & 1 & 1 & 1 & 2 & 0 & 1 & 1 & 2 \\ 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 2 & 2 & 2 \\ 0 & 0 & 1 & 1 & 0 & 1 & 0 & 1 & 2 & 1 & 2 & 1 & 1 & 2 \\ * & * & * & * & * & * & * & * & * & * & * & * & * & * \\ 0 & 0 & 0 & 0 & \frac{1}{2} & -\frac{1}{2} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{2} & -\frac{1}{2} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{3}{4} & -\frac{1}{4} & -\frac{1}{4} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\frac{1}{2} & \frac{1}{2} & -\frac{1}{2} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{2} & -\frac{1}{2} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{2} & -\frac{1}{2} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\frac{1}{4} & -\frac{1}{4} & \frac{3}{4} & 0 & 0 & 0 & 0 & 0 \\ * & * & * & * & * & * & * & * & * & * & * & * & * & * \\ 0 & -1 & -1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & -1 & 0 & 1 & 0 \\ * & * & * & * & * & * & * & * & * & * & * & * & * & * \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 & 13 & 14 & 15 \end{pmatrix}.$$

Figure 2 displays the realm matrix for  $(G_F, G_M, G_C)$  geometrically. Coherency of any prevision (expectation) assertion requires only that the vector  $P(G_F, G_M, G_C)$  lies within the convex hull of the realm members. Algebraically, this means that if  $\mathbf{X}$  is a quantity vector with realm matrix  $\mathbf{R}(\mathbf{X})$ , a cohering prevision vector  $P(\mathbf{X})$  must equal some convex combination of the columns of  $\mathbf{R}$ . That is,  $P(\mathbf{X}) = \mathbf{R}(\mathbf{X}) \mathbf{q}_{15}$ , where  $\mathbf{q}_{15}$  is an element of the unit simplex  $\mathbf{S}^{14} = \{\mathbf{q}_{15} | \text{each } q_i \geq 0 \text{ and } \sum q_i = 1\}$ . Geometrically, the convex hull displayed in Figure 2 is a 3-dimensional polytope produced by removing the twelve “impossible” vertices from the cube of points in  $\{0, 1, 2\}^3$ .

In order to acknowledge the probabilistic content of what genetic theory and observation tell us about the genotypes  $G_F, G_M$ , and  $G_C$ , we need now turn to an algebraic specification of conditional probabilities of the form  $P(G_C = z | (G_F, G_M) = (x, y))$ .

### 3.2 Linear restrictions on $P(G_F, G_M, G_C)$ deriving from genetic theory

Recalling the conditional probabilities induced by genetic theory, we can now introduce them via functions of the  $\mathbf{G}_3$  vector. The bold vector notation  $\mathbf{G}_3$  appearing in the second and third banks of quantities for the realm matrix denotes the vector  $(G_F, G_M, G_C)$  while  $\mathbf{G}_2$  denotes the subvector  $(G_F, G_M)$ . This notation shall be used in the discussion of Section 3.2. Parentheses around any expression that may be true or may be false denotes an event quantity that equals 1 if the expression turns out to be true, and equals 0 if it is found to be false, e.g.,  $(\mathbf{G}_2 = 0, 1)$ .

To begin, consider any one of the conditional probabilities asserted with value 0, such as  $P[G_C = 0 | (G_F, G_M = 0, 2)] = 0$ . The multiplication rule for coherent conditional probabilities that  $P(AB) = P(A|B)P(B)$ , applied to this assertion, yields the requirement that  $P(G_F, G_M, G_C = 0, 2, 0) = P[G_C = 0 | (G_F, G_M = 0, 2)]P(G_F, G_M = 0, 2)$ , which must thus equal 0. However, this condition is already assured by the fact that the column  $(0, 2, 0)^T$  does not appear at all in the realm matrix we have displayed, neither algebraically nor geometrically. This same situation arises for each of the twelve conditional probabilities that equal 0, listed in Table 1.

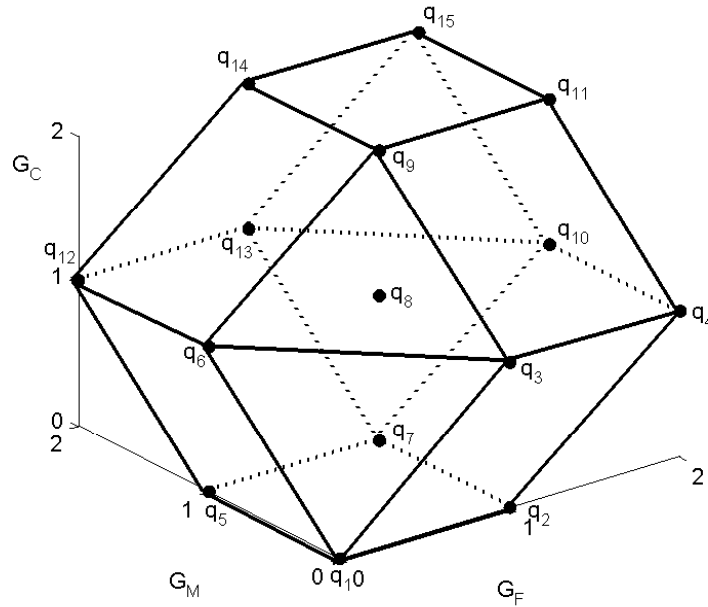


Figure 2: Convex hull of the 15 points constituting the columns of the realm of  $(G_F, G_M, G_C)^T$ . Column numbers are listed in the row at the bottom of the realm matrix. The labels  $q_i$  on the realm elements identify the convexity weights they would be accorded to identify a coherent prevision vector inside the hull.

Next, consider any one of the conditional probabilities in the Table that are shown assessed as equal to the value 1, for example  $P[G_C = 0 | (G_F, G_M = 0, 0)] = 1$ . In this case the multiplication rule then implies that  $P(G_F, G_M, G_C = 0, 0, 0) = P[G_C = 0 | (G_F, G_M = 0, 0)]P(G_F, G_M = 0, 0)$ , which then must equal  $P(G_F, G_M = 0, 0)$ . This feature can be identified in the convex hull polytope shown in Figure 2 by noticing that the only vertex of the polytope appearing in the  $G_C$  dimension for which  $(G_F, G_M) = (0, 0)$  is the point  $(G_F, G_M, G_C) = (0, 0, 0)$ . This same situation characterises each of the singleton points in the  $G_C$  dimension corresponding to the four conditional probabilities shown equal to 1 in Table 1. These are vertex numbers with coefficient labels of  $q_1, q_4, q_{12}$ , and  $q_{15}$ . Examine which points these are in the Figure.

Finally, consider the genetically motivated conditional probabilities in Table 1 that equal neither 0 nor 1, for examples  $P[G_C = 0 | (G_F, G_M = 0, 1)]$  and  $P[G_C = 1 | (G_F, G_M = 0, 1)]$ , both of which equal  $\frac{1}{2}$ . Applying the multiplication rule to these two probabilities yields the requirements that  $P(G_F, G_M, G_C = 0, 1, 0) = \frac{1}{2}P(G_F, G_M = 0, 1)$  in the former case, and that  $P(G_F, G_M, G_C = 0, 1, 1) = \frac{1}{2}P(G_F, G_M = 0, 1)$  in the latter case. To understand how this information is incorporated into the realm matrix, consider for example the former equality. The linearity of coherent prevision (expectation), applied to this equality implies that  $P[(G_F, G_M, G_C = 0, 1, 0) - \frac{1}{2}(G_F, G_M = 0, 1)] = P(G_F, G_M, G_C = 0, 1, 0) - \frac{1}{2}P(G_F, G_M = 0, 1) = 0$ . Using the summary notation we used to define  $\mathbf{G}_3$  and  $\mathbf{G}_2 = (G_F, G_M)$ , this quantity whose prevision must equal 0 can be identified as the quantity  $[(\mathbf{G}_3 = 0, 1, 0) - \frac{1}{2}(\mathbf{G}_2 = 0, 1)]$ . In any column of the realm matrix  $\mathbf{R}$  for which  $\mathbf{G}_2 \neq (0, 1)$  this quantity equals 0. However when  $\mathbf{G}_3 = (0, 1, 0)$ , this quantity equals  $1 - \frac{1}{2}1 = \frac{1}{2}$ , and when  $\mathbf{G}_3 = (0, 1, 1)$ , this quantity equals  $0 - \frac{1}{2}1 = -\frac{1}{2}$ . This explains why that row of the realm matrix has the values that it does. Similar considerations explain the row values of the remaining six rows of the second panel of the realm matrix.

Following from the same type of derivation, each of the 7 quantities that appears in the second bank of the realm matrix has an assessed prevision equaling 0 on the basis of genetic theory. Denoting possible probabilities for the observation of each of the 15 columns of  $\mathbf{R}(\mathbf{G}_3)$  by the letters  $\{q_i\}_{i=1}^{15}$ , the coherency conditions deriving from these seven conditions are, in order as they appear in the rows of the realm matrix,  $q_5 = q_6$ ,  $q_2 = q_3$ ,  $3q_7 = q_8 + q_9$ ,  $q_8 = q_7 + q_9$ ,  $q_{12} = q_{13}$ ,  $q_{10} = q_{11}$ , and  $3q_9 = q_7 + q_8$ . The four equalities of individual  $q_i$ 's in this list are easily understood. The three equalities that involve sums contain one redundancy, and are better understood by their equivalent conditions that  $q_7 = q_9$  and  $q_8 = 2q_7$ .

Geometrically, these algebraic conditions on the vertex probabilities of the realm matrix are displayed in Figure 3. For example, the condition that  $q_5 = q_6$  means that the convexity coefficients on vertices 5 and 6 in Figure 2 can be replaced by a single coefficient on a vertex of the constrained polytope in Figure 3 that is equidistant between them. A similar reduction is made for each of the other 3 direct equalities  $q_i = q_j$  induced by the genetic conditions. Moreover, the three summation conditions containing one redundancy mean that the three coefficients on the vertices numbered 7, 8 and 9 become reduced to a single coefficient attached to

the center point of the polytope,  $(1, 1, 1)$ . Recognising these reductions implied by genetic theory, any cohering assertion of  $P(G_F, G_M, G_C)^T$  must lie on the rectangular plane that sits inside the convex hull of the realm elements, as seen in Figure 3.

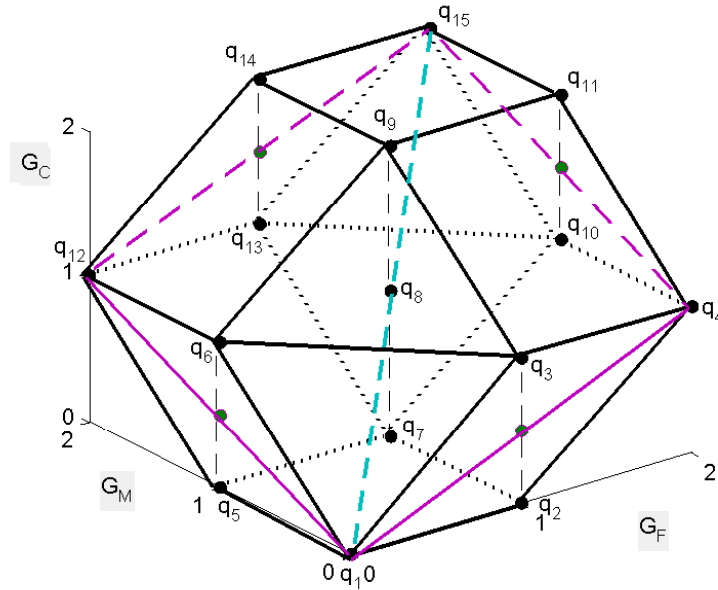


Figure 3: The reduced polytope of coherent previsions  $(P(G_F), P(G_M), P(G_C))$  induced by the seven conditional probabilities motivated by genetic theory is the inlaid magenta coloured plane. It includes the centerpoint  $(1, 1, 1)$ . Further reduction of cohering  $P(G_F, G_M, G_C)$  possibilities to the diagonal bluish-coloured line within this plane derives from regarding  $(G_F, G_M)$  exchangeably, discussed in Section 3.3.

### 3.3 Implications of regarding $G_F$ and $G_M$ exchangeably

At this stage we should note again that I categorically deny the independence of the quantities  $G_F$  and  $G_M$  that is presumed by causal network theorists. The values of  $G_F$  and  $G_M$  are definitely informative about each other. They denote genetic observations for two members of their gene pool with whom we would regard them exchangeably. Asserting the exchangeability of these two would amount to three conditions: that  $P(G_F, G_M = 0, 1) = P(G_F, G_M = 1, 0)$ , that  $P(G_F, G_M = 0, 2) = P(G_F, G_M = 2, 0)$ , and that  $P(G_F, G_M = 1, 2) = P(G_F, G_M = 2, 1)$ . In terms of the vertex coefficients, these conditions amount to the restrictions that  $q_2 + q_3 = q_5 + q_6$ ,  $q_4 = q_{12}$ , and that  $q_{10} + q_{11} = q_{13} + q_{14}$ . This can be seen by examining the columns of the realm matrix that correspond to these specific values of  $(G_F, G_M = x, y)$ . It should be apparent that these three further restrictions on the convexity coefficients reduce the domain of coherent prevision for the  $\mathbf{G}_3$  vector to the diagonal line running from  $(0, 0, 0)$  through to  $(2, 2, 2)$ .

Our analysis of the situation corresponding to the proposed DAG in Figure 1 is now complete. The convexity coefficients  $\mathbf{q}_{15}$  have been reduced to only five free components. These are identifiable in six constrained groups:  $q_1$ ;  $q_2 = q_3 = q_5 = q_6$ ;  $q_4 = q_{12}$ ;  $q_7 = q_9 = q_8/2$ ;  $q_{10} = q_{11} = q_{13} = q_{14}$ ; and  $q_{15}$ . Of course all 15  $q_i$ 's must sum to 1, so this reduces the six free components of  $\mathbf{q}_{15}$  to five. Specifying the values of these  $q_i$ 's would be equivalent to specifying probabilities for the genetic composition of any two members of the gene pool. The six relevant possibilities for  $\mathbf{G}_2$  would be  $(0,0)$ ,  $(0,1)$ ,  $(0,2)$ ,  $(1,1)$ ,  $(1,2)$ , and  $(2,2)$ . Undefined notions of causality are irrelevant.

### 3.4 On the relation of $G_C$ to the test statistic $T$

My second comment on the DAG of Figure 1 concerns the proclaimed causal relation of the genotype  $G_C$  to the test result,  $T$ . More generally, it concerns the coherent implications of conditional probability assertions pertaining to *any* array of quantities relevant to a problem of uncertain information. The analysis is couched in terms that involve only  $G_C$  and  $T$ . However it should be recognised that this is just a part of a complete analysis of all the quantities involved, including those we have already discussed. If the event  $T$  were appended to the vector of quantities whose realm we have identified, the realm matrix for the full vector would be composed of two side-by-side copies of the realm we have already identified. The final row of this concatenated matrix would contain fifteen 0's followed by fifteen 1's. This would denote that no matter which of the fifteen columns of the

realm is the one that corresponds to the actual value of  $(G_F, G_M, G_C)^T$ , the test result  $T$  might be equal to either 0 or 1. This merely recognizes the possibility of false positive and false negative test results.

Suppose we denote the event that the child carries the disease in question by  $D \equiv (G_C > 0)$ . We shall consider its information structure with the event  $T$ , denoting a positive result on the test for presence of the disease. Asserting conditional probabilities of such as  $P(T|D) = .8$  and  $P(T|\bar{D}) = .3$  would place two cohering linear conditions on probabilities  $P(D)$ ,  $P(T)$ , and  $P(DT)$ . Deriving from the multiplication rules, these would be  $P(DT) = .8P(D)$  and  $P(\bar{D}T) = .3P(\bar{D})$ . The latter is equivalent to the statement  $P(DT) = P(T) + .3P(D) - .3$ .

The realm matrix of possibilities for the vector of quantities  $(D, T, DT)$  contains only four columns:

$$\mathbf{R} \begin{pmatrix} D \\ T \\ DT \end{pmatrix} = \begin{pmatrix} 0 & 0 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{pmatrix}.$$

The convex hull of these column vectors is displayed as the boldly outlined tetrahedron in Figure 4, and contains all coherent probability assertions for this unknown vector of events.

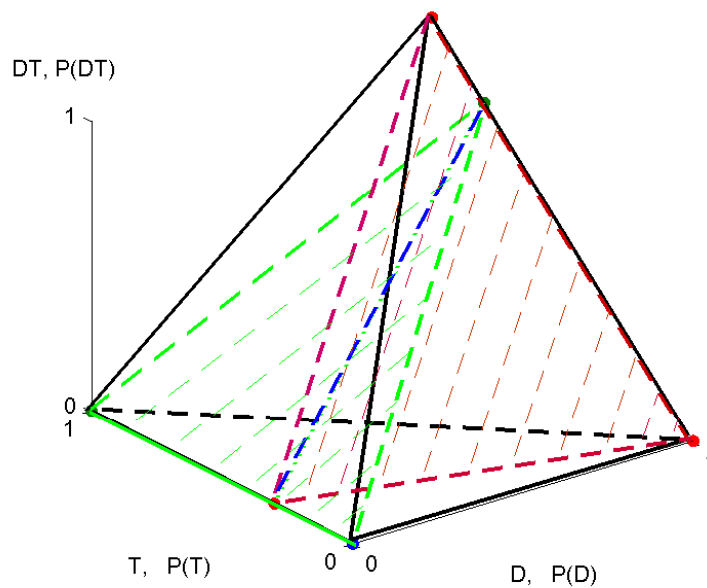


Figure 4: The convex tetrahedron contains all coherent probability vectors for the events  $D$  (the child carries the dominant gene),  $T$  (the test result is positive), and the product of these two events,  $DT$  (the conjunction of  $D$  and  $T$ ). Points on the green plane contain all such vectors cohering with the assertion  $P(T|D) = .8$ ; points on the reddish plane contain all vectors cohering with the assertion  $P(T|\bar{D}) = .3$ . The dashed blue line connecting the points  $(0, .3, 0)$  and  $(1, .8, .8)$  is the intersection of these planes, identifying all probability vectors that cohere with both of these assertions.

However, the two asserted conditional probabilities  $P(T|D) = .8$  and  $P(T|\bar{D}) = .3$  specify the two linear relations among the cohering probabilities  $P(D)$ ,  $P(T)$ , and  $P(DT)$ , which we noted above. These linear relations are represented in Figure 4 by the green and red lined triangular planes as they intersect the hull. Thus, any vector of probabilities  $P(D, T, DT)$  that coheres with *both* of these conditional probability assertions must lie on the intersection of these two planes, the line segment connecting the points  $(0, .3, 0)$  and  $(1, .8, .8)$ . A more detailed presentation of this type of geometrical analysis can be found in the text of Lad (1996, Chapter 3).

The substantive point to be appreciated here is that the concept of cause is completely irrelevant to either the motivation for the conditional probabilities asserted in the problem or to their technical algebraic/geometrical consequences.  $P(T|D)$  and  $P(T|\bar{D})$  represent only someone's (or the scientific community's, "our") assessment of the information content of a positive and a negative test conducted on a carrier and on a non-carrier of the gene in question. The very notion of a "direction" in a DAG such as shown in Figure 1 appears completely arbitrary, both in respect to the relation of the child's genetic condition with the test result, and also with respect to the parents' and the child's genotypes. Conditional probabilities of the reverse form, such as  $P(D|T)$  and  $P(G_F = x|G_C = z)$ , are embedded into any probability assessment of the problem, even if it is supposed to be representable by the DAG proposed in Figure 1. With the limited extent of probability specification we have addressed in this problem, the conditional probability  $P(D|T)$  may lie anywhere within the interval  $[0, 1]$ ,

according to the linear bound on the the probability vector  $(P(D), P(T), P(DT))$  that we found to govern the coherent implications of the assertions  $P(T|D) = .8$  and  $P(T|\bar{D}) = .3$ .

## 4 Concluding remarks

A joint probability mass function for a vector of  $N$  quantities can be factored into the product of conditional mass functions in  $N!$  different ways. Each of these factorisations can be represented by a graph. This much is agreed by everyone. Causal network theorists attribute a preeminent character to the shortest graph among all these possibilities, and ascribe “causal” properties to the relations that are exhibited at some nodes. They then proclaim various types of (conditional) independence relations to be required among quantities that appear around these nodes, both among the ancestors of nodal quantities and among their progeny.

I regard the attribution of the shortest graph with special unobservable causal properties, and the declaration of (conditional) independence properties among certain configurations of these graphs to be arbitrary and misleading. I hope to have displayed here an example of how the substantive probabilistic content of the type of problems they consider can be treated coherently without any reference at all to the meaningless assertion of cause.

The operational subjective construction of probability specifies a linear programming structure as appropriate to resolve computationally the coherent implications of *any* array of probability and conditional probability assertions for any other assertions of interests. The basis for the specification derives from de Finetti’s fundamental theorem of prevision. The limited structures of coherent assessment that adhere to all specifications merited in a DAG representation can be handled in a straightforward way by this computational programme. The causal direction arrows are irrelevant to this procedure. Probabilistic restrictions on inferential conclusions must be motivated by the real setup of the problem that is being assessed, rather than by arbitrary “rules of causation”.

It is true that many applied problems would imply very large computations for the FTP procedures if they are set up in a naive and ham-fisted way. Nonetheless, independence assertions of the severity that are proposed by causal DAG structures cannot be motivated merely by the desire to get out a numerical result. Whenever (conditional) independencies *are* appropriate, suitable linear programming routines can take advantage of the speed of computation they would naturally allow. There are several ways to deal with computational prescriptions of operational subjective statistical analysis. There have been major advances in the computational practicality of large problems using software such as GAMS, which are worth your investigation. An application to the diagnosis of asbestosis via x-rays assessed by three radiologists appears in the article of Capotorti et al. (2007). “Ballpark” computations can be achieved in the manner of full Bayesian analysis using complete distributions motivated by relevant theory specific to applied problems. An example appears in Lad and Brabyn (1993). Finally, computational flexibility can be achieved in subjective Bayesian analysis by approximate linear procedures such as those exposed by Goldstein and Wooff (2007). But that would take us to still another topic.

Many thanks to the ISBrA chapter of ISBA for your invitation to present these ideas to you. I hope they will stimulate serious discussion.

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## Eventos

- **Statistics2013 - The International Year of Statistics**  
([www.statistics2013.org](http://www.statistics2013.org))

Como dito no número anterior, o ano de 2013 foi escolhido como o Ano Internacional da Estatística, uma celebração mundial em reconhecimento das contribuições da estatística. Através de um esforço conjunto de diversas organizações mundiais, o *Statistics2013* pretende promover a importância da estatística para a comunidade científica, estudantes, empresas, governo, política, mídia e o público em geral.

Os objetivos do *Statistics2013* incluem a sensibilização do público para o poder e o impacto das estatísticas sobre todos os aspectos da sociedade; fortalecer a estatística como uma profissão, especialmente entre os jovens; e promover a criatividade e o desenvolvimento das áreas de probabilidade e estatística. Um vídeo de divulgação foi criado pelo *SAS Institute*, retratando as muitas maneiras que a estatística afeta nossas vidas.

Muitos eventos estão programados ao redor do mundo e podem ser encontrados na seção *Activities* do site do *Statistics2013*. Não é possível citar todos esses eventos e apenas uma amostra dessas atividades são apresentadas ao longo dessa seção.

- **29<sup>th</sup> European Meeting of Statisticians**, Budapeste – Hungria, 20 a 25 de julho de 2013.  
([ems2013.eu/](http://ems2013.eu/))

O *European Meeting of Statisticians* é a maior e mais prestigiada reunião de estatísticos na Europa. Além de propiciar um ambiente para a troca de ideias entre estatísticos e probabilistas europeus, nessa edição a organização está se esforçando para

que pesquisadores da Índia, China, Sudeste Asiático, Oriente Médio, América do Norte e América Latina participem em maior número que o habitual. Há também uma ambição dos organizadores de que as disciplinas de probabilidade e estatística sejam igualmente representadas no evento.

O ano de 2013 marca o aniversário de 300 anos das publicações póstumas de Jacob Bernoulli, “*Ars Conjectandi*” e o Paradoxo de São Petersburgo. Além disso, ocorre o 250<sup>o</sup> aniversário da publicação póstuma do ensaio de Thomas Bayes sobre o problema da probabilidade inversa pela *Royal Society*. A *Bernoulli Society* vê o EMS2013 como a ocasião perfeita para celebrar esses acontecimentos.

- **58<sup>a</sup> RBRAS e 15<sup>o</sup> SEAGRO**, Campina Grande – Brasil, 20 a 26 de julho de 2013.  
([www.rbras.org.br/rbras58/](http://www.rbras.org.br/rbras58/))

A 58<sup>a</sup> Reunião Anual da Região Brasileira da Sociedade Internacional de Biometria (RBras) e o 15<sup>o</sup> Simpósio de Estatística Aplicada à Experimentação Agronômica (SEAGRO) serão realizados na cidade de Campina Grande, Estado da Paraíba, durante os dias 22 a 26 de Julho de 2013. A organização do evento está a cargo do Departamento de Estatística da Universidade Estadual da Paraíba - UEPB.

As reuniões da RBras ocorrem anualmente e, a cada dois anos, é realizada conjuntamente com o SEAGRO. A 58<sup>a</sup> Reunião Anual da RBras focará o tema “Modelagem Estatística em áreas multidisciplinares: Impactos causados pelas mudanças climáticas na Região Nordeste”. O programa científico contemplará palestrantes do Brasil e do Exterior, minicursos, tutoriais, sessões temáticas, comunicações e pôsteres. Tradicionalmente, duas outras sessões ocorrerão no evento: a Sessão da Associação Brasileira de Estatística (ABE) e a Sessão

EMBRAPA. A participação da Embrapa no evento é de fundamental importância, pelo fato da interação com a instituição promover o contato dos estatísticos com a extensa base de dados da empresa permitindo uma discussão rica com possibilidade de aprimoramento de metodologias, com reflexos positivos para pesquisa agrônoma brasileira, em especial no Nordeste. A Embrapa é líder em pesquisa no tema agricultura tropical no mundo, tendo grande responsabilidade frente à sociedade. Assim, a participação da Embrapa é oportuna para se estabelecerem parcerias com as universidades, instituições de pesquisas atraírem professores, estudantes de graduação e pós-graduação para formação de equipes multidisciplinares.

- **SPA 2013 - 36<sup>th</sup> Stochastic Processes and Applications**, Boulder – EUA, 29 de julho a 02 de agosto de 2013. ([math.colorado.edu/spa2013/](http://math.colorado.edu/spa2013/))

SPA é uma conferência internacional anual, organizada pela Sociedade Bernoulli de Estatística Matemática e Probabilidade, co-patrocinado pela IMS.

Esse ano, a ISBA está endossando uma sessão em inferência em processos estocásticos, organizada por Gareth Roberts (*University of Warwick*, Reino Unido). Além disso, a ISBA patrocinará uma sessão, com Sergio Bacallado (*Stanford University*, EUA), Peter Orbanz (*Columbia University*, EUA) e Matteo Ruggiero (*University de Torino*, Itália) como palestrantes.

- **XV Escola de Séries Temporais e Econometria**, Teresópolis – Brasil, 11 a 14 de agosto de 2013. ([www.este2013.dme.ufrj.br](http://www.este2013.dme.ufrj.br))

Escola de Séries Temporais e Econometria é realizada a cada dois anos, promovido pela Associação Brasileira de Estatística (ABE) e pela Sociedade Brasileira de Econometria (SBE). A organização desta edição do evento está sob responsabilidade do Departamento de Métodos Estatísticos da Universidade Federal do Rio de Janeiro (UFRJ), com apoio do Departamento de Estatística da Universidade Federal Fluminense (UFF).

O evento contribui para o desenvolvimento de séries temporais e econometria no Brasil, integrando pesquisadores de todas as áreas de séries temporais e econometria de diversas instituições, estudantes de pós-graduação de áreas correlatas, profissionais de empresas públicas e privadas e também estudantes de graduação de universidades públicas e privadas.

- **4<sup>th</sup> ESOBE - European Seminar on Bayesian Econometrics**, Oslo –

Noruega, 22 a 23 de agosto de 2013.

([www.norges-bank.no/en/about/conferences/2013-esobe/](http://www.norges-bank.no/en/about/conferences/2013-esobe/))

Organizado pelo Norges Bank, em colaboração com o ESOBE, e apoiada pela Seção de Economia, Finanças e Negócios (EFaB) da ISBA, esse evento pretende ser um fórum de discussão sobre pesquisas recentes em uma vasta gama de tópicos de econometria sob a abordagem bayesiana.

O programa científico inclui palestras proferidas pelo professor Christopher Sims (*Princeton University*, EUA, ganhador do Prêmio Nobel de Economia em 2011) e pelo professor Tilmann Gneiting (*University of Heidelberg*, Alemanha), além de uma sessão especial sobre “problemas e desafios em macroeconomia estrutural” com o Professor Frank Schorfheide (*University of Pennsylvania*, EUA).

- **59<sup>th</sup> WSC - World Statistics Congress**, Hong Kong – China, 25 a 30 de agosto de 2013. ([www.isi2013.hk/en/](http://www.isi2013.hk/en/))

Organizado pelo *International Statistics Institute* (ISI), a 59<sup>th</sup> WSC fornece uma plataforma para a comunidade estatística internacional compartilhar os mais recentes conhecimentos em estatística. O programa científico inclui uma ampla gama de tópicos, facilitando intercâmbios profissionais e compartilhamento entre os especialistas e profissionais em várias áreas da estatística. Uma série de sessões serão organizadas em um “dia temático” na WSC, onde o tema “Juventude” será abordado a partir de várias perspectivas da estatística.

Como um encontro satélite da WSC, ocorrerá o *ISI Young Statisticians Meeting* (YSI 2013), nos dias 23 e 24 de agosto. A YSI dará a oportunidade para os jovens estatísticos apresentarem seus trabalhos em um ambiente mais compacto e informal, proporcionando-lhes um fórum onde podem construir laços científicos com líderes em suas respectivas áreas. Maiores informações podem ser encontradas em [www.saasweb.hku.hk/conference/ysi2013/](http://www.saasweb.hku.hk/conference/ysi2013/)

- **ICNAAM 2013 - 11<sup>th</sup> International Conference of Numerical Analysis and Applied Mathematics**, Rhodes – Grécia, 21 a 27 de setembro de 2013. ([www.icnaam.org](http://www.icnaam.org))

O objetivo ICNAAM 2013 é reunir os principais cientistas da comunidade internacional na área de matemática numérica e aplicada e atrair trabalhos de pesquisa originais de alta qualidade.

Os tópicos abordados no evento incluem quase todas as áreas da análise numérica e matemática aplicada e computacional. Em destaque, está a sessão “*Highlights in Copula Modeling*”, organizada pela professora Verónica Andrea González-López da Unicamp.

Os trabalhos podem ser submetidos até o dia 20 de Julho e, se aceitos, serão publicados no AIP (*American Institute of Physics*) Conference Proceedings.

- **AS 2013 - 10<sup>th</sup> Applied Statistics**, Bled – Eslovênia, 22 a 25 de setembro de 2013. ([conferences.nib.si/AS2013](http://conferences.nib.si/AS2013))

O principal objetivo da conferência *Applied Statistics 2013* é proporcionar uma oportunidade para que pesquisadores de estatísticas e outros profissionais de diversas áreas relacionadas à estatística se reúnam, apresentem suas pesquisas e aprendam uns com os outros. Um programa de quatro dias consiste de apresentações de palestrantes convidados, seções de diversos temas, e com um workshop.

Os artigos completos podem ser enviados para publicação na *Advances in Methodology and Statistics*, uma revista da Sociedade de Estatística da Eslovênia.

- **XLI Coloquio Argentino de Estadística**, Mendoza – Argentina, 15 a 18 de outubro de 2013. ([www.xlicoloquiodeestadistica.com/](http://www.xlicoloquiodeestadistica.com/))

Este ano, o *Coloquio Argentino de Estadística* será realizado na Faculdade de Economia da *Universidad Nacional de Cuyo*, na cidade de Mendoza. Este evento pretende envolver expoentes estatísticas nacionais e internacionais, como Maria Dolores Ugarte (*Universidad Pública de Navarra*, Espanha).

A submissão de resumos estendidos para apresentação oral pode ser feita até dia 31 de julho e os resumos para apresentação de posters podem ser enviados até dia 31 de agosto.

- **IV ESAMP - Escola de Amostragem e Metodologia de Pesquisa**, Brasília – Brasil, 05 a 08 de novembro de 2013. ([www.xlicoloquiodeestadistica.com/](http://www.xlicoloquiodeestadistica.com/))

A IV ESAMP tem como principal objetivo oferecer uma oportunidade para congregarmos estatísticos, pesquisadores e profissionais de pesquisa social das universidades e de diversos órgãos produtores de informação visando discutir suas experiências à luz dos mais recentes desenvolvimentos metodológicos em planejamento amostral e análise de dados de levantamentos amostrais.

Como na edição anterior, o evento contará com cursos curtos, conferências, sessões temáticas e apresentações de trabalhos em sessões orais e pôster. A realização é do Departamento de Estatística da UnB e o evento conta com o apoio da ABE.

A submissão de trabalhos pode ser realizada até o dia 12 de agosto.

- **O-Bayes 2013: Celebrating 250 Years of Bayes**, Durham – EUA, 15 a 19 de dezembro de 2013. ([bayesian.org/sections/OB/obayes-2013-celebrating-250-years-bayes](http://bayesian.org/sections/OB/obayes-2013-celebrating-250-years-bayes))

Esta *O-Bayes* é uma celebração aos 250 anos da publicação póstuma do artigo de Thomas Bayes introduzindo seu famoso teorema e quase 200 anos de aniversário de Laplace.

Além disso, a décima edição do encontro marca uma transição; doravante o *O-Bayes* será o encontro bi-anual oficial da Seção Objetiva da ISBA.

É possível submeter posters e não há um deadline oficial. Contudo, trabalhos enviados tardiamente podem não entrar no livro de resumos.

- **EFaB@Bayes 250**, Durham – EUA, 15 a 17 de dezembro de 2013. ([bayesian.org/sections/EFaB/efab-bayes-250-workshop](http://bayesian.org/sections/EFaB/efab-bayes-250-workshop))

Esta é a primeira reunião da nova seção ISBA em Economia, Finanças e Negócios (EFaB).

Esta reunião inaugural inclui tutoriais ministrados por importantes nomes nestas áreas, palestras em sessões científicas abrangendo uma vasta gama de tópicos de pesquisa e aplicações, uma sessão especial para novos pesquisadores, apresentações de pôsteres e muito mais. Premiações para estudantes e novos pesquisadores, incluindo a *EFaB@Bayes250 BEST* e *IBM Awards*, serão anunciadas no banquete do *Bayes 250 Day*.

O prazo para a submissão de trabalhos é dia 15 de setembro.

- **Bayes 250 Day**, Durham – EUA, 17 de dezembro de 2013. ([bayesian.org/meetings/Bayes250](http://bayesian.org/meetings/Bayes250))

A ISBA anuncia uma celebração especial do 250<sup>o</sup> aniversário da publicação (23 de dezembro de 1763) do artigo *An Essay towards solving a Problem in the Doctrine of Chances* de Thomas Bayes, que será realizada na *Duke University*, EUA, em conjunto com o *O-Bayes 13* e o *EFaB@Bayes250*.

Os palestrantes convidados são importantes contribuidores para a literatura bayesiana: Stephen Fienberg (*Carnegie-Mellon University*, EUA), Michael Jordan (*University of California, Berkeley*, EUA), Christopher Sims (*Princeton University*, EUA), Adrian Smith (*University of London*, Reino Unido) e Stephen Stigler (*University of Chicago*, EUA).

Haverá um banquete à noite, com um discurso de Sharon Bertsch McGrayne, conhecida jornalista



e escritora que contribuiu com esse número do boletim.

- **2013 ICSA International Conference**, Hong Kong, 20 a 23 de dezembro de 2013.

([www.math.hkbu.edu.hk/ICSA2013/](http://www.math.hkbu.edu.hk/ICSA2013/))

A 9ª Conferência Internacional trienal da Associação Internacional de Estatística Chinesa (ICSA), será realizada na *Hong Kong Baptist University* no período de 20 a 23 de dezembro. O evento é co-patrocinado pela *American Statistical Association* (ASA) e do *Institute of Mathematical Statistics* (IMS). O comitê organizador é co-presidido pelo Jiqian Fang (*Sun Yat-Sen University at Guangzhou*, China), Ji Zhu (*University of Michigan*, EUA) e Lixing Zhu (*Hong Kong Baptist University*, China).

Os seis palestrantes principais serão Raymond Carroll (*Texas A&M University*, EUA), Ching-Shui Cheng (*University of California, Berkeley and Academia Sinica*, EUA), Hengjian Cui (*Capital Normal University*, China), Peter Hall (*Melbourne University*, Austrália), Tze Leung Lai (*Stanford University*, EUA), Howell Tong (*London School of Economics*, Reino Unido). Haverá cerca de 60 sessões técnicas e os tópicos incluem a estatística bayesiana, bioestatística, ensaios clínicos, biologia computacional, dados de grande dimensão, probabilidade, estatística espacial, ensino de estatística, teoria estatística e estatística em economia e finanças.

Trabalhos podem ser submetidos até o dia 31 de agosto.

- **MCMSki IV**, Chamonix Mont-Blanc – França, 06 a 08 de Janeiro de 2014.

([www.pages.drexel.edu/~mw125/mcmski/](http://www.pages.drexel.edu/~mw125/mcmski/))

A quarta edição do MCMSki será realizado em Chamonix Mont-Blanc, França, em janeiro de

2014. Como nos eventos anteriores, a realização é uma parceria entre o *Institute of Mathematical Statistics* (IMS) e a ISBA, e será a primeira reunião oficial da recém-criada seção BayesComp da ISBA. Vai concentrar-se em todos os aspectos teóricos e metodológicos do MCMC, incluindo áreas afins como Monte Carlo sequencial, computação bayesiana aproximada (ABC) e Monte Carlo Hamiltoniano. Em contraste com as reuniões anteriores, vai mesclar o evento principal com o workshop satélite Adap'ski, por ter sessões paralelas sobre os diferentes temas.

- **2014 American Statistical Association Conference on Statistical Practice**, Tampa – EUA, 20 a 22 de Fevereiro de 2014.

([www.amstat.org/meetings/csp/2014/](http://www.amstat.org/meetings/csp/2014/))

*Statistical Practice 2014* pretende reunir centenas de profissionais de estatística, incluindo analistas de dados, pesquisadores e cientistas, que se dedicam à aplicação da estatística para resolver problemas do mundo real em seu dia a dia. A conferência será uma oportunidade para aprender sobre as mais recentes metodologias e melhores práticas de planejamento, análise, programação e consultoria estatística.

A submissão de resumos para a apresentação de posters pode ser feita de 15 a 28 de agosto.

- **ISBA 2014 - Twelfth World Meeting of ISBA**, Cancun – México, 14 a 18 de Julho de 2014.

([bayesian.org/content/twelfth-world-meeting-isba-isba2014](http://bayesian.org/content/twelfth-world-meeting-isba-isba2014))

O 12º encontro mundial da ISBA, em 2014, deverá ocorrer em Cancun, no México. A data provisória é de 14 a 18 de julho. Novas informações devem ser disponibilizadas em breve no site da ISBA.

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#### Diretoria da ISBrA:

PRESIDENTE: *Adriano Polpo* (DEs – UFSCar)  
 SECRETÁRIO: *Francisco Louzada Neto* (ICMC – USP)  
 TESOUREIRA: *Laura Ramos Rifo* (IMECC – Unicamp)  
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