

indirectly by observing the remnants of the physical processes that underlie its existence; for example, the low value of the cosmological constant today could be such a hint. The problem here is that a multiverse proposal cannot in general be disproved this way, because if all possibilities exist somewhere in the multiverse, as some claim, then it can explain any observations, whatever they are. For example, no observations of anisotropy in the cosmic background radiation can disprove the multiverse hypothesis because all possible anisotropies will be generated in the different expanding universe domains; you just have to live in the right one.

The particular multiverse version proposed by Susskind, however, has the great virtue of being testable in one respect. It is supposed to have started out by quantum tunnelling, resulting in a spatially homogenous and isotropic universe with negative spatial curvature, and hence with a total density parameter $\Omega_0 < 1$. The best observationally determined value for this parameter, taking all the data into account, is $\Omega_0 = 1.02 \pm 0.02$. Taken at face value, this seems to contradict the proposed theory. But given the statistical uncertainties, the observations do not definitively exclude $\Omega_0 < 1$, so the theory survives; nevertheless, the observed value should be taken seriously in this era of 'precision cosmology'. These data are not discussed in the book — a symptom of some present-day cosmology, where faith in theory tends to trump evidence. Presumably the hope is that this observational result will go away as more evidence is collected.

The Cosmic Landscape is extremely well written, provides an excellent non-technical overview of the relevant physics, and tackles important questions in a lively way. However, it confuses the event horizon in the expanding universe with particle and visual horizons. In addition, like many multiverse writings, it uses the concept of infinity with gay abandon, when there is good reason — as pointed out by mathematician David Hilbert — to claim that it is not a good physical concept. The book also tries to justify the multiverse idea in terms of the 'many worlds' interpretation of quantum theory — an unproven and totally profligate viewpoint that many find difficult to take seriously.

As a philosophical proposal, the multiverse idea is interesting and has considerable merit. The challenge facing cosmologists now is how to put on a sound basis the attempts to push science beyond the boundary where verification is possible — and what label to attach to the resultant theories. Physicists indulging in this kind of speculation sometimes denigrate philosophers of science, but they themselves do not yet have rigorous criteria to offer for proof of physical existence. This is what is needed to make this area solid science, rather than speculation. Until then, the multiverse situation seems to fit St Paul's description: "Faith is the substance of things hoped for, the

evidence of things not seen." In this case, it is faith that enormous extrapolations from tested physics are correct; hope that correct hints as to the way things really are have been identified from all the possibilities, and that the present marginal evidence to the contrary will go

away. This book gives a great overview of this important terrain, as seen from an enthusiast's viewpoint. ■

George Ellis is in the Department of Mathematics, University of Cape Town, Cape Town 7701, South Africa.

Pet project

The Dog and Its Genome

edited by Elaine A. Ostrander, Urs Giger & Kerstin Lindblad-Toh

Cold Spring Harbor Laboratory Press: 2005. 584 pp. \$135, £80

Stephen J. O'Brien

Genome technology has found its way into the living room with the completion of the whole-genome sequence of the domestic dog *Canis familiaris*, from a female boxer called Tasha. Finished just a year after its initiation in 2003, the remarkably complete sequence (representing an estimated 99% of the dog's 2.4 billion base pairs) achieves 7.5-fold coverage of the genome and is a major advance over the 1.5-fold sequence of a poodle published by Celera in 2003. The dog is now a front-line model for the discovery of disease genes, for gene annotation, and for probing the evolutionary roots of our mammalian origins. *The Dog and Its Genome*, edited by Elaine Ostrander, Urs Giger and Kerstin Lindblad-Toh, celebrates the completion of the dog sequence with 26 chapters on the genomic biology of man's best friend.

The book should appeal to dog fanciers, to genome biologists who wonder about the sequence's applications, and to students of comparative genomics. It presents well written and concise discussions of the history of dog breeds — there are generally estimated to be between 350 and 1,000, of which the American Kennel Club recognizes about 150 that do not exchange genes. As many as 20 breeds were developed by 1750, increasing to 76 by 1905. Yet the domestication of dogs can be traced back 14,000 years on the evidence of archaeological remains, maybe even 40,000 years based on molecular comparisons with wolves. Clearly, dogs are the oldest domesticated species, as detailed in two of the book's chapters, and the phylogenetic ancestry of dog breeds is described in three chapters.

Years from now, as dog genomics matures, this volume will be remembered as the starting point, with vivid pieces on the vast phenotypic variation described for dogs. The latest interpretation of dog genome status is presented for experts and aficionados alike. The remarkable history of inbreeding has led to a mosaic genome of alternating homozygous and heterozygous/polymorphic segments specific for each breed; these are particularly useful for linkage disequilibrium-based association mapping of complex or multifactorial traits.



NHGR/MIT

Boxer tricks: Tasha's genome will help researchers to understand human genetic diseases.

And dogs certainly have complex traits, notably the vast morphologic variation found in dog breeds as disparate as the chihuahua and the great dane. Dogs also have hard-wired behavioural acumen that allow them to herd livestock, locate missing persons and even sniff out human cancers at early stages. And of course they are loving companions like no other animals.

Generations of veterinary clinicians have identified nearly 500 human hereditary disease homologues in dogs, nearly all breed-specific; the 50 reviewed here have a confirmed genetic basis. Several have been treated successfully with futuristic gene-therapy protocols that should whet the appetite of the medical community. The book describes a cancer registry that documents the incidence and pathologies of a dozen neoplasms that account for 23% of deaths in the 65 million pet dogs in the United States. The challenge now will be to use the genome to detail the genetic bases of behaviours, morphological breed distinctiveness and the disposition of breed-specific cancers.

Researchers already have 'bibles' that define gene-based phenotypes suitable for interrogation by mouse, rat, fruitfly and human genetics. *The Dog and Its Genome* does the same for the canine genomics community. It should be consumed by researchers and their students quickly before forthcoming advances render it dated on their bookshelves. ■

Stephen J. O'Brien is in the Laboratory of Genomic Diversity, National Cancer Institute, Frederick, Maryland 21702-1201, USA.