verb 'entanglement' has two meanings, both leading to paradoxical situations which were recognized way back by Einstein, Podolsky and Rosen in 1935, also known (according to the author 'affectionately') as the EPR paradox. At this point the author asks the question 'how do we know that entangled states exist at all?' He proceeds to demonstrate that in the helium atom the two electrons, obey Pauli's exclusion principle, that anti-symmetrizes the multi-electron wave function, which in turn implies entanglement. This property is of course obeyed by Fermions. At this point the author becomes eloquent and states that

> 'in lay man term, Fermions hate being like the other guys, are individualistic; if there is a Fermion nearby that does something and we happen to be an identical Fermion, we will do our best to be different, dress differently, drive a different car, look the other way and preferably get out of the neighborhood as soon as possible. On the other hand Bosons love to be together and to be alike; 'I am having what she is having'. If a Boson is driving on a freeway, a whole pack of Bosons soon will be driving in the same direction, right next to each other – this is how super fluidity works: cats are Fermions and dogs are Bosons; beautiful, eloquent.

The author examines in detail the question 'Are the qubits really entangled' and after detailed discussion of non-locality and separate-ability criterion, comes to the conclusion that to entangle two qubits we must have a non-trivial rank two coupling between them. Such a coupling is indeed provided in NMR as the J-coupling. Non-unitary evolution giving rise to depolarization or decoherence is discussed in detail. The colourful story of the Schrödinger's cat, whether 'dead' or 'alive' is explained in a manner that takes the 'magic' out of it.

Chapter 6 deals with controlled-NOT gate, which is the heart of most quantum computing. The author points out that the controlled-NOT gate, sometimes called the 'measurement' gate, since it can be used to measure a qubit while looking at the other, is only true in classical digital computing. In quantum systems it does not allow us to carry out non-demolition measurement. Furthermore, the controlled-NOT creates entanglement if the control qubit is in coherent superposition state (eq. (6.15)). Later, the author describes general bi-qubit unitary gates. Three qubit gates and the Deutsch gate lead to the Toffoli gate, all of which are discussed in great detail. Experimental demonstration of controlled-NOT operations is discussed with reference to linear Paul trap of ions (Cirac–Zoller gate) using laser cooling, Doppler cooling, and superconducting controlled-NOT gate by the Japanese group and Dutch group.

In the final chapter, use of the controlled-NOT gate in quantum computations is described. First the Deutsch oracle is discussed in great detail and its experimental implementation using ion trap is described. Deutsch–Jozsa oracle is also discussed in great details. The later part of the chapter in which the author defends 'NMR quantum computing', is most enjoyable (to me). The author systematically defends NMR quantum computing as 'quantum', even though it uses a classical apparatus. The nuclear spins individually behave as quantum objects and even their collective behaviour is quantum in nature. They can be placed in coherent superposition state. The coherent superposition state in NMR (the free induction decay) is long-lived, and can even be 'controlled' and allowed to dephase slowly using error correction routines. The Hadamard gate in NMR is just a 90° pulse and can be selectively applied to one, two, any or all qubits. The controlled-NOT gate uses refocusing pulses for controlling the number of qubits participating in the Hamiltonian evolution and each gate can be selectively applied. Several algorithms such as the Deutsch–Jozsa, Grover's search and Shor's prime factorization algorithms have been demonstrated by NMR, and by implication the author admits that NMR quantum computing has demonstrated maximum progress.

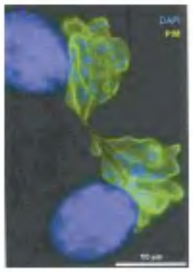
In conclusion, this is an excellent book. However, in an attempt to demystify the 'magic' from quantum computations, it creates its own web of arguments which are tedious and will need a whole semester, to work through its many equations. It is an enlightening book to read, but let me warn you, not an easy one to read.

ANIL KUMAR

Department of Physics and
NMR Research Centre,
Indian Institute of Science,
Bangalore 560 012, India
e-mail: anilnmr@physics.iisc.ernet.in

Annual Review of Microbiology, 2008. Susan Gottesman and Caroline S. Harwood (eds). Annual Reviews, 4139 El Camino Way, P.O. Box 10139, Palo Alto, CA 94303-0139, USA. Vol. 62. 491 pp. Price not mentioned.

This volume covers 23 diverse topics, representing a broad spectrum of themes ranging from basic aspects (RNA polymerase elongation factors) to population microbiology (population structure of *Toxoplasma gondii).* Among these, the one that attracted me at the outset was 'The Fortunate Professor', the prefatory chapter by Stanley Falkow (one of the editors). He begins like a best-selling novelist. He mentions, 'Well, I guess they wanted to invite me before it is too late', alluding to the fact that he was diagnosed with a bone marrow disease. His personal reminiscences have a lot for everyone and the scholarly style of writing is a refreshing reading.



Falkow's thoughts about biotechnology are: 'I have always thought that biotechnology was the direct result of the research funding philosophy of 1950–1980, which was to encourage individual creativity and to invest in the best people no matter what their precise area of scientific expertise might be'. The first chapter on intracellular pathogens sets the tone for newer concepts from various authors in the other chapters. Arturo Casadeval states that 'classifying organisms as intracellular and extracellular may be ultimately a futile exercise fraught with error and misconception'. The article by Mark Achtman on genetically monomorphic pathogens reviews an exciting new concept, which clearly shows that monomorphic pathogens have reached the limit of genome reduction, and hence the current strains arose from a minimal genome of their ancestor. The existence of clinical isolates of monomorphic pathogens argues for setting up high-throughput sequencing for SNP discovery in human pathogens, including *Mycobacterium tuberculosis*, which is also

monomorphic. In reality, comparative genome sequencing could be called the post-proteomic era. Kenneth Keiler brings up-to-date the emerging area of *trans*-translation. He points out that this bacteria-specific phenomenon is crucial when the gene expression programme changes as the cells respond to stress, switch carbon sources, differentiate or initiate pathogenesis. Jan-Willem Veening *et al.* review an exciting field of another bacteria-centred phenomenon, namely bet-hedging strategy as an epigenetic mechanism to improve fitness. A review of the halorespiration-dependent Dehalococcoides that survive by anaerobic reductive dehalogenation of polychlorinated biphenyls is an illustrative example of how microbes could salvage our pollution problems. The last review on the four apicomplexans, viz. Toxoplasma, Plasmodium, Cryptosporidium and Theileria, shows how the host machinery is effectively utilized by successful intracellular pathogens to evade host defence. There are other equally exciting reviews and this volume is a treasurehouse for a microbiologist as well as the general researcher. Indeed, 'The Fortunate Professor' must be a compulsory reading for all researchers, young and old, as well as students aspiring to become microbiologists.

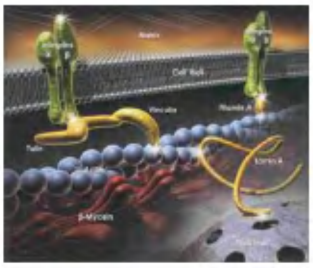
K. DHARMALINGAM

Department of Genetic Engineering,
Madurai Kamaraj University,
Madurai 625 021, India
e-mail: kdharmalingam@vsnl.com

Annual Review of Genomics and Human Genetics, 2008. Aravinda Chakravarti and Eric Green (eds). Annual Reviews, 4139 El Camino Way, P.O. Box 10139, Palo Alto, CA 94303-0139, USA. Vol. 9. 446 pp. Price not mentioned.

This volume of the *Annual Review of Genomics and Human Genetics*, edited by Chakravarti and Green, is a treasure house of 21 articles contributed by 53 authors. The editors have done a commendable job of putting together reviews on contemporary topics. Since the editorial note is missing, it is difficult to assess whether the order of the articles has any thematic basis and therefore, we have reviewed them under broader areas of (i) genome organization, function and analysis, (ii) disease genetics and genomics, (iii) functional genomics, (iv) genomic information and future of medicine and (v) legal, ethical and policy issues.

The volume starts with an informative and illustrative overview of human telomere structure and its biology, focusing more on sub-telomere structure, a core expertise of the author. However, to make it more relevant, the author could have devoted a subsection on telomere biology and diseases. The sixth article describes how sequencing of avian genomes and its global analysis provide new insights into dosage compensation in the ZZ/ZW system, which is different from the XX/XY systems. The next article provides a plethora of intimidating mathematical equations which any researcher involved in linkage disequilibrium-based association studies would have to be aware about and at the same time reiterating that genomic biology is not the domain of only biologists. In the next article, Kelley and Swanson introduce the readers to the methods of identification of regions and genes that are under positive selection through analysis of genomic variations across different human populations. The authors, through examples of FOXP2 (related to cognition) and LCT (lactase persistence) genes, show how genomic signatures 'relate to post agricultural selective pressures' and reflect older events unique to human lineage after the human chimpanzee split. This article on positive selection is timely, given the enormous amount of population variation data available in the public domain (http://www.ncbi.nlm.nih.gov/projects/SNP/; www.hapmap.org), including those from India (www.igvdb.res.in). The article provides a direction for applicability of variation data to understand population migrations, biological selections, etc.



A jump to chapter 12 provides another facet to the opportunities and challenges of the analysis of genome sequence variations for inferring phylogenetic relationships between species. This is especially pertinent as more and more genomes are getting sequenced and newer methods of faster and cost-effective whole-genome sequencing technologies (lucidly described in article 20) are being made available. Article 11 gives a comprehensive account of mechanisms of genomic imprinting across diverse species ranging from plants to mammals, expounding on the theme that genome-wide imprinting is more common than previously envisaged and can now be addressed through genomic methods like CHiP-Seq and model systems like zebra fish, *Drosophila* and *Caenorhabditis elegans*, where imprinting does not occur naturally.

Covering the theme of 'Disease genetics and genomics', a few articles have highlighted the involvement of molecules like aminoacyl-tRNA synthetase, multi subunit complexes like cohesin and organelles like lysosomes and cell types like chondrocytes, osteoblasts and osteoclasts in syndromic diseases. Article 5, one of the best written articles in this edition, covers extensively the diseases caused by mutations in aminoacyl-tRNA synthetase, both in the cytoplasm and mitochondria. It also highlights that despite their ubiquitous expression and critical role in protein synthesis, the effects of mutations in these genes are mostly confined to neurological phenotypes such as peripheral neuropathies, encephalopathy and ataxia. Article 16 illustrates how mutation in the components of the cohesin ring complex that holds together the sister chromatids during mitosis and meiosis can lead to developmental anomalies like Cornelia de Lange syndrome, Roberts-SC phocomelia, etc. The authors highlight that the involvement of cohesin in long-range regulation of gene expression and chromatin remodeling are likely the more critical mechanisms of developmental control. Article 19 deals with clinical and molecular genetic aspects of disorders of lysosome-related organelles (LRO) like melanosome, lamellar bodies, MHC Class II compartment, ruffled border, etc. The authors list the involvement of 30 different genes of different protein complexes in human or animal LRO disorders. They have elaborated how new experimental tools like *in vitro* expression and transport assays, gene silencing, fluorescent imaging and whole genome sequencing have been instrumental in defining molecular and cellular events that regulate LRO biogenesis and trafficking. These insights provide clues for therapeutic interventions for many LRO-associated disorders. Article 14 gives a