

BOOK REVIEW

Genomics – what's up doc?

Genomic Technologies: Present and Future

DJ Galas and SJ McCormack

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Reviewed by HM Wain

Genomics is an expanding field encompassing both large-scale, high-throughput laboratory technologies and hard core, number crunching computer programmes to enable us to extract data and interpret a variety of genomes. This book aims to provide examples from both sides of the equation, with genuine practical advice on laboratory techniques and details of the computational methods that can be used for data analysis. However, it is difficult to decide at whom this book is targeted, although my guess would be the ever-moving post-doc who is to embark on yet another new area of research!

This book covers many areas in a variety of detail, including transgenic technology, chips, mass spectrometry and SNPs, and abstracts of each chapter can be found at the website: <http://www.horizonpress.com/hsp/abs/absfggt.html>. Genomics is a truly fascinating field, although the first chapter somehow does not quite capture the real excitement that is present. However, as with any book that is composed of differently authored chapters, it gains considerably by input from some really excellent scientific writers. Lisa Stubbs' chapter on 'Genome Comparison Techniques' is a prime example of well-written and enlightening science. Describing some of her own work and others', she reviews both the tools and the lessons learned from their application to mammalian genomic sequence. Particularly useful are the descriptions and examples of Pipmaker and VISTA for multispecies comparisons. Typically, her conclusions give a view of the future, which I feel encompasses the reality of genomics and how the scientific mind works, as they are full of questions, fantastic!

The chapter on 'DNA sequence analysis and annotation', currently one of the most interesting areas for

genomics researchers, describes in detail the Genome Channel, one of a number of resources that can be used. Unfortunately, Ensembl, the UCSC Genome Browser and NCBI's browser, while mentioned, are not described in any detail, which I feel is an unfortunate omission.

I found the final chapter by Yanai *et al* the most absorbing: 'Beyond sequence similarity, or sequence analysis in the age of the genome'. Here, part of the future of genomics is presented with details of what further functional insight we may gain from cross-species comparisons. The system of Clusters of Orthologous Groups (COG) is described and the patterns generated are considered for their potential to identify function. An approach to phylogenetic trees is also shown and how this may identify patterns and subsequently predict function using profiling. There is also much emphasis placed on 'location, location, location' and the functional information that can be derived from neighbouring genes. For example, the co-occurrence of a methyl transferase gene with any restriction enzyme gene has enabled scientists to identify new and highly divergent restriction enzyme genes by their co-localisation with the highly conserved motif of the methyl transferase gene. The uses of gene fusion and expression pattern similarity are also discussed as methods of linking genes and identifying function. While looking towards the future, they mention methods of functional analysis by the identification of co-occurrence in text sources, and I think this '*in libro*' approach may well prove to be an insight of significance.

Each chapter in this book is well referenced, and from that point alone it is a worthwhile investment. Unfortunately, this book is somewhat spoiled by poor copy-editing, which does nothing but infuriate the reader. However, in general, the basic structure is a useful mix of sound practical advice, costing strategies, and the advantages and disadvantages of the technologies described.

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