

# Editorial

I would like to welcome you to Volume 4, Issue 1 of *Human Genomics* and announce several changes to the *journal*: it will now be bi-monthly rather than quarterly, several new members have joined our Editorial Board and we have introduced a new section — ‘Genome Databases’.

The reason why we have decided to proceed with six issues per year instead of the four that we had in Volume 3 is because of an increase in the number of submissions, as well as in the time and efforts of the members of the Editorial Board, which have been invaluable.

We would like to welcome Richard G.H. Cotton (Genomic Disorders Research Centre, Howard Florey Institute; Human Variome Project, Australia) and Takashi Gojobori (National Institute of Genetics, Centre for Information Biology; DNA Data Bank of Japan National Institute of Genetics, Japan) to our Editorial Board. In addition, we have Tzu Lip Phang (Division of Pulmonary Sciences and Critical Care Medicine, University of Colorado, Denver, CO, USA) as a Software Review Editor and Panagiotis A. Tsonis (Center for Tissue Regeneration and Engineering, University of Dayton, Dayton, OH, USA) as a Book Review Editor.

Starting with this issue, we have a new section that will include descriptions and/or reviews of Genome Databases; the first paper of this new feature is the description of the Cytochrome P450 Homepage, by David Nelson. This issue also includes an original research paper describing a regression-based approach to simultaneously use families and individuals combined to established association between a genetic marker and quantitative or binary trait. Also in this issue is a review of the use of pathway information in molecular epidemiology; Software Review Editor, Mike Weale, comments on how we can keep up to date in the rapidly changing world of genomic software; there is a review of Joram Piatigorsky’s book *Gene Sharing* and, finally, in the Genome Review section, Brocker and colleagues explore the evolutionary divergence and functions of the *ADAM* and *ADAMTS* gene families.

*Vasilis Vasiliou*  
Editor

*Human Genomics*  
University of Colorado, Denver, CO, USA