Editorial

I would like to welcome you to Volume 3, Issue 3 of *Human Genomics*. As the journal has progressed over the course of this Volume, the efforts and time of the members of the Editorial Board have been invaluable and become ever stronger. I would like to welcome two new members, Elspeth Bruford (Project Coordinator, Human Gene Nomenclature Committee, European Bioinformatics Institute) and Michel Tibayrenc (Directeur de Recherche Classe Excepionnelle IRD [Institut de Recherche pour le Développement]).

In this issue of *Human Genomics*, a number of topics are covered, including the existence of *ALDH2*2* in the Indian population, novel prediction methods for transcription factor binding sites, molecular technologies and bioinformatic tools, as well as *Hox* gene expression.

Published in this issue is a very interesting study by Vaswani *et al.*, exploring genes involved in alcohol metabolism that may be linked with alcoholism in the Indian population. Ethanol is metabolised to acetaldehyde mainly by alcohol dehydrogenase enzymes, and acetaldehyde is then metabolised to acetic acid by aldehyde dehydrogenases (ALDH). The ALDH2 gene *product* is a mitochondrial protein responsible for acetaldehyde clearance. The *ALDH2*2* allele (E487K) protects against alcoholism and is a determinant of alcohol avoidance in some East Asian populations. This is the first report of the existence of *ALDH2*2* in the Indian population, and of a high frequency of *ALDH2*2/*2* in Indian alcoholics.

Wang *et al.* have developed a novel prediction method that employs genomic features related to the presence of regulatory elements to enable more accurate and efficient prediction of transcription factor binding sites (TFBSs). In their study, they used the transcription factor upstream stimulatory factor 1 (USF1) to evaluate the performance of this novel TFBS prediction method because of its known genetic association with coronary artery disease and the recent availability of USF1 chromatin immunoprecipitation microarray (ChIP-chip) results. This method can be also used for other transcription factors involved in human disease studies to help further our understanding of the biology of complex disease.

An increased number of (TG/CA) repeats, especially in the first intron, have been suggestively associated with the regulation of the transcription of several cancer- and disease-related genes, including the genes encoding the epidermal growth factor receptor (*EGFR*), hydroxysteroid (11-beta) dehydrogenase 2 (*HSD11B2*) and interferon-gamma (*IFNG*). Zhang *et al.* have performed a genome-wide search to address the question of whether these dinucleotide repeats represent a novel class of universal regulators of gene expression. Their analysis, based on the expression profiles of these genes in the HapMap CEU samples, revealed no evidence for a significant association between these repeats and gene expression.

Recent molecular technologies, combined with bioinformatics tools, are currently used to improve the sensitivity and reliability of microbial community analysis. Such tools and techniques range from those that attempt to understand a microbial community from their length heterogeneity profiles to those that help to identify the strains and species of a random sampling of the microbes in a given sample. Doud and colleagues review technologies using the microbial communities present in the lungs of cystic fibrosis patients as a paradigm.

Pharmacogenetics could serve as the basis for a personalised antidepressant treatment capable of maximizing the probability of a good response and minimizing side effects. Drago *et al.*, in a review of pharmacogenetic perspectives of antidepressant drugs, report that this goal may not be achievable at the moment.

One of the most important issues of the clustered *Hox* gene expression is its collinearity with the

location of the genes on the chromosome. These *Hox* genes (ie *HoxD13–HoxD9*) are located adjacent to each other and they are expressed sequentially during development. Papageorgiou, in his letter to the Editor, describes a theoretical approach to explain this phenomenon by the use of physical charges.

Protein interactions play critical roles in many biological processes, and identification of such interactions is crucial in understanding protein function, elucidating signal transduction networks and in designing drug studies. In the Software Review section, Lehne and Schlitt have retrieved protein–protein interactions from six major databases (BioGRID, MINT, BIND, DIP, IntAct and HPRD), and integrated and compared the results. They found that with respect to human protein–protein interaction data, HPRD seems to be the most comprehensive. To obtain a complete dataset, however, interactions from all six databases have to be combined.

Finally, in the Gene Annotation section, Vasiliou and colleagues review the ABC transporter (ABC) superfamily that encodes membrane-bound transporters. There are 49 human ABC transporter genes and 21 pseudogenes.

Vasilis Vasiliou
Editor of Human Genomics
University of Colorado Denver