

Editor's Introduction to This Issue

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This issue contains diverse research topics in genomics and bioinformatics. Although the information about genetic variations has increased, we still have a limited understanding about the control mechanisms of how the different tissues and cells within an individual have tissue or cell type-specific gene expression. Regarding this issue, Drs. Shrutii Sarda and Sridhar Hannenhalli, University of Maryland, review the biological implications of the epigenome and the impact of NGS technology on epigenomics research. Drs. Semi Kim and Jung Weon Lee review the epithelial-mesenchymal transition, one of the important mechanisms for understanding the invasion and metastasis of cancer, by focusing on TMPRSS4 and TM4SF5. Dr. Quang Vinh Nguyen's group, University of Western Sydney, reports an interesting and useful tool to support interactive visualization, with which we can extract knowledge from complex genetic and clinical data. This tool supports patient-to-patient analysis from an overview of the patient population

in the similarity space to detailed views of genes. Both Dr. Byeong-Chul Kang's group, Insilicogen, Inc., and Dr. Byungwook Lee's group, Korean BioInformation Center, report genetic variation-based population genetics studies. The Insilicogen group reports a semantic model for ethnic disparity-associated SNPs using HapMap data, and the KOBIC group reports ethnic variant SNPs and copy number polymorphisms in Asians.

To get better accessibility, we changed *Genomics & Informatics* to an e-Journal. At this time, three outstanding scientists from Canada, France, and Egypt have joined as new editorial board members. From this issue, 50 editorial board members from 6 countries across the world will lead this journal. *Genomics & Informatics* is already available in PubMed Central and PubMed. Based on these efforts together, we expect broader international visibility of *Genomics & Informatics*.

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