

Editor's Introduction to This Issue

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This is a special issue, consisting over 10 selected dissertations that were awarded in 3 genome analysis competitions (KOGO Young Scientist Best Paper Award, KNIH KARE Data Analysis Award, and KOBIC Bioinformatics Software Award), hosted by KOGO (Korea Genome Organization) in 2014. A dissertation (In-Pyo Baek *et al.*) on developing software that defines and visualizes phenotype-related single-nucleotide variants (SNVs) among whole SNVs through next-generation sequencing (NGS) won the grand prize for the KOBIC award, and the KNIH KARE award was given to the elucidation of epigenetic interactions of genes regulated by non-coding elements in complex diseases by Min Kyung Sung *et al.* The other 8 consist of dissertations regarding GAWS, genomewide classification of miRNA, and short-read phasing for constructing haplotypes in certain genomic loci that are associated with BMI. In addition, there are 4 review papers on diverse genome research issues. Dr. Feng Zhang's group of Fudan University reviewed the genomic architecture, synthesis mechanism,

and biological roles of copy number variants. Dr. Hyun-Seok Park's group of Ewha Womans University reviewed the design of hidden Markov models and their application in solving various computational problems in epigenetics. Drs. Seon-Hee Yim and Yeun-Jun Chung reviewed current issues in direct-to consumer genetic testing. Dr. Perumal Elumalai reviewed the chemo-preventive potential of nimbolide for cancer treatment. Several genetic association studies in hyperuricemia, maturity-onset diabetes, BMI, and insulin levels will be interesting for readers. In silico characterization of a drug target candidate enzyme in legionellosis, rifampicin resistance mechanisms in tuberculosis treatment, and a study of phytochemicals for the treatment of type 1 diabetes will be useful information for researchers in this field.

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