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Seiya Imoto is currently an Associate Professor of Human Genome Center, Institute of Medical Science, University of Tokyo. He received BS, MS, and Ph.D. in Mathematics from Kyushu University in 1996, 1998 and 2001, respectively. His current research interests cover Bayesian analysis of high-dimensional heterogeneous data, DNA microarray gene expression data analysis, network analysis for life sciences, data assimilation for pathway simulation model construction and computational drug target discovery.