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## Editorial

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**Biographical notes:** Timothy B. Patrick, PhD is Chair of the Department of Health Informatics and Administration, College of Health Sciences, University of Wisconsin-Milwaukee. His research focuses on ontology and interoperability of information.

Hamid Alinejad-Rokny is working at UNSW, Australia. He is the author/co-author of more than 55 publications in technical journals and conferences. He served on the program committees of several national and international conferences. He is Editor-in-Chief at JBML, Deputy Editor-in-Chief at *International Journal of Software Engineering and Computing* and he is editorial board member at *IJSEI*, *IJFIPM*, *IJSCIP*, *IJCSCS*, *IJCDS*, *IJCNT*. His research interests are in the areas of data mining, bioinformatics and artificial intelligence and biological computing.

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This special section addresses three key computational problems in bioinformatics.

There are three articles included in this special section. The first article, ‘Enzyme classification using reactive motifs’, addresses the need for a generalisation method to make reactive motifs more effective representations of proteins in a functional similarity set. The authors demonstrate that “...a fuzzy concept lattice (FCL) may provide an efficient representation of both single-value and multi-value biological background knowledge and an efficient computational support for reactive motif generalisation”.

The second article, ‘Inference of domain-domain interactions by matrix factorisation and domain-level features’, focuses on the problem of “...identifying interacting domains among proteins to elucidate hidden functions for protein-protein interactions”. The authors show that false positive predictions of domain-domain interactions are reduced by use of a “...link prediction approach [based on a] leaning model including low rank matrices as latent features in combination with biological features and topological features of the domain network”.

The third article, ‘Accurate single individual haplotyping based on HuRef dataset using HapSAT algorithm’, addresses the NP-Hard Haplotype Assembly problem of “...reconstructing two haplotypes for an individual using a set of aligned SNP fragments from the two haplotypes (related to a particular chromosome).... An optimised reimplementation of HapSAT algorithm is used to find haplotypes for HuRef dataset” and shows “...significantly superior results compared to previously proposed algorithms”.