Call for papers for a special issue of

Information Fusion

An International Journal on Multi-Sensor, Multi-Source Information Fusion

An Elsevier Publication

On

“NATURAL COMPUTING IN BIOINFORMATICS”

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Bioinformatics is a fast growing interdisciplinary scientific area aimed at managing, analyzing and interpreting information from biological data, sequences and structures, with promising applications to Biomedicine. Often, data analysis problems in Bioinformatics concern the fusion of multisensor outputs, such as in the case of oligonucleotide microarrays or the fusion of multi-source information, when one must integrate different kinds of biological data. A very powerful approach to those tasks lies in Natural Computing, especially for its fast generation of good solutions with the desired level of precision.Natural Computing is a general term pertaining to the computing going on in Nature as well as the computing inspired by Nature. Over the past few years many Natural Computing strategies, ranging from Neural Networks, Evolutionary Computation, Fuzzy Sets, Support Vector Machines to Ant Colony Optimization, Particle Swarm Optimization, etc., have been applied successfully to the solution of complex problems. These include signal and image processing, classification, clustering, feature selection, data visualization, data mining, and information fusion.

*Manuscripts (**which should be original and not previously published or presented even in a more or less similar form under any other forum**) highlighting recent advances in the applications of Natural Computing based techniques for information fusion in Bioinformatics, from improving protein-protein interaction to pharmacogenomic systems, from clustering to data visualization and mining, are invited. It is necessary that all submissions relate their work to the overall scope of Information Fusion Journal.*

Topics appropriate for this special issue include, but are not limited to, Natural Computing applications in the following aspects of Bioinformatics:

- *Sequence homology and Phylogenetics*
- *Primary genomic sequence*
- *Protein structure prediction*
- *Folding, Docking and Drug design*
- *Gene expression analysis*
- *Sequential and structural motif discovery*
- *Gene/Metabolic pathway regulatory network*

*Manuscripts should be submitted electronically online at http://ees.elsevier.com/inffus. The corresponding author will have to create a user profile if one has not been established before at Elsevier. **Simultaneously, please also send without fail an electronic copy (PDF format preferred), to the Guest Editor(s) listed below**.*

Guest Editors

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