

## Special Issue on Soft Computing for Analysis of Biomedical Data

# CALL FOR PAPERS

Soft computing (SC) techniques can be used to tackle problems characterized by imprecision, uncertainty, and partial truth to achieve tractability and robustness at a low computational cost.

These features represent the main differences between SC and hard computing techniques and provide SC strategies with the ability to deal with ambiguous situations like imprecision and uncertainty. For this reason, SC techniques can obtain approximate solutions to problems which have no known methods to compute an exact solution. The main SC paradigms include fuzzy systems, evolutionary computation, artificial neural computing, metaheuristics, and swarm intelligence.

Those features render SC particularly suitable for analyzing medical data, which is typically characterized by imprecision and the presence of noise. Moreover, SC techniques allow easily integrating human knowledge, which can help achieve better solutions. Biomedical data may be of different nature: texts, images, signals, and so forth, which typically contain a high presence of noise.

The overall aim of this special issue is to compile the latest research and development, up-to-date issues, and challenges in the field of SC and its applications to biomedical data.

Potential topics include but are not limited to the following:

- ▶ Medical imaging, signal processing, and text analysis
- ▶ Data mining medical data and records
- ▶ Clinical expert systems
- ▶ Modelling and simulation of medical processes
- ▶ Drug description analysis
- ▶ Patient-centric care
- ▶ Rational drug design and personalized medicine
- ▶ Biomedical text/data mining and visualization
- ▶ Network biology/medicine
- ▶ Interpreting genomic or metagenomic data
- ▶ Gene expression analysis
- ▶ Discovering regulatory or expression pathways
- ▶ Modeling ecosystems or population dynamics
- ▶ Discovering genome-disease or genome-phenotype associations
- ▶ Omics data analysis and functional genomics for complex diseases
- ▶ Gene-gene interactions and gene-environment interactions for disease association
- ▶ analysis
- ▶ Protein structure prediction
- ▶ Phylogenetics
- ▶ Assembling next generation sequence data

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/cmmm/scbm/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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