

# CALL FOR PAPERS

## IEEE SIGNAL PROCESSING MAGAZINE

### Special Issue on Genomic and Proteomic Signal Processing in Biomolecular Pathways

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Since the first full draft of the human genome we have seen an explosion of genomic and proteomic exploration technologies. Massive amounts of data are available for research in molecular biology and medicine. A dedicated issue to the role of signal processing in the acquisition and analysis of this data was published in the IEEE Signal Processing Magazine earlier (Volume:24 Issue:1 Date:Jan. 2007). The rapid evolution of the field and exciting new developments mandate an update on the state-of-the-art and future challenges for signal processing in genomics and proteomics defining its role in current systems biology.

A structured engineering approach is needed to solve difficult signal processing problems in molecular and systems biology. Recent high-throughput studies probe regulatory mechanisms through gene and non-coding RNA expression (e.g. miRNA), genomic single nucleotide and gene copy number variations, DNA methylation, histone methylation and other modifications and chromatin remodeling. Microarray technologies target over one million loci across the genome. Latest second generation sequencing technology is fast producing new data (RNA-seq, CHIP-seq, DNA-seq and methyl-seq) on a whole genome scale at a single nucleotide resolution level. Sensitivity allows sequencing of the genome from a single cell (e.g. in cancer). Whole genome sequencing is approaching wide affordability. New approaches in quantitative proteomics allow establishing the amounts and post-translational modification status of proteins allowing the building of dynamic models as functions of time, species origin and internal or external perturbation. These developments create new opportunities for signal processing in genomics and proteomics.

We invite papers that use signal processing algorithms and technologies for high throughput discovery in life sciences or medicine with emphasis on regulatory aspects. Topics can include, but are not limited to:

1. Efficient high throughput whole genome microarray and sequencing data analysis
2. Cross-modal data analysis (gene expression, methylation, copy number, genotype...)
3. Multigenome sequence alignment
4. Metagenomics
5. Clustering large scale molecular data
6. Probabilistic network scaling and modeling
7. Integration of genomic and proteomic networks
8. Cross-species comparison of biological networks and pathways
9. Quantitative proteomics
10. Dynamic model building

**Submission.** Prospective authors should submit a two-page white paper to the web submission system at <http://mc.manuscriptcentral.com/spmag-ieee>.

The publication schedule is as follows:

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|----------------------------|------------------|----------------------------|---------------|
| • White paper due:         | November 1, 2010 | • Acceptance notification: | June 15, 2011 |
| • Invitation notification: | December 1, 2010 | • Final manuscript due:    | July 15, 2011 |
| • Manuscript due:          | January 31, 2011 | • Publication date:        | January, 2012 |