Research Letters in Signal Processing

Journal Menu

- Abstracting and Indexing
- Aims and Scope
- Article Processing Charges
- Articles in Press
- Author Guidelines
- Bibliographic Information
- Contact Information
- Editorial Board
- Editorial Workflow
- Reviewers Acknowledgment
- Subscription Information

Call for Proposals for
Special Issues

Research Letter

Is Subcellular Localization Informative for Modeling Protein-Protein Interaction Signal?

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Abstract

Statistical methods have been intensively applied in genomic signal processing (Dougherty et al. 2005). For budding yeast *Saccharomyces cerevisiae* with around 6000 proteins, genome-wide protein-protein-interaction (PPI) (Fromont-Racine et al. 2000, Ito et al. 2001, Newman et al. 2000, and Uetz et al. 2000 among others) and protein subcellular localization (PSL) (Huh et al. 2003) data recently became available and for the latter the presence of 4152 proteins is experimentally tested in each of the 22 subcellular compartments. Recent work shows that multiple biological sources are helpful for both PSL and PPI predictions, and this paper studies statistical feasibility of modeling PPI from PSL since PSLs may play different marginal or joint roles in the complex regulatory network. However, our results indicate that PSL may be controversial for this purpose as an independent source.