STATUS OF THE IT TRANSACTIONS
Mailing dates

Jan 1/3
Feb 1/22
Mar 2/21
Apr 3/20
May 4/24
Jun 5/23
Jul 6/19
## Sub-to-Pub data

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## Submission data

Papers submitted, January to June 2008: 484
Papers submitted, January to June 2007: 456
AE performance I (December 20, 2007)
AE performance I (December 20, 2007)

weeks to publication (ave = 50)

30-day load (ave = 2.8)
Associate Editors lineup

New entries: Franz Hlawatsch (Detection and Estimation), Rei Safavi-Naini, (Complexity and Cryptography), Michael Gastpar, (Shannon Theory/Network Info. Th.), Keith Martin, (Complexity and Cryptography), Patrick Hayden, (Quantum Information Theory), Adriaan van Wijngaarden, (Communications)
CALL FOR PAPERS: Special Issue of the IEEE Transactions on Information Theory on Molecular Biology and Neuroscience

Recently, information theory has gained significant attention in various areas of life sciences, most prominently in bioinformatics, computational molecular biology, and neurosciences. But despite the fact that information theoretic methods have successfully employed by biologists to predict the association between DNA mutations and disease, identifying protein binding sequences in nucleic acids, analyzing neural signal transmission and higher functionalities of cognitive organs, many more problems at the interface of information theory and biology remain unexplored.

In order to address such problems — including identifying the information content of shapes, complex patterns, and self-organizing networks; designing special-trained data sets for humans, and formalizing the notion of information content — new information-theoretic tools, techniques, and unified frameworks are required.

As natural sciences are becoming increasingly related to other fields and disciplines, a broader set of tools and methods must be developed. The idea of 'Information Theory' as a unified theory for understanding the interactions between the various fields of neurosciences and molecular biology has the potential to establish the field of bioinformatics and molecular biology, and these two disciplines can benefit from other fields as well.

The purpose of this special issue is to provide the reader with a broad overview of the most important problems in molecular biology and neuroscience, to foster the development of new research directions and to accelerate progress in these fields. The special issue will consist of a mixture of invited and contributed papers.

The following list represents the major advances in the area of bioinformatics and neuroscience that will be invited to provide the interested reader with comprehensive, yet highly approachable writings to the biological fields of interest. In the latter case, please invite the following issues: medicine and behavior analysis.

- Statistical and information-theoretic analysis of DNA and protein sequence DNA and protein sequence comparison, nucleotide binding, DNA sequencing, and nucleotide sequence analysis.
- Coding genetic problems in design and analysis of DNA, RNA, and DNA sequence data analysis.
- In silico transcription networks, e.g., examples of regulatory networks, and examples of regulatory network interactions and structure.
- Escherichia coli and other disease microorganisms. Chemical models for DNA, RNA, and protein interactions.
- New information-theoretic tools for analyzing complex sequences, and complex sequences and complex systems.
- Inference and model simulation problems, e.g., models of regulatory networks, and synthetic regulatory networks.
- Control and information theory in neuroscience systems.

IMPORTANT DATES
Paper proposals submission deadline: November 17, 2008
Paper submission deadline: January 2009
Completion of first round of review: April 2009
Final review and selection of papers: August 2009
Final manuscripts due to IEEE October 2009
Publication of the Special Issue: December 2009

INSTRUCTIONS FOR MANUSCRIPT SUBMISSION:
In order to ensure the highest quality of published papers, authors will be asked to submit their paper proposals, not exceeding 4 pages in length. The proposals will be reviewed by experts in the field of information theory, and only those papers deemed adequate will make it into the final review.

GUEST EDITORS (AND EDITORIAL BOARD):
- C. Albrecht, Harvard Medical School (Massachusetts Institute of Technology)
- Carolé Babot, INRIA, Université de Tours, France
- Joel F. Cohen, Max Planck Institute of Neurobiology
- Jonatan Dros, University of Illinois at Urbana-Champaign
- Helen Gaskin, University of Heidelberg
- Miroslav Ramon, Harvard Medical School
- Hyo Min Shin, University of Washington, Seattle
- Wojciech Szpankowski, Portland University

Digital Object Identifier (DOI): 10.1109/TIT.2008.928698
PAREJA vs. MANUSCRIPT CENTRAL
Feature: Reviewer search

**Pareja**

- User must enter three fields (first and last name, email). Searches the records that start exactly with those fields. Entering only the last name or part of it is not enough.
- Sometimes returns unwanted results and may insert records with erroneous email addresses.
- Visualization requires painful window scrolling in order to get to the needed record.
- Interface is not intuitive. The button “update/add reviewer” has multiple behaviors and is used to search or add reviewer.

**Manuscript Central (CL version)**

- Has a frame for reviewer search that allows better scanning of the database.
- There is a button to insert the reviewer found.
- There is a button to insert a new reviewer.
- Visualizes up to eight reviewers in a short frame (no need to scroll) without disturbing details of address and phone numbers. Everything is available at a glance.
Feature: User interface

Pareja

- Primitive, does not summarize information at different levels but always provides the maximum details available. Users have to scroll up and down in order to find the information needed.

Manuscript Central (CL version)

- Frame-based, separates information in different areas and provides different levels of detail as needed.
Feature: E-mail

Pareja

- Generates emails of limited length (the insertion of the abstract would exceed this length).
- Requires the insertion of email templates to be generated from scratch by the AE.
- **Does not store emails**

Manuscript Central (CL version)

- All emails to reviewers are stored in the system.
- Provides sophisticated handling of reminders.
- Email templates are customized on a journal-wide basis even though AE’s may modify them.
- As a result, correspondence from the journal to the authors is more systematic and professional.
Feature: Management

- The system owner can probably see everything (including reviewer names) while the EiC has limited access, cannot access AEs’ record.
- The EiC has full control on every feature of the system.