

Special Session on Computational Intelligence for Biological Feature Induction

Analysis of large biological data sets is sometimes routine, but there is often a need to select effective features for classification or analysis of biological data. These features can be as diverse as a SNP panel, motifs, or a numerical feature derived from the biological data via an algorithmic process. Many biological data sets come with natural features like QSARS in chemoinformatics or substring statistics for sequence data. In other problems, value has been demonstrated in going beyond feature selection to feature induction. *Induced features* are ones that are derived from data to meet specific needs.

This special session solicits high quality manuscripts on computational intelligence techniques for feature induction from biological data. Papers should use computational intelligence techniques to induce novel, useful features computable from biological data. This includes but is not limited to:

- Deep learning of features.
- Side Effect Machines.
- Complex string kernels, e.h. woven string kernels.
- Genetic programming based feature induction.
- Induced network motifs and graph kernels.
- Interacting ecosystem measurements that serve as features.
- Complex system for feature induction such as liquid state automata and do-what's possible systems.
- Advanced SNP selection including groups of SNPs that interact to form features.
- Representations and comparisons of representations for feature induction.
- Feature induction for chemoinformatics.
- Feature induction for diagnostics.
- Comparisons of feature induction systems.
- Comparison of the effectiveness of induced and standard features.

Manuscripts should conform to conference submission guidelines and be submitted under the special session.

Organizer Biographies

Daniel Ashlock

Professor Daniel Ashlock has a doctorate in mathematics from CalTech. He is a member of the IEEE Technical Committee on Bioinformatics and Bioengineering and serves as an associate editor for the IEEE Transactions of Evolutionary Computation and the IEEE/ACM Transactions on Bioinformatics and Computational Biology. Dr. Ashlock has twice served as the General Chair of CIBCB and has been on the organizing committee more years than not. His awards include a CIBCB Best Paper award in 2016 and a Lifetime Achievement award in 2015. Dr. Ashlock has over 250 peer reviewed publications, the majority of which are related to computational intelligence or bioinformatics. Dr. Ashlock's primary research areas are representations, bioinformatics, and games.

Wendy Ashlock

Dr. Wendy Ashlock has an AB in mathematics from the University of Chicago, an MA in mathematics from the University of Guelph, and a PhD in Computer Science from York University in Toronto. She is currently the Bioinformatics and Bioengineering Technical Chair for IEEE CIS and is Finance Chair for IEEE CIBCB 2017. She works as the Chief Data Scientist for Ashlock & McGuinness Consulting, Inc. Her research areas include: machine learning, computational genomics, and modeling.

Andrew McEachern

Andrew McEachern has a doctorate in mathematics from the University of Guelph. He is currently a post-doctoral researcher at Queen's University researching games, bioinformatics and mathematical education practices at the secondary and tertiary level. His research includes techniques for feature induction in sequence data.

Anticipated number of contributed papers

Given the number of regular CIBCB participants already contacted, four submissions seem certain and as many as ten are possible.