

TCBB Special Section on the Brazilian Symposium on Bioinformatics 2013

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THIS issue of *TCBB* contains extended versions of works that were originally presented at the *Brazilian Symposium on Bioinformatics 2013* (BSB 2013), held in Recife, Brazil, November 3-6, 2013. The Proceedings of BSB 2013 have been published by Springer Verlag, in volume 8213 of the *Lecture Notes in Bioinformatics* series (series editors: S. Istrail, P. Pevzner, and M. Waterman). Eighteen papers were presented at BSB 2013; four of these were invited for submission to a special section of *TCBB*. The invitation stipulated that the papers would have to be substantially expanded, and would undergo a new round of peer review. These four manuscripts were carefully evaluated by 11 international experts. The four papers now published are the result of this process.

Braga and Stoye study the well-known Double-cut-and-join (DCJ)-indel theoretical model of genome evolution in "Sorting Linear Genomes with Rearrangements and Indels". They present several new results concerning the computation of an evolutionary distance between two genomes under this model. Their main result is a proof that distances computed under a restricted version of the model and an unrestricted version are the same.

Hoener zu Siederdisen, Hofacker, and Stadler present a theory of algebraic operations over linear grammars in "Product Grammars for Alignment and Folding". This theory and its implementation make it possible to "multiply together" dynamic programming algorithms, a widely used technique in computational biology. The authors demonstrate that this framework provides a powerful tool for developing programs that would otherwise require a complex ad-hoc approach. As an example, they elegantly apply their framework to the problem of aligning protein sequences to DNA sequences in the presence of "editing frameshifts," a real problem observed in the mitochondria of *Physarum polycephalum*, a slime mold, which is a model organism for studying RNA editing.

RNA molecules, in contrast to DNA, can take many different three-dimensional shapes. This is one reason why we find so many different kinds of RNAs in the cell, performing varied functions. Hoksza and Svozil present the program MultiSETTER, which allows multiple alignment of RNA sequences taking into account three-dimensional structural information in "Multiple 3D RNA Structure

Superposition Using Neighbor Joining". This program is an extension of their previously-published pairwise-alignment program SETTER. The paper presents extensive experimental results, which show that MultiSETTER has accuracy as good as or in some case better than SETTER, while being substantially faster.

The BLAST program for sequence comparison is arguably the most widely used computational tool used in all science. There are two basic elements to this success: the speed with which comparisons are made and the statistics of sequence similarity scores, encapsulated in the e-value statistic. Carroll, Williams, Davis, and Spouge improve on this venerable practice by introducing the false discovery rate (FDR) statistic into BLAST and PSI-BLAST in "Improving Retrieval Efficacy of Homology Searches Using the False Discovery Rate". They show that their FDR-versions of these programs are better at separating relevant from irrelevant results, a welcome development for BLAST users.

Together, these four papers cover a wide arc of results, from the most theoretical to the very practical, and are thus an excellent showcase of the work presented at BSB 2013 and of computational biology in general. We finalize by thanking the BSB 2013 program committee members as well as the reviewers for the papers invited to this special issue for their invaluable help in the review process.

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Guest Editors



João C. Setubal received the PhD degree in computer science from the University of Washington in 1992. He is a professor of bioinformatics in the Chemistry Institute, University of São Paulo (USP), Brazil, and an adjunct faculty in the Virginia Bioinformatics Institute. He is the director of the Computational Biology and Genomics Research Center, USP and an ACM distinguished speaker.



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