SPECIAL ISSUE

BIOINFORMATICS OF DNA
Edited by L. S. Heath, H. C. Bravo, M. Caccamo, and M. Schatz

422 Building and Improving Reference Genome Assemblies
By K. Meltz Steinberg, V. A. Schneider, C. Alkan, M. J. Montague, W. C. Warren, D. M. Church, and R. K. Wilson
[INVITED PAPER] This paper reviews the problems and algorithms of assembling a complete genome from millions of short DNA sequencing reads.

436 Short Read Mapping: An Algorithmic Tour
By S. Canzar and S. L. Salzberg
[INVITED PAPER] This paper discusses the challenge of mapping short DNA reads to an existing target genome, covering the approaches and the current tools for addressing this problem.

459 Reading the Underlying Information From Massive Metagenomic Sequencing Data
By X. Zhang, S. Liu, H. Cui, and T. Chen
[INVITED PAPER] This paper addresses the computational processing of metagenomic data, describing the typical pipeline of a variety of software tools for the task and the current state of the art.

474 De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue
By V. Jamilloux, J. Daron, F. Choulet, and H. Quesneville
[INVITED PAPER] This paper introduces a computational method for annotating an important class of repetitive sequences, called transposable elements, in the wheat genome.

482 A Novel Pathway Analysis Approach Based on the Unexplained Disregulation of Genes
By S. Ansari, C. Voichita, M. Donato, R. Tagett, and S. Draghici
[INVITED PAPER] This paper describes a new computational analysis method for gene expression data that utilizes all the data effectively for identifying the dynamics of biological pathways.

496 DANUBE: Data-Driven Meta-ANalysis Using UnBiased Empirical Distributions—Applied to Biological Pathway Analysis
By T. Nguyen, C. Mitrea, R. Tagett, and S. Draghici
[INVITED PAPER] This paper proposes DANUBE, a new unbiased method of statistical meta-analysis that is applied to combine the results of multiple experiments performed for the same biological condition.

516 Linking Statistical and Ecological Theory: Hubbell’s Unified Neutral Theory of Biodiversity as a Hierarchical Dirichlet Process
By K. Harris, T. L. Parsons, U. Z. Ijaz, L. Lahti, I. Holmes, and C. Quince
[INVITED PAPER] This paper addresses the issue of a species occupying a specific ecological niche by introducing a new algorithmic model that overcomes shortcomings of the traditional neutral models.

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On the Cover: Our cover image this month captures the essence of this special issue with a DNA double helix featured against the backdrop of gene sequences.
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530 Bridging Histology and Bioinformatics—Computational Analysis of Spatially Resolved Transcriptomics
   By M. Mignardi, O. Ishaq, X. Qian, and C. Wählby
   [INVITED PAPER] This paper reviews image processing techniques for measuring gene expression in different regions of tissue samples.

542 A Parallel Algorithm for N-Way Interval Set Intersection
   By R. M. Layer and A. R. Quinlan
   [INVITED PAPER] This paper proposes a parallel algorithm for computing the intersection of multiple sets of genomic sequences.

552 Manual for Using Homomorphic Encryption for Bioinformatics
   By N. Dowlin, R. Gilad-Bachrach, K. Laine, K. Lauter, M. Naehrig, and J. Wernsing
   [INVITED PAPER] This paper provides a new homomorphic encryption algorithm and associated software for bioinformatics to enhance the security and privacy associated with computing on human genomes.