

SPECIAL ISSUE

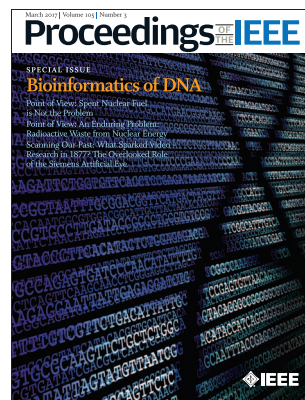
BIOINFORMATICS OF DNA

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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 By P. F. Peterson
- 415 An Enduring Problem: Radioactive Waste From Nuclear Energy**
 By M. V. Ramana
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- 568 SCANNING OUR PAST**
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 By M. Schubin
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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. Wahlby*

|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.

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