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Altri autori (Persone)	McLysaghtAoife HusonDaniel H
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Nota di contenuto	Lower Bounds for Maximum Parsimony with Gene Order Data -- Genes Order and Phylogenetic Reconstruction: Application to ?-Proteobacteria -- Maximizing Synteny Blocks to Identify Ancestral Homologs -- An Expectation-Maximization Algorithm for Analysis of Evolution of Exon-Intron Structure of Eukaryotic Genes -- Likely Scenarios of Intron Evolution -- OMA, A Comprehensive, Automated Project for the Identification of Orthologs from Complete Genome Data: Introduction and First Achievements -- The Incompatible Desiderata of Gene Cluster Properties -- The String Barcoding Problem is NP-Hard -- A Partial Solution to the C-Value Paradox -- Individual Gene Cluster Statistics in Noisy Maps -- Power Boosts for Cluster Tests -- Reversals of Fortune

-- Very Low Power to Detect Asymmetric Divergence of Duplicated Genes -- A Framework for Orthology Assignment from Gene Rearrangement Data.

Sommario/riassunto

The complexity of genome evolution poses many exciting challenges to developers of mathematical models and algorithms, who have recourse to a spectrum of algorithmic, statistical and mathematical techniques, ranging from exact, heuristic, fixed-parameter and approximation algorithms for problems based on parsimony models to Monte Carlo Markov Chain algorithms for Bayesian analysis of problems based on probabilistic models. The annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB ComparativeGenomics) is a forum on all aspects and components of this field, ranging from new quantitative discoveries about genome structure and process to theorems on the complexity of computational problems inspired by genome comparison. The informal steering committee for this meeting consists of David Sankoff, Jens Lagergren and Aoife McLysaght. This volume contains the papers presented at the 3rd RECOMB Comparative Genomics meeting, which was held in Dublin, Ireland, on September 18-20, 2005. The first two meetings of this series were held in Minneapolis, USA (2003) and Bertinoro, Italy (2004). This year, 21 papers were submitted, of which the Program Committee selected 14 for presentation at the meeting and inclusion in this proceedings. Each submission was refereed by at least three members of the Program Committee. After completion of the referees' reports, an extensive Web-based discussion took place for making decisions. The RECOMB Comparative Genomics 2005 Program Committee consisted of the following 27 members: Vineet Bafna, Anne Bergeron, Mathieu Blanchette, Avril Coghlan, Dannie Durand, Nadia El-Mabrouk, Niklas Eriksen, Aaron Halpern, Rose Hoberman, Daniel Huson, Jens Lagergren, Giuseppe Lancia, Emmanuelle Lerat, Aoife McLysaght, Istvan Miklos, Bernard Moret, Pavel Pevzner, Ben Raphael, Marie-France Sagot, David Sankoff, Cathal Seoighe, Beth Shapiro, Igor Sharakhov, Mike Steel, Jens Stoye, Glenn Tesler and Louxin Zhan. We would like to thank the Program Committee members for their dedication and hard work.