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| Record Nr. | UNISA996384940603316 |
| Autore | Eudes Morton |
| Titolo | Catholique traditions. Or A treatise of the beliefe of the Christians of Asia, Europa, and Africa, in the principall controuersies of our time [[electronic resource] ] : In fauour of the louers of the catholicke trueth, and the peace of the Church. Written in French by Th. A.I.C. and translated into English, by Lewis Owen |
| Pubbl/distr/stampa | London, : Printed by W. Stansby, for Henry Fetherstone, and are to be sold at his shoppe in Pauls Church-yard, at the signe of the Rose, 1610 |
| Descrizione fisica | [16], 96, 99-235, [3] p |
| Altri autori (Persone) | OwenLewis <1572-1633.> |
| Soggetti | Theology, Doctrinal |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Note generali | A translation of "Tradition catholique", attributed to Morton Eudes.<br>Variant: title page has: translated into English, by L.O.<br>Another variant (STC 10561) is dated 1609.<br>Reproduction of the original in the British Library. |
| Sommario/riassunto | eebo-0018 |

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| 2. | Record Nr. | UNINA9910346696203321 |
| | Autore | Russ B Altman |
| | Titolo | Biocomputing 2010 - Proceedings of the Pacific Symposium |
| | Pubbl/distr/stampa | World Scientific Publishing Co, 2009<br>[Place of publication not identified], : World Scientific Publishing Company Incorporated, 2009 |
| | ISBN | 1-282-76350-4<br>9786612763502<br>981-4295-29-9 |
| | Descrizione fisica | viii, 487 p. : ill. (some col.) |
| | Altri autori (Persone) | AltmanRuss <1961-> (Russell Biagio)<br>DunkerA. Keith <1943-> (Alan Keith)<br>HunterLawrence <1961-> |
| | Disciplina | 572.8 |
| | Soggetti | Bioinformatics<br>Genomics |
| | Lingua di pubblicazione | Inglese |
| | Formato | Materiale a stampa |
| | Livello bibliografico | Monografia |
| | Note generali | Bibliographic Level Mode of Issuance: Monograph |
| | Nota di bibliografia | Includes bibliographical references. |
| | Nota di contenuto | Computational challenges in comparative genomics. Session introduction / Bernard Moret ... [et al.]. Accurate taxonomic assignment of short pyrosequencing reads / Jose C. Clemente , Jesper Jansson, Gabriel Valiente. Benchmarking BLAST accuracy of genus/phyla classification of metagenomic reads / Steven D. Essinger, Gail L. Rosen. Guided genome halving : provably optimal solutions provide good insights into the preduplication ancestral genome of Saccharomyces cerevisiae / Haris Gavranovic, Eric Tannier. A practical algorithm for estimation of the maximum likelihood ancestral reconstruction error / Glenn Hickey, Mathieu Blanchette. Optimization methods for selecting founder populations for captive breeding of endangered species / Webb Miller ... [et al.] -- Computational studies of non-coding RNAs. Session introduction / Rolf Backofen ... [et al.]. RNA structural segmentation / Ivan Dotu ... [et al.]. RNAz 2.0 : improved noncoding RNA detection / Andreas R. Gruber ... [et al.]. Identification and classification of small RNAs in transcriptome sequence data / D. Langenberger ... [et al.]. Improvement of structure conservation index |

with centroid estimators / Yohei Okada, Kengo Sato, Yasubumi Sakakibara. Dynamic programming algorithms for RNA structure prediction with binding sites / Unyanee Poolsap, Yuki Kato, Tatsuya Akutsu. An algorithm for the energy barrier problem without pseudoknots and temporary arcs / Chris Thachuk ... [et al.] -- Dynamics of biological networks. Session introduction / Tanya Y. Berger-Wolf ... [et al.]. Local optimization for global alignment of protein interaction networks / Leonid Chindelevitch, Chung-Shou Liao, Bonnie Berger. Identification of coordinately dysregulated subnetworks in complex phenotypes / Salim A. Chowdhury, Mehmet Koyuturk. Subspace differential coexpression analysis : problem definition and a general approach / Gang Fang ... [et al.]. Estimation of protein and domain interactions in the switching motility system of Myxococcus xanthus ... [et al.]. Exploring biological network dynamics with ensembles of graph partitions / Saket Navlakha, Carl Kingsford. Geometric evolutionary dynamics of protein interaction networks / Natasa Przulj ... [et al.]. The steady states and dynamics of Urokinase-mediated plasmin activation / Lakshmi Venkatraman ... [et al.] -- Multi-resolution modeling of biological macromolecules. Session introduction / Samuel Flores ... [et al.]. Multi-resolution approach for interactively locating functionally linked ion binding sites by steering small molecules into electrostatic potential maps using a haptic device / Olivier Delalande ... [et al.]. Predicting RNA structure by multiple template homology modeling / Samuel C. Flores ... [et al.]. Constructing multi-resolution Markov State Models (MSMs) to elucidate RNA hairpin folding mechanisms / Xuhui Huang ... [et al.]. Multiscale dynamics of macromolecules using normal mode langevin / Jesus A. Izaguirre, Christopher R. Sweet, Vijay S. Pande. Insights into the intra-ring subunit order of TriC/CCT : structural and evolutionary analysis / Nir Kalisman, Michael Levitt. "Cross-graining :" Efficient multi-scale simulation via Markov state models / Peter Kasson, Vijay Pande. Toward understanding allosteric signaling mechanisms in the ATPase domain of molecular chaperones / Ying Liu, Ivet Bahar. 3D-blast : 3D protein structure alignment, comparison, and classification using spherical polar Fourier correlations / Lazaros Mavridis. David W. Ritchie. Structural prediction of protein-RNA interaction by computational docking with propensity-based statistical potentials / Laura Perez-Cano ... [et al.] -- Personal genomics. Session introduction / Can Alkan ... [et al.]. Improving the prediction of pharmacogenes using text-derived gene-drug relationships / Yael Garten, Nicholas P. Tatonetti, Russ B. Altman. Finding unique filter sets in PLATO : a precursor to efficient interaction analysis in GWAS data / Benjamin J. Grady ... [et al.]. Enabling personal genomics with an explicit test of epistasis / Casey S. Greene ... [et al.]. Loss of post-translational modification sites in disease / Shuyan Li ... [et al.]. Detecting genome-wide haplotype polymorphism by combined use of mendelian constraints and local population structure / Xin Li, Yixuan Chen, Jing Li. Sequence Feature Variant Type (SFVT) analysis of the HLA genetic association in juvenile idiopathic arthritis / Glenys Thomson ... [et al.]. Cokgen : a software for the identification of rare copy number variation from SNP microarrays / Gokhan Yavas ... [et al.] -- Reverse engineering and synthesis of biomolecular systems. Session introduction / Gil Alterovitz ... [et al.]. Co-design in synthetic biology : a system-level analysis of the development of an environmental sensing device / David A. Ball ... [et al.]. Critical analysis of transcriptional and post-transcriptional regulatory networks in multiple myeloma / Marta Biasiolo ... [et al.]. A computational model of gene expression in an inducible synthetic circuit / Francesca Ceroni, Simone Furini, Silvio Cavalcanti. Retrovirus

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| | HTLV-1 gene circuit : a potential oscillator for eukaryotes / Alberto Corradin ... [et al.]. Emulsion based selection of T7 promoters of varying activity / Eric A. Davidson ... [et al.]. Clustering context-specific gene regulatory networks / Archana Ramesh ... [et al.]. Writing and compiling code into biochemistry / Adam Shea ... [et al.]. Synthesis of pharmacokinetic pathways through knowledge acquisition and automated reasoning / Luis Tari ... [et al.] -- Workshops. In silico biology / Richard Goldstein ... [et al.]. Genomic standards consortium workshop : Metagenomics, Metadata and Metaanalysis (M3) / Peter Sterk ... [et al.]. Extraction of genotype-phenotype-drug relationships from text : from entity recognition to bioinformatics application / Adrien Coulet ... [et al.]. |
| Sommario/riassunto | The Pacific Symposium on Biocomputing (PSB) 2010 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in problems of biological significance. Presentations are rigorously peer reviewed and are published in an archival proceedings volume. PSB 2010 will be held on January 4 - 8, 2010 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2010 will bring together top researchers from the US, Asia Pacific, and around the world to exchange research results and address pertinent issues in all aspects of computational biology. It is a forum for the presentation of work in databases, algorithms, interfaces, visualization, modeling, and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology. The PSB has been designed to be responsive to the need for critical mass in sub-disciplines within biocomputing. For that reason, it is the only meeting whose sessions are defined dynamically each year in response to specific proposals. PSB sessions are organized by leaders of research in biocomputing's "hot topics". In this way, the meeting provides an early forum for serious examination of emerging methods and approaches in this rapidly changing field. |