

12th Asia-Pacific Bioinformatics Conference 2014

(APBC 2014)

**Shanghai, China
17-19 January 2014**

ISBN: 978-1-62993-835-6

Printed from e-media with permission by:

Curran Associates, Inc.
57 Morehouse Lane
Red Hook, NY 12571



Some format issues inherent in the e-media version may also appear in this print version.

All papers Copyright© (2014) by their respective authors; licensee BioMed Central. These are Open Access articles distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Printed by Curran Associates, Inc. (2014)

For further information, please contact BioMed Central Ltd at the address below. The collection is available online at <http://www.biomedcentral.com/1471-2105/11?issue=S1>

BioMed Central Ltd
236 Gray's Inn Road
London WC1X 8HB
UK

Phone: +44 (0)20 3192 2000
Fax: +44 (0)20 3192 2010

Email: info@biomedcentral.com
Web: www.biomedcentral.com

Additional copies of this publication are available from:

Curran Associates, Inc.
57 Morehouse Lane
Red Hook, NY 12571 USA
Phone: 845-758-0400
Fax: 845-758-2634
Email: curran@proceedings.com
Web: www.proceedings.com

TABLE OF CONTENTS

AUTOMATIC CLASSIFICATION OF PROTEIN STRUCTURES USING LOW-DIMENSIONAL STRUCTURE SPACE MAPPINGS.....	1
<i>Daniel Asarnow, Rahul Singh</i>	
ON THE SELECTION OF APPROPRIATE DISTANCES FOR GENE EXPRESSION DATA CLUSTERING.....	20
<i>Pablo A. Jaskowiak, Ricardo J.G.B. Campello, Ivan G. Costa</i>	
USING DISTANCES BETWEEN TOP-N-GRAM AND RESIDUE PAIRS FOR PROTEIN REMOTE HOMOLOGY DETECTION.....	37
<i>Bin Liu, Jinghao Xu, Quan Zou, Ruifeng Xu, Xiaolong Wang, Qingcai Chen</i>	
EXTRACTING RATE CHANGES IN TRANSCRIPTIONAL REGULATION FROM MEDLINE ABSTRACTS.....	47
<i>Wenting Liu, Kui Miao, Guangxia Li, Kuiyu Chang, Jie Zheng, Jagath C. Rajapakse</i>	
TOWARDS INTEGRATIVE GENE FUNCTIONAL SIMILARITY MEASUREMENT.....	59
<i>Jiajie Peng, Yadong Wang, Jin Chen</i>	
PREDICTION OF HETEROTRIMERIC PROTEIN COMPLEXES BY TWO-PHASE LEARNING USING NEIGHBORING KERNELS.....	69
<i>Peiyang Ruan, Morihiro Hayashida, Osamu Maruyama, Tatsuya Akutsu</i>	
PROTEIN FOLDING IN HP MODEL ON HEXAGONAL LATTICES WITH DIAGONALS.....	75
<i>Dipan Lal Shaw, A.S.M. Shohidull Islam, M. Sohel Rahman, Masud Hasan</i>	
COLLECTIVE PREDICTION OF PROTEIN FUNCTIONS FROM PROTEIN-PROTEIN INTERACTION NETWORKS.....	88
<i>Qingyao Wu, Yunming Ye, Michael K Ng, Shen-Shyang Ho, Ruichao Shi</i>	
TRANSCRIPTIONAL REGULATION PREDICTION OF ANTIESTROGEN RESISTANCE IN BREAST CANCER BASED ON RNA POLYMERASE II BINDING DATA.....	98
<i>Denan Zhang, Guohua Wang, Yadong Wang</i>	
AN IMPROVED CHIP-SEQ PEAK DETECTION SYSTEM FOR SIMULTANEOUSLY IDENTIFYING POST-TRANSLATIONAL MODIFIED TRANSCRIPTION FACTORS BY COMBINATORIAL FUSION, USING SUMOYLATION AS AN EXAMPLE.....	116
<i>Chia-Yang Cheng, Chia-Han Chu, Hung-Wei Hsu, Fang-Rong Hsu, Chung Yi Tang, Wen-Ching Wang, Hsing-Jien Kung, Pei-Ching Chang</i>	
PROPOSING A HIGHLY ACCURATE PROTEIN STRUCTURAL CLASS PREDICTOR USING SEGMENTATION-BASED FEATURES.....	130
<i>Abdollah Dehzangi, Kuldip Paliwal, James Lyons, Alok Sharma, Abdul Sattar</i>	
STRUCTURAL INSIGHTS INTO MODE OF ACTIONS OF NOVEL NATURAL MYCOBACTERIUM PROTEIN TYROSINE PHOSPHATASE B INHIBITORS.....	143
<i>Jaspreet Kaur Dhanjal, Sonam Grover, Sudhanshu Sharma, Ajeet Kumar Singh, Abhinav Grover</i>	
TOWARDS SEQUENCE-BASED PREDICTION OF MUTATION-INDUCED STABILITY CHANGES IN UNSEEN NON-HOMOLOGOUS PROTEINS.....	152
<i>Lukas Folkman, Bela Stantic, Abdul Sattar</i>	
CLUSTER BASED PREDICTION OF PDZ-PEPTIDE INTERACTIONS.....	164
<i>Kousik Kundu, Rolf Backofen</i>	
ACCUMULATION OF CTCF-BINDING SITES DRIVES EXPRESSION DIVERGENCE BETWEEN TANDEMLY DUPLICATED GENES IN HUMANS.....	175
<i>Ben-Yang Liao, Andrew Ying-Fei Chang</i>	
SPECTRAL PROBABILITIES OF TOP-DOWN TANDEM MASS SPECTRA.....	182
<i>Xiaowen Liu, Matthew W Segar, Shuai Cheng Li, Sangtae Kim</i>	
SUPERVISED CATEGORICAL PRINCIPAL COMPONENT ANALYSIS FOR GENOME-WIDE ASSOCIATION ANALYSES.....	191
<i>Meng Lu, Hye-Seung Lee, David Hadley, Jianhua Z Huang, Xiaoning Qian</i>	
GENOME SEQUENCING OF HIGH-PENICILLIN PRODUCING INDUSTRIAL STRAIN OF PENICILLIUM CHRYSOGENUM.....	201
<i>Fu-Qiang Wang, Jun Zhong, Ying Zhao, Jingfa Xiao, Jing Liu, Meng Dai, Guizhen Zheng, Li Zhang, Jun Yu, Jiayan Wu, Baoling Duan</i>	
METACLUSTER-TA: TAXONOMIC ANNOTATION FOR METAGENOMIC DATA BASED ON ASSEMBLY-ASSISTED BINNING.....	213
<i>Yi Wang, Henry Chi Ming Leung, Siu Ming Yiu, Francis Yuk Lun Chin</i>	

APPLICATION OF MICRORNA AND MRNA EXPRESSION PROFILING ON PROGNOSTIC BIOMARKER DISCOVERY FOR HEPATOCELLULAR CARCINOMA	222
<i>Lin Wei, Baofeng Lian, Yuannv Zhang, Wei Li, Jianren Gu, Xianghuo He, Lu Xie</i>	
SEQUENCE ALIGNMENT BY PASSING MESSAGES	235
<i>Byung-Jun Yoon</i>	
INFERRING TRANSCRIPTION FACTOR COLLABORATIONS IN GENE REGULATORY NETWORKS	243
<i>Sherine Awad, Jin Chen</i>	
PRIORITIZING PROTEIN COMPLEXES IMPLICATED IN HUMAN DISEASES BY NETWORK OPTIMIZATION	253
<i>Yong Chen, Thibault Jacquemin, Shuyan Zhang, Rui Jiang</i>	
PATHWAY-GENE IDENTIFICATION FOR PANCREATIC CANCER SURVIVAL VIA DOUBLY REGULARIZED COX REGRESSION	263
<i>Haijun Gong, Tong Tong Wu, Edmund M Clarke</i>	
GENES ASSOCIATED WITH GENOTYPE-SPECIFIC DNA METHYLATION IN SQUAMOUS CELL CARCINOMA AS CANDIDATE DRUG TARGETS	272
<i>Ryoichi Kinoshita, Mitsuo Iwadate, Hideaki Umeyama, Y-H Taguchi</i>	
DETECTION OF TYPE 2 DIABETES RELATED MODULES AND GENES BASED ON EPIGENETIC NETWORKS	289
<i>Hui Liu, Tongtong Wang, Hongbo Liu, Yanjun Wei, Guofeng Zhao, Jianzhong Su, Qiong Wu, Hong Qiao, Yan Zhang</i>	
IDENTIFYING DISEASE ASSOCIATED GENES BY NETWORK PROPAGATION	305
<i>Yu Qian, Søren Besenbacher, Thomas Mailund, Mikkel Heide Schierup</i>	
ON CONTROL OF SINGLETON ATTRACTORS IN MULTIPLE BOOLEAN NETWORKS: INTEGER PROGRAMMING-BASED METHOD	312
<i>Yushan Qiu, Takeyuki Tamura, Wai-Ki Ching, Tatsuya Akutsu</i>	
MATHEMATICAL MODELING OF GATA-SWITCHING FOR REGULATING THE DIFFERENTIATION OF HEMATOPOIETIC STEM CELL	322
<i>Tianhai Tian, Kate Smith-Miles</i>	
JOINT CLUSTERING OF PROTEIN INTERACTION NETWORKS THROUGH MARKOV RANDOM WALK	334
<i>Yijie Wang, Xiaoning Qian</i>	
COMPARISON ON EXTREME PATHWAYS REVEALS NATURE OF DIFFERENT BIOLOGICAL PROCESSES	347
<i>Yanping Xi, Yue Zhao, Li Wang, Fei Wang</i>	
Author Index	