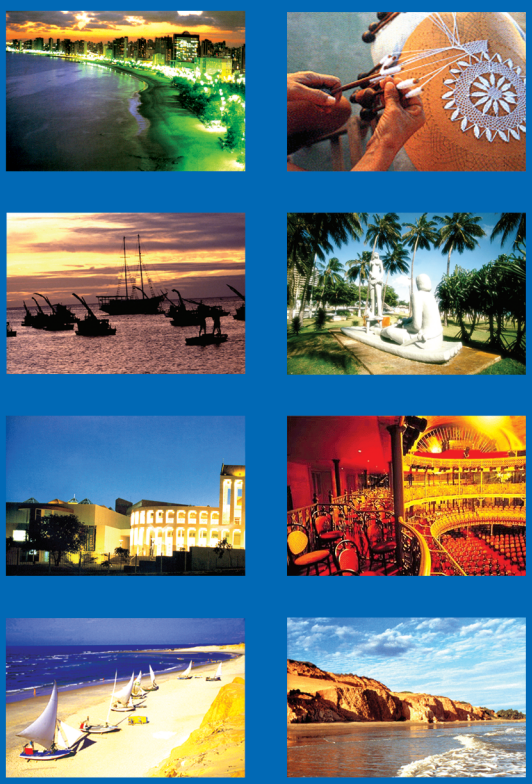
www.iscb.org/ismb2006



ISMB 2006

Intelligent Systems for Molecular Biology

and 2nd Annual AB³C Conference: X-Meeting

august 6-10, 2006

fortaleza, brazil

Program

the 14th annual meeting of the international society for computational biology

ISCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

Embrapa Agriculture Informatics

Laboratório Nacional de Computação Científica

Dear Delegate,

On behalf of the International Society for Computational Biology, I am pleased to welcome you to ISMB 2006, the fourteenth annual international conference on Intelligent Systems for Molecular Biology. The program at this year's meeting, thanks to conference chair Goran Neshich and vice chair Ana Tereza Ribeiro de Vasconcelos, and scientific program chairs Phil Bourne and Søren Brunak, is exceptionally strong including 67 papers, 24 PLoS Track presentations, over 550 posters, 40 software demonstrations, 12 tutorials and four associated satellite and SIG meetings.

Please join me in thanking the members of the scientific advisory committee, Amos Bairoch, Barry Honig, and Nobohiro Go, the program committee area chairs, and the close to 400 paper reviewers for their work in assembling an excellent program. I especially thank the members of the local organizing committee Goran Neshich, Paula Kuzer Falcão, Álvaro Seixas Neto, Gonçalo A. G. Pereira, João Carlos Setubal, João Paulo Kitajima, José Antonio Maranho, Junior Barrera, Sandro José de Souza, Glacius Oliva, Richard Charles Garrat, Diana Magalhães de Oliveira, Fernando Barroso and Sergio Verjovski-Almeida whose work has made the success of this meeting possible.

I hope you find the meeting both enjoyable and illuminating, and I urge you to express your congratulations to the organizers on a fine effort.

Sincerely,

Michael Gribskov
President, ISCB

9500 Gilman Drive, MC 0505 • La Jolla, CA 92093-0505 • USA
www.iscb.org • admin@iscb.org • +1-858-822-0852

Welcome to Brazil
Welcome to Fortaleza

On behalf of the organizing committees of ISMB 2006, together with the International Society for Computational Biology (ISCB) and the "Associação Brasileira de Bioinformatica e Biologia Computacional" (AB³C) we wish you a warm welcome to ISMB 2006, the X-meeting and to Fortaleza.

You are participating in the first ISMB conference held in a tropical country, a country belonging to the "developing world". This is an achievement of fantastic proportions for ISCB, a show of care for its global membership. AB³C, a young organization, has the honor to co-organize its annual X-meeting together with ISMB. This is truly a remarkable occasion for the scientific community and we wish to set the mark in terms of how important it is to integrate scientists from around the world in a place such as Fortaleza.

Our Program Committee took a very challenging job, to select from 404 submitted papers, 67 for oral presentation. To complement and enrich the program, ISMB 2006 includes 24 selected PLoS Track oral presentations. The Poster Session Committee approved 567 posters, covering a broad spectrum of computational biology interests and corresponding applications. In addition there will be a presentation of late breaking research as part of the Late Breaking Poster session. The Software Demo Committee has evaluated and approved 40 presentations. All of these presentations compose an excellent program, covering both the traditional and novel applications of computational biology.

This year we celebrate the participation of eight fantastic keynote speakers, three of them Nobel Laureates, setting ISMB 2006 apart from earlier conferences.

Continuing to build on an ISMB tradition of conference events including Special Interest Group meetings (SIGs), Satellite Meeting and 12 Tutorials, the Scientific Committee introduced two new sessions to the program. The New Frontiers (set as a panel discussion following the presentation by five prominent scientists) and the Latin America Bioinformatics (set in format of the AB³C X-meeting) add to the exciting conference program.

We would like to specially thank Embrapa, the Brazilian Agricultural Research Corporation, and the LNCC, National Laboratory for Scientific Computation, for hosting the organization of this Conference.

Finally, we would like to thank everyone who supported the conference; the conference delegates, our sponsors and exhibitors from around the world, and the Brazilian Science funding agencies.

We wish you all a nice stay in Fortaleza, and we hope that you enjoy as much as possible all aspects of this event. We are confident that you will enjoy your stay in Fortaleza, not only through the exciting scientific program, but also as an opportunity for creating working contacts with Latin American and Brazilian researchers. Take time to get to know the wonderful Brazilian people, their customs, their warm climate and in particular their way of entertainment.

Yours sincerely,

Dr Goran Neshich
ISMB 2006 Conference Chair

Dr. Ana Tereza Ribeiro de Vasconcelos
ISMB 2006 Vice Chair

International Society for Computational Biology (ISCB) Meeting Schedule

ISCB Business Meeting

All ISMB Conference delegates are invited to participate in the ISCB Business Meeting

Monday, August 7
12:45 p.m. - 1:45 p.m.

ISCB Business Meeting	Room E2

Committee Meetings

All ISMB Conference delegates are invited to participate in any ISCB Committee Meetings as listed below:

Monday, August 7
10:00 a.m. - 11:00 a.m.

SIG Coordinators Meeting	Room P

6:00 p.m. - 7:00 p.m.

ISCB Public-Affairs Committee Meeting	Room B6
ISCB Conferences Committee Meeting	Room P

Tuesday, August 8
6:00 p.m. - 7:00 p.m.

ISCB Publications Committee Meeting	Room B4
ISCB Affiliates & SIGs Committee Meeting	Room B6
ISCB Education Committee Meeting	Room P

Thursday, August 10
9:00 a.m. – 9:45 a.m.

Sponsor and Exhibitors Meeting	Room P

12:45 p.m. - 1:45 p.m.

ISCB Finance & Business Development Committee Meeting	Room B6

Board of Directors Meeting (Open to ISCB Board members only)

Saturday, August 5
6:00 p.m. – 10:00 p.m.

ISCB Board Meeting	Room Pedro Lazar 3, Oasis Hotel

Sunday, August 6
9:00 a.m. – 12:00 p.m.

ISCB Board Meeting	Room Pedro Lazar 3, Oasis Hotel

Conference Venue

Centro de Convenções do Ceará (Ceará Convention Center)
Av. Washington Soares, 1141
Cep 60.811-341
Fortaleza Ceará Brazil
Phone: 55-85-34883903

Registration Hours

Friday, August 4 - Thursday, August 10
Registration: Ceará Convention Center - Hall G

Friday, August 4
7:30 a.m. - 6:00 p.m.

Saturday, August 5
7:30 a.m. - 6:00 p.m.

Sunday, August 6
7:30 a.m. - 6:00 p.m.

Monday, August 7
7:30 a.m. - 7:30 p.m.

Tuesday, August 8
7:30 a.m. - 7:30 p.m.

Wednesday, August 9
7:30 a.m. - 1:30 p.m.

Thursday, August 10
7:30 a.m. - 5:00 p.m.

Delegate Shuttle Schedule

Complimentary shuttle service for ISMB delegates is available to and from the convention center from the hotels noted below. Delegates not staying at these hotels are encouraged to walk to the closest hotel (check the number at Avenida Beira Mar as a guide).

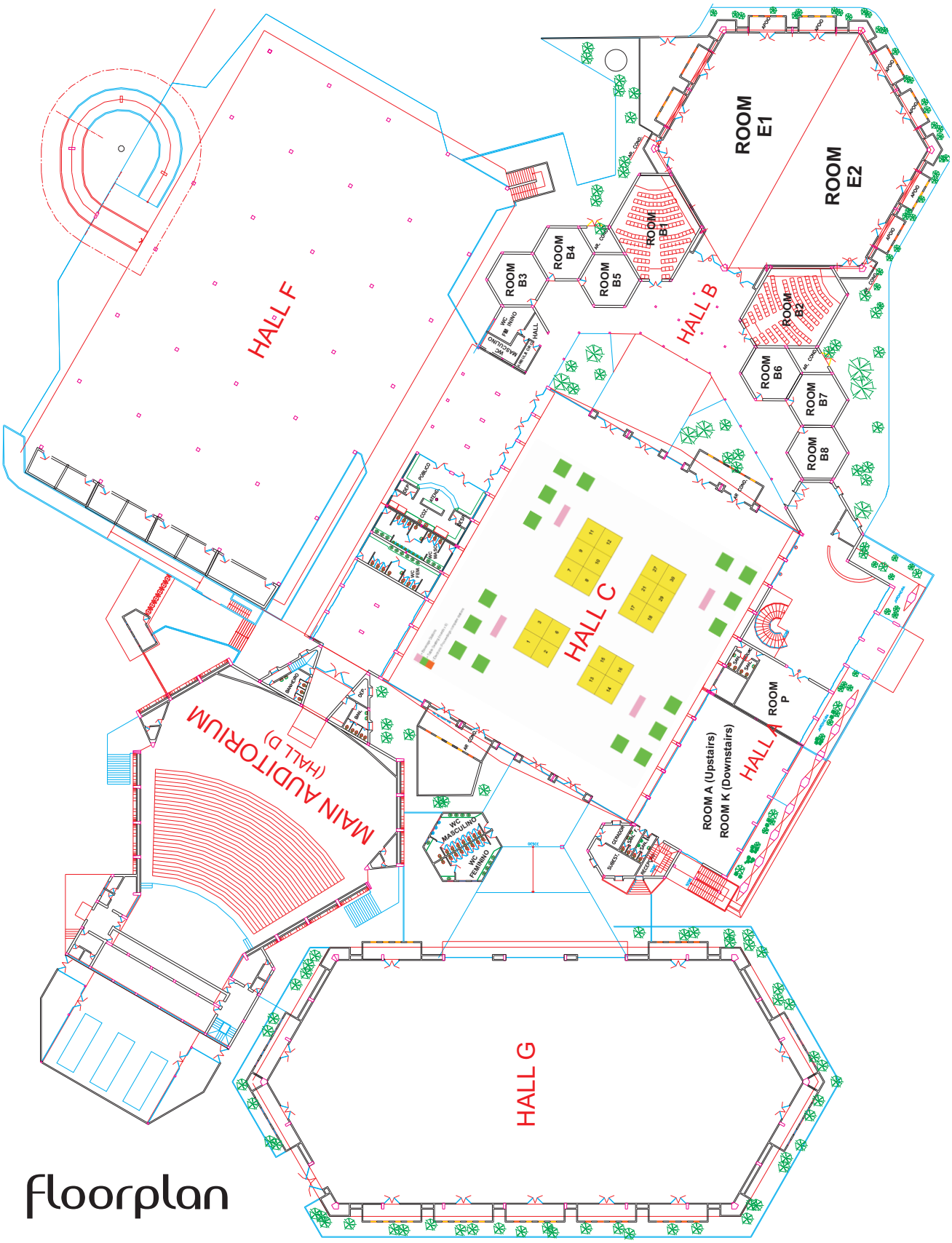
Hotel Iracema: Av. Almirante Barroso, 734
Hotel Holiday Inn: Av. Raimundo Girão, 800
Hotel Costa do Mar: Av. Raimundo Girão, 1338
Hotel Oasis: Av Beira Mar, 2500
Hotel Seara: Av. Beira Mar, 3080
Hotel Gran Marquise: Av. Beira Mar, 3980

	Depart Hotel	Depart Convention Center
Friday, August 4	7:00 a.m.	6:30 p.m.
Saturday, August 5	7:00 a.m.	6:30 p.m.
Sunday, August 6	7:00 a.m.	6:00 p.m.
Monday, August 7	7:00 a.m.	9:30 p.m.
Tuesday, August 8	7:00 a.m.	9:30 p.m.
Wednesday, August 9*	7:45 a.m.	12:30 p.m. - 1:15 p.m.
Thursday, August 10	7:45 a.m.	5:15 p.m.

***Note:** Beach Park Event Shuttles**:**

- Non-Delegates with tickets for the Beach Park event will be transported from hotels noted above at 12:00 (noon) to the convention center and then to Beach Park.
- Delegates NOT attending the Beach Park event will be transported from the convention center to hotels at 12:30 p.m.
- Delegates and guests with tickets going to Beach Park will go directly from the convention center at 12:30 p.m. Buses will return to hotels at 6:30 p.m.

general information



floorplan

	Room A (2nd Floor)	
7:00 a.m.		
7:30 a.m. - 6:00 p.m.		
9:00 a.m. - 10:30 a.m.	3Dsig Satellite Meeting	
10:30 a.m. - 11:00 a.m.		
11:00 a.m - 12:00 p.m.	3Dsig Satellite Meeting	
12:00 p.m. - 1:00 p.m.		
1:00 p.m. - 3:30 p.m.	3Dsig Satellite Meeting	
3:30 p.m. - 4:00 p.m.		
4:00 p.m. - 6:30 p.m.	3Dsig Satellite Meeting	
6:30 p.m.		

Friday (August 4)

Room B1	Room E1
Shuttles depart Hotels to Convention Center	
Registration - Hall G	
Alternative Splicing SIG	BOSC SIG
Coffee Break - Satellite & SIG meetings (available outside meeting rooms)	
Alternative Splicing SIG	BOSC SIG
Lunch - Satellite and SIG meetings (Hall F)	
Alternative Splicing SIG	BOSC SIG
Coffee Break - Satellite & SIG meetings (available outside meeting rooms)	
Alternative Splicing SIG	BOSC SIG
Shuttles depart Convention Center to Hotels	

	Room A (2nd Floor)	
7:00 a.m.		
7:30 a.m. - 6:00 p.m.		
9:00 a.m. - 10:30 a.m.	3Dsig Satellite Meeting	Alter
10:30 a.m. - 11:00 a.m.		
11:00 a.m - 12:00 p.m.	3Dsig Satellite Meeting	Alter
12:00 p.m. - 1:00 p.m.		
1:00 p.m. - 3:30 p.m.	3Dsig Satellite Meeting	Alter
3:30 p.m. - 4:00 p.m.		
4:00 p.m. - 6:30 p.m.	3Dsig Satellite Meeting	Alter
6:30 p.m.		
7:30 p.m.	3Dsig Satellit	

saturday (august 5)

Room B1	Room B2	Room E1
Shuttles depart Hotels to Convention Center		
Registration - Hall G		
lternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
Coffee Break - Satellite & SIG meetings (available outside meeting rooms)		
lternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
Lunch - Satellite and SIG meetings (Hall F)		
lternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
Coffee Break - Satellite & SIG meetings (available outside meeting rooms)		
lternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
Shuttles depart Convention Center to Hotels		
ellite Meeting - Dinner (3Dsig Delegates and ticket holders) - Oasis Hotel (Brazil Room)		

	Room A (2nd Floor)	Room B1	Room B2	Ro
7:00 a.m.				
7:30 a.m. - 6:00 p.m.				
8:30 a.m. - 10:30 a.m.	Student Council Symposium (SCS2)	Tutorial *AM2:* Genomes, Browsers and Databases: Tools For Automated Data Integration Across Multiple Genomes *Peter Schattner*	Tutorial *AM4:* Chemoinformatics *Pierre Baldi*	*AM1:* Literature Min Information R Biological *Lars J*
10:30 a.m. - 10:45 a.m.				
10:45 a.m. - 12:30 p.m.	SCS2 Continued	Tutorial *AM2* Continued	Tutorial *AM4* Continued	*AM1*
12:30 p.m. - 2:00 p.m.	Lunch for delegates a			
2:00 p.m. - 4:00 p.m.	SCS2 Continued	Tutorial *PM11:* Computational Biology Of Post-Transcriptional Gene Regulation: At The Interplay Of Genomes, Networks And Evolution *Uwe Ohler and Dirk Holste*	Tutorial *PM13:* Protein-Protein Interactions: Structure and Systems Approaches to Analyze Diverse Genomic Data *Anna Panchenko and Benjamin Shoemaker*	
4:00 p.m. - 4:15 p.m.				
4:15 p.m. - 6:00 p.m.	SCS2 Continued	Tutorial *PM11* Continued	Tutorial *PM13* Continued	
6:00 p.m. - 6:30 p.m.				

sunday (august 6)

Room B3	Room B5	Room B6	Room E1	Room E2
Shuttles depart Hotels to Convention Center				
Registration - Hall G				
Tutorial *AM1:* Biological Mining - From on Retrieval to ical Discovery *ars Juhl Jensen*	Tutorial *AM3:* Python Programming for Life Science Researchers *Sebastián Bassi*	Tutorial *AM7:* Exploring Computational Biology with a Massively Parallel High Performance Computing Environment *Kirk Jordan and Scott Emrich*	Tutorial *AM5:* Computing Biological Function: Bioinformatics Approach to the Analysis and Prediction of Protein Function *Yanay Ofran and Marco Punta*	Tutorial *AM6:* Integration and Analysis of Diverse Genomic Data *Olga Troyanskaya*
Coffee Break - Tutorials and Student Council Symposium (available outside meeting rooms)				
Tutorial *AM1* Continued	Tutorial *AM3* Continued	Tutorial *AM7* Continued	Tutorial *AM5* Continued	Tutorial *AM6* Continued
s attending Student Council Symposium, delegates attending 2 tutorials and ticket holders - Hall F				
	Tutorial *PM10:* Introduction to Computational Proteomics - Open Problems *Jacques Colinge*		Tutorial *PM8:* Bayesian Networks For Bioinformatics: An Introduction To Inference And Learning *Chris Needham and James Bradford*	Tutorial *PM9:* From Pathways Databases to Network Models *Baltazar Aguda and Andrew Goryachev*
Coffee Break - Tutorials and Student Council Symposium (available outside meeting rooms)				
	Tutorial *PM10* Continued		Tutorial *PM8* Continued	Tutorial *PM9* Continued
Shuttles depart Convention Center to Hotels				

	Main Auditorium (Hall D)	Room E1	Room E2
7:00 a.m.			
7:30 a.m. - 7:30 p.m.			
8:45 a.m. - 10:05 a.m.			
9:00 a.m. - 9:00 p.m.			
10:05 a.m. - 10:30 a.m.			
10:30 a.m. - 10:55 a.m.	Structural Bioinformatics *Paper 1:* ZPRED: Predicting the distance to the membrane center for residues in alpha-helical membrane proteins *Erik Granseth, Håkan Viklund, Arne Elofsson*	Database and Data Integration *Paper 2:* An experimental metagenome data management and analysis system *Victor Markowitz, Natalia Ivanova, Krishna Palaniappan Ernest Szeto, Frank Korzeniewski, Athanasios Lykidis, Iain Anderson, Konstantinos Mavrommatis, Victor Kunin, Hector Garcia Martin, Inna Dubchak, Phil Hugenholtz, Nikos Kyrpides*	Systems Biology *Paper 3:* Create and assess protein networks through molecular characteristics of individual proteins *Yanay Ofran, Guy Yachdav, Eyal Mozes, Ta-tsen Soong, Rajesh Nair, Burkhard Rost*
10:55 a.m. - 11:20 a.m.	Structural Bioinformatics *Paper 4:* A combinatorial pattern discovery approach for the prediction of membrane dipping (re-entrant) loops *Gorka Lasso, John Antoniw, Jonathan Mullins*	Database and Data Integration *Paper 5:* Distance based algorithms for small biomolecule classification and structural similarity search *Emre Karakoc, Artem Cherkasov, S. Cenk Sahinalp*	Systems Biology *Paper 6:* Dense subgraph computation via stochastic search: application to detect transcriptional modules *Logan Everett, Li-San Wang, Sridhar Hannenhalli*
11:20 a.m. - 11:45 a.m.	Structural Bioinformatics *Paper 7:* Comparative footprinting of DNA-binding proteins *Bruno Contreras-Moreira, Julio Collado-Vides*	Database and Data Integration *Paper 8:* springScape: Visualisation of microarray and contextual bioinformatic data using spring embedding and an information landscape *Timothy Ebbels, Bernard Buxton, David Jones*	Systems Biology *Paper 9:* A decompositional approach to parameter estimation in pathway modeling: A case study of the Akt and MAPK pathways and their crosstalk *Geoffrey Koh, Huey Fern Carol Teong, Marie-Veronique Clement, David Hsu, P S Thiagarajan*

monday (august 7)

Room A (2nd Floor)	Room B1	Room B2	Room B3
Shuttles depart Hotels to Convention Center			
Registration - Hall G			
Opening Welcome and Introduction of Keynote 1 - Main Auditorium (Hall D) Keynote 1: Robert Huber - Molecular machines for protein degradation			
Posters on Display - Hall G - 9:00 a.m. - 9:00 p.m.			
Coffee Break with Exhibitors - Hall C			
Software Demo ArrayExpress	Software Demo Integrated Microbial Genomes (IMG) System	Software Demo SSAHA2	Software Demo GINsim: a software for the qualitative

	Main Auditorium (Hall D)	Room E1	Room E2
11:45 a.m. - 12:10 p.m.	Structural Bioinformatics *Paper 10:* The iRMSD: A local measure of sequence alignment accuracy using structural information *Fabrice Armougom, Sebastien Moretti, Vladimir Keduas, Cedric Notredame*	Database and Data Integration *Paper 11:* SNP Function Portal: a web database for exploring the function implication of SNP alleles *Pinglang Wang, Manhong Dai, Weijian Xuan, Richard C McEachin, Anne U Jackson, Laura J Scott, Brian Athey, Stanley J. Watson, Fan Meng*	Systems Biology *Paper 12:* Bistable Switching and Excitable Behaviour in the Activation of Src at Mitosis *Hendrik Fuß, Werner Dubitzky, Stephen Downes, Mary Jo Kurth*
12:10 p.m. - 12:35 p.m.	Structural Bioinformatics *Paper 13:* Improved pruning algorithms and divide-and-conquer strategies for dead-end elimination, with application to protein design *Ivelin Georgiev, Ryan Lilien, Bruce Donald*	Database and Data Integration *Paper 14:* Integrating structured biological data by kernel Maximum Mean Discrepancy *Karsten Borgwardt, Arthur Gretton, Malte Rasch, Hans-Peter Kriegel, Bernhard Schoelkopf, Alex Smola*	Systems Biology *Paper 15:* Identification of metabolic units induced by environmental signals *Jose Nacher, Jean-Marc Schwartz, Minoru Kanehisa, Tatsuya Akutsu*
12:35 p.m. - 2:00 p.m.	Lunch - Hall F		ISCB Open Business Meeting (12:45 p.m.- 1:45 p.m)
2:00 p.m. - 2:25 p.m.	Structural Bioinformatics *Paper 16:* Modelling sequential protein folding under kinetic control using hp lattice models *Fabien Huard, Charlotte Deane, Graham Wood*	Human Health *Paper 17:* Predicting the prognosis of breast cancer by integrating clinical and microarray data with Bayesian networks *Olivier Gevaert, Frank De Smet, Dirk Timmerman, Yves Moreau, Bart De Moor*	Systems Biology *Paper 18:* Inferring functional pathways from multi-perturbation data *Nir Yosef, Alon Kaufman, Eytan Ruppin*
2:25 p.m. - 2:50 p.m.	Structural Bioinformatics *Paper 19:* A probabilistic approach to protein backbone tracing in electron density maps *Frank DiMaio, Jude Shavlik, George Phillips*	Human Health *Paper 20:* ACIAP, Autonomous hierarchical agglomerative Cluster Analysis based Protocol to partition conformational datasets *Giovanni Bottegoni, Walter Rocchia, Maurizio Recanatini, Andrea Cavalli*	Systems Biology *Paper 21:* Dynamical analysis of a generic Boolean model for the control of the mammalian cell cycle *Adrien Fauré, Aurélien Naldi, Claudine Chaouiya, Denis Thieffry*
2:50 p.m. - 3:15 p.m.	Structural Bioinformatics *Paper 22:* Learning MHC binding *Nebojsa Jojic, M. Reyes-Gomez, D. Heckerman, C. Kadie, O. Furman-Schueler*	Human Health *Paper 23:* Integrating copy number polymorphisms into array CGH analysis using a robust HMM *Sohrab Shah, Xiang Xuan, Ron DeLeeuw, Mehrnoush Khojasteh, Wan Lam, Raymond Ng, Kevin Murphy*	Systems Biology *Paper 24:* Computational inference of the molecular logic for synaptic connectivity in C. elegans *Vinay Varadan, David Miller III, Dimitris Anastassiou*

monday (august 7)

Room A (2nd Floor)	Room B1	Room B2	Room B3
Software Demo Web Services at the European Bioinformatics Institute	Software Demo HP/Synamatix: Enhancement and Acceleration of Genome Assembly using Novel Pattern Indexing and Retrieval Application	Software Demo Pygr, the Python Graph Database Framework for Bioinfomatics	
Birds of a Feather Flock Together	Birds of a Feather Flock Together	Birds of a Feather Flock Together	Birds of a Feather Flock Together
Software Demo EBI: Text Mining	Software Demo TreeDomViewer: A tool for the visualization of phylogeny and protein domain structure	Software Demo PATIKAweb	Software Demo BioModels Database

	Main Auditorium (Hall D)	Room E1	Room E2
3:15 p.m. - 3:40 p.m.			
3:40 p.m. - 4:05 p.m.	New Frontiers Panel Introduction and Session Chair: *Goran Neshich, Embrapa/CNPTIA* Key Challenges in exploiting biomolecular data for Medicine and Agriculture *Janet Thornton, European Bioinformatics Institute, Wellcome Trust* Conceptual questions and key challenges in computational biology *Chris Sander, Memorial Sloan-Kettering Cancer Center*	Human Health *Papaer 25:* Decoding non-unique oligonucleotide hybridization experiments of targets related by a phylogenetic tree *Alexander Schliep, Sven Rahmann*	Systems Biology *Paper 26:* An integrative approach for causal gene identification and gene regulatory pathway inference *Zhidong Tu, Li Wang, Michelle Arbeitman, Ting Chen, Fengzhu Sun*
4:05 p.m. - 4:30 p.m.		*PLoS Track 1:* Knowledge-Based Analysis of Genome-Wide SNP Scanning Data *Fan Meng*	Systems Biology *Paper 27:* An equilibrium partitioning model connecting gene expression and cis-motif content *Joe Mellor, Charles DeLisi*
4:30 p.m. - 4:55 p.m.	New Frontiers Session Continued	*PLoS Track 2:* Datamining the Fourth Dimension from Crystal Structures: Function-Structure-Entropy Relationships in Membrane Proteins *Ilan Samish*	*PLoS Panel:* BioTermNet: a system for biomedical text mining *(Asako Koike)* Imitating manual curation of text-mined facts in biomedicine *(Raul Rodriguez-Esteban)* SherLoc: Comprehensive Prediction of Protein Subcellular Localization by Integrating Clues from Sequence Data and the Literature *(Hagit Shatkay)*
4:55 p.m. - 5:50 p.m.			
6:00 p.m. - 9:00 p.m.			
9:30 p.m.			

monday (august 7)

Room A (2nd Floor)	Room B1	Room B2	Room B3
Coffee Break with Exhibitors - Hall C			
Software Demo Genome Expression Pathway Analysis Tool (GEPAT)	Software Demo PIRSF Protein Classification System (PCS)	Software Demo GenePro	
Introduction of Keynote 2 - Main Auditorium (Hall D)			
Keynote 2: Tom Blundell - Structural biology, informatics and the discovery of new medicines			
Poster Session with Authors (Odd Numbers) & Reception - Hall G			
Shuttles depart Convention Center to Hotels			

	Main Auditorium (Hall D)	Room E1	Room E2
7:00 a.m.			
7:30 a.m. - 7:30 p.m.			
8:45 a.m. - 9:55 a.m.			Morning
9:00 a.m. - 9:00 p.m.			
9:55 a.m. - 10:20 a.m.	New Frontiers Session Continued The future of the funding for biomolecular data and knowledge infrastructures: proposition for a "Fortaleza declaration" *Amos Bairoch, Swiss Institute of Bioinformatics*	Sequence Analysis *Paper 28:* Indel seeds for homology search *Denise Mak, Yevgeniy Gelfand, Gary Benson*	Molecular and Supramolecular Dynamics *Paper 29:* DynaPred: A structure and sequence based method for the prediction of MHC class I binding peptide sequences and conformations *Iris Antes, Shirley Siu, Thomas Lengauer*
10:20 a.m. - 10:50 a.m.			
10:50 a.m. - 11:15 a.m.		Sequence Analysis *Paper 30:* Interpreting anonymous DNA samples from mass disasters --- probabilistic forensic inference using genetic markers *Tien-ho Lin, Eugene W. Myers, Eric P. Xing*	Text Mining & Information Extraction *Paper 31:* Accessing Images in Bioscience Literature through User-Interface Designs and Natural Language Processing *Hong Yu, Minsuk Lee*
11:15 a.m. - 11:40 a.m.	New Frontiers Session Continued The changing face of scientific dissemination as it applies to computational biology *Phil Bourne, University of California*	Sequence Analysis *Paper 32:* BaCelLo: a balanced subcellular localization predictor *Andrea Pierleoni, Pier Luigi Martelli Piero Fariselli, Rita Casadio*	Text Mining & Information Extraction *Paper 33:* Finding the evidences for protein-protein interactions from PubMed abstracts *Hyunchul Jang, Jaesoo Lim, Joon-Ho Lim, Soo-Jun Park, Kyu-Chul Lee, Seon-Hee Park*

tuesday (august 8)

	Room A (2nd Floor)	Room B1	Room B2	Room B3
Shuttles depart Hotels to Convention Center				
Registration - Hall G				
ng Welcome, Promotion - ISMB/ECCB 2007 - Introduction of Keynote 3 - Main Auditorium (Hall D) Keynote 3: Kurt Wüthrich - Computational Aspects of NMR Studies with Proteins in Solution				
Posters on Display - Hall G - 9:00 a.m. - 9:00 p.m.				
d r s A e e l s s l, r				
Coffee Break with Exhibitors - Hall C				
n n n n d g e				
n n e n d s n, k, k	Software Demo OpenMS - A Software Platform for Shotgun Proteomics	Software Demo IBM: Inferring Common Origins	Software Demo Biological Concept Diagram Editor (BCDE)	Software Demo myGrid and ToolBus/PathPort Interoperability

	Main Auditorium (Hall D)	Room E1	Room E2
11:40 a.m. - 12:05 p.m.		Sequence Analysis *Paper 34:* On counting position weight matrix matches in a sequence, with application to discriminative motif finding *Saurabh Sinha*	Text Mining & Information Extraction *Paper 35:* Novel unsupervised feature filtering of biological data *Roy Varshavsky, Assaf Gottlieb, Michal Linial, David Horn*
12:05 p.m. - 12:30 p.m.	New Frontiers Session Continued	Sequence Analysis *Paper 36:* Finding regulatory motifs with maximum density subgraph *Eugene Fratkin, Brian Naughton, Douglas Brutlag, Serafim Batzoglou*	Text Mining & Information Extraction *Paper 37:* Integrating image data into biomedical text categorization *Hagit Shatkay, Nawei Chen, Dorothea Blostein*
12:30 p.m. - 2:00 p.m.		Lunch - Hall F	EBI User's Forum
2:00 p.m. - 2:25 p.m.	Transcriptomics *Paper 38:* Statistical mechanical modeling of genome-wide transcription factor occupancy data by MatrixREDUCE *Barrett Foat, Alexandre Morozov, Harmen Bussemaker*	Sequence Analysis *Paper 39:* Apples to apples: improving the performance of motif finders and their significance analysis in the Twilight Zone *Patrick Ng, Niranjan Nagarajan, Neil Jones, Uri Keich*	*PLoS Track 3*: Gene Expression Trees in Blood Cell Development *Ivan Costa*
2:25 p.m. - 2:50 p.m.	Transcriptomics *Paper 40:* Quantification of transcription factor expression from arabidopsis images *Daniel Mace, Ji-Young Lee, Richard Twigg, Juliette Colinas, Philip Benfey, Uwe Ohler*	Sequence Analysis *Paper 41:* CONTRAfold: RNA secondary structure prediction without physics-based models *Chuong Do, Daniel Woods, Serafim Batzoglou*	*PLoS Track 4:* Pervasive unproductive splicing of SR proteins associated with ultraconserved elements *Steven Brenner*

tuesday (august 8)

Room A (2nd Floor)	Room B1	Room B2	Room B3
ISCB Student Council Open Meeting	Birds of a Feather Flock Together Cancer Biomedical Informatics Grid (caBIG), *Peter Covitz*	Birds of a Feather Flock Together Semantic types: towards a common annotation schema for biomedical literature, *D. Rebholz-Schuhman*	Birds of a Feather Flock Together Bioinformatics Core Facilities, *Fran Lewitter*
Software Demo STING_RDB	Software Demo Extend Your Bioinformatics with Accelrys: Integration of new tools in a common workflow environment expands capabilities and biological context	Software Demo GeneChip Analysis System (WGAS)	Software Demo GNARE

	Main Auditorium (Hall D)	Room E1	Room E2
2:50 p.m. - 3:15 p.m.	Transcriptomics *Paper 42:* Identifying cycling genes by combining sequence homology and expression data *Yong Lu, Roni Rosenfeld, Ziv Bar-Joseph*	Sequence Analysis *Paper 43:* Context-specific independence mixture modeling for positional weight matrices *Benjamin Georgi, Alexander Schliep*	*PLoS Track 5*: Population Sequencing from Chromatogram Data *Nebojsa Jojic*
3:15 p.m. - 3:40 p.m.	Transcriptomics *Paper 44:* Analysis of sample set enrichment scores: assaying the enrichment of sets of genes for individual samples in genome-wide expression profiles *Elena Edelman, Alessandro Porrello, Justin Guinney, Bala Balakumaran, Andrea Bild, Phillip Febbo, Sayan Mukherjee*	Sequence Analysis *Paper 45:* ARTS: Accurate recognition of transcription starts in human *Soeren Sonnenburg, Alexander Zien, Gunnar Raetsch*	*PLoS Track 6:* Sm/Lsm genes: a glimpse into early Eukaryotic evolution *Stella Veretnik*
3:40 p.m. - 4:05 p.m.			
4:05 p.m. - 4:30 p.m.	Transcriptomics *Paper 46:* Efficient identification of DNA binding partners in a sequence database *Tobias Mann, William Noble*	Sequence Analysis *Paper 47:* Informative priors based on transcription factor structural class improve de novo motif discovery *Leelavati Narlikar, Raluca Gordan, Uwe Ohler, Alexander Hartemink*	*PLoS Track 7:* Comparative analysis of the complete transcriptome of the ENCODE regions in chimpanzees and humans *Philipp Khaitovich*
4:30 p.m. - 4:55 p.m.	Transcriptomics *Paper 48:* Semi-supervised analysis of gene expression profiles for lineage-specific development in the Caenorhabditis elegans embryo *Yuan Qi, Patrycja Missiuro, Ashish Kapoor, Craig Hunter, Tommi Jaakkola, David Gifford, Hui Ge*	Sequence Analysis *Paper 49:* ProfilePSTMM: capturing tree-structure motifs in carbohydrate sugar chains *Kiyoko Aoki-Kinoshita, Nobuhisa Ueda, Hiroshi Mamitsuka, Minoru Kanehisa*	*PLoS Track 8:* The strength of selection on ultraconserved elements *Christina Chen*
4:55 p.m. - 5:50 p.m.	Keynote 4: Overton Award		
6:00 p.m. - 9:00 p.m.			
9:30 p.m.			

tuesday (august 8)

Room A (2nd Floor)	Room B1	Room B2	Room B3
	Software Demo Genetic Marker Search Engine for Medline	Software Demo GObase	
Coffee Break with Exhibitors - Hall C			
Software Demo PRIDE and the Ontology Lookup Service	Software Demo Talk to Sun about Life Sciences	Software Demo BlueStar STING - A multiplatform environment for protein structure analysis	Software Demo HARLEM (Hamiltonians to Research LargE Molecules)
Introduction of Keynote 4 - Main Auditorium (Hall D)			
ard: Mathieu Blanchette - What mammalian genomes tell us about our ancestors, and vice-versa			
Poster Session with Authors (Even Numbers) & Reception - Hall G			
Shuttles depart Convention Center to Hotels			

	Main Auditorium (Hall D)	Room E1	Room E2
7:30 a.m. - 1:30 p.m.			
7:45 a.m.			
8:45 a.m. - 9:50 a.m.			
9:00 a.m. - 1:00 p.m.			
9:50 a.m. - 10:15 a.m.	Evolution & Phylogeny *Paper 50:* Constructing near-perfect phylogenies with multiple homoplasy events *Ravi Vijaya Satya, Amar Mukherjee, Gabriela Alexe, Laxmi Parida, Gyan Bhanot*	Ontologies *Paper 51:* A top-level ontology of functions and its application in the Open Biomedical Ontologies *Patryk Burek, Robert Hoehndorf, Frank Loebe, Johann Visagie, Heinrich Herre, Janet Kelso*	*PLoS Track 9:* Automated Cell Biology in Drug Discovery: Extracting Biological Information from Images of Cell *Eugeni Vaisberg*
10:15 a.m. - 10:40 a.m.	Evolution & Phylogeny *Paper 52:* BNTagger: Improved tagging snp selection using bayesian networks *Phil Hyoun Lee, Hagit Shatkay*	Ontologies *Paper 53:* An ontology for a robot scientist *Larisa Soldatova, Amanda Clare, Andrew Sparkes, Ross King*	*PLoS Track 10:* Predicting Biological Networks from Diverse Data: a New Role for the Hsp90 Complex *Chad Myers*
10:40 a.m. - 11:05 a.m.	Evolution & Phylogeny *Paper 54:* Mutation parameters from sequence data using graph theoretic measures on lineage trees *Reuma Magori Cohen, Yoram Louzoun, Steven Kleinstein*	Ontologies *Paper 55:* Protein classification using ontology classification *Katherine Wolstencroft, Phillip Lord, Lydia Tabernero Andy Brass, Robert Stevens*	*PLoS Track 11:* Gene Expression of C. elegans Neurons Carries Significant Information on Their Synaptic Connectivity *Alon Kaufman*
11:05 a.m. - 11:35 a.m.			
11:35 a.m. - 12:30 p.m.			
12:30 p.m.	Shuttles depart for Hotels		
6:30 p.m.			

wednesday (august 9)

Room A (2nd Floor)	Room B1	Room B2	Room B3
Registration - Hall G			
Shuttles depart Hotels to Convention Center			
Morning Welcome and Introduction of Keynote 5 - Main Auditorium (Hall D) Keynote 5: Elena Conti - Molecular mechanisms in RNA degradation			
Posters on Display - Hall G - 9:00 a.m. - 2:00 p.m.			
Software Demo The BioMAZE System	Software Demo IMG/M: An Experimental Metagenome Data Management and Analysis System	Software Demo MARSMotif: Deciphering Transcriptional Subnetworks from Microarray Expression Data using Regression Splines	Software Demo STRING database
Coffee Break with Exhibitors - Hall C			
Introduction of Keynote 6 - Main Auditorium (Hall D) Keynote 6: Charles DeLisi - New Approaches to Biomarker Discovery			
els and/or Beach Park for Delegates and off-site event ticket holders - 1:15 p.m. Last Departure			
Shuttles depart to hotels from Beach Parkt			

	Main Auditorium (Hall D)	Room E1	Room E2	
7:30 a.m. - 5:30 p.m.				
7:45 a.m.				
8:30 a.m. - 4:00 p.m.				
8:45 a.m. - 9:50 a.m.				
9:50 a.m. - 10:15 a.m.	Proteomics *Paper 56:* Semi-Supervised LC/MS alignment for differential proteomics *Bernd Fischer, Jonas Grossmann, Volker Roth, Wilhelm Gruissem, Sacha Baginsky, Joachim M. Buhmann*	Comparative Genomics *Paper 57:* Hairpins in a haystack: recognizing microrna precursors in comparative genomics data *Jana Hertel, Peter F. Stadler*	*PLoS Track 12:* Splice Form Prediction using Machine Learning *Gunnar Rätsch*	
10:15 a.m. - 10:40 a.m.	Proteomics *Paper 58:* Annotating proteins by mining protein interaction networks *Mustafa Kirac, Gultekin Ozsoyoglu, Jiong Yang*	Comparative Genomics *Paper 59:* Comparative genomics reveals unusually long motifs in mammalian genomes *Neil Jones, Pavel Pevzner*	*PLoS Track 13:* The consequences of alternative splicing on biological pathways *Melissa Cline*	
10:40 a.m. - 11:10 a.m.				
11:10 a.m. - 11:35 a.m.	Proteomics *Paper 60:* A model-based approach for mining membrane protein crystallization trials *Sitaram Asur, Srinivasan Parthasarathy, Pichai Raman, Matthew Eric Otey*	Comparative Genomics *Paper 61:* Relative contributions of structural designability and functional diversity in fixation of gene duplicates *Boris Shakhnovich*	*PLoS Track 14:* Analysis of pleiotropy during C. elegans development and interpretation with interactome networks *Hui Ge*	
11:35 a.m. - 12:00 p.m.	Proteomics *Paper 62:* Peptide sequence tag-based blind identification of post-translational modification with point process model *Chunmei Liu, Bo Yan, Yinglei Song, Ying Xu, Liming Cai*	Comparative Genomics *Paper 63:* Automatic clustering of orthologs and inparalogs shared by multiple proteomes *Andrey Alexeyenko, Ivica Tamas, Gang Liu, Erik Sonnhammer*	*PLoS Track 15:* Integrative Analysis of NCI-60 Panel Reveals Candidate Key Genetic Regulators Affected by Genomic Alterations *Doron Lipson*	E

thursday (august 10)

	Room A (2nd Floor)	Room B1	Room B2	Room B3
				Registration - Hall G
				Shuttles depart Hotels to Convention Center
				Posters on Display - Hall G
				Morning Welcome and Introduction of Keynote 7 - Main Auditorium (Hall D) Keynote 7: Rich Roberts - The need of Bioinformatics for experimental biologists
	Latin American BioInformatics Introduction Session	Software Demo Pathway Knowledge Management System (PKMS)	Software Demo UniProtKB and InterPro	Software Demo The PANTHER Classification System
				Coffee Break with Exhibitors - Hall C
	Latin American BioInformatics Session Continued	Software Demo IntAct - an extensible open source framework for molecular interactions	Software Demo CEP: Conformational epitope prediction server	

	Main Auditorium (Hall D)	Room E1	Room E2	
12:00 p.m. - 1:45 p.m.	Lunch R			
1:45 p.m. - 2:10 p.m.	Proteomics *Paper 64:* Rapid knot detection and application to protein structure prediction *Firas Khatib, Matt Weirauch, Carol Rohl*	Comparative Genomics *Paper 65:* A Sequence-based filtering method for ncRNA identification and its application to searching for Riboswitch Elements *Shaojie Zhang, Ilya Borovok, Yair Aharonowitz, Roded Sharan, Vineet Bafna*	*PLoS Track 16:* Integration of FRAP experiments and 3D simulations of diffusion in the lumen and surface of Endoplasmic Reticulum *Petros Koumoutsakos*	
2:10 p.m. - 2:35 p.m.	Proteomics *Paper 66:* A computational approach toward label-free protein quantification using predicted peptide detectability *Haixu Tang, Randy Arnold, Pedro Alves, Zhiyin Xun, David Clemmer, Milos Novotny, James Reilly, Predrag Radivojac*	Comparative Genomics *Paper 67:* Finding novel genes in bacterial communities isolated from the environment *Lutz Krause, Naryttza N. Diaz, Daniela Bartels, Robert A. Edwards, Alfred Pühler, Forest Rohwer, Folker Meyer, Jens Stoye*	*PLoS Track 17:* Comparison of Alternative Splicing Structures in Eukaryotes *Michael Sammeth*	E
2:35 p.m. - 3:00 p.m.	*PLoS Track 18:* Comparative Genomics of GPCRs: ET-Guided Annotation and Re-design of Aminergic Receptors *Olivier Lichtarge*	*PLoS Track 19:* DOE Hanford Site Metagenome: A multiple extreme environment that hosts wide diversity of microbes and radiotolerant bacteria *Mustafa Syed, Natalia Maltsev*	*PLoS Track 20:* Probabilistic Genetic Networks analysis of three Plasmodium falciparum strains from dynamical expression signals *Hernando del Portillo and Roberto Cesar Junior Barrera*	
3:00 p.m. - 3:25 p.m.	*PLoS Track 21:* Recursive Top-Down Quantum Clustering of Biological Data *Michal Linial*	*PLoS Track 22:* Simplified Models of Evolution lead to Improved Prediction of Functional Linkage from Correlated Gain and Loss of Genes among Eukaryotes *Daniel Barker*	*PLoS Track 23:* A Probabilistic Functional Gene Network of Worm: An Extensive and Accurate Systemic Model of a Multi-cellular Organism *Insuk Lee*	E
3:25 p.m. - 3:55 p.m.				
3:55 p.m. - 4:50 p.m.	Keynote			
4:50 p.m. - 5:15 p.m.				
5:15 p.m.				

thursday (august 10)

	Room A (2nd Floor)	Room B1	Room B2	Room B3
n Reception & Late Breaking Poster Session with Authors - Hall G / Lunch with Exhibitors - Hall C				
f D e f n s	Latin American BioInformatics Session Continued	Software Demo VisANT	Software Demo Swiss-Prot Protein Knowledgebase: ready for the future	
f s s h				
c f n l s d a	Latin American BioInformatics Session Continued			
c f d a n e				
Coffee with Exhibitors - Hall C				
Introduction of Keynote 8 - Main Auditorium (Hall D)				
note 8: Sr. Scientist Accomplishment Award: Michael Waterman - Whole Genome Optical Mapping				
Conference Awards and Closing				
Shuttles depart Convention Center to Hotels				

Comparative Genomics

Poster A-1

Comparative genomics of *Ciona savignyi* and *Ciona intestinalis*

Lesheng Kong (Temasek Life Sciences Laboratory); Balamurugan Kumarasamy (Temasek Life Sciences Laboratory); Elia Stupka (Telethon Institute of Genetics and Medicine); Arend Sidow (Stanford University Medical Center); Kerrin Small (Stanford University Medical Center); Michael Brudno (University of Toronto); Alan Christoffels (Temasek Life Sciences Laboratory)

Poster A-2

Gland expression profile derived from ESTs

Eduardo R Capanema (UFMG); Maurício A Mudado (UFMG); J Miguel Ortega (UFMG)

Poster A-3

Correlation between the expression of splicing factors and the presence of specific patterns of alternative splicing in human and mouse.

Júlio César Nunes (Ludwig Institute For Cancer Research - São Paulo Branch); Pedro Alexandre Favoretto Galante (Ludwig Institute For Cancer Research - São Paulo Branch); Sandro J. de Souza (Ludwig Institute For Cancer Research - São Paulo Branch)

Poster A-4

The strength of selection on ultraconserved elements

Christina TL Chen (Washington University at Saint Louis); Barak A. Cohen (Washington University at Saint Louis)

Poster A-5

Annotation, comparative and evolutionary analysis of fungal Carbohydrate Active enZymes (CAZymes)

Etienne G.J. Danchin (AFMB, CNRS); Pedro M. Coutinho (AFMB, CNRS); Corinne Rancurel (AFMB, CNRS); Bernard Henrissat (AFMB, CNRS)

Poster A-6

Identification of conserved TAF1 promoters with functional roles in human Embryonic Stem cells

Victor M. Ruotti (WiCell Research Institute); Aaron Darling (Dept. of Computer Science, University of Wisconsin-Madison); Ron Stewart (WiCell Research Institute); Tae Hoon Kim (. Ludwig Institute for Cancer Research, UCSD School of Medicine); Bing Ren (. Ludwig Institute for Cancer Research, UCSD School of Medicine); James Thomson (WiCell Research Institute)

Poster A-7

Breakpoint Re-use and Generalized Transpositions Depend on Synteny Block Size in Mammalian Genome Rearrangements

Oliver Attie (Department of Infectious Diseases, Mount Sinai School of Medicine, NY, NY 10029); Aaron E. Darling (Department of Computer Science, University of Wisconsin-Madison, Madison, WI 53706); John Sikorski3 (Regeneron Pharmaceuticals, Tarrytown, NY10591); Sophia Yancopoulos (Chiorazzi Lab, Feinstein Institute for Medical Research, Manhasset, NY 11030)

Poster A-8

Multiple Sample Methodology for Determining Significant Within-Class Concordance of Aberration in Array CGH Data

Mitchell Guttman (Computational Biology and Informatics Lab, University of Pennsylvania); Carolyn Mies (Department of Pathology, University of Pennsylvania); Katarzyna Dudycz-Sulicz (Department of Pathology, University of Pennsylvania); Sharon Diskin (Division of Oncology, Children); Don Baldwin (Microarray Facility, University of Pennsylvania); Gregory R. Grant (Computational Biology and Informatics Lab, University of Pennsylvania)

Poster A-9

Genomic coevolution of syntenic genes in Rhizobiales

Humberto Peralta (CCG UNAM); Gabriela Guerrero (CCG UNAM); Alejandro Aguilar (CCG UNAM); Jaime Mora (CCG UNAM)

Poster A-10

Codon instability at high GC level in the comparison between Human and Chimpanzee

Rosina Piovani (Laboratorio de Organización y Evolución del Genoma. Sección Biomatemática. Facultad de Ciencias, Uni); Hugo Naya (Laboratorio de Organización y Evolución del Genoma. Sección Biomatemática. Facultad de Ciencias, Uni); Victor Sabbía (Laboratorio de Organización y Evolución del Genoma. Sección Biomatemática. Facultad de Ciencias, Uni); Héctor Musto (Laboratorio de Organización y Evolución del Genoma. Sección Biomatemática. Facultad de Ciencias, Uni)

Poster A-11

Identification and Analysis of Retroid Agents in the Insect Genomes: Drosophila melanogaster, Anopheles gambiae, and Apis mellifera.

Holly A. Basta (Montana State University, Bozeman, MT); Marcella A. McClure (Montana State University, Bozeman, MT)

Poster A-12

Annotating the Eukaryotic Retrome

Marcella A. McClure (MSU); Crystal Hepp (MSU); Holly Basta (MSU); Tara Swope (MSU); Steve Martin (MSU); Anoop Winston (MSU); Alex Buzak (MSU)

Poster A-13

Construction and Analysis of Protein-Protein Interaction Network of *Aspergillus fumigatus* Proteins

Alper Soyler (Department of Food Engineering, Middle East Technical University); Tolga Can (Department of Computer Engineering, Middle East Technical University); Zumrut B. Ogel (Department of Food Engineering, Middle East Technical University)

Poster A-14

A rapid genome re-annotation system for comparative study of bacterial genomes

Satoshi Tamaki (Institute for Advanced Biosciences, Keio University, Kanagawa 252-8520, Japan); Kazuharu Arakawa (Japan Society for the Promotion of Science); Masaru Tomita (Institute for Advanced Biosciences, Keio University, Kanagawa 252-8520, Japan)

Poster A-16

Conservation of genomic neighbourhood is related to the rate by which intraparalogous proteins evolve in two bacterial species

Vasilis J. Promponas (University of Cyprus, Cyprus); Nikolas Papanikolaou (University of Crete, Greece); Ioannis Iliopoulos (University of Crete, Greece)

Poster A-17

Alternative Splicing Events of Stress Responsive Genes in Arabidopsis and Rice Universal Stress Protein Domains

Shaneka S. Simmons (Department of Biology, Jackson State University, Jackson, Mississippi 39217, USA); Raphael D. Isokpehi (Department of Biology, Jackson State University, Jackson, Mississippi 39217, USA)

Poster A-18

3D-ANNOTATE: A Web Portal for Structure-based Protein Annotation using Grid Technology

Shikta Das (Imperial College London)

Poster A-19

Logical and probabilistic reasoning for the functional annotation of genomic comparisons.

Keith Flanagan (University of Newcastle); Matthew Pocock (University of Newcastle); Phil Lord (University of Newcastle); Robert Stevens (University of Manchester); Anil Wipat (University of Newcastle)

Poster A-20

Comparative analysis of environmental sequences

Konrad U Foerstner (European Molecular Biology Laboratory); Christian von Mering (European Molecular Biology Laboratory); Sean D Hooper (European Molecular Biology Laboratory); Peer Bork (European Molecular Biology Laboratory)

Poster A-21

Anchor-based whole genome divergence and phylogeny: Analysis of Mycobacterial genomes

Anchal Vishnoi (Research Scholar); Rahul Roy (Professor); Alok Bhattacharya (Professor)

Poster A-22

Comparison of Alternative Splicing Structures in Eukaryotes

Sammeth, M (GRIB - IMIM); Foissac, S (GRIB - CRG); Guigó, R (GRIB - IMIM)

Poster A-23

Phylogenetic profiling approach to generate RNA-regulated protein networks in *E. coli*

Nozomu Yachie (Institute for Advanced Biosciences, Keio University); Koji Numata (Institute for Advanced Biosciences, Keio University); Yoshiteru Negishi (Institute for Advanced Biosciences, Keio University); Hiroyuki Nakamura (Institute for Advanced Biosciences, Keio University); Junichi Sugahara (Institute for Advanced Biosciences, Keio University); Rintaro Saito (Institute for Advanced Biosciences, Keio University); Masaru Tomita (Institute for Advanced Biosciences, Keio University)

Poster A-24

A multi-species study of chromosomal domains of co-expression

Aditya Ramani (Department of Computer Science, University of Illinois at Urbana-Champaign); Kilannin Krysiak (School of Molecular and Cell Biology, University of Illinois at Urbana-Champaign); Chengxiang Zhai (Department of Computer Science, University of Illinois at Urbana-Champaign); Lei Liu (W. M. Keck Center for Comparative and Functional Genomics, University of Illinois at Urbana-Champaig)

Poster A-25

Patterns of Gene Colocalization in the Human Genome

Par Engstrom (Computational Biology Unit, Bergen Center for Computational Science, University of Bergen, Bergen, N); David Fredman (Computational Biology Unit, Bergen Center for Computational Science, University of Bergen, Bergen, N); Boris Lenhard (Computational Biology Unit, Bergen Center for Computational Science, University of Bergen, Bergen, N)

Poster A-26

Plasticity of transcriptional regulatory machinery revealed from whole genome comparison

Sarath Chandra Janga (Program of Computational Genomics, CCG-UNAM); Ernesto Perez-Rueda (Department of Cellular Engineering & Biocatalysis, IBT-UNAM)

Poster A-27

Prediction of Non-Coding RNAs Using Drosophila Whole-Genome Alignments

Yuri Bendana (Bioengineering Graduate Group, UC Berkeley/UCSF); Ian Holmes (Bioengineering, UC Berkeley)

Poster A-28

Delineating the Functional Components of Eukaryotic Genomes

Jonathan M. Keith (Department of Mathematics, University of Queensland); Stuart Stephen (Institute for Molecular Bioscience, University of Queensland); Peter Adams (Department of Mathematics, University of Queensland); John S. Mattick (Institute for Molecular Bioscience, University of Queensland)

Databases & Data Integration

Poster B-1

MPVAD: System of integration of biological data

R Puga (Faculty of Medicine of Ribeirão Preto, Department of Genetic, University of São Paulo, Ribeirão Preto); S Amui (Faculty of Pharmaceutical Sciences, University of São Paulo, Ribeirão Preto, SP, Brazil); D Jorge (Faculty of Medicine of Ribeirão Preto, Department of Genetic, University of São Paulo, Ribeirão Preto); M Junior (Department of Biotechnology, University of Ribeirão Preto, Ribeirão Preto, SP, Brazil); A Soares (Faculty of Pharmaceutical Sciences, University of São Paulo, Ribeirão Preto, SP, Brazil); S Giuliatti (Faculty of Medicine of Ribeirão Preto, Department of Genetic, University of São Paulo, Ribeirão Pret)

Poster B-2

IDconverter and IDClight: Conversion and enrichment of

Patricio Yankilevich (Centro Nacional de Investigaciones Oncologicas (CNIO)); Andreu Alibés (Centro Nacional de Investigaciones Oncologicas (CNIO)); Andrés Cañada (Centro Nacional de Investigaciones Oncologicas (CNIO)); Ramón Diaz Uriarte (Centro Nacional de Investigaciones Oncologicas (CNIO))

Poster B-3

A Graph-relational Integrated Database of Human and Mouse Omics data

Junaid Gamieldien (NBN South Africa); Darren Otgaar (NBN South Africa); Nadeen Southgate (NBN South Africa); Daniel A. Jacobson (NBN South Africa)

Poster B-4

Cyberinfrastructure for Emerging and Re-Emerging Infectious Diseases

Oswald R. Crasta (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Eric Snyder (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Stephen Cammer (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Darius Dziuda (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Zhangjun Fei (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Mike Czar (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Eric Nordberg (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Boyu Yang (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Chengdong Zhang (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Chaitanya Kommidi (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Ranjan Jha (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Yan Zhang (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Anjan Purkayastha (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Rebecca Wattam (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Kelly Williams (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Ron Kenyon (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Rebecca Will (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Joao Setubal (Group, Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta); Bruno W. Sobral (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and Sta)

Poster B-5

UniProt: the Universal Protein Resource

Raja Mazumder (Protein Information Resource, Georgetown University); Claire ODonovan (European Bioinformatics Institute)

Poster B-6

NMR Manager – Metabolomics software for interpreting NMR spectra

Robert Stones (Central Science Laboratory); Adrian Charlton (Central Science Laboratory); James Donarski (Central Science Laboratory)

Poster B-8

The BioMAZE System: an environment for representation and analysis of biological processes

Christian LEMER (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Hassan ANHEROUR (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Fabian COUCHE (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Simon DE KEYZER (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Yves DEVILLE (Computing Science and Engineering Department, Université catholique de Louvain, Place Saint-Barbe 2,); Frederic FAYS (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Olivier HUBAUT (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Jacques VAN HELDEN (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Br); Shoshana J. WODAK (Department of Biochemistry and Structural Biology, Department of Medical Genetics, University of Tor)

Poster B-9

MiDaR: Microarray Database Resource for Customized Chip Design

Eric C. Rouchka (Department of Computer Engineering and Computer Science, University of Louisville); Ravishrikanth Gundlapalli (Department of Computer Engineering and Computer Science, University of Louisville); Nigel G.F. Cooper (Deparment of Anatomical Sciences and Neurobiology, University of Louisville)

Poster B-10

PhenoLink - Linking phenotype to genotype

Pieter Neerincx (Laboratory of Bioinformatics, WUR); Blaise Alako (Laboratory of Bioinformatics, WUR); Jack Leunissen (Laboratory of Bioinformatics, WUR)

Poster B-11

Implementation of a query processing model and view based data integration system

Myung-Eun Lim (Bioinformatics Team, Electronics and Telecommunications Research Institute); Myung-Guen Chung (Bioinformatics Team, Electronics and Telecommunications Research Institute); Yong-Ho Lee (Bioinformatics Team, Electronics and Telecommunications Research Institute); Soo-jun Park (Bioinformatics Team, Electronics and Telecommunications Research Institute)

Poster B-12

Integr8 – Access to Complete Genomes and Proteomes

Manuela Pruess (EMBL Outstation - European Bioinformatics Institute (EBI)); Lawrence Bower (EMBL Outstation - European Bioinformatics Institute (EBI)); Paul Kersey (EMBL Outstation - European Bioinformatics Institute (EBI)); Rajesh Radhakrishnan (EMBL Outstation - European Bioinformatics Institute (EBI)); Rolf Apweiler (EMBL Outstation - European Bioinformatics Institute (EBI))

Poster B-13

Development of Data Templates for Data Collection, Storage and Database Submission

Miguel Anducho (Crop Research Informatics Laboratory, CIMMYT.); Kyle Braak (Crop Research Informatics Laboratory, CIMMYT.); Richard Bruskiewich (Crop Research Informatics Laboratory, IRRI.); Victoria Carollo (Center for Computational Biology, Montana State University.); Tom Hazekamp (International Plant Genetic Resources Institute.); Andrew Farmer (National Center for Genomic Resources.); David Marshall (Scottish Crop Research Center.); Dave Matthews (GrainGenes, Cornell University.); Ayton Meintjes (Bioinformatics and Computational Biology Unit, University of Pretoria.); Thomas Metz (Crop Research Informatics Laboratory, IRRI.); Jane Morris (African Centre for Gene Technologies.); Manuel Ruiz (TropDB, CIRAD.); Mary Schaeffer (MaizeGDB, University of Missouri.); Theo van Hintum (Centre for Genetic Resources, The Netherlands.); Susan McCouch (Gramene, Cornell University.); Guy Davenport (Crop Research Informatics Laboratory, CIMMYT.)

Poster B-14

Contextual Analysis and Visualization of High Throughput Experimental Data

Nenad Bartonicek (Bioinformatics Group, Faculty of Science, Zagreb University, Horvatovac 102a, 10000 Zagreb, Croatia.); Igor Segota (Department of Physics, Faculty of Science, Zagreb University, Bijenička cesta 32, 10000 Zagreb,); Kristian Vlahovicek (Bioinformatics Group, Faculty of Science, Zagreb University, Horvatovac 102a, 10000 Zagreb, Croatia.)

Poster B-15

Patho-Gene and Pathos Databases – Support for Biodefense and Emerging Infectious Disease Research

Elizabeth M. Glass (Argonne National Laboratory); Mark D'Souza (University of Chicago); Alexis Rodriguez (Argonne National Laboratory); Dinanath Sulakhe (University of Chicago); Mustafa Syed (Argonne National Laboratory); Natalia Maltsev (Argonne National Laboratory)

Poster B-16

MamPol: Mammalia Polymorphism Database

Raquel Egea (Departament de Genetica i Microbiologia, Universitat Autonoma de Barcelona); Sonia Casillas (Departament de Genetica i Microbiologia, Universitat Autonoma de Barcelona); Antonio Barbadilla (Departament de Genetica i Microbiologia, Universitat Autonoma de Barcelona)

Poster B-18

The TIGR Rice Genome Annotation Database

Shu Ouyang (The Institute for Genomic Research); Haining Lin (The Institute for Genomic Research); Kevin L. Childs (The Institute for Genomic Research); Wei Zhu (The Institute for Genomic Research); John Hamilton (The Institute for Genomic Research); Dan Lee (The Institute for Genomic Research); Mathew Campbell (The Institute for Genomic Research); Renae Malek (The Institute for Genomic Research); Li Zheng (The Institute for Genomic Research); Joshua Orvis (The Institute for Genomic Research); Brian Haas (The Institute for Genomic Research); Jennifer Wortman (The Institute for Genomic Research); Robin Buell (The Institute for Genomic Research)

Poster B-19

APID: Agile Protein Interaction DataAnalyzer

Prieto C. (Cancer Research Center (CIC, CSIC/USAL)); De Las Rivas J. (Cancer Research Center (CIC, CSIC/USAL))

Poster B-20

The PIRSF system for protein classification, rule-based annotation, and ontology mapping

Darren A. Natale (PIR/GUMC); Cecilia Arighi (PIR/GUMC); Winona Barker (PIR/GUMC); Zhangzhi Hu (PIR/GUMC); Hongzhan Huang (PIR/GUMC); Robel Kahsay (PIR/GUMC); Raja Mazumder (PIR/GUMC); Anastasia Nikolskaya (PIR/GUMC); Sona Vasudevan (PIR/GUMC); C. R. Vinayaka (PIR/GUMC); Lai-Su Yeh (PIR/GUMC); Cathy H. Wu (PIR/GUMC)

Poster B-21

INOH pathway data ontologies

Ken FUKUDA (CBRC, AIST); Satoko YAMAMOTO (BIRD, JST); Noriko SAKAI (BIRD, JST); Hiromi NAKAMURA (Information and Mathematical Science Laboratory, Inc.); Toshihisa TAKAGI (Graduate School of Frontier Sciences, University of Tokyo)

Poster B-22

Online dynamic visualization and statistical analyses of rat phenome data

Anne E Kwitek (Medical College of Wisconsin); Zhanchi Wang (Medical College of Wisconsin); Allen W. Cowley Jr. (Medical College of Wisconsin); Andrew S. Greene (Medical College of Wisconsin); Richard J. Roman (Medical College of Wisconsin); Howard J. Jacob (Medical College of Wisconsin)

Poster B-23

A cell type transcriptional atlas database for rice

Matthew Holford (Yale University); Teresa Ceserani (Yale University); Mei Chen (Yale University); Neeru Gandotra (Yale University); Yuling Jiao (Yale University); Naixin Li (Yale University); Tie Liu (Yale University); Ligeng Ma (Yale University); Ning Sun (Yale University); Susan Tausta (Yale University); Xing-Wang Deng (Yale University); Hongyu Zhao (Yale University); Timothy Nelson (Yale University)

Poster B-24

WebLab: a workflow-based platform integrating bioinformatics resources

Jianmin Wu (Center of Bioinformatics, Peking University, Beijing 100871, China); Ge Gao (Center of Bioinformatics, Peking University, Beijing 100871, China); Xiaoqiao Liu (Center of Bioinformatics, Peking University, Beijing 100871, China); Lei Kong (Center of Bioinformatics, Peking University, Beijing 100871, China); Zhe Li (Center of Bioinformatics, Peking University, Beijing 100871, China); Di Liu (Center of Bioinformatics, Peking University, Beijing 100871, China); Wen Tang (Center of Bioinformatics, Peking University, Beijing 100871, China); Jingchu Luo (Center of Bioinformatics, Peking University, Beijing 100871, China)

Poster B-25

eSLDB: eukaryotic Subcellular Localization DataBase

Andrea Pierleoni (Biocomputing Group, Department of Biology, University of Bologna); Pier Luigi Martelli (Biocomputing Group, Department of Biology, University of Bologna); Piero Fariselli (Biocomputing Group, Department of Biology, University of Bologna); Rita Casadio (Biocomputing Group, Department of Biology, University of Bologna)

Poster B-26

NUDLE: A Tool for Inferring Nutrient Disease Relationships from Metabolic Networks

Anoop Kumar (Department of Computer Science, Tufts University, Medford, MA, USA); Jennifer S. Buell (Friedman School of Nutrition Science and Policy, Tufts University, Boston, MA, USA); Lenore J. Cowen (Department of Computer Science, Tufts University, Medford, MA, USA); Inga Peter (Institute for Clinical Research and Health Policy Studies, Tufts-New England Medical Center, Boston)

Poster B-27

Development of Computational Tools for a Dynamic Association between Genomic and Proteomic Data and Metabolic Pathways

Renato Milani (Department of Biochemistry - Unicamp); Itaraju J. B. Brum (Department of Biochemistry - Unicamp); Anderson R. Martins (Alellyx Applied Genomics); Eduardo Galembeck (Department of Biochemistry - Unicamp)

Poster B-28

A Computational Pipeline for the Analysis of Data from a 500,000 SNP Whole Genome Association Study of Multiple Sclerosis

David Sexton (Center for Human Genetics Research, Vanderbilt University, International Multiple Sclerosis Genetics); Jacob McCauley (Center for Human Genetics Research, Vanderbilt University, International Multiple Sclerosis Genetics); Justin Giles (Center for Human Genetics Research, Vanderbilt University, International Multiple Sclerosis Genetics); Yuki Bradford (Center for Human Genetics Research, Vanderbilt University, International Multiple Sclerosis Genetics); Jonathan Haines (Center for Human Genetics Research, Vanderbilt University, International Multiple Sclerosis Genetics)

Poster B-29

UniHI: Unifying Large-Scale Maps of the Human Protein Interactome

Gautam Chaurasia (Max-Delbrück-Centrum); Christian Hänig (Max-Delbrück-Centrum); Hanspeter Herzel (Institute for Theoretical Biology); Erich Wanker (Max-Delbrück-Centrum); Matthias E. Futschik (Institute for Theoretical Biology)

Poster B-30

Prediction from complex bioinformatic databases, with application to protein--protein interactions

Berzuini Carlo (MRC BSU); Tom M.W. Nye (MRC BSU); Sarah A. Teichmann (MRC LMB)

Poster B-31

MS-PED: A Management System for Proteomics Experimental Data

W. Yan (Bioinformatics User Facility, University of California, Los Angeles, CA); S. Than (School of Dentistry, University of California, Los Angeles, CA); R. Qiao (School of Medicine, University of Southern California, Los Angeles, CA); D.S. Parker (Department of Computer Science, University of California, Los Angeles, CA); D. Wong (School of Dentistry, University of California, Los Angeles, CA)

Poster B-32

A Classification for Conceptually Layouting Protein-Protein Interaction Networks

SunLee Bang (Electronics & Telecommunications Research Institute); JaeHun Choi (Electronics & Telecommunications Research Institute); JongMin Park (Electronics & Telecommunications Research Institute); SooJun Park (Electronics & Telecommunications Research Institute)

Poster B-33

STING Database Quality Assessment

Stanley R. M. Oliveira (Embrapa Agricultural Informatics); Paula R. K. Falcão (Embrapa Agricultural Informatics); Michel E. B.Yamagishi (Embrapa Agricultural Informatics); Goran Neshich (Embrapa Agricultural Informatics); Diego N. Rodrigues (Embrapa Agricultural Informatics); Kassyus R. R. Souza (Embrapa Agricultural Informatics); Douglas U. Morita (Embrapa Agricultural Informatics); Gustavo V. Almeida (Embrapa Agricultural Informatics); Ivan Mazoni (Embrapa Agricultural Informatics); Edgard H. Santos (Embrapa Agricultural Informatics); Fábio D. Vieira (Embrapa Agricultural Informatics); José G. Jardine (Embrapa Agricultural Informatics)

Poster B-34

A computational system to select candidate genes for complex human traits

Kyle J Gaulton (Department of Genetics, University of North Carolina); Karen L Mohlke (Department of Genetics, University of North Carolina); Todd J Vision (Department of Biology, University of North Carolina)

Poster B-35

FlagelLink – An integrated organellar database dealing with refined pattern recognition of specific motifs/domains targeted to the eukaryotic flagellum

Fabiana Freire de Araújo (NUGEN-UECE); Wesley Jefferson Oliveira Alcoforado (NUGEN-UECE); João David de Lira (NUGEN-UECE); Dácio Barros Tavares (NUGEN-UECE); Ana Luiza Bessa de Paula Barros (LARCES-UECE); Diana Magalhães de Oliveira (NUGEN-UECE)

Poster B-36

XMLPipeDB: A Reusable, Open Source Tool Chain for Building Relational Databases from XML Sources

Kam D. Dahlquist (Loyola Marymount University); Joey Barrett (Loyola Marymount University); Joe Boyle (Loyola Marymount

University); Adam Carasso (Loyola Marymount University); David Hoffman (Loyola Marymount University); Babak Naffas (Loyola Marymount University); Jeffrey Nicholas (Loyola Marymount University); Roberto Ruiz (Loyola Marymount University); Scott Spicer (Loyola Marymount University); John David N. Dionisio (Loyola Marymount University)

Poster B-37

InterProScan New and Planned Features

Sarah Hunter (European Bioinformatics Institute); Nicola Mulder (European Bioinformatics Institute); Alberto Labarga (European Bioinformatics Institute)

Poster B-38

Novel "shim" Service to Develop Fexible Workflows with Web Services

Toshiaki Katayama (University of Tokyo); Minoru Kanehisa (Kyoto University)

Poster B-39

Automating the Maintenance of Bioinformatics Services with Aap

Estienne Swart (National Bioinformatics Network (South Africa)); Ruediger Brauning (National Bioinformatics Network (South Africa))

Poster B-40

Middleware approach to data integration for plant genomics

Pierre Larmande (Phd Student); Isabelle Mougenot (Assitant Professor); Christine Tranchant-Dubreuil (Ingineer); Manuel Ruiz (Phd); Therese Libourel (Professor)

Poster B-41

Context-sensitive Evidence Integration for Predicting Biological Networks

Chad L. Myers (Lewis-Sigler Institute for Integrative Genomics, Department of Computer Science); Olga G. Troyanskaya (Lewis-Sigler Institute for Integrative Genomics, Department of Computer Science)

Poster B-42

Evidence handling in EMBL Third Party Annotation: a two-tiered structure

Cochrane G.R. (EMBL-EBI); Bates K. (EMBL-EBI); Faruque N. (EMBL-EBI); Kanz C. (EMBL-EBI); Kulikova T. (EMBL-EBI); Zhu W. (EMBL-EBI); Apweiler R (EMBL-EBI)

Poster B-44

An Integrated database of structural parameters for protein analysis

Stanley R. M. Oliveira (Embrapa Agricultural Informatics); Gustavo V. Almeida (Embrapa Agricultural Informatics); Kassyus R. R. Souza (Embrapa Agricultural Informatics); Diego N. Rodrigues (Embrapa Agricultural Informatics); Goran Neshich (Embrapa Agricultural Informatics); Paula R. Kuser-Falcão (Embrapa Agricultural Informatics); Michel E. B.Yamagishi (Embrapa Agricultural Informatics); Edgard H. Santos (Embrapa Agricultural Informatics); Fábio D. Vieira (Embrapa Agricultural Informatics); José G. Jardine (Embrapa Agricultural Informatics)

Poster B-45

Digr: A web interface for mining Digrabase graph databases

Kieran O'Neill (National Bioinformatics Network); Dan Jacobson (National Bioinformatics Network); Hugh Murrell (University of KwaZulu-Natal)

Poster B-46

GEMINA: Genomic Metadata for Infectious Agents

Aaron Gussman (The Institute for Genomic Research, Rockville, Maryland 20850, USA.); Sam Angiuoli (The Institute for Genomic Research, Rockville, Maryland 20850, USA.); Lynn M. Schriml (The Institute for Genomic Research, Rockville, Maryland 20850, USA.The Institute for Genomic Researc); Kumar Hari (Ibis Division of Isis Pharmaceuticals, 1891 Rutherford Rd., Carlsbad, CA 92008, USA.); Alan Goates (Ibis Division of Isis Pharmaceuticals, 1891 Rutherford Rd., Carlsbad, CA 92008, USA.); Kathy Phillippy (The Institute for Genomic Research, Rockville, Maryland 20850, USA.); Tanja Davidsen (The Institute for Genomic Research, Rockville, Maryland 20850, USA.); Anu Ganapathy (The Institute for Genomic Research, Rockville, Maryland 20850, USA.); Steven Salzberg (Center for Bioinformatics and Computational Biology, University of Maryland Institute for Advanced C); Owen White (The Institute for Genomic Research, Rockville, Maryland 20850, USA.); Neil Hall (The Institute for Genomic Research, Rockville, Maryland 20850, USA.)

Poster B-47

A Web-based Workbench for Conducting "In-Silico" Experiments Using Microarray Data

Cheryl Hornbaker (Department of Pharmacology, University of Colorado Health Sciences Center); Lawrence Hunter (Department of Pharmacology, University of Colorado Health Sciences Center); Tzu Phang (Department of Pharmacology, University of Colorado Health Sciences Center); Sanjiv Bhave (Department of Pharmacology, University of Colorado Health Sciences Center); Ravan Lapadat (Department of Pharmacology, University of Colorado Health Sciences Center); Laura Saba (Department of Pharmacology, University of Colorado Health Sciences Center); Jeanette Gaydos (Department of Pharmacology, University of Colorado Health Sciences Center); Daniel McGoldrick (Department of Pharmacology, University of Colorado Health Sciences Center); Andrew Dolbey (Department of Pharmacology, University of Colorado Health Sciences Center); Brian Soriano (Department of Pharmacology, University of Colorado Health Sciences Center); John Belnap (Behavioral Neuroscience, Oregon Health & Science University); Aaron Gabow (Department of Pharmacology, University of Colorado Health Sciences Center); Allison Ellington (Department of Pharmacology, University of Colorado Health Sciences Center); Eric Ellington (Department of Pharmacology, University of Colorado Health Sciences Center); Kendra Jones (Department of Pharmacology, University of Colorado Health Sciences Center); Paula Hoffman (Department of Pharmacology, University of Colorado Health Sciences Center); Boris Tabakoff (Department of Pharmacology, University of Colorado Health Sciences Center)

Poster B-48

SOAP-based services provided by the European Bioinformatics Institute

Alberto Labarga (European Bioinformatics Institute - EMBL); S. PIlai (European Bioinformatics Institute - EMBL); M. Anderson (European Bioinformatics Institute - EMBL); F. Valentin (European Bioinformatics Institute - EMBL); H. McWilliam (European Bioinformatics Institute - EMBL); P. Stoehr (European Bioinformatics Institute - EMBL); K. Henrick (European Bioinformatics Institute - EMBL); P. Rice (European Bioinformatics Institute - EMBL); R. Lopez (European Bioinformatics Institute - EMBL)

Poster B-49

BISI: an integrative, extensible and minable database of South African wildlife and indigenous livestock biomaterial information

Athlee Maclear (National Bioinformatics Network); Darren Otgaar (National Bioinformatics Network); Dr. Junaid Gamieldien (National Bioinformatics Network); Dr. Paul Bartels (National Zoological Gardens/BioBankSA); Dan Jacobson (National Bioinformatics Network); Dr. Antoinette Kotze (National Zoological Gardens, South Africa)

Poster B-51

Arabidopsis Functional Genomics Data Integration

Nicolas Tsesmetzis (Computational Biology Department, John Innes Centre); Matthew Couchman (Computational Biology Department, John Innes Centre); Sean Walsh (Computational Biology Department, John Innes Centre)

Poster B-52

CUDXML: Codon Usage Database in XML Format

Denis Shestakov (Turku Centre for Computer Science); Tapio Salakoski (University of Turku)

Poster B-53

GAFFA: Genome Annotation Framework for Flexible Analysis

Anders Lanzén (Computational Biology Unit, Bergen Center for Computational Science, University of Bergen); Svenn Helge Grindhaug (Computational Biology Unit, Bergen Center for Computational Science, University of Bergen); Pål Puntervoll (Computational Biology Unit, Bergen Center for Computational Science, University of Bergen)

Poster B-54

SNP-Ontology for semantic integration of genomic variation data

Adrien Coulet (KIKA Medical, 35 rue de Rambouillet 75012 Paris, France. LORIA (UMR 7503 CNRS-INPL-INRIA-Nancy2-UHP)); Malika Smaïl-Tabbone (LORIA (UMR 7503 CNRS-INPL-INRIA-Nancy2-UHP)); Pascale Benlian (Université Pierre et Marie Curie - Paris6, INSERM UMRS 538, Biochimie - Biologie Moléculaire, Paris,); Amedeo Napoli (LORIA (UMR 7503 CNRS-INPL-INRIA-Nancy2-UHP)); Marie-Dominique Devignes (LORIA (UMR 7503 CNRS-INPL-INRIA-Nancy2-UHP))

Poster B-56

A Functional Genomics Information Management System

Meintjes, AP (University of Pretoria); Schriek, CA (University of Pretoria); De Bruin, J (University of Pretoria); Harrison, CM (University of Pretoria); Tiedt, DA (University of Pretoria); Ganesan, H (University of Pretoria); Hefer, CA (University of Pretoria); de Beer, TAP (University of Pretoria); Burger, PB (University of Pretoria); Joubert, F (University of Pretoria)

Poster B-57

Generation Challenge Programme (GCP) Domain Modeling and Crop Information Platform

Kyle Braak (Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT)); Richard M. Bruskiewich (International Rice Research Institute (IRRI)); Guy Davenport (Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT)); Alexis Dereeper (Centre de coopération Internationale en Recherche Agronomique pour le Développement (CIRAD)); Andrew Farmer (National Center for Genome Resources (NCGR)); Tom HazeKamp (International Plant Genetic Resources Institute (IPGRI)); Graham Mclaren (International Rice Research Institute (IRRI)); Thomas Metz (International Rice Research Institute (IRRI)); Sebastian Ritter (Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT)); Manuel Ruiz (Centre de coopération Internationale en Recherche Agronomique pour le Développement (CIRAD)); Martin Senger (International Rice Research Institute (IRRI)); Reinhard Simon (Centro Internacional de la Papa (CIP)); Masaru Takeya (National Institute for Agrobiological Sciences (NIAS)); Theo Van Hintum (Wageningen Universiteit & Researchcentrum (WUR))

Poster B-58

Development of BioMOBY and its Associated Applications

Mylah Rystie Anacleto (International Rice Research Institute (IRRI)); Kyle Braak (Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT)); Richard Bruskiewich (International Rice Research Institute (IRRI)); Mathieu Rouard (International Plant Genetic Resources Institute (IPGRI)); Martin Senger (International Rice Research Institute (IRRI)); Milko Skofic (International Plant Genetic Resources Institute (IPGRI))

Poster B-59

Design Principles of Ontology-based Query and Development of Ontology Wrapper

Myung-Guen Chung (Electronics and Telecommunications Research Institute); Myung-Eun Lim (Electronics and Telecommunications Research Institute); Myung-Nam Bae (Electronics and Telecommunications Research Institute); Yong-Ho Lee (Electronics and Telecommunications Research Institute); Soo-Jun Park (Electronics and Telecommunications Research Institute)

Poster B-60

Classification of snake venon-neutralizing effects of medicinal plants via artificial neural networks

Gabriela Félix dos Santos (Department of Physics and Mathematics of Ribeirão Preto - University of São Paulo); Renato Tinós (Department of Physics and Mathematics of Ribeirão Preto - University of São Paulo); Silvana Giuliatti (Faculty of Medicine of Ribeirão Preto - University of São Paulo)

Poster B-61

Genome-wide Comparison of DNA Melting Bubbles and Ensembl's Genomic Annotations

Geir Ivar Jerstad (Dept. of Informatics, University of Oslo); Eivind Tøstesen (Dept. of Tumor Biology, Norwegian Radium Hospital); Torbjørn Rognes (Dept. of Informatics, University of Oslo); Eivind Hovig (Dept. of Tumor Biology, Norwegian Radium Hospital)

Poster B-62

Database PROBACTER: proteomes of plants-associated bacteria

Fernanda Nascimento Almeida (Labindo, LNCC); Rangel Celso Souza (Labindo, LNCC); Alexandre Rossi Paschoal (Labindo, LNCC); Ana Tereza Ribeiro de Vasconcelos (Labindo, LNCC); Claudia Barros Monteiro-Vitorello (Labindo, LNCC)

Poster B-63

2D Maps of Protein Surface

Marcelo Gonçalves Narciso (Embrapa Informática Agropecuária); Michel E. B. Yamagishi (Embrapa Informática Agropecuária); Paula R. Kuser-Falcão (Embrapa Informática Agropecuária); Goran Neshich (Embrapa Informática Agropecuária)

Poster B-64

Expression Databases for Three Crop Species: Maize, Rice and Potato

Jia Liu (TIGR); Eugene Ly (TIGR); Li Zheng (TIGR); Amy Hart (TIGR); Shu Ouyang (TIGR); Kimberly Rehfeld (TIGR); Willem Rensink (TIGR); Robin Buell (TIGR); Qiaoping Yuan (TIGR); Hue Vuong (TIGR)

Poster B-65

CocoaGen DB, an Integrative Information System to Exploit both Phenotypic and Genomic Data on Cocoa

Xavier Argout (CIRAD); Manuel Ruiz (CIRAD); Mathieu Rouard (INIBAP); Chris Turnbull (School of Plant Sciences, University of Reading); Claire Lanaud (CIRAD); Eric Rosenquist (ARS, USDA); Brigitte Courtois (CIRAD)

Poster B-66

TraceSearch: Implementation and Applications.

Adam Spargo (WTSI); Steve Leonard (WTSI); Guy Coates (WTSI); Jody Clements (WTSI); Roger Pettett (WTSI); Antony Cox (WTSI); Martin Widlake (WTSI); Zemin Ning (WTSI)

Poster B-67

Disease Portals: A Platform for Genetic and Genomic Research

Andrew Patzer (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Weihong Jin (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Mary Shimoyama (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Simon Twigger (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Anne Kwitek (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Howard Jacob (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Victoria Petri (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin); Jiali Chen (Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin)

Evolution and Phylogeny

Poster C-1

Elucidating the complex nature of gene fusion events for moving towards automatic quantification of protein function

Ashwin Sivakumar (Bioinformatics group, Division of Genetics, Institute of Biotechnology, University of Helsinki PO B); Christopher Wilton (Bioinformatics group, Division of Genetics, Institute of Biotechnology, University of Helsinki PO Bo); Swapan Mallick (Bioinformatics group, Division of Genetics, Institute of Biotechnology, University of Helsinki PO Bo); Liisa Holm (Bioinformatics group, Division of Genetics, Institute of Biotechnology, University of Helsinki PO Bo)

Poster C-2

Phylogenetic Analysis On Five STR- Loci Of Chromosome Y In Homo Sapiens Sapiens, Pan Troglodytes And Macaca Tonkeana

Everty M. Rocha (LASP/FIOCRUZ); Flora M. C. Fernandes (LASP/FIOCRUZ)

Poster C-3

Phylogenetic Analysis Of The Mitochondrial DNA HVS2 Loci

Thiago J Santana (LASP/FIOCRUZ); Flora M.C. Fernandes (LASP/FIOCRUZ)

Poster C-4

A phylogenetic reconstruction method based on genetic algorithms and hierarchical clustering

Ryosuke Watanabe (Computer Science Department, ITESM Campus Estado de México); Edgar E. Vallejo (Computer Science Department, ITESM Campus Estado de México); Enrique Morett (Department of Cellular Engineering and Biocatalysis, IBT UNAM)

Poster C-5

Generation and evolutionary fate of insertions of organelle DNA in the nuclear genome of rice and Arabidospsis

Christos Noutsos (AG Leister, Botanik I, Biologie, Ludwig Maximillian University); Dario Leister (AG Leister, Botanik I, Biologie, Ludwig Maximillian University)

Poster C-6

Intracellular transporters evolve slowly

Hajime Ohyanagi (Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics); Takashi Gojobori (Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics)

Poster C-7

In silico identification and analysis of new Artemis/Artemis-like sequences from fungal and metazoan species

Diego Bonatto (Universidade de Caxias do Sul); Martin Brendel (Universidade Estadual de Santa Cruz); João Antonio Pêgas Henriques (Universidade de Caxias do Sul)

Poster C-8

Molecular recognition and evolution in the olfactory receptor gene superfamily

Tsviya Olender (Department of Molecular Genetics and the Crown Human Genome Center, Weizmann Institute of Science); Ester Feldmesser (Department of Molecular Genetics and the Crown Human Genome Center, Weizmann Institute of Science); Ronny Aloni (Department of Molecular Genetics and the Crown Human Genome Center, Weizmann Institute of Science); Doron Lancet (Department of Molecular Genetics and the Crown Human Genome Center, Weizmann Institute of Science)

Poster C-9

How protein evolution measured by similarity change and stop codon incidence depends on the genetic code

Francisco Prosdocimi (UFMG); Henrique Melo (UFMG); Eduardo R Capanema (UFMG); J Miguel Ortega (UFMG)

Poster C-10

Evolutionary History of Multi-Domain Proteins

Diana Ekman (Stockholm Bioinformatics Center, Stockholm University); Åsa Björklund (Stockholm Bioinformatics Center, Stockholm University); Arne Elofsson (Stockholm Bioinformatics Center, Stockholm University)

Poster C-11

Evolution of Death-domain-superfamily in apoptosis pathway

Juilee Thakar (Department of Bioinformatics, University of Wuerzburg and Department of Physics, Pennsylvania state); Yogeshwar Kelkar (Integrated biosciences,Department of Biology, Pennsylvania state university); Christoph Borner (Center for biochemistry and molecular cell biology, University of Freiburg); Thomas Dandekar (Department of Bioinformatics, Wuerzburg)

Poster C-12

Do Genome-Escale Phylogenies Actually Detect True Trees?

Karla Yotoko (PUC-RS); Sandro Bonatto (PUC-RS)

Poster C-13

Rhogap Domain-containing Proteins Phylogeny – An Bayesian Approach

Marcelo Mendes Brandão (hematology And Hemotherapy Center - Unicamp); Karina Lucas Da Silva-brandão (zoology Department - Unicamp); Fernando Ferreira Costa (hematology And Hemotherapy Center - Unicamp); Sara Terezinha Olalla Saad (hematology And Hemotherapy Center - Unicamp)

Poster C-14

A new approach for using genome scans to detect recent positive selection in the human genome

Tang, Kun (Max Planck Institute for Evolutionary Anthropology); Stoneking, Mark (Max Planck Institute for Evolutionary Anthropology)

Poster C-15

Molecular evolution and structural aspects of plant alcohol dehydrogenase

Claudia Elizabeth Thompson (Universidade Federal do Rio Grande do Sul); Loreta Brandão de Freitas (Universidade Federal do Rio Grande do Sul); Francisco Mauro Salzano (Universidade Federal do Rio Grande do Sul); Osmar Norberto de Souza (Pontifícia Universidade Católica do Rio Grande do Sul)

Poster C-16

Comparative analysis of nucleotide polymorphism levels across different taxonomic units

Natalia Petit (Departamento de Genètica i Microbiología. Facultat de Ciències, Universitat Autònoma de Barcelona); Sonia Casillas (Departamento de Genètica i Microbiología. Facultat de Ciències, Universitat Autònoma de Barcelona); Raquel Egea (ica i Microbiología. Facultat de Ciències, Universitat Autònoma de Barcelona); Alfredo Ruiz (ica i Microbiología. Facultat de Ciències, Universitat Autònoma de Barcelona); Antonio Barbadilla (ica i Microbiología. Facultat de Ciències, Universitat Autònoma de Barcelona)

Poster C-17

Simplified Models of Evolution lead to Improved Prediction of Functional Linkage from Correlated Gain and Loss of Genes among Eukaryotes

Daniel Barker (School of Biology, University of St Andrews); Andrew Meade (School of Biological Sciences, University of Reading); Mark Pagel (School of Biological Sciences, University of Reading)

Poster C-18

reconstructing prokaryotic phylogeny applying a novel integrative approach

naryttza n. diaz (center for biotechnology (cebitec), universität bielefeld); lutz krause (center for biotechnology (cebitec), universität bielefeld); alfred pühler (lehrstuhl für genetik, universität bielefeld); kasten niehause (lehrstuhl für genetik, universität bielefeld); timm w. nattkemper (technische fakultät, universität bielefeld)

Poster C-20

Maximum likelihood inference of ancestral gene content for the bacterial septosome

Robson Francisco de Souza (Departament of Biochemistry, University of São Paulo, Brazil); Sandro José de Souza (Computational Biology Laboratory - Ludwig Institute for Cancer Research - São Paulo Branch, Brazil); Frederico José Gueiros Filho (Departament of Biochemistry, University of São Paulo, Brazil)

Poster C-21

C.A.S.S.I.O.P.E.

Lopez rascol (EA 3781); Gouret (EA 3781); Grusea (EA 3781); Danchin (AFMB); Pontarotti (EA 3781)

Poster C-22

Comparative Genomic Profiling of an Emerging Pathogen using a 7 Genomes Escherichia coli Microarray

Hanni Willenbrock (Center for Biological Sequence Analysis); Camilla Sekse (Norwegian School of Veterinary Science); Kristoffer Kiil (Center for Biological Sequence Analysis); Yngvild Wasteson (Norwegian School of Veterinary Science); David W. Ussery (Center for Biological Sequence Analysis)

Poster C-23

Conformational diversity and evolutionary sequence divergence of proteins

Maria Silvina Fornasari (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Gustavo Parisi (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes)

Poster C-24

Comparative sequence analysis of microbial genomes to identify potential virulence genes in Mycobacterium tuberculosis

Gordon Jamieson (IIDMM); Halimah Rabiu (IIDMM); Venu Vuppu (IIDMM); Nicola Mulder (IIDMM)

Poster C-25

Evolutionary mechanisms involved in the origin of a natural mutant rat from an inbred rat strain.

B.Kiran Kumar (NIN); Dr.N.Vijaya Bhanu (NIN); Dr.N.V.Giridharan (NIN); Dr.Vishnu Vardhan Rao (NIN)

Poster C-26

3D Phylogeny Explorer: Distinguishing paralogs, lateral transfer, and violations of the "molecular clock" assumption with 3D visualization

Namshin Kim (Molecular Biology Institute, Center for Genomics and Proteomics, Department of Chemistry and Biochem); Christopher Lee (Molecular Biology Institute, Center for Genomics and Proteomics, Department of Chemistry and Biochem)

Poster C-27

LOSS: an heuristic approach to incorporate prior information into prokaryotic genomic GC prediction

Hugo Naya (Unidad de Bioinformática, Institut Pasteur de Montevideo, Uruguay); Héctor Romero (Laboratorio de Organización y Evolución del Genoma, Sección Biomatemética, Facultad de Ciencias, Uru)

Poster C-28

Modeling the evolution of gene and protein interactions

Todd A. Gibson (University of Colorado Health Sciences Center); Debra S. Goldberg (University of Colorado)

Poster C-29

PhyloTree – An Integrated and Automatic Tool to Generate Phylogenetic Trees

Ana Luiza Bessa de Paula Barros (Computação-UECE); Gerardo Valdísio Rodrigues Viana (Computação-UECE); Tariana Mara Fernandes Batista (Computação-UECE); Gustavo Agusto de Lima Campos (Computação-UECE); Raimundo Bezerra da Costa (NUGEN-UECE); Rodrigo Maggioni (NUGEN-UECE); Diana Magalhães de Oliveira (NUGEN-UECE)

Poster C-30

Evolutionary inferences from the amino acid sequence of HC-Pro, a plant virus multifunctional protein

Antonio Sergio Kimus Braz (Depto Genetica - IBB - UNESP Botucatu); Ivan de Godoy Maia (Depto Genetica - IBB - UNESP Botucatu)

Poster C-31

Evolutionary Patterns At Different Codon Positions

Lee Bofkin (Cambridge University, European Bioinformatics Institute); Nick Goldman (European Bioinformatics Institute)

Poster C-32

Clustering to minimize genetic overlap between clades

Mukund Narasimhan (Microsoft Corp.); Nebojsa Jojic (Microsoft Corp.)

Poster C-33

Evolutionary Trends in Proteomes: exploring the Multidimensional Contributions

Tekaia (Institut Pasteur); Yeramian (Institut pasteur)

Poster C-34

Parallelizing Computationally Intensive Bootstrap Phylogenetic Analyses

Ricardo Gonzalez-Mendez (Department of Radiological Sciences, University of Puerto Rico School of Medicine); Hugh B. Nicholas (NRBSC, Pittsburgh Supercomputing Center); Alexander J. Ropelewski (NRBSC, Pittsburgh Supercomputing Center)

Poster C-35

Phylogenetic studies on UniProtKB/Swiss-Prot families and data from complete proteomes

Boeckmann (SIB); Kriventseva (University of Geneva); Amendolia (SIB); Bairoch (SIB & University of Geneva)

Poster C-36

Life with 22 amino acids

Hector Romero (Fac. Ciencias - UdelaR); Hector Musto (Fac. Ciencias - UdelaR); Vadim Gladyshev (University of Nebraska); Gustavo Salinas (Fac. Química - UdelaR)

Poster C-37

Genome alignment with lineage-specific rearrangement and gene flux rates

Aaron E. Darling (Dept. of Computer Science, Univ. of Wisconsin-Madison); Bob Mau (Dept. of Animal Health and Biomedical Sciences, Univ. of Wisconsin-Madison); Nicole T. Perna (Dept. of Animal Health and Biomedical Sciences and Genome Center, Univ. of Wisconsin-Madison)

Poster C-38

Comparison Between Complete Genomes of Vibrio Species

Patrícia P. Côgo (Institute of Computing, University of Campinas); João Meidanis (Institute of Computing, University of Campinas); Fabiano Thompson (Department of Genetics, Institute of Biology, Federal University of Rio de Janeiro)

Poster C-39

Evaluation of Brazilian web based program for classification of HIV-1 sequences

Luciano V Araujo (Department of Computer Science - Department of Computer Science - University of São Paulo); João E Ferreira (Department of Computer Science - University of São Paulo); Sabri S Sanabani (Fundação Pro-Sangue, Hemocentro, São Paulo, Brazil); Ester C Sabino (Fundação Pro-Sangue, Hemocentro, São Paulo, Brazil)

Poster C-40

Evaluating Orthology Detection Approaches in the Absence of a Gold Standard

Feng Chen (Biological Chemistry Graduate Program, University of Pennsylvania); Aaron J Mackey (Department of Biology, and Genomics Institute, University of Pennsylvania); Jeroen K Vermunt (Department of Methodology and Statistics, Tilburg University, Netherlands); David S Roos (Department of Biology, and Genomics Institute, University of Pennsylvania)

Poster C-41

Metamorphosis - Sorting by Weighted Inversions, Transpositions, and Inverted Transpositions

Martin Bader (University of Ulm); Simon Gog (University of Ulm); Enno Ohlebusch (University of Ulm)

Poster C-42

Anâtaxis, a Simple Deterministic Phylogenetic Reconstruction Algorithm

Bernhard Sonderegger (Département d'informatique, Université de Genève, Swiss Institute of Bioinformatics); Gabriel Bittar (Swiss Institute of Bioinformatics); Bastien Chopard (Département d'informatique, Université de Genève, Swiss Institute of Bioinformatics)

Poster C-44

Bayesian Partitioning for Phylogenetic Footprinting

Yussanne Ma (Division of Molecular Biosciences, Imperial College London); Dr. Maria De Iorio (Division of Epidemiology, Public Health and Primary Care, Imperial College London); Dr. Michael Stumpf (Division of Molecular Biosciences, Imperial College London)

Poster C-45

On the origin of microbial ORFans: Quantifying the strength of the evidence for viral lateral transfer

Yanbin Yin (University at Buffalo); Daniel Fischer (University at Buffalo)

Poster C-46

In-paralogs analysis of Insecta

Stanislav Vershenya (Bioinformatics, University of Wuerzburg); Joerg Schultz (Bioinformatics, University of Wuerzburg)

Human Health

Poster D-1

Development of prediction system in TYPE 2 DIABETES using molecular epidemiological data

Ju-young Lee (nih,korea); Seung-Woo Shin (nih,korea); Seol-hee Bae (nih,korea); Keun-Joon Park (nih,korea); In Ae Hur (nih,korea); Jeoung Ho Cha (nih,korea); Haesook Min (nih,korea); Eun Ji Hwang (nih,korea); Keun yong Park (nih,korea); Hyun-Woo Han (nih,korea); Hang-Suk Choi (nih,korea)

Poster D-2

A time series analysis tool for the analysis of neuronal activity in Parkinson disease

Patricio Yankilevich (Departmento de Ciencias de la Computación, Facultad de Ciencias Exactas y Naturales, Universidad de); Gustavo Murer (Departamento de Fisiología, Facultad de Medicina, Universidad de Buenos Aires); Luis Riquelme (Departamento de Fisiología, Facultad de Medicina, Universidad de Buenos Aires)

Poster D-3

Mixture Modeling in Fused Genotype and Phenotype Data

Benjamin Georgi (Max-Planck Institute for Molecular Genetics); M. Anne Spence (University of California at Irvine); Pam Flodman (University of California at Irvine); Alexander Schliep (Max-Planck Institute for Molecular Genetics)

Poster D-4

Discovering cell dynamics in pancreas fibrosis by means of microarray gene expression profiling

Aenne Glass (Bioinformatics Core Facility, Medical Faculty, University of Rostock); Thomas Karopka (Bioinformatics Core Facility, Medical Faculty, University of Rostock)

Poster D-5

Gene prioritization via genomic data fusion

Peter Van Loo (Human Genome Laboratory, Department of Human Genetics, Flanders Interuniversity Institute for Biotec); Stein Aerts (Laboratory of Neurogenetics, Department of Human Genetics, Flanders Interuniversity Institute for Bi); Diether Lambrechts (The Center for Transgene Technology and Gene Therapy, Flanders Interuniversity Institute for Biotech); Sunit Maity (The Center for Transgene Technology and Gene Therapy, Flanders Interuniversity Institute for Biotech); Bert Coessens (Bioinformatics group, K.U.Leuven ESAT-SCD); Frederik De Smet (The Center for Transgene Technology and Gene Therapy, Flanders Interuniversity Institute for Biotech); Leon-Charles Tranchevent (Bioinformatics group, K.U.Leuven ESAT-SCD); Bart De Moor (Bioinformatics group, K.U.Leuven ESAT-SCD); Peter Marynen (Human Genome Laboratory, Department of Human Genetics, Flanders Interuniversity Institute for Biotec); Bassem Hassan (Laboratory of Neurogenetics, Department of Human Genetics, Flanders Interuniversity Institute for Bi); Peter Carmeliet (The Center for Transgene Technology and Gene Therapy, Flanders Interuniversity Institute for Biotech); Yves Moreau (Bioinformatics group, K.U.Leuven ESAT-SCD)

Poster D-6

Analysis for Single nucleotide polymorphism related type 2 diabetes in insulin signaling pathway

Hang Suk Choi (NIH Korea); Seung-Woo Shin (NIH Korea); Eun Jung Jang (NIH Korea); Hyo-jeong Ban (NIH Korea); Keun-Joon Park (NIH Korea); Ji Hong Kim (NIH Korea); Chang-Bum Hong (NIH Korea); Sung-Hoon Lee (NIH Korea); Keun yong Park (NIH Korea); Hyun-Woo Han (NIH Korea); Ju-young Lee (NIH Korea)

Poster D-7

Exploratory analysis of multi-modal data including breast cancer microarray data

Christian Martin (Technical Faculty, Bielefeld University); Harmen grosse Deters (Technical Faculty, Bielefeld University); Tim W. Nattkemper (Technical Faculty, Bielefeld University)

Poster D-8

Genome wide analysis of factors regulating gene expression in liver

Andreas Teufel (Department of Medicine I, Johannes Gutenberg University, Mainz, Germany); Arndt Weinmann (Department of Medicine I, Johannes Gutenberg University, Mainz, GermanyDepartment of Medicine I); Markus Krupp (Department of Medicine I, Johannes Gutenberg University, Mainz, Germany); Matthias Budinger (Institute of Medical Biometry, Epidemiology and Informatics (IMBEI), Johannes Gutenberg University,); Peter R Galle (Department of Medicine I, Johannes Gutenberg University, Mainz, Germany)

Poster D-10

Gene Expression Profiling in Autoimmunity: Molecular Signatures of Systemic Lupus Erithematosus, Rheumatoid Arthritis and Type 1 Diabetes Mellitus

Guilherme Liberato Silva (Department of Genetics of Faculty of Medicine of Ribeirão Preto, University of São Paulo); Cristina Moraes Junta (Department of Genetics of Faculty of Medicine of Ribeirão Preto, University of São Paulo); Paula Sandrin Garcia (Department of Genetics of Faculty of Medicine of Ribeirão Preto, University of São Paulo); Diane Meyre Rassi (Department of Genetics of Faculty of Medicine of Ribeirão Preto, University of São Paulo); Eduardo A. Donadi (Department of Medicine of Faculty of Medicine of Ribeirão Preto, University of São Paulo); Geraldo Aleixo S. Passos Junior (Department of Genetics of Faculty of Medicine of Ribeirão Preto, University of São Paulo)

Poster D-11

From systems to symptoms: A combined genomics approach to expression-based breast cancer outcome prediction

Victor J. Weigman (Department of Biology, Program in Bioinformatics and Computational Biology, UNC-CH); Melissa Troester (Department of Pathology and Laboratory Medicine, UNC-CH); Xiaping He (Lineberger Comprehensive Cancer Center, UNC-CH); Chien-Hui Huang (Lineberger Comprehensive Cancer Center,UNC-CH); Charles M. Perou (Department of Pathology and Laboratory Medicine, Department of Genetics, Lineberger Comprehensive Ca)

Poster D-12

Molecular Homologous Modeling Of 3b-hsd2 Mutant Enzyme: Structure-function Aspects Of Pro222gln Mutation Correlates With The Experimental Data From A Patient With Congenital Adrenal Hyperplasia

Lucio Fabio Caldas Ferraz (CBMEG, Unicamp); Fernanda Soardi (CBMEG, Unicamp); Paula Falcão (Embrapa); Goran Neshich (Embrapa); Maricilda Palandi De Mello (CBMEG, Unicamp)

Poster D-13

Ad Hoc Biomedical Computational Tools: An Unfilled Niche

Craig R. Street (Biomedical Informatics Facility, Department of Pathology and Laboratory Medicine, University of Penn); David Wang (Biomedical Informatics Facility, Department of Pathology and Laboratory Medicine, University of Penn); David Birtwell (Biomedical Informatics Facility, Department of Pathology and Laboratory Medicine, University of Penn); Kevin Lux (Biomedical Informatics Facility, Department of Pathology and Laboratory Medicine, University of Penn); Alison W. Loren (Division of Hematology and Oncology, Department of Medicine, University of Pennsylvania, Philadelphi); Eline L. Prak (Department of Pathology and Laboratory Medicine, University of Pennsylvania, Philadelphia, PA 19104); David Fenstermacher (Biomedical Informatics Facility, Department of Pathology and Laboratory Medicine, University of Penn)

Molecular and Supramolecular Dynamics

Poster E-3

Analysis of Prion Protein: deeper understanding of protein motion from the molecular dynamics simulation

Masakazu Sekijima (Computational Biology Research Center / AIST); Chie Motono (Computational Biology Research Center / AIST); Yutaka Akiyama (Computational Biology Research Center / AIST); Tamotsu Noguchi (Computational Biology Research Center / AIST)

Poster E-4

Mutational Effects on Calbindin D9k Investigated by Molecular Dynamics Simulations

Sérgio Modesto Vechi (Instituto de Química e Biotecnologia, Universidade Federal de Alagoas); Fernando Luis Barroso da Silva (Faculdade de Ciências Farmacêuticas de Ribeirão Preto, Universidade de São Paulo)

Poster E-6

Flexibility adaptation of enzymes to low temperatures

Adrian Kalstein (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Sandra Maguid (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Gustavo Parisi (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Sebastian Fernandez-Alberti (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes)

Poster E-7

Sequence-structure-flexibility relationship in protein evolution

Sandra Maguid (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Gustavo Parisi (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Sebastian Fernandez-Alberti (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Julian Echave (Instituto Nacional de Investigaciones Fisicoquimicas Teoricas y Aplicadas, Universidad Nacional de L)

Poster E-8

Dynamics of catalysis and inhibition in oligopeptidases: Natural peptide structures as promising antihypertensive agents

Jorge H. Fernandez (Center of Applied Toxinology –Instituto Butantan, S.P., Brazil); Vanessa Rioli (Center of Applied Toxinology –Instituto Butantan, S.P., Brazil); Goran Neshich (Structural Bioinformatics Laboratory, CNPTIA – EMBRAPA, Campinas, S.P., Brazil); Emmer S. Ferro (Departamento de Biologia Celular e Desenvolvimento, ICB - USP, S.P., Brazil); Fernanda C. Portaro (Center of Applied Toxinology –Instituto Butantan, S.P., Brazil); Antonio C. M. Camargo (Center of Applied Toxinology –Instituto Butantan, S.P., Brazil)

Poster E-9

Dynamical System Modeling of the Estrogen Transcription Control Network

Marcelo Ris (IME-USP); Junior Barrera (IME-USP); Helena Brentani (Hospital do Câncer)

Poster E-10

Structural Comparative Studies of Brazilian HIV-1 Protease Mutants: Molecular Modeling and X-Ray Data

Paulo Ricardo Batista (IBCCF / UFRJ); Pedro A. G. Lapido Loureiro (IBCCF / UFRJ); Mario Sanches (Physics Department / USP / Sao Carlos); Igor Polikarpov (Physics Department / USP / Sao Carlos); Pedro Geraldo Pascutti (IBCCF / UFRJ)

Poster E-11

Simulation of Amino Acid Solvation Structure in Transmembrane Helices and Implications for Membrane Protein Folding

Anna Johansson (Stockholm Bioinformatics Center, Stockholm University); Erik Lindahl (Stockholm Bioinformatics Center, Stockholm University)

Poster E-12

A Hierarchical Approach to Predict Protein Conformational Changes in terms of Localized Rearrangements using Temporal and Spatial Constraints

Arvind Ramanathan (Department of Computational Biology, Carnegie Mellon University); Tatyana Mamonova (Department of Chemistry, Carnegie Mellon University); Maria Kurnikova (Department of Chemistry, Carnegie Mellon University);

Ontologies

Poster F-1

Time-courses of gene expression during development of murine tooth germs by analysis of microarray data

Harald Osmundsen (Univ. of Oslo); Maria (Landin); Steinar (Risnes)

Poster F-3

Protein Structure Homology Modelling assisted by Ontology

Kellen Pinagé (Computing Science Department, Federal University of Amazonas); Virgínia Brilhante (Computing Science Department, Federal University of Amazonas)

Poster F-5

GOLIAS: Gene Ontology Library Analyzer for SAGE

Gustavo GL Costa (Universidade Estadual de Campinas- Hemocentro); Anderson Ferreira da Cunha (Universidade Estadual de Campinas- Hemocentro); Tarcísio de Souza Peres (Universidade Estadual de Campinas- Hemocentro); Tiago Ferraz Machado (Universidade Estadual de Campinas- Hemocentro); Fernando Ferreira Costa (Universidade Estadual de Campinas- Hemocentro)

Proteomics

Poster G-1

An Integrated Strategy In 2DE Maps Analysis For The Identification Of Potential Discriminants Between Different Clinical Conditions

Pattini L (Bioengineering Department, Polytechnic University of Milan, Milan, Italy); Cannistraci CV (Bioengineering Department, Polytechnic University of Milan, Milan, Italy); Conti A (Proteome Biochemistry, San Raffaele Scientific Institute, Milan, Italy); Iannaccone S (Neurology Department, San Raffaele Scientific Institute, Milan, Italy); Alessio M (Proteome Biochemistry, San Raffaele Scientific Institute, Milan, Italy); Cerutti S (Bioengineering Department, Polytechnic University of Milan, Milan, Italy)

Poster G-2

Comparison of Gene Expression in Murine Retina by SAGE and 2D-PAGE

Tim Alcon (Bioinformatics and Computational Biology, Iowa State University); Heather West Greenlee (Biomedical Sciences, Iowa State University); Vasant Honavar (Computer Science, Iowa State University)

Poster G-3

Molecular mechanics studies of pyrophosphorylase, template enzyme involved in chitin metabolic pathway

Manoelito C. Dos Santos Junior (Programa de Pós-Graduação em Biotecnologia); Sandra A. Assis (Departamento de Saúde); Aristóteles Goes Neto (Departamento de Biologia); Sandra Helena Cruz (Universidade de São Paulo); Alex Guterres Taranto (Departamento de Saúde)

Poster G-4

Sequence structure of the proteins based on the conservative elements

Yehoshua Sobolevsky (Genome Diversity Center, Haifa University); Edward N. Trifonov (Genome Diversity Center, Haifa University)

Poster G-6

Proteomics Approach for Exploring Sperm Antigens Involved in Epididymal Maturation

Amol R. Suryawanshi (Department of Gamete Immunobiology, National Institute for Research in Reproductive Health (ICMR), M); Shagufta A. Khan (Department of Gamete Immunobiology, National Institute for Research in Reproductive Health (ICMR), M); Priyanka P. Parte (Department of Gamete Immunobiology, National Institute for Research in Reproductive Health (ICMR), M); Vrinda V. Khole (Department of Gamete Immunobiology, National Institute for Research in Reproductive Health (ICMR), M)

Poster G-7

Learning Classifiers for Assigning Protein Sequences to Subcellular Localization Families

Carson Andorf (Iowa State University); Drena Dobbs (Iowa State University); Vasant Honavar (Iowa State University)

Poster G-8

Prediction system for chemical structures of glycolipids using MALDI-TOF MS and MS/MS data

Masahiro ITO (Department of Bioscience and Bioinformatics, Ritsumeikan University); Yuki Matsumuro (Department of Bioscience and Bioinformatics, Ritsumeikan University)

Poster G-9

Study on the role of bgl operon of E.coli in stationary phase

Ranjna Madan (Indian Institute of Science); S. Mahadevan (Indian Instiute of Science)

Poster G-10

Detection of post-translational modifications of proteins by mass shift decomposition in peptide mass fingerprints

Axel Rack (Max Planck Institute for Infection Biology); Peter R. Jungblut (Max Planck Institute for Infection Biology); Klaus-Peter Pleissner (Max Planck Institute for Infection Biology)

Poster G-12

Beating the Noise: New Statistical Methods for Detecting Signals in MALDI-TOF Spectra below Noise Level

Tim OF Conrad (Free University of Berlin, Department of Mathematics and Computer Science); Alexander Leichtle (Institute of Laboratory Medicine, Clinical Chemistry and Molecular Diagnostics, University Hospital); Andre Hagehuelsmann (Microsoft Research); Elmar Diederichs (Free University of Berlin, Department of Mathematics and Computer Science); Sven Baumann (Institute of Laboratory Medicine, Clinical Chemistry and Molecular Diagnostics, University Hospital); Joachim Thiery (Institute of Laboratory Medicine, Clinical Chemistry and Molecular Diagnostics, University Hospital); Christof Schuette (Free University of Berlin, Department of Mathematics and Computer Science)

Poster G-13

A Wrapper-based Approach for Protein Identification in PPI Networks

YongHo Lee (Electronics and Telecommunications Research Institute (ETRI)); JaeHun Choi (Electronics and Telecommunications Research Institute (ETRI)); MyungEun Lim (Electronics and Telecommunications Research Institute (ETRI)); SooJun Park (Electronics and Telecommunications Research Institute (ETRI))

Poster G-14

Storage, management and exchange of experimental and validated proteomics data considering HUPO-PSI standards

Klaus-Peter Pleissner (Max Planck Institute for Infection Biology , Berlin, Germany); Benjamin Arndt (University of Applied Sciences, Berlin, Germany); Daniel Paape (Max Planck Institute for Infection Biology , Berlin, Germany); Toni Aebischer (Max Planck Institute for Infection Biology , Berlin, Germany); Monika Schmid (Max Planck Institute for Infection Biology , Berlin, Germany); Robert Stein (Max Planck Institute for Infection Biology , Berlin, Germany); Peter R. Jungblut (Max Planck Institute for Infection Biology , Berlin, Germany)

Poster G-15

Modified Random Forest Algorithm for Biomarker Identification in Clustered Mass Spectrometry Data

Yuliya Karpievitch (Dept. of Biostatistics and Applied Mathematics, M. D. Anderson Cancer Center, University of Texas); Elizabeth Hill (Dept. of Biostatistics, Bioinformatics and Epidemiology, Medical University of South Carolina); Timothy Millar (Dept. of Gastroenterology and Hepatology, Medical University of South Carolina); Adam Smolka (Dept. of Gastroenterology and Hepatology, Medical University of South Carolina); Jonas Almeida (Dept. of Biostatistics and Applied Mathematics, M. D. Anderson Cancer Center, University of Texas); Brenda Hoffman (Dept. of Gastroenterology and Hepatology, Medical University of South Carolina)

Poster G-16

Evaluation of predicted human protein networks

Mario Albrecht (Max Planck Institute for Informatics); Fidel Ramirez (Max Planck Institute for Informatics); Andreas Schlicker (Max Planck Institute for Informatics); Yassen Assenov (Max Planck Institute for Informatics); Hagen Blankenburg (Max Planck Institute for Informatics); Carola Huthmacher (Max Planck Institute for Informatics); Thomas Lengauer (Max Planck Institute for Informatics)

Poster G-17

SuperQual: A tool to assess similarity of liquid chromatography mass spectrometry data

Lukas Mueller (IMSB); Markus Mueller (IMSB); Reto Ossola (IMSB); Ruedi Aebersold (IMSB)

Poster G-18

Comparative Assessment of Large-Scale Maps of the Human Protein Interactome

Matthias E. Futschik (Institute for Theoretical Biology, Humboldt-University); Gautam Chaurasia (Max-Delbrück-Centrum)

Poster G-19

Identification of Thermostability in Microorganisms using Compression Algorithms

Van der Linden, M. G. (Laboratório Nacional de Computação Científica); Batista, L. V. (Universidade Federal da Paraíba); Farias, S. T. (Universidade Federal de Minas Gerais); Marques, J. R. T. (Universidade Federal da Paraíba)

Poster G-20

Enhanced protein identification and gene annotation from MS/MS data

Jens Allmer (Institute for Plant Biochemistry and Biotechnology, Westfälische Wilhelms University, Münster, Germa); Bianca Naumann (Institute for Plant Biochemistry and Biotechnology, Westfälische Wilhelms University, Münster, Germa); Monica Zhang (Institute for Plant Biochemistry and Biotechnology, Westfälische Wilhelms University, Münster, Germa); Michael Hippler (Institute for Plant Biochemistry and Biotechnology, Westfälische Wilhelms University, Münster, Germa)

Poster G-21

The iProXpress Knowledge System for Proteomic Studies

Hongzhan Huang (Georgetown University Medical Center); Zhang-Zhi Hu (Georgetown University Medical Center); Xin Yuan (Georgetown University Medical Center); Peter McGarvey (Georgetown University Medical Center); An Chi (University of Virginia); Satya Saxena (National Institute on Aging); Cathy H. Wu (Georgetown University Medical Center)

Poster G-22

From peptides - identified by mass spec - to biomolecular pathways

Claus A. Andersen (Sienabiotech SpA); Stefano Gotta (Sienabiotech SpA); Roberto Raggiaschi (Sienabiotech SpA); Andreas Kremer (Sienabiotech SpA); Eduardo Gonzalez Couto (Sienabiotech SpA); Rainer Kern (Sienabiotech SpA); Georg C. Terstappen (Sienabiotech SpA)

Poster G-23

Alignment-Independent Homology Estimator

Avihay Apatoff (The Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan University); Eddo Kim (The Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan University); Yossef Kliger (Compugen Ltd.)

Poster G-24

Mapping epitope candidates from HIV-1 Brazilian sequences for vaccine Development

Artur T.L. Queiróz (LASP/CPqGM/FIOCRUZ, Salvador, Bahia, Brazil.); Luciane A. Santos (LASP/CPqGM/FIOCRUZ, Salvador, Bahia, Brazil.); Tulio de Oliveira (Oxford University, U.K.); Ramon Moreau (LASP/CPqGM/FIOCRUZ, Salvador, Bahia, Brazil.); Bernardo Galvão-Castro (LASP/CPqGM/FIOCRUZ, Salvador, Bahia, Brazil; FBDC/EBMSP, Salvador, Bahia, Brazil.); Luis Carlos Alcântara (LASP/CPqGM/FIOCRUZ, Salvador, Bahia, Brazil; FBDC/EBMSP, Salvador, Bahia, Brazil.)

Poster G-26

Bioinformatic analysis of Gluconacetobacter diazotrophicus proteome

Lery, LMS (IBCCF/UFRJ); von Kruger, WMA (IBCCF/UFRJ); Bisch, PM (IBCCF/UFRJ)

Poster G-27

IntAct - An extensible open source framework for molecular interactions

H. Hermjakob (EBI); S Kerrien (EBI)

Sequence Analysis

Poster H-1

Analysis of the Conservation of Regulation Systems in Firmicutes

Nicolas Sierro (The Institute of Medical Science, The University of Tokyo); Kenta Nakai (The Institute of Medical Science, The University of Tokyo)

Poster H-2

GINGA - Graphical INterface for comparative Genome Analysis

Alexandre Rossi Paschoal (LabInfo, LNCC); Marcelo Marques Zerillo (Institute of Biology, USP); Luiz Gonzaga Paula de Almeida (LabInfo, LNCC); Oberdan de Lima Cunha (LabInfo, LNCC); Ana Tereza Ribeiro de Vasconcelos (LabInfo, LNCC); Claudia Barros Monteiro-Vitorello (LabInfo, LNCC)

Poster H-3

Splice Form Prediction using Machine Learning

Gunnar.Raetsch@tuebingen.mpg.de (Friedrich Miescher Laboratory of the Max Planck Society); Sören Sonnenburg (Fraunhofer FIRST); Jagan Srinivasan (Caltech); Klaus-Robert Müller (Fraunhofer FIRST); Ralf Sommer (MPI Developmental Biology); Bernhard Schölkopf (MPI Biological Cybernetics)

Poster H-4

Machine Learning Algorithms for Polymorphism Detection

Georg Zeller (Friedrich Miescher Laboratory of the Max Planck Society); Gabriele Schweikert (MPI Biological Cybernetics); Richard Clark (MPI Developmental Biology); Stefan Ossowski (MPI Developmental Biology); Norman Warthman (MPI Developmental Biology); Paul Shinn (The Salk Institute); Kelly Frazer (Perlegen Sciences Inc.); Joe Ecker (The Salk Institute); Daniel Huson (University of Tübingen); Detlef Weigel (MPI Developmental Biology); Bernhard Schölkopf (MPI Bilogical Cybernetics); Gunnar Rätsch (Friedrich Miescher Laboratory of the Max Planck Society)

Poster H-5

Accurate Global Alignment Statistics: An Application to Searching for Protein Domains

Maricel G. Kann (NCBI); Sergey L. Sheetlin (NCBI); Yonil Park (NCBI); Stephen H. Bryant (NCBI); John L. Spouge (NCBI)

Poster H-6

Regulatory Content of Vertebrate Enhancers

Altuna Akalin (Computational Biology Unit, Bergen Center for Computational Science, Univ. of Bergen, Norway); Boris Lenhard (Computational Biology Unit, Bergen Center for Computational Science, Univ. of Bergen, Norway)

Poster H-7

Classification of HCV Using Whole Genome Method

Raymond Wan (Gilead Sciences Inc.); Eugenia Bastos (SAS Institute)

Poster H-8

Prediction of Peptide Binding to MHC Class I Using Sliding Motifs and Regression Trees

Ana Paula Sales (Computational Biology and Bioinformatics Program, Duke University); Georgia D. Tomaras (Department of Surgery, Duke University Medical Center); Thomas B. Kepler (Department of Biostatistics and Bioinformatics, Duke University)

Poster H-9

Improved membrane protein topology prediction by domain assignments

Andreas Bernsel (Stockholm Bioinformatics Center, Stockholm University); Gunnar von Heijne (Department of Biochemistry and Biophysics, Stockholm University)

Poster H-10

Successful clustering of ortholog groups by Bidirectional Best Hit (BBH) using organisms modeled from a single ancestral via stepwise mutation

Francisco Prosdocimi (UFMG); Maurício A Mudado (UFMG); J Miguel Ortega (UFMG)

Poster H-11

Hidden Markov Models for Gene Finding in Viral Genomes

Saskia de Groot (Department of Statistics, University of Oxford); Stephen McCauley (Department of Statistics, University of Oxford); Jotun Hein (Department of Statistics, University of Oxford)

Poster H-12

Regulatory motif discovery pipeline for co-regulated gene sets and chromatin-IP data: from motifs to functional instances

Laurence Ettwiller (EMBL); Benedict Paten (EBI); Mirana Ramialison (EMBL); Ewan Birney (EBI); Jochen Wittbrodt (EMBL)

Poster H-13

Combined ab initio and comparative analysis of putative cis regulatory modules (CRMs)

Nora (Pierstorff); Rodrigo (Nunes da Fonseca); Casey (Bergman); Thomas (Wiehe)

Poster H-14

Markov Models of Genome Segmentation

Vivek Thakur (School of Information Technology, Jawaharlal Nehru University, India); R. K. Azad (Dept. of Biological Sciences, University of Pittsburgh, USA); R. Ramaswamy (School of Physical Sciences, Jawaharlal Nehru University, India)

Poster H-16

RASTA-Bacteria: a tool for the annotation of Toxin/Antitoxin modules in bacterial genomes

Emeric SEVIN (UMR6061-CNRS); Frédérique Barloy-Hubler (UMR6061-CNRS)

Poster H-17

Construction of dephosphorylation site prediction system

Seong-Jin Park (Hanyang university); Soo-Young Cho (Hanyang university); Young-Seek Lee (Hanyang university)

Poster H-18

Evolution of the Inorganic Pyrophosphatase Family

Joel Hedlund (IFM Bioinformatics, Linköping university, Linköping, Sweden); Roberto Cantoni (CGB, Karolinska Institute, Stockholm, Sweden; Department of physical sciences, "Federico II" Univers); Margareta Baltscheffsky (Arrhenius Laboratories, Stockholm university, Stockholm, Sweden); Herrick Baltscheffsky (Arrhenius Laboratories, Stockholm university, Stockholm, Sweden); Bengt Persson (IFM Bioinformatics, Linköping university, Linköping, Sweden; CGB, Karolinska Institute, Stockholm, S)

Poster H-19

Regular Expression Pattern Matching Using Suffix Array amd Its Application to Motif Search

Aki Hasegawa (Informatics Infrastructure Team, Genome Core Technology Facilities, Genomic Sciences Center, RIKEN); Akihiko Konagaya (Informatics Infrastructure Team, Genome Core Technology Facilities, Genomic Sciences Center, RIKEN)

Poster H-20

A De Bruijn Subgraph Approach to Repeat Identification in Incompletely Sequenced Genomes

José Augusto Amgarten Quitzau (University of Bielefeld); Jens Stoye (University of Bielefeld)

Poster H-21

n-Nucleotide Frequency Analysis for Detecting Conserved String Pattern in Mus musculus Genome

Fumikazu KONISHI (RIKEN GSC); Aki Hasegawa (RIKEN GSC); Akihiko KONAGAYA (RIKEN GSC)

Poster H-22

Protein solubility assessment using support vector machine

Pawel Smialowski (Technical University Muenchen); Antonio Martin-Galiano (Technical University Muenchen); Tobias Girschick (Technical University Muenchen); Dmitrij Frishman (Technical University Muenchen)

Poster H-23

Are competitive tandem splice donors utilized to shift out-of-frame and trigger nonsense-mediated decay?

Ralf H. Bortfeldt (Friedrich Schiller University of Jena); Stefan Schuster (Friedrich Schiller University of Jena); Dirk Holste (Institute of Molecular Pathology Vienna)

Poster H-24

Characterization of putative chromosomal rearrangements related to chromosomes ends between Leishmania species. An in silico approach

Patrícia de Cássia Ruy (FMRP/FFCLRP-USP); Loislena Oliveira Brito (FMRP-USP); Elton José Rosas de Vasconcelos (FMRP-USP); Raony Guimarães Correa do Carmo Lisboa Cardenas (FMRP/FFCLRP-USP); Ângela Kaysel Cruz (FMRP-USP); Jeronimo Conceição Ruiz (FMRP-USP)

Poster H-25

ProtComp: Hybrid approach of predicting sub-cellular localization of animal, plants and bacterial proteins

Victor Solovyev (Royal Holloway, University of London, Egham, Surrey,TW20 0EX, UK); Alexander Bachinsky (Softberry Inc., 116 Radio Circle, Suite 400, Mount Kisco, NY,10549,USA)

Poster H-26

Evolution of the Inorganic Pyrophosphatase Family

Joel Hedlund (IFM Bioinformatics, Linköping University, Linköping, Sweden); Roberto Cantoni (CGB, Karolinska Institute, Stockholm, Sweden; Department of Physical Sciences, "Federico II" Univers); Margareta Baltscheffsky (Arrhenius Laboratories, Stockholm University, Stockholm, Sweden); Herrick Baltscheffsky (Arrhenius Laboratories, Stockholm University, Stockholm, Sweden); Bengt Persson (IFM Bioinformatics, Linköping University, Linköping, Sweden; CGB, Karolinska Institute, Stockholm, S)

Poster H-27

Predicting Nuclear Localization

John Hawkins (University of Queensland); Mikael Boden (University of Queensland)

Poster H-28

On the the fidelity of assembly, binning and gene calling of metagenomes using simulated datasets

Konstantinos Mavromatis (Joint Genome Institute); Natalia Ivanova (Joint Genome Institute); Kerrie Barry (Joint Genome Institute); Harris Shapiro (Joint Genome Institute); Eugene Goltsman (Joint Genome Institute); Alice McHardy (IBM Thomas J. Watson Research Center.); Isidore Rigoutsos (IBM Thomas J. Watson Research Center.); Asaf Salamov (Joint Genome Institute); Frank Korzenieski (Joint Genome Institute); Miriam Land (Oak Ridge National Laboratory); Philip Hugenholtz (Joint Genome Institute); Nikos C Kyrpides (Joint Genome Institute)

Poster H-29

Gnomon - NCBI gene prediction tool for eukaryotic genomes

Alexander Souvorov (NCBI); Yuri Kapustin (NCBI); Boris Kiryutin (NCBI); Vyacheslav Chetvernin (NCBI); Tatiana Tatusova (NCBI); David Lipman (NCBI)

Poster H-30

Prediction of Transcription Factor Binding Sties by a Novel Computational Algorithm

Daekwan Seo (Virginia Commonwealth University); Moritoshi Yasunaga (University of Tsukuba); Insook Kim (University of Araknsas Medical Sciences); Jung H. Kim (University of Arkansas)

Poster H-31

Microarray Layout and the Quadratic Assignment Problem

Sergio A. de Carvalho Jr (Graduiertenkolleg Bioinformatik and International NRW Graduate School in Bioinformatics and Genome R); Sven Rahmann (Algorithms and Statistics for Systems Biology group, Genome Informatics, Technische Fakultät, Bielef)

Poster H-32

Characterization of homogeneous and heterogeneous regions in the human genome and compositional features of individual chromosomes

Victor Sabbia (Laboratorio de Organización y Evolución del Genoma); Rosina Piovani (Laboratorio de Organización y Evolución del Genoma); Hugo Naya (Insituto Pasteur Montevideo); Hector Musto (Laboratorio de Organización y Evolución del Genoma)

Poster H-33

Probabilistic reasoning on occurrences of related binding site model matches

Rainer Pudimat (University of Freiburg); Rolf Backofen (University of Freiburg)

Poster H-34

An in silico and in vivo study on the Caulobacter crescentus SOS regulon

Apuã C. M. Paquola (Depto. de Microbiologia, Instituto de Ciências Biomédicas, Universidade de São P aulo); Raquel P. Rocha (Depto. de Microbiologia, Instituto de Ciências Biomédicas, Universidade de São P aulo); Rodrigo S. Galhardo (Depto. de Microbiologia, Instituto de Ciências Biomédicas, Universidade de São P aulo); Carlos F. M. Menck (Depto. de Microbiologia, Instituto de Ciências Biomédicas, Universidade de São P aulo)

Poster H-35

Identifying functional domains in a family of restriction endonucleases where DNA recognition, methyltransferase and endonuclease functions reside in a single polypeptide.

Richard D. Morgan (New England Biolabs)

Poster H-36

Sequence Comparison by Sequence Harmony Identifies Sub-type Specific Sites for Smad Receptor Binding

Walter Pirovano (IBIVU, Free University Amsterdam); K. Anton Feenstra (IBIVU, Free University Amsterdam); Jaap Heringa (IBIVU, Free University Amsterdam)

Poster H-37

TreeDomViewer: A tool for the visualization of phylogeny and protein domain structure

Blaise T.F Alako (Laboratory of Bioinformatics, Wageningen University); Daphne Rainey (Keygene NV); Harm Nijveen (Laboratory of Bioinformatics, Wageningen University); Jack A.M. Leunissen (Laboratory of Bioinformatics, Wageningen University)

Poster H-38

A Motif Sampler for the Discovery of Conserved Motif Pairs with Periodic Spacing

Erik Larsson (Department of Biomedicine, Göteborg University); Olle Nerman (Department of Mathematical Statistics, Chalmers University of Technology); Per Lindahl (Department of Biomedicine, Göteborg University)

Poster H-39

Comparative structure-based analysis of amino acid composition in proteins adapted to cold and hot environments

Gisle Sælensminde (University of Bergen); Inge Jonassen (University of Bergen)

Poster H-40

GFMerge - A method for merging of gene predictions

Sebastian Spiegler (Technical University Ilmenau, Germany; Wellcome Trust Sanger Institute, Cambridge, UK); Marie-Adele Rajandream (Wellcome Trust Sanger Institute, Cambridge, UK); Neil Hall (The Institute for Genomic Research (TIGR), Maryland, USA); Kim Rutherford (Genetics Department, Cambridge University, UK); Arnaud Kerhornou (Genome Bioinformatics Research Group, Barcelona, Spain)

Poster H-41

Large-scale detection of mutations potentially responsible of genetic disorders

Kais Ghedira (Institute Pasteur of Tunis); Walid Bedhiafi (Institut Pasteur de Tunis); Hela Ouaili (Ecole de Supérieure des Statistique et de l'Analyse de l'Information); Koussay Dellagi (Institute Pasteur of Tunis); Alia Benkahla (Institute Pasteur of Tunis)

Poster H-42

Discriminatory features of sequence profiles for transcription factor binding site discovery

Gerald Quon (Department of Biochemistry, University of Toronto); Shoshana Wodak (Structural Biology and Biochemistry, The Hospital for Sick Children)

Poster H-43

Vector Graphics to improve Blast graphic representations

Rafael Jimenez (NBN)

Poster H-44

"Co-transcriptional" prediction of splice sites and analysis of spliceosomal introns in human pre-mRNAs

Kai Wang (Center for Biological Sequence Analysis, Biocentrum, Technical University of Denmark); Rasmus Wernersson (Center for Biological Sequence Analysis, Biocentrum, Technical University of Denmark); Søren Brunak (Center for Biological Sequence Analysis, Biocentrum, Technical University of Denmark)

Poster H-45

yrGATE: Web Based Community Gene Annotation for Eukaryotes

Matthew Wilkerson (Department of Genetics, Development, and Cell Biology, Iowa State University); Shannon Schlueter (Department of Genetics, Development, and Cell Biology, Iowa State University); Volker Brendel (Department of Genetics, Development, and Cell Biology and Department of Statistics, Iowa State Unive)

Poster H-46

Telomerase RNA searching using an Infernal-based pipeline

Ariane Machado Lima (Instituto de Matemática e Estatística, Universidade de São Paulo); Sean R. Eddy (Department of Genetics, Washington University); Hernando A. del Portillo (Instituto de Ciências Biomédicas II, Universidade de São Paulo); Alan Mitchell Durham (Instituto de Matemática e Estatística, Universidade de São Paulo)

Poster H-47

Development of an integrated Comparative Genomics environment

Hamilton Ganesan (Bioinformatics, University of Pretoria); Fourie Joubert (Bioinformatics, University of Pretoria)

Poster H-48

Chaos Game Representation and Vector Quantization (CGR-VQ): a new computational tool for the identification of transcription factor binding sites

Dominik Beck (Biomathematics Group, ITQB-UNL / INESC-ID); Jonas S Almeida (Dept Biostatistics and Applied Mathematics, Univ. Texas MDAnderson Cancer Center / Biomathematics Gr); Ana Teresa Freitas (IST/ INESC-ID); Arlindo L. Oliveira (IST/ INESC-ID); Susana Vinga (INESC-ID /FCM-UNL)

Poster H-49

New EST trimming procedure applied to SUCEST sequences

Christian Baudet (Institute of Computing - Unicamp); Zanoni Dias (Institute of Computing - Unicamp)

Poster H-50

M-Coffee: combining multiple sequence alignment methods with T-Coffee

Iain Wallace (University College Dublin,Ireland); Orla OSuillivan (University College Dublin,Ireland); Desmond Higgins (University College Dublin,Ireland); Cedric Notredame (Laboratoire Information Génomique et Structurale, CNRS Marseille,France)

Poster H-51

Constrained Alignment Using Cluster Tree Elimination

Sebastian Will (University of Freiburg); Anke Busch (University of Freiburg); Rolf Backofen (University of Freiburg)

Poster H-52

Web Based Computational Tools for Predicting G-quadruplexes in Mammalian Genes

Oleg Kikin (Ramapo College of NJ); Rumen Kostadinov (University of Pennsylvania); Nishtha Malhotra (Ramapo College of NJ); Manuel Viotti (Ramapo College of NJ); Lawrence DAntonio (Ramapo College of NJ); Paramjeet S. Bagga (Ramapo College of NJ)

Poster H-53

Using latent semantic indexing (LSI) to evaluate the similarity of sets of sequences without multiples alignments character-by-character

Braulio RGM Couto (UNI-BH); Ana Paula Ladeira (UNI-BH)

Poster H-54

Software usage testing for studies of genetic variability in marine shrimp aquaculture

Michel Toth Kamimura (NUGEN-UECE); Samara Cardoso da Silva (NUGEN-UECE); Fátima de Cássia Evangelista de Oliveira (NUGEN-UECE); Sara Ramos Medeiros (NUGEN-UECE); Daniel Pascoalino Pinheiro (NUGEN-UECE); Rodrigo Maggioni (NUGEN-UECE); Diana Magalhães de Oliveira (NUGEN-UECE)

Poster H-55

HMM-based subsequence feature map for Protein Classification and Remote Homology Detection

Omer Sinan Sarac (Dept. of Computer Engineering, Middle East Technical Univeristy); Volkan Atalay (Dept. of Computer Engineering, Middle East Technical Univeristy); Rengul Cetin-Atalay (Dept. of Molecular Biology and Genetics, Bilkent Univeristy)

Poster H-56

ARTS: Accurate Recognition of Transcription Starts

Sören Sonnenburg (Fraunhofer FIRST); Alexander Zien (MPI for biological Cybernetics and Friedrich Miescher Laboratory); Fabio de Bona (Friedrich Miescher Laboratory); Gunnar Rätsch (Friedrich Miescher Laboratory)

Poster H-57

Construction of multiple transcription factor prediction system

Min-Young Park (Hanyang university); Soo-Young Cho (Hanyang university); Young-Seek Lee (Hanyang university)

Poster H-58

An Automated Combination of Sequence Motif Kernels for Protein Subcellular Localization

Alexander Zien (MPI for Biological Cybernetics); Cheng Soon Ong (Friedrich Miescher Laboratory and MPI for Biological Cybernetics)

Poster H-59

XGrid Implementation of the InterProScan for the Epichloe festucae Genome Project

Wayne E. Beech (Computing Services, University of Kentucky); V. Cody Bumgardner (Department of Computer Science, University of Kentucky); Uliana Hesse (Plant Pathology, University of Kentucky); Ch. David Van Horn (Department of Computer Science, University of Kentucky); Jerzy W. Jaromczyk (Department of Computer Science, University of Kentucky); Christopher Schardl (Plant Pathology, University of Kentucky)

Poster H-60

Improvements in ELM Resource Filtering and Web Service Technology Implementation

Claudia Chica (EMBL); Kate Gould (EMBL); Allegra Via (University of Rome Tor Vergata); Jan Christian Bryne (Bergen Centre for Computational Science); Francesca Diella (EMBL); Pal Puntervoll (Bergen Centre for Computational Science); Rein Aasland (University of Bergen); Manuela Helmer-Citterich (University of Rome Tor Vergata); Toby Gibson (EMBL)

Poster H-61

Identification of replication origins in archaea using a moving window model along the double strands

Yonghong Wang (Department of Physics, Tianjin University, Tianjin, 300072, China; School of Computer Science and I); Xiaolei Liu (Department of Physics, Tianjin University, Tianjin, 300072, China)

Poster H-62

Chisel - a Framework for Identification and Characterization of Taxonomic and Phenotypic Versions of Enzymes

Alexis Rodriguez (Argonne National Laboratory); Yi Zhang (Argonne National Laboratory); Natalia Maltsev (Argonne National Laboratory); Elizabeth Marland (Argonne National Laboratory)

Poster H-64

Precisely Mapping Structural Variations in the Human Genome by Splitting Shotgun Reads

Zemin Ning (The Wellcome Trust Sanger Institute)

Poster H-65

DP-BIND: a sequence-based application of multiple machine learning methods to predict DNA-binding sites in DNA-binding proteins.

Igor Kuznetsov (University at Albany); Seungwoo Hwang (University at Albany); Zhenkun Gou (University at Albany)

Poster H-66

Analyzing the effects of generalizations implicit within the BLAST algorithm

Mileidy Gonzalez (University of Maryland Baltimore County); Stephen J. Freeland (University of Maryland Baltimore County)

Poster H-67

Decomposition of DNA Sequences into Hidden Components: Applications to Human Genome's Promoter Recognition

Yasuo Matsuyama (Waseda University); Kenji Onuki (Waseda University); Youichi Ito (Waseda University); Yugo Ishihara (Waseda University); Kouhei Kawasaki (Waseda University); Takayuki Hasegawa (Waseda University)

Poster H-68

A Comparison a New Genetic Algorithm With Existing Methods For Determining a Consensus Sequence

Josh W Gilkerson (University of Kentucky, Dept. of Computer Science); Dr. Jerzy W. Jaromczyk (University of Kentucky, Dept. of Computer Science)

Poster H-69

On the Quality of Motifs for Protein Phosphorylation Site Prediction

Yasser EL-Manzalawy (Artificial Intelligence Laboratory, Department of Computer Science, Iowa State University); Cornelia Caragea (Artificial Intelligence Laboratory, Department of Computer Science, Iowa State University); Drena Dobbs (Department of Genetics, Development and Cell Biology, Bioinformatics and Computational Biology Gradu); Vasant Honavar (Artificial Intelligence Laboratory, Department of Computer Science, Bioinformatics and Computationa)

Poster H-70

Computational identification of structural variation in genomes

David Fredman (Bergen Center for Computational Science); Boris Lenhard (Bergen Center for Computational Science)

Poster H-71

A composite benchmark for local gapped alignments and scoring systems based on extended alphabets

Lorenzo Cerutti (Swiss Institute of Bioinformatics); Marco Pagni (Swiss Institute of Bioinformatics)

Poster H-72

MAVIANT – a Multi-purpose Alignment Vlewing and (SNP) Annotation Tool

Panitz, F (Dept. Genetics and Biotechnology, Danish Institute of Agricultural Sciences); Stengaard, H (Dept. Genetics and Biotechnology, Danish Institute of Agricultural Sciences); Bendixen, C (Dept. Genetics and Biotechnology, Danish Institute of Agricultural Sciences)

Poster H-73

Unusually Large Conserved Syntenic Blocks at the Vertebrate Hox loci are associated with Conserved Regulatory Elements Within and Outside Hox clusters

B.Venkatesh (Institute of Molecular and Cell Biology); Alison Lee (Institute of Molecular and Cell Biology); Esther E.G.L. Koh (Institute of Molecular and Cell Biology); Alice Tay (Institute of Molecular and Cell Biology); Sydney Brenner (Institute of Molecular and Cell Biology)

Poster H-75

In silico characterization of sequence conservation in the 5' and 3' untranslated regions between Leishmania species

Elton José Rosas de Vasconcelos (FMRP - USP); Patrícia de Cássia Ruy (FMRP/FFCLRP - USP); Loislene Oliveira Brito (FMRP - USP); Raony Guimarães Correa do Carmo Lisboa Cardenas (FMRP/FFCLRP - USP); Angela Kaysel Cruz (FMRP - USP); Jeronimo Conceição Ruiz (FMRP - USP)

Poster H-76

Sequence Analysis Of The Riboflavin Biosynthesis Genes From Acidithiobacillus Ferrooxidans.

Marcos Tadeu Santos (CBMEG, Unicamp); Lucio Fabio Caldas Ferraz (CBMEG, Unicamp); Fernanda De Castro Reis (CBMEG, Unicamp); Ana Paula Felício (IQ, Unesp); Paula Falcão (Embrapa); Maria Teresa Marques Novo (Ufscar); Goran Neshich (Embrapa); Oswaldo Garcia Jr (IQ, Unesp); Laura Maria Mariscal Ottoboni (CBMEG, Unicamp)

Poster H-77

Biological signal prediction using Stochastic Regular Grammar

Andre Kashiwabara (IME-USP); Alan Durham (IME-USP)

Poster H-78

Evaluating ORF Function Predictions using Domain-specific Knowledge

Sivakumar Kannan (Robert Cedergren Centre for Bioinformatics and Genomics, Département de Biochimie, Université de Mon); Gertraud Burger (Robert Cedergren Centre for Bioinformatics and Genomics, Département de Biochimie, Université de Mon)

Poster H-79

CONTRAlign 2: Discriminative Training for Multiple Sequence Alignment

Chuong B. Do (Stanford University); Samuel S. Gross (Stanford University); Robert C. Edgar (Stanford University); Kazutaka Katoh (Kyoto University); Serafim Batzoglou (Stanford University)

Poster H-80

An integrated custom design tool for PCR resequencing

Daniel Ingber (Applied Biosystems); Jingwei Ni (Applied Biosystems); Mary Ann Rydland (Applied Biosystems); Robert Sanders (Applied Biosystems); Xiaoying Lin (Applied Biosystems)

Poster H-81

TOFI: A Software Tool for Oligonucleotide Fingerprint Identification

Waibhav Tembe (Biotechnology HPC Institute, US Army Medical Research and Materiel Command); Nela Zavaljevski (Biotechnology HPC Institute, US Army Medical Research and Materiel Command); Elizabeth Bode (Diagnostic Systems Division, US Army Medical Research Institute of Infectious Diseases); Catherine Chase (Diagnostic Systems Division, US Army Medical Research Institute of Infectious Diseases); Jeanne Geyer (Diagnostic Systems Division, US Army Medical Research Institute of Infectious Diseases); Leonard Wasieloski (Diagnostic Systems Division, US Army Medical Research Institute of Infectious Diseases); Gary Benson (Departments of Biology and Computer Science, Boston University); Jaques Reifman (Biotechnology HPC Institute, US Army Medical Research and Materiel Command)

Poster H-82

An Integrated System for High Throughput Genome Annotation and Comparative Genome Analysis

Samuel V Angiuoli (TIGR); Jonathan Crabtree (TIGR); Joshua Orvis (TIGR); Jennifer R Wortman (TIGR); Owen R White (TIGR)

Poster H-83

Conserved genes in a path from commensalism to pathogenicity

ZhiWei Cao (Shanghai Center for Bioinformation Technology, 100 Qinzhou Road, Shanghai, China); Wu Wei (Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences; Graduate School of the Chi)

Poster H-84

A functional genomics sequence analysis workbench

CA Hefer (University of Pretoria); F Joubert (University of Pretoria)

Poster H-85

Motif Discovery with Arbitrary Insertions and Deletions

Martin C Frith (IMB / RIKEN); Timothy L Bailey (IMB)

Poster H-86

GREENPHYL: A Generic Phylogenomic Pipeline for Ortholog Prediction Between two Model Plant Species Arabidopsis thaliana and Oryza sativa

Matthieu Conte (CIRAD); Sylvain Gaillard (CIRAD); Brigitte Courtois (CIRAD); Manuel Ruiz (CIRAD); Emmanuel Guiderdoni (CIRAD); Christophe Perin (CIRAD)

Poster H-87

CaPSuLo, an integrative web tool for predicting the subcellular location of proteins

Perret (Swiss Institute of Bioinformatics); Bairoch (Swiss Institute of Bioinformatics); Veuthey (Swiss Institute of Bioinformatics)

Poster H-88

Porter+: A Server for Protein Structural Motif Prediction

Catherine Mooney (UCD); Gianluca Pollastri (UCD); Alessandro Vullo (UCD)

Poster H-89

Conservation and Correlation Analyses of the V3 Sequences of HIV-1 Envelope Proteins

Shuo L. Lin (Wyeth Vaccines Research); Robert Zagursky (Wyeth Vaccines Research)

Poster H-90

PCR primer design for 2,4-D degradation genes using BLOCKS and the CDD database

Vianez Junior, J. L. S. G (Departamento de Microbiologia Geral, LBSBM, UFRJ); Macrae, A (Departamento de Microbiologia Geral, LBSBM, UFRJ)

Poster H-91

A Digital Northern tool for assessment of Citrus differentially expressed genes

Marcelo S. Reis (Centro APTA Citros "Sylvio Moreira"); Marco A. Takita (Centro APTA Citros "Sylvio Moreira"); Alessandra A. Souza (Centro APTA Citros "Sylvio Moreira"); Irving J. Berger (Centro APTA Citros "Sylvio Moreira"); Juliana Freitas-Astua (Embrapa Milho e Sorgo, and Centro APTA Citros "Sylvio Moreira"); Marcos A. Machado (Centro APTA Citros "Sylvio Moreira")

Structural Bioinformatics

Poster I-1

Modelling of S1 Subunits of Three Different Avian Infectious Bronchitis Coronavirus Strains

Caio Júlio Martins Veloso (UFMG/PUCMG); Josiane Tavares de Abreu (UFMG/PUCMG); Jose Sergio de Resende (EMV/UFMG); Marcelo Santoro (ICB/UFMG)

Poster I-2

Protein function prediction based on 'reverse engineering' of the protein fold-recognition approach:examples from CASP6

Michal Andrzej Kurowski (Genesilico, IIMCB)

Poster I-3

Designing C2H2 Zinc Finger Proteins to Target Specific Genomic Sites

Jeff Sander (Iowa State University); Peter Zaback (Iowa State University); Fengli Fu (Iowa State University); Daniel Voytas (Iowa State University); Drena Dobbs (Iowa State University)

Poster I-4

Crystal structure of PrTX-I complexed with alpha-tocopherol and comparison studies with native Lys49-PLA2s

Juliana Izabel dos Santos (Depto. de Física e Biofísica - Iinstituto de Biociências, UNESP / Botucatu); Andreimar Martins Soares (Depto. de Análises Clínicas, Bromatológicas e Toxicológicas, FCFRP, USP / Ribeirão Preto); Marcos Roberto de Mattos Fontes (Depto. de Física e Biofísica - Iinstituto de Biociências, UNESP / Botucatu)

Poster I-5

Protein structure topology comparison based on contact maps

Raquel C. Melo (UFMG); Ivan Mazoni (Embrapa); Goran Neshich (Embrapa); Marcelo M. Santoro (UFMG); Wagner Meira Jr (UFMG)

Poster I-6

Contacts as the key elements for comparing two protein structures

Raquel C. Melo (UFMG); Ivan Mazoni (Embrapa); Goran Neshich (Embrapa); Marcelo M. Santoro (UFMG); Wagner Meira Jr (UFMG)

Poster I-7

Analyzing high-throughput biological data: complexities, issues, challenges and some lessons learned

Fazel Famili (IIT); Sieu Phan (IIT); Ziying Liu (IIT); Junjun Ouyang (IIT); Youlian Pan (IIT); Alan J. Barton (IIT)

Poster I-8

Genome-wide de novo structure prediction for over 100 genomes and automatic integration of structure prediction with Gene Ontology database

Lars Malmström (University of Washington); David Baker (University of Washington); Richard Bonneau (NYU, Dept of Computer Science)

Poster I-9

A one-shot algorithm for visualizing large-scale RNA structures with pseudoknots as planar graphs

Kyungsook Han (Inha University); Yanga Byun (Inha University)

Poster I-10

Negative Result on Maximum Common Subgraph of Two Graphs

Xiuzhen Huang (Department of Computer Science, Arkansas State University)

Poster I-12

Predicting co-evolving pairs in Pfam based on Mutual Information of mutation events measured along the phylogenetic tree

Scooter willis (Department of Computer and Information Science and Engineering, University of Florida);

Poster I-13

Predicting Enzyme Class From Protein Structural Parameters Using STING_DB parameters and Bagging Predictors

Michel E. B. Yamagishi (Embrapa Informática); Stanley R. M. Oliveira (Embrapa Informática); Luiz C. Borro (Embrapa Informática); Edgard H. Santos (Embrapa Informática); José G. Jardine (Embrapa Informática); Fábio D. Vieira (Embrapa Informática); Ivan Mazoni (Embrapa Informática); Marcelo G. Narciso (Embrapa Informática); Paulo R. Kuser-Falcão (Embrapa Informática); Goran Neshich (Embrapa Informática)

Poster I-14

Analysing Protein-Protein Interface using JPIV

Michel E. B. Yamagishi (Embrapa Informática); Paula R. Kuser-Falcão (Embrapa Informática); Luiz C. Borro (Embrapa Informática); Stanley R. M. Oliveira (Embrapa Informática); Edgard H. Santos (Embrapa Informática); José G. Jardine (Embrapa Informática); Fábio D. Vieira (Embrapa Informática); Ivan Mazoni (Embrapa Informática); Marcelo G. Narciso (Embrapa Informática); Goran Neshich (Embrapa Informática)

Poster I-17

Identification of novel imprinted genes in human

Jorge E. S. de Souza (Pós-Graduação em Bioinformática - Universidade de São Paulo); Pedro A. F. Galante (Bioquímica - Universidade de São Paulo); Lilian C. Pires (Biologia Molecular e Genômica - Instituto Ludwig de Pesquisa sobre o Câncer); Sandro J. de Souza (Biologia Computacional - Instituto Ludwig de Pesquisa sobre o Câncer); Anamaria A. Camargo (Biologia Molecular e Genômica - Instituto Ludwig de Pesquisa sobre o Câncer)

Poster I-18

Identification of Druggabable "Hot Spots" in Ligand Binding Pockets by Computational Solvent Mapping of Proteins

Melissa R. Landon (Graduate Program in Bioinformatics, Boston University); Spencer C. Thiel (Graduate Program in Bioinformatics, Boston University); David R. Lancia, Jr. (Department of Biomedical Engineering, Boston University); Sandor Vajda (Department of Biomedical Engineering, Boston University)

Poster I-19

A Trypanosoma cruzi Genome Study by Sequence-Structure HighThroughput Comparative Modelling: A First Step Towards the Identification of Potential Molecular Targets for Chagas Disease

Priscila V. S. Z. Capriles (LNCC/MCT); Shaila C. Rössle (Ludwig - Maximilians - University of Munich); Ana C. R. Guimarães (DBBM/FIOCRUZ); Marcos Catanho (DBBM/FIOCRUZ); Paulo M. Bisch (IBCCF/UFRJ); Wim Degrave (DBBM/FIOCRUZ); Laurent E. Dardenne (LNCC/MCT)

Poster I-20

Effects of amino acid composition, finite size of proteins and sparse statistics on distance-dependent statistical pair potentials

Dmitry Rykunov (Albert Einstein College of Medicine); Andras Fiser (Albert Einstein College of Medicine)

Poster I-21

Structural Parameters To Filter Crucial Catalytic Site Aminoacids From Fructose 1,6-bisphosphate Aldolase

Marcelo Mendes Brandão (Hemotherapy and Hematology Center - UNICAMP); Paula R. Kuser (Embrapa information technology); Goran Neshich (Embrapa information technology)

Poster I-22

BlueStar STING - A multiplatform environment for protein structure analysis

Paula Kuser (EMBRAPA); Michel E. B. Yamagishi (EMBRAPA); Stanley R. M. Oliveira (EMBRAPA); Ivan Mazoni (EMBRAPA); Edgard H. Santos (EMBRAPA); Fábio D. Vieira (EMBRAPA); José G. Jardine (EMBRAPA); Luiz C. Borro (EMBRAPA); Goran Neshich (EMBRAPA)

Poster I-23

INFO-RNAseq - Fast Inverse RNA Folding Satisfying Sequence Constraints

Anke Busch (Albert-Ludwigs-University Freiburg, Inst. of Computer Science, Chair for Bioinformatics); Rolf Backofen (Albert-Ludwigs-University Freiburg, Inst. of Computer Science, Chair for Bioinformatics)

Poster I-24

How parallel are the helices of your favourite protein?

Peter Røgen (Department of Mathematics, Technical University of Denmark); Per W. Karlsson (Department of Mathematics, Technical University of Denmark)

Poster I-26

Using Knowledge-Based Constraints To Optimise Comparative Models Of Protein Structure

Braddon K. Lance (Macquarie University, Department of Statistics); Graham R. Wood (Macquarie University, Department of Statistics); Charlotte M. Deane (University of Oxford, Department of Statistics)

Poster I-28

Protein-Protein Docking Guided by Biochemical Data

Domantas Motiejunas (EML Research); Ting Wang (UC Davis); Anna Feldman-Salit (EML Research); Tim Johann (EML Research); Razif Gabdoulline (EML Research); Rebecca Wade (EML Research)

Poster I-29

VSM-G: the Virtual Screening Manager platform for computational Grids. Use for the identification of putative ligands of the Liver X Receptor

Alexandre Beautrait (Mr); Bernard Maigret (Mr)

Poster I-30

Automatically Clustering Protein Structure Using the Distribution of Atom Bonds in Backbone

Sung Hee Park (ETRI bioinformatics team); Chan Yong Park (ETRI bioinformatics team); Dae Hee Kim (ETRI bioinformatics team); Soo Jun Park (ETRI bioinformatics team)

Poster I-31

Prediction of functional residues from Plasmodium falciparum plasmepsins: implications in the antimalarial drugs design.

Pedro Alberto Valiente Flores (Centro de Estudios de Proteínas (CEP), Facultad de Biología, Universidad de La Habana, Cuba.); Amaury Pupo Meriño (Centro de Estudios de Proteínas (CEP), Facultad de Biología, Universidad de La Habana, Cuba.); Tirso Pons Hernández (Centro de Estudios de Proteínas (CEP), Facultad de Biología, Universidad de La Habana, Cuba.); Pedro G. Pascutti (Instituo de Biofísica Carlos Chagas Filho, Universidade Federal do Rio de Janeiro, Brasil.)

Poster I-32

Homology modeling of Chromobacterium violaceum and Thiobacillus ferrooxidans atypical ArsR proteins

Rafael S. Rocha (Laboratório de Polimorfismo de DNA, CCB-UFPa, Belém-PA, Brasil); Marta P. Carepo (Centro de Química Fina e Biotecnologia FCT/UNL Portugal); Evonnildo C. Gonçalves (Laboratório de Polimorfismo de DNA, CCB-UFPa, Belém-PA, Brasil); Artur Silva (Laboratório de Polimorfismo de DNA, CCB-UFPa, Belém-PA, Brasil); Cláudio N. Alves (Laboratório de Química, CCEN-UFPa, Belém-PA, Brasil); Maria P. Schneider (Laboratório de Polimorfismo de DNA, CCB-UFPa, Belém-PA, Brasil)

Poster I-33

Information-Theoretic Analysis of Protein Fold Potentials

Armando D. Solis (Mount Sinai School of Medicine); S. Rackovsky (Mount Sinai School of Medicine)

Poster I-34

Structural Analysis of proplasmepsin from the human malarial pathogen plasmodium vivax

Juliana M. Papine (Faculdade de Ciências Farmacêuticas-PUCCampinas,); Mariana S. Vieira (Faculdade de Ciências Farmacêuticas-PUCCampinas,); José G. Jardine (Embrapa); Goran Neshich (Embrapa); Paula R. Kuser-Falcão (Embrapa); Michel E. B.Yamagishi (Embrapa); Stanley R. M. Oliveira (Embrapa); Ivan Mazoni (Embrapa); Fábio D. Vieira (Embrapa); Edgar H. Santos (Embrapa)

Poster I-35

Structural Analysis of the Protein Twitching Motility

Jose Gilberto Jardine (Embrapa Information Technology); Goran Neshich (Embrapa Information Technology); Paula R. Kuser-Falcão (Embrapa Information Technology); Michel E. B.Yamagishi (Embrapa Information Technology); Stanley R. M. Oliveira (Embrapa Information Technology); Ivan Mazoni (Embrapa Information Technology); Edgard H. Santos (Embrapa Information Technology); Fábio D. Vieira (Embrapa Information Technology); Sérgio Marangoni (Departamento de Bioquímica, UNICAMP); Daniel Martins (Departamento de Bioquímica, UNICAMP); Flavia V. Winck (Departamento de Bioquímica, UNICAMP); José C. Novello (Departamento de Bioquímica, UNICAMP); Juliana M. Papine (Faculdade de Ciências Farmacêuticas-PUCCampinas); Mariana S. Vieira (Faculdade de Ciências Farmacêuticas-PUCCampinas)

Poster I-36

DomainDiscovery: A Novel Algorithm for Protein Domain Boundary Assignment Using Support Vector Machine

Abdur R Sikder (Advanced Networks Research Group, School of Information Technologies, University of Sydney, NSW 2006); Stella Veretnik (San Diego Supercomputer Center, University of California San Diego, 9500 Gilman Drive, La Jolla, CA); Albert Y Zomaya (Advanced Networks Research Group, School of Information Technologies, University of Sydney, NSW 2006); Philip E Bourne (Department of Pharmacology, University of California San Diego, 9500 Gilman Drive, La Jolla, CA 9209)

Poster I-38

Structural and Evolutionary analysis of Importin-alpha and its interaction with the nuclear localization sequence peptides

Agnes Alessandra Sekijima Takeda (Dept. de Física e Biofísica, Instituto de Biociências, UNESP, Botucatu-SP, Brasil); Antônio Sergio Kimus Braz (Laboratório de Biotecnologia e Genética Molecular (BIOGEM), Dept. de Genética, Instituto de Biociênc); Bostjan Kobe (Dept .Biochemistry and Molecular Biology, University of Queensland, Brisbane,QLD, Australia); Marcos Roberto de Mattos Fontes (Dept. de Física e Biofísica, Instituto de Biociências, UNESP, Botucatu-SP, Brasil)

Poster I-41

Single-family analysis of binding site structural similarities

Rafael Najmanovich (EBI); Richard Morris (EBI); Janet Thornton (EBI)

Poster I-42

Use of docking tools and MD simulations to predict the interaction between the MH2 domain of Smad3 and the PDZ domain of Erbin

Matthieu Chavent (eDAM group); Claire Nourry (Inserm - UMR 599 - Molecular Pharmacology); Nadine Deliot (Inserm - UMR 599 - Molecular Pharmacology); Jean Paul Borg (Inserm - UMR 599 - Molecular Pharmacology); Bernard Maigret (eDAM group)

Poster I-43

Novel Protein Structural Classification by Discovering Coherence in Hydrophobicity Scales

Sumeet Dua (College of Engineering and Science, Louisiana Tech University); Pradeep Chowriappa (College of Engineering and Science, Louisiana Tech University); Ramakrishnan Rajagopalan (College of Engineering and Science, Louisiana Tech University)

Poster I-44

Protein Dynamics from X-Ray Crystallography Data: Modeling Structural Heterogeneity with Inverse Kinematics

Henry van den Bedem (Stanford Linear Accelerator Center); Ankur Dhanik (Stanford University); Ashley M. Deacon (Stanford Linear Accelerator Center); Jean-Claude Latombe (Stanford University)

Poster I-45

Profiling Tertiary Protein Motifs Using PHMM

Jalal Mahmud (Department of Computer Science, Stony Brook University, Stony Brook , NY 11794, USA); Chang Zhao (Department of Computer Science, Stony Brook University, Stony Brook , NY 11794, USA); I.V. Ramakrishnan (Department of Computer Science, Stony Brook University, Stony Brook , NY 11794, USA)

Poster I-46

Protein Designability in the 2-D Triangular Lattice

Myron F. Peto (ISU); Robert L. Jernigan (ISU); Andrzej Kloczkowski (ISU)

Poster I-47

The Cry 1Ac Protein from Bacillus thuringiensis and its structure stability centers

Katia Regina Evaristo de Jesus (EMBRAPA CNPMA); Paula Kuser (EMBRAPA CNPTIA); Goran Neshich (EMBRAPA CNPTIA)

Poster I-48

Serine Proteases analysis based on phylogenetic trees constructed from the sequence and structure alignments

Cristina Ribeiro (UFMG); Paula Kuser (EMBRAPA CNPTIA); Goran Neshich (EMBRAPA CNPTIA); Marcelo Santoro (UFMG)

Poster I-49

Protein Ligand Contacts Analysed In An Integrated Environment With Other Structure And Sequence Related Parameters

Paula Kuser (Embrapa Cnptia); Luiz Cesar Borro (Embrapa Cnptia); Ivan Mazoni (Embrapa Cnptia); Michel Yamagishi (Embrapa Cnptia); José G. Jardine (Embrapa Cnptia); Edgard H. dos Santos (Embrapa Cnptia); Stanley R. M. Oliveira (Embrapa Cnptia); Goran neshich (Embrapa Cnptia)

Poster I-50

MSSP: simultaneous comparison of the same structure descriptor for different protein structures

Ivan Mazoni (Embrapa CNPTIA); Paula Kuser (Embrapa CNPTIA); Michel Yamagishi (Embrapa CNPTIA); Luiz Borro (Embrapa CNPTIA); Jose Jardine (Embrapa CNPTIA); Edgard H. dos Santos (Embrapa CNPTIA); Stanley R. M. Oliveira (Embrapa CNPTIA); Goran Neshich (Embrapa CNPTIA)

Poster I-51

Comparisson Of The Amino Acids Co-evolution And The Correlated Structure Descriptors

Ivan Mazoni (Embrapa CNPTIA); Paula Kuser (Embrapa CNPTIA); Michel Yamagishi (Embrapa CNPTIA); Luiz Borro (Embrapa CNPTIA); Jose Jardine (Embrapa CNPTIA); Edgard H. dos Santos (Embrapa CNPTIA); Stanley R. M. Oliveira (Embrapa CNPTIA); Goran Neshich (Embrapa CNPTIA); Marcelo Narciso (Embrapa CNPTIA)

Poster I-52

Insights into protein-protein interfaces using a Bayesian network prediction method

James Bradford (University of Leeds); Chris Needham (University of Leeds); Andrew Bulpitt (University of Leeds); David Westhead (University of Leeds)

Poster I-53

A computational method to identify amino acid residues involved in protein-RNA interactions

Michael Terribilini (Iowa State Univeristy); Jeffry Sander (Iowa State Univeristy); Byron Olson (Iowa State Univeristy); Jae-Hyung Lee (Iowa State Univeristy); Robert Jernigan (Iowa State Univeristy); Vasant Honavar (Iowa State Univeristy); Drena Dobbs (Iowa State Univeristy)

Poster I-54

RNA Secondary structure prediction

Stéfan Engelen (IBISC -CNRS. University of Evry/Genopole); Fariza Tahi (IBISC -CNRS. University of Evry/Genopole)

Poster I-55

Discrimination of beta-barrel Membrane Proteins based on Statistical Methods and Machine Learning Algorithms

M. Michael Gromiha (CBRC, AIST); Makiko Suwa (CBRC, AIST)

Poster I-56

Fast Structural Similarity Search based on Topology String Matching

Sung Hee Park (Bioinformatics Research Centre, Department of Computing Science, University of Glasgow); Keun Ho Ryu (Database Laboratory, Department of Computer Science, Chungbuk National University); David Gilbert (Bioinformatics Research Centre, Department of Computing Science, University of Glasgow)

Poster I-57

Targeting Proteins from the Human Cancer Protein Interaction Network (HCPIN) for Structural Genomics

Y. J. Huang (Department of Molecular Biology and Biochemistry, Center for Advanced Biotechnology and Medicine, Ru); L. J. Lu (Department of Molecular Biology and Biochemistry,Yale University,Northeast Structure Genomics Consor); M. B. Gerstein (Department of Molecular Biology and Biochemistry,Yale University,Northeast Structure Genomics Consor); G. T. Montelione (Department of Molecular Biology and Biochemistry, Center for Advanced Biotechnology and Medicine, Ru)

Poster I-58

i-BioS: A system for Inverse Biological Virtual Screening Based on Inverse Docking Approach

Julio CD Lopes (Cheminformatics and Medicinal Chemistry Group - Departamento de Química - UFMG)

Poster I-59

Prediction of protein complexes using evolutionary information

Richard Bickerton (Department of Biochemistry, University of Cambridge); Tom Blundell (Department of Biochemistry, University of Cambridge); David Burke (Department of Biochemistry, University of Cambridge)

Poster I-60

Docking protein domains in contact space

Stefano Lise (University College London); Alice Walker-Taylor (University College London); David T Jones (University College London)

Poster I-61

Expected packing density allows to predict both amyloidogenic and unfolded regions in protein chain

Galzitskaya (Institute of Protein Research); Garbuzynskiy (Institute of Protein Research); Lobanov (Institute of Protein Research)

Poster I-62

Self-organizing Maps - the Heuristic Approach for Understanding Ligand-protein Interactions in Vitamin D Receptor

Ferdinand Molnár (Department of Biochemistry, Universitz of Kuopio)

Poster I-63

The Influence of Alternative Splice Sites in Protein Structure

Elza H.A.B. Durham (IME -USP/LICR); Richard Garrat (IFSC-USP); Sandro J. de Souza (LICR)

Poster I-64

Structural classification and prediction of reentrant regions in alpha-helical transmembrane proteins: application to complete genomes

Håkan Viklund (Stockholm University); Erik Granseth (Stockholm University); Arne Elofsson (Stockholm University)

Poster I-65

Visualization and clustering of Protein Local Conformational Space using Geometric Invariant Theory

Ashish V Tendulkar (KReSIT, IIT Bombay); Pramod P Wangikar (Dept of Chemical Engg, IIT Bombay)

Poster I-66

Crystal structure of hemoglobin from Cerdocyon thous at 2.2 Å resolution using syncrotron radiation

Esteves, G. F. (Universidade de Brasília); Freitas, S. M. (Universidade de Brasília)

Poster I-67

3D Model quality evaluation using evolutionary information

Nicolas Palopoli (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Ezequiel Juritz (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes); Diego Gomez-Casati (IIB-INTECH, UNSAM-CONICET); Gustavo Parisi (Centro de Estudios e Investigaciones, Universidad Nacional de Quilmes)

Poster I-68

Prediction of order and disorder at the domain level

Zsuzsanna Dosztanyi (Institute of Enzymology); Mark Sandor (Institute of Enzymology); Istvan Simon (Institute of Enzymology)

Poster I-69

Datamining the Fourth Dimension from Crystal Structures: Function-Structure-Entropy Relationships in Membrane Proteins

Ilan Samish (Dept of Biochemistry & Biophysics, School of Medicine & Dept of Chemistry, School of Arts and Science); Avigdor Scherz (Weizmann Institute of Science, Rehovot, Israel)

Poster I-70

Dimeric Lys49-Phospholipases A2: Which Is The Correct Biological Assembly?

Mário T. Murakami (Departamento de Física, IBILCE, UNESP, São José do Preto-SP, Brazil); Raghuvir K. Arni (Departamento de Física, IBILCE, UNESP, São José do Preto-SP, Brazil); Marcos R.M. Fontes (Departamento de Física e Biofísica, Instituto de Biociências, UNESP, Botucatu-SP, Brazil)

Poster I-71

In Silico Identification of Radial Spoke Proteins and Prediction of their Arrangement Patterns towards Assembly of the Flagellar Axoneme in *Leishmania spp*

Allan Rodrigo Soares Maia (NUGEN-UECE); Ana Carolina Landim Pacheco (NUGEN-UECE); Hálisson Lucas Ribeiro (NUGEN-UECE); George de Paulo Ferreira (NUGEN-UECE); Ana Luiza Bessa de Paula Barros (LARCES-UECE); Raimundo Bezerra da Costa (NUGEN-UECE); Rodrigo Maggioni (NUGEN-UECE); Diana Magalhaes de Oliveira (NUGEN-UECE)

Poster I-72

Protein Active Site Comparison and Retrieval System Based on 3D Pattern Matching

Dae-Hee Kim (Electronics and Telecommunications Research Institute); Sung-Hee Park (Electronics and Telecommunications Research Institute); Chan-Yong Park (Electronics and Telecommunications Research Institute); Soo-Jun Park (Electronics and Telecommunications Research Institute); Seon-Hee Park (Electronics and Telecommunications Research Institute)

Poster I-73

A Filtering Approach for Improved Modelling of Predicted Contact Maps

Alberto J. Martin (School of Computer Science and Informatics University College Dublin); A. Vullo (School of Computer Science and Informatics University College Dublin); G. Pollastri (School of Computer Science and Informatics University College Dublin)

Poster I-74

Molecular dynamic and structural analysis from the ab initio model of HC-Pro, a plant virus multifunctional protein

Antonio Sergio Kimus Braz (Depto Genetica - IBB - UNESP Botucatu); Sérgio Oyama Jr. (Centro de Biologia Molecular Estrutural, Laboratório Nacional de Luz Síncrotron); Ivan de Godoy Maia (Depto Genetica - IBB - UNESP Botucatu)

Poster I-75

A set of approaches for analysis of functional relationship in proteins

Joanna M. Sasin (International Institute of Molecular and Cell Biology); Janusz M. Bujnicki (International Institute of Molecular and Cell Biology)

Poster I-76

Structural Annotation Pipeline for Malarial proteomes

Yolandi Joubert (Department Biochemistry, University of Pretoria); Fourie Joubert (Department Biochemistry, University of Pretoria)

Poster I-77

LIGLIB: Generation of in silico analogous ligand libraries

Wolf Cochrane (University Pretoria); Fourie Joubert (University Pretoria)

Poster I-78

Structural and phylogenetic studies with a theoretical model of the BjussuMP-I, a metalloprotease isolated from the *Bothrops jararacussu* venom

Angelo J. Magro (Departamento de Física e Biofísica - Instituto de Biociências de Botucatu - UNESP - Botucatu/SP - Br); Antônio S. K. Braz (Departamento de Genética - Instituto de Biociências de Botucatu - UNESP - Botucatu/SP - Brasil); Andreimar M. Soares (Departamento de Análises Clínicas, Toxicológicas e Bromatológicas - Faculdade de Ciências Farmacêuti); Marcos R. M. Fontes (Departamento de Física e Biofísica - Instituto de Biociências de Botucatu - UNESP - Botucatu/SP - Br)

Poster I-79

Conformational changes in the structure of Shikimate Kinase from *Mycobacterium tuberculosis* caused for ions and substrates

Marcio Vinicius Bertacine (Ibilce - UNESP); Livia Maria Faim (Ibilce - UNESP); Igor Bordim Vasconcelos (PUC - Porto Alegre RS); Jaim Simões de Oliveira (PUC - Porto Alegre RS); Luis Augusto Basso (PUC - Porto Alegre RS); Diógenes Santiago Santos (PUC - Porto Alegre RS); Walter Filgueira de Azevedo Jr. (PUC - Porto Alegre RS)

Poster I-80

XXStout: Improving the Prediction of Long range residue contacts

Ian Walsh (University College Dublin School of Computer Science and Informatics); Alessandro Vullo (University College Dublin School of Computer Science and Informatics); Gianluca Pollastri (University College Dublin School of Computer Science and Informatics)

Poster I-81

Improvement of Portable virtual reality system with haptic device for molecular modeling and education

Isao Okada (Tokyo Medical and Dental University); Takayuki Ohnishi , (Tokyo Medical and Dental University); Hiroshi Nagata, (Tokyo Medical and Dental University); Hiroshi Tanaka (Tokyo Medical and Dental University); Hiroshi Mizushima (Tokyo Medical and Dental University)

Poster I-82

Protein Structure Prediction Aided Text Mining for Functional Inference

Andreas Rechtsteiner (CGB, Indiana University); Jeremy Luinstra (B-Div, Los Alamos National Lab); Judith D. Cohn (B-Div, Los Alamos National Lab); Charlie E. M. Strauss (B-Div, Los Alamos National Lab)

Poster I-83

Chemoinformatics approach to Differential Drug Response of the Tyrosine Kinase Domain BCR-ABL to Imatinib in Chronic Myeloid Leukemia Patients

Sergio de Alencar (UFMG); Julio Lopes (UFMG); Abdrelly Martins (UFMG)

Poster I-85

A Study of SNPs in Sirtuins Structures

Beatriz J. Pinto (Faculty of Medicine of Ribeirão Preto - University of São Paulo); André L. T. Vinci (Faculty of Medicine of Ribeirão Preto - University of São Paulo); Marcela C. de Santo (Laboratory of Bioinformatics - University of Ribeirão Preto); Milton Faria Jr (Laboratory of Bioinformatics - University of Ribeirão Preto); Silvana Giuliatti (Faculty of Medicine of Ribeirão Preto - University of São Paulo)

Poster I-86

Comparative Analysis of Human SIRT Proteins Tertiary Structures

André L. T. Vinci (Faculty of Medicine of Ribeirão Preto - University of São Paulo); Beatriz J. Pinto (Faculty of Medicine of Ribeirão Preto - University of São Paulo); Marcela C. de Santo (Laboratory of Bioinformatics - University of Ribeirão Preto); Milton Faria Jr (Laboratory of Bioinformatics - University of Ribeirão Preto); Silvana Giuliatti (Faculty of Medicine of Ribeirão Preto - University of São Paulo)

Poster I-87

Using a computer model of human CYP21 to correlate structural features with clinical severity

Jonas Carlsson (IFM Bioinformatics, Linköping University); Tiina Robins (Molecular Medicine and Surgery, Centre of Molecular Medicine, (CMM), KI / KS); Maria Sunnerhagen

(Molecular Biotechnology, IFM, Linköping University); Anna Wedell (Molecular Medicine and Surgery, Centre of Molecular Medicine, (CMM), KI / KS); Bengt Persson (IFM Bioinformatics, Linköping University; Centre for Genomics and Bioinformatics, Karolinska Institu)

Poster I-88

Protein Structural Analysis Made Easy

Tjaart de Beer (University of Pretoria); Fourie Joubert (University of Pretoria)

Poster I-89

Tsallis Statistics Applied to Protein Folding, Protein Model Refinement and Molecular Complex Optimization

Pedro G. Pascutti (Instituto de Biofísica Carlos Chagas Filho - Universidade Federal do Rio de Janeiro - Brasil); Tacio V. Amorim Fernandes (Instituto de Biofísica Carlos Chagas Filho - Universidade Federal do Rio de Janeiro - Brasil); Flávia P. Agostini (Laboratório Nacional de Computação Científica/CNPq - Petrópolis-RJ - Brasil)

Poster I-90

Molecular Modeling Of The Riboflavin Genes From *Acidithiobacillus ferrooxidans*

Lucio Fabio Caldas Ferraz (CBMEG, Unicamp); Fernanda De Castro Reis (CBMEG, Unicamp); Marcos Tadeu Santos (CBMEG, Unicamp); Ana Paula Felício (IQ, Unesp); Paula Falcão (Embrapa); Maria Teresa Marques Novo (Ufscar); Goran Neshich (Embrapa); Oswaldo Garcia Jr (IQ, Unesp); Laura Maria Mariscal Ottoboni (CBMEG, Unicamp)

Poster I-93

Anti-tick vaccines: homology modeling of a tick antigen Bm91 from Boophilus microplus

Jurgens de Bruin (Bioinformatics,University of Pretoria); Anabella R.M. Gaspar (Biochemistry,University of Pretoria); Albert W.H. Neitz (Biochemistry,University of Pretoria)

Poster I-94

In Silico Comparative Macromolecular Modeling of the Leishmania Flagellum: 3D Perspective of an Axonemal Nanomachine

Cleilton Lima Rocha (NUGEN-UECE); Marcília Pinheiro da Costa (NUGEN-UECE); George de Paulo Ferreira (Computação-UECE); Fabiana Freire de Araújo (Computação-UECE); Allan Rodrigo Soares Maia (NUGEN-UECE); Patricy de Andrade Salles (NUGEN-UECE); Hálisson Lucas Ribeiro (Computação-UECE); Ana Luiza Bessa de Paula Barros (Computação-UECE); Diana Magalhães de Oliveira (NUGEN-UECE)

Poster I-95

Molecular Modeling Of Polypeptide Deformylase From *Acidithiobacillus ferrooxidans*

Fernanda De Castro Reis (CBMEG, Unicamp); Lúcio Fábio Caldas (CBMEG, Unicamp); Marcos Tadeu Dos Santos (CBMEG, Unicamp); Paula K. Falcão (Embrapa Informática Agropecuária); Goran Neshich (Embrapa Informática Agropecuária); Laura M. M. Ottoboni (CBMEG, Unicamp)

Poster I-96

Ab Initio Modelling of Protein C-alpha Traces Through Structural Constraints Predicted by Machine Learning

Davide Bau (School of Computer Science and Informatics, UCD Dublin); Alessandro Vullo (School of Computer Science and Informatics, UCD Dublin); Gianluca Pollastri (School of Computer Science and Informatics, UCD Dublin)

Poster I-97

Fast Protein Structure Alignment by Joining Similar Substructure Pair

Chan-Yong Park (ETRI); Sung-Hee Park (ETRI); Dae-Hee Kim (ETRI); Soo-Jun Park (ETRI); Hong-Ro Lee (Chung Nam University); Chi-Jung Hwang (Chung Nam University)

Poster I-98

Sequence based prediction of distortion in alpha-helix using Support Vector Machine

Ashish V Tendulkar (KReSIT, IIT Bombay); Pramod P. Wangikar (Dept of Chemical Engg, IIT Bombay)

Poster I-99

FILTREST3D: a simple method for discrimination of multiple structural models against spatial restraints

Michal J. Gajda (Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell); Marta Kaczor (Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell); Anastasia Bakulina (Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell); Andrzej Kasperski (Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell); Alan M. Friedman (Department of Biological Sciences, Purdue University, West Lafayette, IN, USA); Chris Bailey-Kellogg (Department of Computer Science, Dartmouth College, Hanover, NH, USA); Janusz M. Bujnicki (Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell)

Poster I-100

Meta-MQAP: an SVM-based meta-server for the quality assessment of protein models

Marcin Pawlowski (International Institute of Molecular and Cell Biology in Warsaw); Ryszard Matlak (International Institute of Molecular and Cell Biology in Warsaw); Janusz Bujnicki (International Institute of Molecular and Cell Biology in Warsaw)

Poster I-101

High resolution crystal structure of BthTX-I-BPB and comparison analysis with native BthTX-I - insights into the lack of the toxic activities

Marchi-Salvador, D.P. (IBB-UNESP); Fernandes, C.A.H. (IBB-UNESP); dos Santos, J.I. (IBB-UNESP); Amui, S.F. (FCF-USP); Soares, A.M. (FCF-USP); Fontes, M.R.M. (IBB-UNESP)

Poster I-102

Classifiers of the protein interactions with their substrate/inhibitors

Vera S. Garcia (Unicamp/Embrapa); Paula Kuser Falcão (Embrapa)

Poster I-103

Screening the human UTR database for stabilized RNA secondary structures

Sven Siebert (Department of Bioinformatics, Institute of Computer Science, Albert-Ludwigs University Freiburg); Rolf Backofen (Department of Bioinformatics, Institute of Computer Science, Albert-Ludwigs University Freiburg)

Poster I-104

Self-consistent Assignment of Asparagine and Glutamine Side-Chain Amide Rotamers

Christian X. Weichenberger (Dept. of Molecular Biology, University of Salzburg); Manfred J. Sippl (Dept. of Molecular Biology, University of Salzburg)

Systems Biology

Poster J-1

BiologicalNetworks: integrated environment for system level analysis and predictive modeling of molecular machines. Case study of eukaryotic early meiosis

Michael Baitaluk (San Diego Supercomputer Center, UCSD); Mayya Sedova (San Diego Supercomputer Center, UCSD); Biranchi Patra (Keck Graduate Institute); Kirilynn Svay (Keck Graduate Institute); Amarnath Gupta (San Diego Supercomputer Center, UCSD); Animesh Ray (Keck Graduate Institute)

Poster J-2

Analysis of pleiotropy during C. elegans development and interpretation with interactome networks

Lihua Zou (Harvard University); Brian Ross (Whitehead Institute); Jun Liu (Harvard Univeristy); Hui Ge (Whitehead Institute)

Poster J-3

Searching for Genes Involved in Novel Mechanisms of Tumor Cell Death Triggered by FGF2: Introducing New Methodological Approaches

F. Nakano (BIOINFO-USP, SP, Brasil); P. F. Asprino (Instituto

de Química, Universidade de São Paulo, São Paulo, SP, Brasil); C. H. A. Higa (Instituto de Matetmática e Estatística, Universidade de São Paulo, SP, Brasil); R. F. Hashimoto (nstituto de Matetmática e Estatística, Universidade de São Paulo, SP, Brasil); H. A. Armelin (Instituto de Química, Universidade de São Paulo, São Paulo, SP, Brasil)

Poster J-4

Systematic Analysis of Phenotypes of E. coli Single Gene Deletion Mutants

Hirotada Mori (Nara Institute of Science and Technology); Hiroko Matsui (Mitsubishi space Co. Ltd.); Hiroaki Gobara (Nara Institute of Science and Technology); Shigeki Tanishima (Mitsubishi space Co. Ltd.); Sivasundaram Suharnan (Axio Helix Co. Ltd.); Shigehiko Kanaya (Nara Institute of Science and Technology); Barry L. Wanner (Purdue University)

Poster J-6

Dynamical Modeling of the Gene Regulatory Network of Halobacterium from Diverse Global Systems Biology Datasets

David J Reiss (Institute for Systems Biology); Vesteinn Thorsson (Institute for Systems Biology); Paul Shannon (Institute for Systems Biology); Lee Hood (Institute for Systems Biology); Nitin S Baliga (Institute for Systems Biology); Richard Bonneau (Depts. of Biology and Computer Science, New York University)

Poster J-7

Statistical Analysis of Retroviral Insertional Mutagenesis Data

Jeroen de Ridder (Information and Communication Theory Group, Delft University of Technology); Jaap Kool (Division of Molecular Genetics, The Netherlands Cancer Institute); Anthony Uren (Division of Molecular Genetics, The Netherlands Cancer Institute); Lodewyk Wessels (Division of Moleculat Biology, The Netherlands Cancer Institute); Marcel Reinders (Information and Communication Theory Group, Delft University of Technology)

Poster J-8

Inferring transcriptional modules from ChIP-chip-, motif- and microarray data

Karen Lemmens (Dept. Electrical Engineering, K.U.Leuven); Thomas Dhollander (Dept. Electrical Engineering, K.U.Leuven); Tijl De Bie (Dept. Psychology); Pieter Monsieurs (Dept. Electrical Engineering, K.U.Leuven); Kristof Engelen (ept. Microbial and Molecular Systems, K.U.Leuven); Bart De Moor (Dept. Electrical Engineering, K.U.Leuven); Kathleen Marchal (ept. Microbial and Molecular Systems, K.U.Leuven)

Poster J-9

In silico motif search along with in vivo confirmation of NF-kB regulated gene sets in NPC microarray data

Yuching Lai (Life Science Department, Chang Gung University); Greg Tyrelle (Life Science Department, Chang Gung University); Kuang-Den Chen (Life Science Department, Chang Gung University)

Poster J-10

Dedicated Computer System for Genome Wide Simulation of Signal Transduction Networks

Tetsuya Maeshiro (University of Tsukuba); Katsunori Shimohara (Doshisha University)

Poster J-11

Computational predicted protein associations of Mycobacteriun tuberculosis under hypoxic conditions associated with latency

Christian Solis Calero (Facultad de Farmacia y Bioquímica - Universidad Nacional Mayor de San Marcos); Luisa Negron Ballarte (Facultad de Farmacia y Bioquímica - Universidad Nacional Mayor de San Marcos)

Poster J-12

GEM System version 2 for the analysis of metabolic pathways

Kazuharu Arakawa (Institute for Advanced Biosciences, Keio University, and Japan Society for the Promotion of Science); Nobuaki Kono (Institute for Advanced Biosciences, Keio University); Satoshi Tamaki (Institute for Advanced Biosciences, Keio University); Hiromi Yoshida (Institute for Advanced Biosciences, Keio University); Masaru Tomita (Institute for Advanced Biosciences, Keio University)

Poster J-13

A computational genomics approach to identify cis-regulatory modules from chromatin immunoprecipitation microarray data – a case study of E2F1

Victor X Jin (UC Davis Genome Center); Alina Rabinovich (UC Davis Genome Center); Sharon L. Squazzo (UC Davis Genome Center); Peggy J. Farnham (UC Davis Genome Center)

Poster J-14

Metabolic Flux Analysis To Study The Production Of Cda, By *Streptomyces coelicolor*

Raul Munoz-Hernandez (The University of Manchester); Ana Katerine de Carvalho Lima Lobato (The University of Manchester); Ferda Mavituna (The University of Manchester)

Poster J-15

The Role of LIMK1 in Endothelial Barrier Function

Matvey Gorovoy (University of Illinois); Tatyana Voyno-Yasenetskaya (University of Illinois)

Poster J-16

Computational analysis of gene regulatory elements

Reddy, D. A. (University of Hyderabad); Mitra, C. K. (University of Hyderabad)

Poster J-17

An Agent-based Model of T cell Proliferatin Experiments

Beatriz Stransky (UFRJ); Eduardo Auilar (UFRJ); Luis Alfredo V Carvalho (UFRJ); Alberto Nobrega (UFRJ)

Poster J-18

Regulation of E.coli respiration: molecular genetic network reconstruction and mathematical modeling

Alexander V. Ratushny (Institute of Cytology and Genetics SB RAS); Tamara M. Khlebodarova (Institute of Cytology and Genetics SB RAS); Vitaly A. Likhoshvai (Institute of Cytology and Genetics SB RAS)

Poster J-19

Probabilistic comparison of gene sets for detecting key metabolic pathways in the stress response of yeast

Jean-Marc Schwartz (Kyoto University); Claire Gaugain (University of Bordeaux); Jose Nacher (Kyoto University); Antoine de Daruvar (University of Bordeaux); Minoru Kanehisa (Kyoto University)

Poster J-20

Does the Yeast PPI Network Look Like a Jellyfish?

Shaohua Zhou (Department of Developmental and Cell Biology, University of California Irvine); Arthur D. Lander (Department of Developmental and Cell Biology, University of California, Irvine); Natasa Przulj (Department of Computer Science, University of California Irvine)

Poster J-21

Biological Organization and Information

Maurício V. Kritz (LNCC/MCT)

Poster J-22

Beyond classical statistics - A systems biology approach for pathway level analysis

Sorin Draghici (Karmanos Cancer Institute and Dept. of Comp. Science, Wayne State Univ.); Kashyap Amin (Dept. of Comp. Science,); Arina Done (Dept. of Comp. Science); Purvesh Khatri (Dept. of Comp. Science)

Poster J-23

Small Molecule Regulation of Metabolic Networks

Alex Gutteridge (Kyoto University); Susumu Goto (Kyoto University); Minoru Kanehisa (Kyoto University)

Poster J-24

SymBioSys: K.U.Leuven Center for Computational Systems Biology

Yves Moreau (K.U.Leuven ESAT-SCD); Sigrid De Keersmaeker (K.U.Leuven BIW-CMPG); Kathleen Marchal (K.U.Leuven BIW-CMPG); Chantal Mathieu (K.U.Leuven MED-Legendo); Frans Schuit (K.U.Leuven MED-GEU); Jos Vanderleyden (K.U.Leuven BIW-CMPG); Iven Van Mechelen (K.U.Leuven PSY-QuantPsy); Geert Verbeke (K.U.Leuven MED-BioStat); Joris Vermeesch (K.U.Leuven MED-CME-UZ); Mieke Verstuyf (K.U.Leuven MED-Legendo); Bart De Moor

(K.U.Leuven ESAT-SCD)

Poster J-25

Biological Network Comparison Using Graphlet Degree Distribution

Natasa Przulj (UC Irvine, Computer Science)

Poster J-26

Studying microRNA-target interactions using gene expression data

Gabor Halasz (Columbia Univesity); Harmen J Bussemaker (Columbia Univesity)

Poster J-27

KEGG-based pathway visualization tool for complex omics data

Nobuaki Kono (Institute for Advanced Biosciences, Keio University); Kazuharu Arakawa (Japan Society for the Promotion of Science); Yohei Yamada (Institute for Advanced Biosciences, Keio University); Hirotada Mori (Nara Institute of Science and Technology); Masaru Tomita (Institute for Advanced Biosciences, Keio University)

Poster J-28

Evidential Reasoning and Validation for Gene Expression Data

Noppadon Khiripet (National Electronics and Computer Technology Center, Thailand)

Poster J-29

Protein Interaction Prediction with Supervised Learning Methods

Oksana Kohutyuk (Department of Comp. Science, Iowa State University); Vasant Honavar (Department of Comp. Science, Iowa State University)

Poster J-30

Cellular sensing machinery for exogenous and endogenous conditions is differentially encoded on the chromosome and poorly conserved across genomes

Heladia Salgado Osorio (CCG/UNAM); Sarath Chandra Janga (CCG/UNAM); Agustino Martínez Antonio (INSERM U511, Université Pierre et Marie Curie, CHU-Pitié Salpetrière Paris, France); Julio Collado Vides (CCG/UNAM)

Poster J-31

PATIKAweb: A Web service for querying, visualizing and analyzing a graph-based pathway database

Asli (Ayaz); Ozgun (Babur); Esat (Belviranli); Ahmet (Cetintas); Recep (Colak); Emek (Demir); Alptug (Dilek); Ugur (Dogrusoz); E.Zeynep (Erson); Erhan (Giral); Kutay (Karatepe); Hande (Kucuk); Cihan (Kucukkececi); Serhat (Tekin)

Poster J-32

Phylogenetic profiles for the prediction of protein-protein interactions: how to select reference organisms?

Jingchun Sun (Virginia Commonwealth University); Yixue Li (Bioinformation Center, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences); Zhongming Zhao (Virginia Commonwealth University)

Poster J-33

A study to identify interactions between transcription factors and non-housekeeping genes to determine expression regulation of cancer genes

Kihoon Yoon (University of Texas at San Antonio); Amitava Karmaker (University of Texas at San Antonio); Stephen Kwek (University of Texas at San Antonio)

Poster J-34

Condition transition analysis reveals TF activity related to nutrient-limitation-specific effects of oxygen presence in yeast

Theo Knijnenburg (Mediamatics,TU Delft); Lodewyk Wessels (Mediamatics,TU Delft / Molecular Biology, The Netherlands Cancer Institute); Marcel Reinders (Mediamatics,TU Delft)

Poster J-35

FunCoup: data integration and the network of functional coupling in Eukaryotes

Andrey V Alexeyenko (Stockholm Bioinformatics Center, Stockholm University); Erik LL Sonnhammer (Stockholm Bioinformatics Center, Stockholm University)

Poster J-36

The consequences of alternative splicing on biological pathways

Melissa Cline (Pasteur Institute)

Poster J-37

A Homology-based Method for Predicting Complexes in Large Protein-Protein Interaction Networks

Jae-Hun Choi (ETRI); Jong-Min Park (ETRI); Soo-Jun Park (ETRI)

Poster J-38

Nonlinear dimesnionalilty reduction in apoptosis signalling networks

Sergii Ivakhno (University of Edinburgh; School of Informatics); Douglas Armstrong (University of Edinburgh; School of Informatics)

Poster J-39

Metabolic flux balance model as a potentially approach for the design and optimization of Cosmomycin production by Streptomyces olindensis ICB20

Ana Katerine de Carvalho Lima Lobato (The School of Chemical Engineering and Analytical Science, The University of Manchester); Raul Munoz-Hernandez (The School of Chemical Engineering and Analytical Science, The University of Manchester); Renata L. Araujo Furlan (University of Sao Paulo); Gabriel Padilla (Institute of Biomedical Sciences, University of Sao Paulo); Leandro M. Garrido (Institute of Biomedical Sciences, University of Sao Paulo); Gorete Ribeiro de Macedo (Department of Chemical Engineering, Federal University of Rio Grande do Norte); Ferda Mavituna (The School of Chemical Engineering and Analytical Science, The University of Manchester)

Poster J-40

Comparative Evaluation of the Accuracy of Reverse Engineering Gene Regulatory Networks with various Machine Learning Methods

Adriano V. Werhli (BioSS); Marco Grzegorczyk (University of Dortmund); Dirk Husmeier (BioSS); Wolfgang Urfer (University of Dortmund)

Poster J-41

Identification of transcription logic-gate dynamics in *Escherichia coli*

Ilaria Mogno (University of Rome La Sapienza); Lorenzo Farina (University of Rome La Sapienza); Timothy Gardner (Boston University)

Poster J-43

On the Creation of Provably-Correct Models of Biological Structure and Process

Randall L. Owen (University of Oxford); Charlotte Deane (University of Oxford)

Poster J-44

GenePro: a Cytoscape Plugin for Advanced Visualization and Analysis of Interaction Networks

Jim Vlasblom (Center for Computational Biology, The Hospital for Sick Children); Samuel Wu (Center for Computational Biology,The Hospital for Sick Children); Shuye Pu (Center for Computational Biology, The Hospital for Sick Children); Mark Superina (Center for Computational Biology, The Hospital for Sick Children); Gina Liu (Center for Computational Biology, The Hospital for Sick Children); Chris Orsi (Center for Computational Biology, The Hospital for Sick Children); Shoshana J. Wodak (Center for Computational Biology, The Hospital for Sick Children, Departments of Biochemistry and Me)

Poster J-45

Assistant Research Fellow

ChungYen Lin (Institute of Information Science, Academia Sinica); Chi-Shiang Cho (National Health Research Institutes); Chia-Ling Chen (National Health Research Institutes); Fan-Kai Lin (National Health Research Institutes); Chieh-Hua Lin (National Health Research Institutes); Pao-Yang Chen (National Health Research Institutes); Shu-Hwa Chen (Institute of Zoology, Academia Sinica); Chen-Zen Lo (National Health Research Institutes); Chao A. Hsiung (National Health Research Institutes)

Poster J-46

Multi-layered network structure of amino acid (AA) metabolism characterized by each essential AA-deficient condition

Nahoko Shikata (Graduate School of Systems Life Sciences, Kyushu University); Yukihiro Maki (Department of Digital Media, Fukuoka International University); Yasushi Noguchi (Research Institute for Health Fundamentals, Ajinomoto Co., Inc.); Masato Mori (Research Institute for Health Fundamentals, Ajinomoto Co., Inc.); Taizo Hanai (Graduate School of Systems Life Sciences, Kyushu University); Michio Takahashi (Research Institute for Health Fundamentals, Ajinomoto Co., Inc.); Masahiro Okamoto (Graduate School of Systems Life Sciences, Kyushu University)

Poster J-47

Relationship between topology and functions in chloroplast metabolic network evolution

Zhuo Wang (Biomedical Instrument Institute, Shanghai Jiao Tong University); Yazhu Chen (Biomedical Instrument Institute, Shanghai Jiao Tong University); Yuanyuan Li (Shanghai Center for Bioinformation Technology); Yixue Li (Shanghai Center for Bioinformation Technology); Lei Liu (W. M. Keck Center for Comparative and Functional Genomics, University of Illinois at Urbana-Champaig)

Poster J-48

Mapping of Escherichia coli transcriptional regulation from a compendium of expression profiles

Jeremiah J Faith (Boston University); Boris Hayete (Boston University); Joshua Thaden (Boston University); Ilaria Mogno (University of Rome); Jamey Wierzbowski (Cellicon Biotechnologies Inc.); Guillaume Cottarel (Cellicon Biotechnologies Inc.); Simon Kasif (Boston University); James Collins (Boston University); Timothy Gardner (Boston University)

Poster J-49

Analysis of Adaptation Behaviour of Fungi Under Biotic Stress Caused by Biofilm Formation

Betul Soyler (Department of Food Engineering); Zumrut B. Ogel (Department of Food Engineering)

Poster J-50

Monet Ontology as a tool to construct and explore integrated biological networks

Ney Lemke (IBB-Unesp); Renata Vieira (Unisinos); João Paulo Müller da Silva (Unisinos); José Guilherme Camargo de Souza (UNISINOS); Marialva Sinigaglia (IF-UFRGS); José Carlos Mombach (IF-UFRGS)

Poster J-51

Combined visualization and analysis of Gene Ontology annotations using multivariate representations of annotations and bipartite networks

Rohan Williams (UNSW); Kai (Kevin) Xu (National ICT Australia); Jane Huang (University of Sydney); Chris Cotsapas (UNSW); Seokhee Hong (National ICT Australia); Geoff McCaughan (University of Sydney); Mark Gorrell (University of Sydney); Peter Little (UNSW)

Poster J-52

Probabilistic Genetic Networks analysis of three *Plasmodium falciparum* strains from dynamical expression signals

Junior Barrera (Instituto de Matemática e Estatística - Universidade de São Paulo); Roberto Marcondes Cesar Jr (Instituto de Matemática e Estatística - Universidade de São Paulo); David Corrêa Martins Jr (Instituto de Matemática e Estatística - Universidade de São Paulo); Ricardo Z. N. Vêncio (Instituto de Matemática e Estatística - Universidade de São Paulo); Carlos A. B. Pereira (Instituto de Matemática e Estatística - Universidade de São Paulo); Hernando A. Del Portillo (Instituto de Ciências Biomédicas - Universidade de São Paulo)

Poster J-53

Using Synthetic Gene Expression Data to Assess Characteristics of Gene Network Inference Algorithms

Tim Van den Bulcke (ESAT-SCD, K.U.Leuven); Koenraad Van Leemput (ISLab, Universiteit Antwerpen); Thomas Dhollander (ESAT-SCD, K.U.Leuven); Bart De Moor (ESAT-SCD, K.U.Leuven); Piet van Remortel (ISLab, Universiteit Antwerpen); Kathleen Marchal (CMPG, K.U.Leuven)

Poster J-54

Identifying Individual Genome-Scale Models: Integrating Reverse Engineering with Classification Analysis

Bahrad A. Sokhansanj (Drexel University); Suman Datta (Drexel University); Diane C. Lim (Drexel University)

Text Mining & Information Extraction

Poster K-1

OAT - Shows the complementarity of MeSH and GO in interpretation of gene lists

Anders Bresell (IFM Bioinformatics, Linköpings Universitet, Sweden); Bo Servenius (AstraZeneca R&D Lund, Sweden); Bengt Persson (IFM Bioinformatics, Linköpings Universitet, Sweden)

Poster K-2

Literature Mining at the Protein Information Resource (PIR)

Hu, ZZ (Protein Information Resource, Georgetown University Medical Center); Liu, H (Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University Medical Cente); Han, B (Center for Information Science and Technology, Temple University); Yuan, X (Protein Information Resource, Georgetown University Medical Center); Obradovic, Z (Center for Information Science and Technology, Temple University); Vijay-Shanker, K (Department of Computer and Information Sciences, University of Delaware); Vucetic, S (Center for Information Science and Technology, Temple University); Wu, CH (Protein Information Resource, Georgetown University Medical Center)

Poster K-3

Disambiguation of large gene/protein terminologies by automatic literature profiling

Roney S Coimbra (GlaxoSmithKline - Cheminformatics); Dana E. Vanderwall (GlaxoSmithKline - Cheminformatics)

Poster K-4

Genotyping and Annotation of Affymetrix SNP Arrays

Philippe Lamy (Bioinformatics Research Center, University of Aarhus); Carsten Wiuf (Bioinformatics Research Center, University of Aarhus); Claus L. Andersen (Molecular Diagnostic Laboratory, Aarhus University Hospital, Skejby); Friedrik P. Wikman (Molecular Diagnostic Laboratory, Aarhus University Hospital, Skejby)

Poster K-5

Title: SAM as a plugin for BASE

Ana Carolina Q. Simoes (Programa de Pós-Graduação Interunidades em Bioinformática & Departamento de Bioquímica, Instituto de); Aline Maria da Silva (Programa de Pós-Graduação Interunidades em Bioinformática & Departamento de Bioquímica, Instituto de)

Poster K-6

Construction and Evaluation of an Abbreviation Dictionary for Normalizing Protein Names

Joon-Ho Lim (ETRI); Jaesoo Lim (ETRI); Hyunchul Jang (ETRI); Soo-Jun Park (ETRI)

Poster K-8

Dynamic query and exploration of literature paths between proteins

Robert Hoffmann (Memorial Sloan-Kettering Cancer Center); Chris Sander (Memorial Sloan-Kettering Cancer Center)

Poster K-9

Human Computer Interface Analysis of Tier1/2/3 Bioinformatics Tools

Annette Greiner (Joint Genome Institute); Kristen Taylor (Joint Genome Institute)

Poster K-10

Recursive Top-Down Quantum Clustering of Biological Data

Varshavsky Roy (School of Computer Science and Engineering, The Hebrew University of Jerusalem, Israel); Horn David (School of Physics and Astronomy, Tel Aviv University, Israel); Linial Michal (Deptartment of Biological Chemistry, The Hebrew University of Jerusalem, Israel)

Poster K-11

Annotation errors and their correction by association rule mining

Artamonova I.I. (Institute for Bioinformatics, GSF - National Research Center for Environment and Health); Frishman G. (Institute for Bioinformatics, GSF - National Research Center for Environment and Health); Gelfand M.S. (Institute of Information Transmission Problems RAS); Frishman D. (Department of Genome Oriented Bioinformatics, Technische Universität Munchen)

Poster K-12

FLAME: Frequency-Based Lexical Analysis of Microarray Gene Lists

Anar K. Khan (AgResearch Ltd., Invermay Agricultural Centre, Puddle Alley, Mosgiel, Otago, New Zealand); Alistair K. Knott (Computer Science Department, University of Otago, 90 Union Place East, Dunedin, New Zealand); Jonathan W. Warren (AgResearch Ltd., Invermay Agricultural Centre, Puddle Alley, Mosgiel, Otago, New Zealand); John C. McEwan (AgResearch Ltd., Invermay Agricultural Centre, Puddle Alley, Mosgiel, Otago, New Zealand)

Poster K-14

BioMint: a database curator's assistant for biomedical text processing

Anne-Lise Veuthey (Swiss Institute of Bioinformatics); Violaine Pillet (Swiss Institute of Bioinformatics); Marc Zehnder (Swiss Institute of Bioinformatics)

Poster K-15

A New Methodology for Regulatory Network Inference

Ígor L. Almeida (PIPCA, Universidade do Vale do Rio dos Sinos - São Leopoldo, Brazil); Adelmo L. Cechin (PIPCA, Universidade do Vale do Rio dos Sinos - São Leopoldo, Brazil); Cláudia K. Barcellos (Hewlett-Packard Labs - Porto Alegre, Brazil); Irene S. Gabashvili (Computational Biosciences Research, Hewlett-Packard Labs - Palo Alto, USA)

Poster K-16

Predicting MEDLINE Abstracts Relevant to Salt Tolerance in Plants

Crystal L. Nevels (Department of Computer Science, Jackson State University, Jackson Mississippi, USA); Charles E. Bland (Department of Computer Science, Jackson State University, Jackson Mississippi, USA); Raphael D. Isokpehi (Department of Biology, Jackson Mississippi, USA)

Poster K-17

Effects of Head Noun Features on Statistical Named Entity Recognition in Biomedical Literatures

Jaesoo Lim (Electronics and Telecommunications Research Institute); Hyunchul Jang (Electronics and Telecommunications Research Institute); Joon-Ho Lim (Electronics and Telecommunications Research Institute); Soo-Jun Park (Electronics and Telecommunications Research Institute)

Poster K-18

Clustering of Medline abstracts using Particle Swarm Optimisation

Ayton Meintjes (Bioinformatics and Computational Biology Unit, University of Pretoria); Fourie Joubert (Bioinformatics and Computational Biology Unit, University of Pretoria)

Poster K-19

Construction of Scoring Functions using Neural Network for Determination of Affinities Constants Receptor-Ligand.

Thaís Gaudencio do Rêgo (Laboratório Nacional de Computação Científica); Marco Antônio Vilela (Laboratório Nacional de Computação Científica); Hélio José Corrêa Barbosa (Laboratório Nacional de Computação Científica); Laurent Emmanuel Dardenne (Laboratório Nacional de Computação Científica);

Poster K-20

From Spectrum to Structure using Machine Learning

Caroline Farrelly (University of Manchester); Prof. Douglas Kell (University of Manchester); Dr. Joshua Knowles (University of Manchester);

Poster K-21

Frame-based Analysis of Complex Relationships in Biomedical Text: Annotating and Extracting Protein Transport Information in GeneRIFs

Zhiyong Lu (Center for Computational Pharmacology, School of Medicine, University of Colorado); William Baumgartner Jr. (Center for Computational Pharmacology, School of Medicine, University of Colorado); Michael Bada (Center for Computational Pharmacology, School of Medicine, University of Colorado); James Firby (Center for Computational Pharmacology, School of Medicine, University of Colorado); Philip Ogren (Center for Computational Pharmacology, School of Medicine, University of Colorado); Kevin Cohen (Center for Computational Pharmacology, School of Medicine, University of Colorado); Lawrence Hunter (Center for Computational Pharmacology, School of Medicine, University of Colorado)

Poster K-22

EBIMed and Protein Corral: EBI's information retrieval and information extraction engines for realtime analysis of Medline abstracts

Arregui (EBI); Gaudan (EBI); Kirsch (EBI); Rebholz-Schuhmann (EBI)

Poster K-24

BioTermNet: a system for biomedical text mining

Asako Koike (Univ. of Tokyo); Toshihisa Takagi (Univ. of Tokyo)

Poster K-25

Search Engine for Mining Biological Significance of Genetic Markers in Medline

Weijian Xuan (Molecular and Behavioral Neuroscience Institute and Department of Psychiatry, University of Michigan); Pinglang Wang (Molecular and Behavioral Neuroscience Institute and Department of Psychiatry, University of Michigan); Stanley J. Watson (Molecular and Behavioral Neuroscience Institute and Department of Psychiatry, University of Michigan); Fan Meng (Molecular and Behavioral Neuroscience Institute and Department of Psychiatry, University of Michigan)

Poster K-26

Imitating manual curation of text-mined facts in biomedicine

Raul Rodriguez-Esteban (Center for Computational Biology and Bioinformatics, Columbia University); Ivan Iossifov (Center for Computational Biology and Bioinformatics, Columbia University); Andrey Rzhetsky (Center for Computational Biology and Bioinformatics, Columbia University)

Poster K-27

Mindmapping literature information: extract, visualize and explore for modeling

Steven Vercruysse (Ghent University - VIB); Martin Kuiper (Ghent University - VIB)

Poster K-28

Mining Provenance Logs from Bioinformatics Workflows

Sérgio Manuel Serra da Cruz (NCE-UFRJ)

Transcriptomics

Poster L-1

A calibration method for estimating absolute expression levels from microarray data

Kristof Engelen (Department of Microbial and Molecular Systems, KULeuven); Hui Zhao (Department of Electrical Engineering, KULeuven); Bart De Moor (Department of Electrical Engineering, KULeuven); Kathleen Marchal (Department of Microbial and Molecular Systems, KULeuven)

Poster L-2

Genome Expression Pathway Analysis Tool - Analysis and Visualization of Microarray Gene Expression Data under Genomic, Proteomic and Metabolic Context

Markus Weniger (Department of Bioinformatics, Biocenter, University Wuerzburg); Joerg Schultz (Department of Bioinformatics, Biocenter, University Wuerzburg)

Poster L-3

Identification of Deuterostomia Conserved Genes in the Human Parasite Schistosoma mansoni

Thiago M. Venancio (Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, Brazil); Ricardo DeMarco (Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, Brazil); Giulliana T. Almeida (Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, Brazil); Katia C.P. Oliveira

(Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, Brazil); João C. Setubal (Virginia Bioinformatics Institute, Virginia Polytechnic Institute and State University, Blacksburg,); Sergio Verjovski-Almeida (Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, Brazil)

Poster L-4

A Large Scale Gene Expression Analysis of the Mouse Brain

Pedro A. F. Galante (Ludwig Institute for Cancer Research and Departamento de Bioquímica - IQ - USP); Sandro José de Souza (Ludwig Institute for Cancer Research); Bettina Malnic (Departamento de Bioquímica - IQ - USP)

Poster L-5

Power CoClustering – detecting multiple regulatory influences in gene expression data

Shay Zakov (Computer Science Department, Ben Gurion University); Avraham A. Melkma (Computer Science Department, Ben Gurion University)

Poster L-6

Kernel-imbedded Gaussian Processes For Microarray Gene Expression Data Analysis

Leo Wang-kit Cheung (Division of Biostatistics and Bioinformatics, Department of Preventive Medicine and Epidemiology, Lo); Xin Zhao (Department of Information and Computer Sciences, University of Hawaii)

Poster L-7

SNPs in NAGNAG Acceptors Are Highly Predictive for Variations of Alternative Splicing

Michael Hiller (Albert-Ludwigs-University Freiburg)

Poster L-8

Detection of the candidates of Alternative promoters and TOP genes using Database of Transcription Start Sites (DBTSS)

Riu Yamashita (HGC, IMS,Univ. of Tokyo); Katsuki Tsuritani (HGC, IMS, Univ. of Tokyo); Yutaka Suzuki (Dep. of Med. Genome. Sci., Univ. of Tokyo); Sumio Sugano (Dep. of Med. Genome. Sci., Univ. of Tokyo); Kenta Nakai (HGC, IMS, Univ. of Tokyo)

Poster L-9

Discovering co-occurrences of gene annotations in large lists of genes

Pedro Carmona-Saez (BioComputing Unit. National Center of Biotechnology); Monica Chagoyen (BioComputing Unit. National Center of Biotechnology); Jose M. Carazo (BioComputing Unit. National Center of Biotechnology); Francisco Tirado (Computer Architecture Department. Universidad Complutense de Madrid); Alberto Pascual-Montano (Computer Architecture Department. Universidad Complutense de Madrid)

Poster L-10

Query-driven Search for Analysis of Large Microarray Collections

Matthew A. Hibbs (Lewis-Sigler Institute for Integrative Genoimcs, Department of Computer Science, Princeton Universit); Kai Li (Department of Computer Science, Princeton University); Olga G. Troyanskaya (Lewis-Sigler Institute for Integrative Genoimcs, Department of Computer Science, Princeton Universit)

Poster L-11

Development of a Rice Genome Database for the Interpretation of Cereal Microarray Data

Philip Law (Bioinformatics and Computational Biology Unit, University of Pretoria); Clotilde Claudel-Renard (Bioinformatics and Computational Biology Unit, University of Pretoria); Fourie Joubert (Bioinformatics and Computational Biology Unit, University of Pretoria); Dave Berger (Department of Botany, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretor);

Poster L-12

Probabilistic Inference of transcription factor concentrations and gene-specific regulatory activities

Guido Sanguinetti (University of Sheffield); Neil Lawrence (University of Sheffield); Magnus Rattray (University of Manchester);

Poster L-13

Cerebellar Ethanol Sensitivity: A Central Role For Creb Transcription Regulation

George K. Acquaah-Mensah (Massachusetts College of Pharmacy & Health Sciences)

Poster L-14

Combining DNA copy number and gene expression data to reveal recurrent genetic abnormalities in pancreatic cancer

Liviu Badea (AI department, National Institute for Research in Informatics); Doina Tilivea (AI department, National Institute for Research in Informatics)

Poster L-15

MDframe: a computational framework for the high-throughput identification of human regulatory motifs

Linyong Mao (Medical University of South Carolina); Omar Moussa (Medical University of South Carolina); John S. Yordy (Medical University of South Carolina); Dennis K. Watson (Medical University of South Carolina); W. Jim Zheng (Medical University of South Carolina)

Poster L-17

Global analysis of antisense transcription in intronic regions of the human genome

Helder I. Nakaya (Departamento de Bioquímica, Instituto de Química, USP); Rodrigo Louro (Departamento de Bioquímica, Instituto de Química, USP); André Lopes (Departamento de Bioquímica, Instituto de Química, USP); Tarik El-Jundi (Departamento de Bioquímica, Instituto de Química, USP); Paulo P. Amaral (Departamento de Bioquímica, Instituto de Química, USP); Angela Fachel (Departamento de Bioquímica, Instituto de Química, USP); Aline M. da Silva (Departamento de Bioquímica, Instituto de Química, USP); Eduardo M. Reis (Departamento de Bioquímica, Instituto de Química, USP); Sergio Verjovski-Almeida (Departamento de Bioquímica, Instituto de Química, USP)

Poster L-18

Non-negative matrix factorization of biological data

Alberto Pascual-Montano (Computer Architecture Department.. Complutense University of Madrid. Spain); Pedro Carmona-Saez (BioComputing Unit. National Center of Biotechnology. Madrid. Spain); Monica Chagoyen (BioComputing Unit. National Center of Biotechnology. Madrid. Spain); Francisco Tirado (Computer Architecture Department.. Complutense University of Madrid. Spain); Jose M. Carazo (BioComputing Unit. National Center of Biotechnology. Madrid. Spain); Roberto D. Pascual-Marqui (The KEY Institute for Brain-Mind Research. Zurich. Switzerland)

Poster L-19

Computational detection of tissue- and process-specific cis-regulatory modules by a maximum specificity method

Peter Van Loo (Department of Human Genetics, Flanders Interuniversity Institute for Biotechnology and University of); Stein Aerts (Department of Human Genetics, Flanders Interuniversity Institute for Biotechnology and University of); Bart De Moor (Bioinformatics group, Department of Electrical Engineering, University of Leuven, Belgium); Yves Moreau (Bioinformatics group, Department of Electrical Engineering, University of Leuven, Belgium); Peter Marynen (Department of Human Genetics, Flanders Interuniversity Institute for Biotechnology and University of)

Poster L-20

Improving nitrogen utilisation and amino acid composition in barley used for animal feed

Carsten Friis (CBS); Michael Hansen (Danish Institute of Agricultural Sciences); E. Vincze (Danish Institute of Agricultural Sciences,); P. B. Holm (Danish Institute of Agricultural Sciences,)

Poster L-21

Integrative Analysis of NCI-60 Panel Reveals Candidate Key Genetic Regulators Affected by Genomic Alterations

Doron Lipson (CS Dept, Technion, Israel); Mark Reimers (National Cancer Institute, Bethesda, MD); Anya Tsalenko (Agilent Laboratories, CA); Amir Ben-Dor (Agilent Laboratories, CA); Kimberly Bussey (National Cancer Institute, Bethesda, MD); William Reinhold (National Cancer Institute, Bethesda, MD); Michael Barrett (Agilent Laboratories, CA); John Weinstein (National Cancer Institute, Bethesda, MD); Zohar Yakhini (Agilent Laboratories, CA)

Poster L-22

Splicing Arrays: Profiling transcriptome by statistical analysis of mRNA isoform expression

Murlidharan Nair (IUSB); Hai-Ri, Li (UCSD); Jessica A Whitaker (IUSB); Xiang-Dong Fu (UCSD)

Poster L-23

Novel Gene Expression Analysis Using SAM and PAM Algorithms to Determine Estrogen-regulated Genes Involved in Response to Neoadjuvant Endocrine Therapy for Breast Cancer

Susan Trapp ("Computational Bioscience Program, Univ. of Colorado Health Sciences"); Tzu Phang ("School of Medicine, Univ. of Colorado Health Sciences"); Djuana Harvell ("Division of Endocrinology, Univ. of Colorado Health Sciences"); Larry Hunter ("Computational Bioscience Program, Univ. of Colorado Health Sciences"); Anthony Elias ("Dept of Oncology, Univ. of Colorado Health Sciences"); Jennifer Richer ("Division of Endocrinology, Univ. of Colorado Health Sciences")

Poster L-24

Fuzzy puzzle of cis-elements in co-regulated promoters – the blueprint of key nodes in signal transduction networks

Nico Voss (BIOBASE GmbH Halchtersche Str. 33, D-38304 Wolfenbüttel, Germany); Tatyana Konovalova (Institute of Cytology and Genetics, Novosibirsk, Russia); Philip Stegmaier (BIOBASE GmbH Halchtersche Str. 33, D-38304 Wolfenbüttel, Germany); Olga Kel-Margoulis (r. 33, D-38304 Wolfenbüttel, Germany); Evelin Katona (University Hospital Regensburg Franz-Josef-Strauss-Allee 11, D-93053 Regensburg, Germany); Thomas Langmann (University Hospital Regensburg Franz-Josef-Strauss-Allee 11, D-93053 Regensburg, Germany); Gerd Schmitz (University Hospital Regensburg Franz-Josef-Strauss-Allee 11, D-93053 Regensburg, Germany); Edgar Wingender (Dept. Bioinformatics, UKG/Univ. Göttingen, Goldschmidtstr. 1, 37077 Göttingen, Germany); Alexander Kel (BIOBASE GmbH Halchtersche Str. 33, D-38304 Wolfenbüttel, Germany)

Poster L-25

ChromoViz-Web: mapping and multimodal visualizing gene expression data with integrated major bio resources onto chromosomes using scalable vector graphics

Do Kyoon Kim (Seoul National University Biomedical Informatics (SNUBI)); Jihoon Kim (Department of Biostatistics, University of Wisconsin); Ju Han Kim (Seoul National University Biomedical Informatics (SNUBI))

Poster L-26

SigWin-finder: an interactive workflow in a virtual laboratory for e-bioscience

Marcia A. Inda (Integrative Bioinformatics Unit, Faculty of Science, University of Amsterdam); Marco Roos (Integrative Bioinformatics Unit, Faculty of Science, University of Amsterdam); Adam S. Z. Belloum (Institute of Informatics, Faculty of Science, University of Amsterdam); Dmitry Vasunin (Institute of Informatics, Faculty of Science, University of Amsterdam); Timo M. Breit (Integrative Bioinformatics Unit, Faculty of Science, University of Amsterdam)

Poster L-27

graPT : A genome resourcing analyzer for Predictive Toxicology

Jung Hoon Woo (Seoul National University Biomedical Informatics, Interdisciplinary Program in Bioinformatics, Seoul); Ju Han Kim (Seoul National University Biomedical Informatics, College of Medicine, Seoul National University)

Poster L-28

The role of membrane proteins in sample classification inferred by genome-wide expression profiling data

Paolo Uva (IRBM (MRL-Rome)); Armin Lahm (IRBM (MRL-Rome)); Emanuele de Rinaldis (IRBM (MRL-Rome));

Poster L-29

Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in Arabidopsis thaliana

Matti Kankainen (University of Helsinki, Institute of Biotechnology); Günter Brader (University of Helsinki, Department of Biological and Environmental Sciences, Division of Genetics); Petri Törönen (University of Helsinki, Institute of Biotechnology); E. Tapio Palva (University of Helsinki, Department of Biological and Environmental Sciences, Division of Genetics); Liisa Holm (University of Helsinki, Institute of Biotechnology);

Poster L-30

Features of sequence composition and population genetical measures of selection to analyse alternatively spliced exons and introns

Ivana Vukusic (University of Cologne, Institute for Genetics); Sushma-Nagaraja Grellscheid (Institute of Human Genetics, International Centre for Life, University of Newcastle upon Tyne); Thomas Wiehe (University of Cologne, Institute for Genetics)

Poster L-31

Large-scale analysis of the impact of alternative splicing on protein isoforms

Johannes Frey-Skött (Stockholm Bioinformatics Center); Arne Elofsson (Stockholm Bioinformatics Center)

Poster L-32

Gene Expression Trees in Blood Cell Development

Ivan G. Costa Filho (Department of Computational Molecular Biology, Max Planck Institute for Molecular Genetics); Stefan Roepcke (Department of Computational Molecular Biology, Max Planck Institute for Molecular Genetics); Alexander Schliep (Department of Computational Molecular Biology, Max Planck Institute for Molecular Genetics)

Poster L-33

Meta-Learning of Clustering Algorithms: Analyzing Gene Expression Time Courses

Francisco A. T. de Carvalho (Centro de Informática, Universidade Federal de Pernambuco); Ricardo B. C. Prudencio (Centro de Informática, Universidade Federal de Pernambuco); Marcílio C. P. de Souto (Departamento de Informática e Matemática Aplicada, Universidade Federal do Rio Grande do Norte); Ivan G. Costa (Dept. of Computational Molecular Biology, Max Planck Institute for Molecular Genetics); Benjamin Georgi (Dept. of Computational Molecular Biology, Max Planck Institute for Molecular Genetics); Teresa Ludermir (Centro de Informática, Universidade Federal de Pernambuco); Stefan Roepcke (Dept. of Computational Molecular Biology, Max Planck Institute for Molecular Genetics); Alexander Schliep (Dept. of Computational Molecular Biology, Max Planck Institute for Molecular Genetics)

Poster L-34

Modeling Transcription Kinetics with Differential Equations

Pablo R. Freire (National Laboratory for Scientific Computation); Ana Tereza R. Vasconcelos (National Laboratory for Scientific Computation)

Poster L-35

Graphical User Interfaces to Microarray Analysis Programs

Keith Satterley (Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research); James Wettenhall (Peter MacCallum Cancer Centre); Ken Simpson (Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research); Gordon K Smyth (Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research)

Poster L-36

Characterization of gene expression during erytrhoid differentiation by Serial Analysis of Gene Expression (SAGE)

Anderson F Cunha (Universidade Estadual de Campinas-Hemocentro); Ana Flávia Brugnerotto (Universidade Estadual de Campinas- Hemocentro); Adriana S S Duarte (Universidade Estadual de Campinas- Hemocentro); Gustavo G L Costa (Universidade Estadual de Campinas-Hemocentro); Marcelo F Carazolle (Universidade Estadual de Campinas- Instituto de Biologia); Gonçalo A G Pereira (Universidade Estadual de Campinas- Instituto de Biologia); Fernando F Costa (Universidade Estadual de Campinas-Hemocentro)

Poster L-37

Fuzzy Biclustering of Microarray Data - borrowing ideas from sequence profiles

Stefan Tomiuk (Miltenyi Biotec GmbH); Michael Brosda (Miltenyi Biotec GmbH); Corinna Scholz (Miltenyi Biotec GmbH); Kay Hofmann (Miltenyi Biotec GmbH)

Poster L-38

Meta Prediction of Human microRNA Targets

Alal Eran (Children's Hospital Informatics Program, Harvard-MIT Division of Health Sciences and Technology); Alvin Kho (Children's Hospital Informatics Program, Harvard-MIT Division of Health Sciences and Technology); Iris Eisenberg

(Howard Hughes Medical Institute, Children's Hospital Boston); Michal Galdzicki (Children's Hospital Informatics Program, Harvard-MIT Division of Health Sciences and Technology); Kamila Naxerova (Children's Hospital Informatics Program, Harvard-MIT Division of Health Sciences and Technology); Marco Ramoni (Children's Hospital Informatics Program, Harvard-MIT Division of Health Sciences and Technology); Louis Kunkel (Howard Hughes Medical Institute, Children's Hospital Boston); Isaac Kohane (Children's Hospital Informatics Program, Harvard-MIT Division of Health Sciences and Technology)

Other

Poster M-1

CUPID: Core and Unique Protein IDentification system

Raja Mazumder (Protein Information Resource, Georgetown University); Darren A. Natale (Protein Information Resource, Georgetown University); Sudhir Murthy (DCWASA- DWT); Rathi Thiagarajan (Protein Information Resource, Georgetown University); Cathy H. Wu (Protein Information Resource, Georgetown University)

Poster M-2

Downregulation of anti-apoptotic gene expression by antisense oligonucleotides induces apoptosis and sensitizes head and neck squamous cell carcinoma cells to chemotherapy

Himani Sharma (Dept. Of Biochemistry, All India Institute Of Medical Sciences, Ansari Nagar, New Delhi. India); Neeta Singh (Dept. Of Biochemistry, All India Institute Of Medical Sciences, Ansari Nagar, New Delhi. India)

Poster M-3

Synthesis And Selection Of Antibacterials Using Codon-Shuffling As Method For De Novo Protein Design.

Alka Rao (ICGEB, New Delhi); Sidharth Chopra (ICGEB, New Delhi); Geeta Ram (ICGEB, New Delhi); Anand Ranganathan (ICGEB, New Delhi)

Poster M-4

Plant Transcription Factors

Diego Mauricio Riano Pachón (Department of Molecular Biology, Institute of Biochemistry and Biology, University of Potsdam); Ingo Dreyer (Department of Molecular Biology, Institute of Biochemistry and Biology, University of Potsdam); Slobodan Ruzicic (Cooperative Research Group, Max Plack Institute of Molecular Plant Physiology); Bernd Mueller-Roeber (Department of Molecular Biology, Institute of Biochemistry and Biology, University of Potsdam)

Poster M-5

Predicting Chemical Properties of Metabolites

Roman Eisner (University of Alberta); Craig Knox (University of Alberta); Russ Greiner (University of Alberta); David Wishart (University of Alberta)

Poster M-6

Identification of Microorganisms Clusters by Using Dynamic Programming to Analyze Antimicrobial Susceptibility Sequences

Braulio RGM Couto (UNI-BH); Ana P Ladeira (UNI-BH); Carlos EF Starling (Hospitais Vera Cruz , Life Center e Baleia)

Poster M-8

An information system to early detect and control plant diseases and other causal agents of damage

Camargo, A. (The University of Liverpool, Department of Electrical Engineering & Electronics, Liverpool, L69 3GJ,); Smith, J. (The University of Liverpool, Department of Electrical Engineering & Electronics, Liverpool, L69 3GJ,);

Poster M-9

Bioinformatics analysis on ChIP-on-chip data to survey global RNA pol II binding and histone H3 acetylation patterns and the effects induced by HDAC inhibition

Richard Cai (Scientific Computing and Statistics, Genome and Proteome Sciences, NIBRI); Shaowen Wang (Molecular Biology, NIBRI); Darrell Ricke (Scientific Computing and Statistics, Genome and Proteome Sciences, NIBRI); Yan Yan-Neale (Drug Discovery II, Oncology, NIBRI); Richard Young (Whitehead Institute, MIT); Dalia Cohen (Molecular Biology, NIBRI);

Poster M-10

Effective strategies for bioinformatics training on genomics resources

Warren C. Lathe III, Ph.D. (OpenHelix); Mary E. Mangan, Ph.D (OpenHelix); Scott M. Lathe (OpenHelix); Ken Klima, Ph.D. (Hebert Research); George Taniwaki, Ph.D. (Hebert Research)

Poster M-11

ASviewer : Visualizing the transcript structure and functional domains of alternatively-spliced genes

Younghee Lee (Ewha Womans University); Wonhyong Chung (National Genome Information Center); Sanghyuk Lee (Ewha Womans University)

Poster M-12

An open-source software platform for the management and analysis of genotyping data

Corne Schriek (Bioinformatics and Computational Biology Unit, University of Pretoria)

Poster M-13

A Computational Framework for Analysis of Dynamic Social Structures

Tanya Y. Berger-Wolf (Department of Computer Science, University of Illinois at Chicago); Ilya R. Fischhoff (Department of Ecology & Evolutionary Biology, Princeton University); Daniel I. Rubenstein (Department of Ecology & Evolutionary Biology, Princeton University); Jared Saia (Department of Computer Science, University of New Mexico, Albuquerque); Siva Sundaresan (Department of Ecology & Evolutionary Biology, Princeton University)

Poster M-15

A Numeric Coding Scheme for Amino Acids

Siwo Geoffrey Henry (Dept. Biochemistry, Egerton University)

Poster M-16

DOE Hanford Site Metagenome: A multiple extreme environment that hosts wide diversity of microbes and radiotolerant bacteria

Syed H Mustafa (Argonne National Laboratory); Natalia Maltsev (Argonne National Laboratory); Fred Brockman (Pacific Northwest National Laboratory); Banu Gopalan (Pacific Northwest National Laboratory)

Poster M-17

Detecting Cell Cycle Regulated Genes of Schizosaccharomyces pombe by using Non-metric Multidimensional Scaling without Sinusoidal Fitting

Y-h. Taguchi, (Department of Physics, Chuo University,)

Poster M-18

A Simple Formula for the High Regularisation Limit of SVMs & Ridge Regression with Application to Gene Selection and Classification of Microarrays

Justin Bedo (ANU); Tiberio Caetano (NICTA); Brian Parker (NICTA); Conrad Sanderson (NICTA); Peter Sunehag (NICTA); Adam Kowalczyk (NICTA)

Poster M-19

Quantitative model of the Mdm2-mediated p53 ubiquitination network

Paul Brazhnik (Virginia Tech); Kurt W. Kohn (NCI NIH)

Poster M-20

Optimized Selection of Short Interfering RNA Target Loci

Istvan Ladunga (Center for Biotechnology & Dept. Statistics, University of Nebraska-Lincoln)

Poster M-22

Choosing the End: Regulation of Alternative 3' Splice Sites

Yael Mandel-Gutfreund (Faculty of Biology, Technion-Israel Institute of Technology); Martin Akerman (Faculty of Biology, Technion-Israel Institute of Technology)

Poster M-23

GMP-RAM v1.1: A Proposed Software Tool To Support The Method For Risk Assessment Of Genetically Modified Plants

Katia Regina Evaristo De Jesus (Embrapa Meio Ambiente); Fábio Danilo Vieira (Embrapa Agriculture Informatics); Denis Ubeda De Lima (Bayer Cropscience Ltda / Bioscience)

ISMB 2006 sponsors

Intelligent Systems for Molecular Biology

Premier

Gold

Best Paper and Poster Presentation sponsored by