ISCB LATIN AMERICA 2016
Buenos Aires, Argentina
November 21 - 23, 2016

Schedule at a Glance
MONDAY - 21 November

08:45	09:00	Morning Welcome
09:00	10:00	Keynote Presentation: *A Mechanistic View of Oncogenic K-Ras Biology* **Ruth Nussinov**, PhD, National Cancer Institute, Maryland, USA
10:00	10:30	Coffee Break
10:30	12:30	**Protein Session**
	10:30	Biomolecular Dynamics in Complex in vivo Environments Garegin Papoian
	10:55	Discovery of Protein Isoforms for Different Stages of Prostate Cancer - Luis Rueda
	11:10	Analysis of cell-cycle regulatory linear motifs bound by the pRb retinoblastoma tumor suppressor - Lucía Chemes
	11:25	Identification and Substantiation of Specificity Determining Residue Networks using small Datasets and MI-promiscuity - Facundo Orts
	11:40	Residue-covariation networks cluster similar functional domains - Franco Simonetti
	11:55	Validation of Assembly and alignment-free method for chloroplast next generation sequences data - Raúl Martín Amado Cattáneo
	12:10	SwissProt Select: The New Protein Superfamily Database for Reliable Function Assignation - Nicolás Stocchi
	12:20	DEPICTViz - Differential Expression and Protein InteraCTions Visualization Tool Nalvo F. Almeida
12:30	14:30	**Lunch on Own**
14:30	16:30	**Data Session**
	14:30	Tech Talk, EMBL-EBI, Overview of EMBL-EBI Services and How We Work with Industry
	14:50	Systematic assessment of multi-gene predictors of pan-cancer tumour sensitivity to drugs exploiting gene expression data - Pedro J. Ballester
	15:10	Drug targets prioritization for neglected diseases - SantiagoVidela
	15:30	A Data-Driven Approach to Estimating the Number of Clusters in Hierarchical Clustering Antoine Emil Zambelli
	15:45	A novel approach for highly-diverse multi-omics data fusion applied to tomato germplasm selection - Georgina Stegmayer
	16:00	Pasteur_galaxy: An open and sustainable Galaxy instance for NGS data analysis Oussama Souiai
	16:15	Graphing genomes in 2D, applications of multivariate statistics on the genomic composition - Maria Camila Martinez
16:30	17:00	**Coffee Break**
17:00	18:00	**Keynote Presentation**: Coding for running speed and computing displacement in the mammalian brain's GPS **Emilio Kropff, PhD**, Researcher at the National Research Council (CONICET), Leloir Institute IIBBA, Buenos Aires, Argentina
18:00	19:30	**Networking and Posters, Odd Poster Presentations** **Poster Abstracts -** http://tinyurl.com/zh55g8m

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Schedule at a Glance
Tuesday– 22 November

08:45	09:00	Morning Welcome and Announcements
09:00	10:00	**Keynote Presentation**: Birdsong to study neural control and biomechanics in a learned sensorimotor task **Ana Amador, PhD,** University of Buenos Aires and IFIBA, National Research Council (CONICET), Buenos Aires, Argentina
10:00	10:30	Coffee Break
10:30	**12:30**	**Machine Learning and Data Mining Session**
	10.30	Tech-Talk, CITES, Latin American Business Incubator located in Sunchales, Santa Fe, Starting UP Bioinformatics
	10:50	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers - Søren Brunak
	11:10	Advanced data mining reveals a non-canonical mode of interaction for MHC class II I ligands - Morten Nielsen
	11:30	Novel microRNA discovery from genome-wide data: a computational pipeline with unsupervised machine learning - Georgina Stegmayer
	11:50	NetPhosPan: a pan specific predictor for phosphorylation site predictions - Emilio Fenoy
	12:03	Machine Learning Tools to Computationally Identify Genomic Elements Melissa Woghiren
	12:16	TAXOFOR: Taxonomic Assignment of 16S rDNA sequences using Fourier Analysis Guillerm Luque y Guzman Saenz
12:30	14:30	**Lunch on Own**
14:30	16:30	**Disease Session**
	14:30	Multi-Cohort Analysis Identifies Cross-Tissue Gene Signature to Predict Lung Function and TFS in Patients with Idiopathic Pulmonary Fibrosis - Scott Madeleine
	14:50	Differential network analysis for the identification of common and specific regulatory mechanisms between idiopathic dilated cardiomyopathy and ischemic cardiomyopathy Mariana Recamonde-Mendoza
	15:10	A bioinformatics approach shows significant overlap of molecular pathology in early p preeclampsia with endometrial diseases - Maria Rabaglino
	15:30	Diagno: an online Clinical Genomics Diagnosis tool - Patricio Yankilevich
	15:45	MultiOmics: an R package to infer genomics and epigenomics mechanisms involved with cancer disease progression - Martin Abba
	16:00	In silico prediction of biological targets of small molecules by a chemical similarity approach - Andreas Schüller
	16:15	Transcriptomic analysis of drug resistant isolates of the parasitic trematode Fasciola hepatica - Jose Tort
16:30	17:00	**Coffee Break**
17:00	18:00	**EMBO Lecture Keynote Presentation**: Systematic Patterns in Millions of 20 Yearlong Individual Patient Disease Trajectories **Søren Brunak, PhD**, Professor, Research Director Novo Nordisk Foundation Center for Protein Research, University of Copenhagen
18:00	19:30	**Networking and Posters, Even numbered posters to be presented, view poster abstracts at** http://tinyurl.com/zh55g8m

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Schedule at a Glance
Wednesday - 23 November

08:45	09:00	Morning Welcome and Announcements
09:00	10:00	**Keynote Presentation**: Data Visualization in Bioinformatics: Exploring the 'Dark' Proteome **Sean I. O'Donoghue, PhD**, CSIRO & Garvan Institute of Medical Research, Sydney, Australia
10:00	10:30	**Coffee Break**
10:30	12:30	**Genes Session**
	10:30	Tech Talk: Heritas, Bioinformatics for clinical diagnostics
	10:50	Extreme learning machines for discovering gene regulatory networks from temporal profiles of expression Mariano Rubiolo
	11:15	Dynamics of tRNA fragments and their targets in aging mammalian brain Andrey Grigoriev
	11:40	Exploring the human virome, new tools, new insights - Alejandro Reyes AND Seeking informative regions in viral genomes - Jaime Leonardo Moreno
	12:05	Bioinformatic sequence analysis tools for the search for new short peptide in "non-coding" sequences - Luciana Ines Escobar
	12:17	Prediction of microRNA targets in Echinococcus - Natalia Macchiaroli
12:30	14:30	**Lunch on Own**
14:30	16:30	**Systems Session**
	14.30	Bioinformatic mapping of microRNAs related with cervical cancer on Human Latinoamerican Genomic Variants Milena Guerrero Flórez
	14:53	An integrative method to unravel the host-parasite interactome: an orthology based approach Yesid Cuesta Astroz
	15:15	Universal attenuators and their interactions with feedback loops in gene regulatory networks Dianbo Liu
	15:30	Combining miRNA and their regulators to understand the formation of diapause as transgenerational defense against pathogens in C. elegant - Alberto Jesus Martin
	15:45	Cellular Information Processing: pre-equilibrium signalling, cooperatively effects and membrane receptor trafficking Federico Sevlever
	16:00	Evaluation of Anti-biofilm activity of synthetic peptides analogous to human cathelicidin LL-37 in clinical isolates of Staphylococcus app - Fredy Alexander Guevara Agudelo
	16:15	From in silico modelling to comprehension of agroecosystems: towards a complex index to study of microbial diversity and its relation of soil health - Arsenio J Rodriguez
16:30	17:00	**Awards and Closing**