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 - Lucia 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
                   Assignment - 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 - Santiago Videla
            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
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 Brünak

11:10  Advanced data mining reveals a non-canonical mode of interaction for MHC class II 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

12:16  TAXOFOR: Taxonomic Assignment of 16S rDNA sequences using Fourier Analysis

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 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](http://tinyurl.com/zh55g8m)
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| 09:00 | **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 | Coffee Break                                                          |
| 10:30 | **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 | Lunch on Own                                                          |
| 14:30 | **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 | Awards and Closing                                                    |