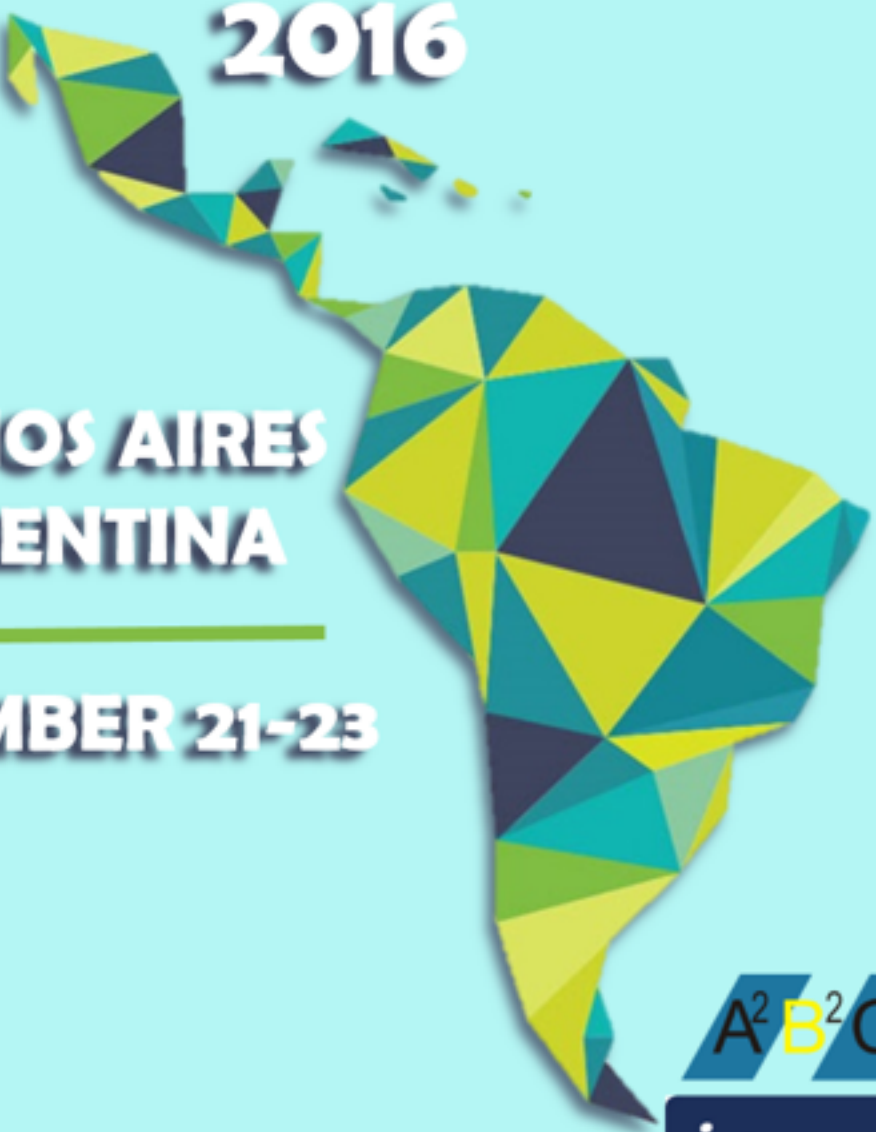
# A2B2C
# ISCB LATIN AMERICA BIOINFORMATICS CONFERENCE
# 2016



BUENOS AIRES
ARGENTINA

NOVEMBER 21-23

$A^2B^2C$

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

## CONFERENCE PROGRAM

# Schedule at a Glance

## MONDAY – 21 November

08:00 19:30 Registration

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 - 10:55 Biomolecular Dynamics in Complex in vivo Environments
  Garaging Papoian
- 10:55 - 11:10 Discovery of Protein Isoforms for Different Stages of Prostate Cancer
  Luis Rueda
- 11:10 - 11:25 Analysis of cell-cycle regulatory linear motifs bound by the
  pRb retinoblastoma tumor suppressor - Lucia Chemes
- 11:25 - 11:40 Identification and Substantiation of Specificity Determining Residue
  Networks using small Datasets and MI-promiscuity - Facundo Orts
- 11:40 - 11:55 Residue-covariation networks cluster similar functional domains
  Franco Simonetti
- 11:55 - 12:10 Validation of Assembly and alignment-free method for chloroplast next
  generation sequences data - Raúl Martín Amado Cattáneo
- 12:10 - 12:20 SwissProt Select: The New Protein Superfamily Database for Reliable
  Function Assignation - Nicolás Stocchi
- 12:20 - 12:30 DEPICTViz - Differential Expression and Protein
  InteraCTions Visualization Tool - Nalvo F. Almeida

12:30 14:30 **Lunch on Own**

***MONDAY - 21 November Cont.***

| | | |
|---|---|---|
| 14:30 16:30 | | **Data Session** |
| | 14:30 14:50 | Tech Talk, EMBL-EBI, Overview of EMBL-EBI Services and How We Work with Industry |
| | 14:50 15:10 | Systematic assessment of multi-gene predictors of pan-cancer tumour sensitivity to drugs exploiting gene expression data<br>Pedro J. Ballester |
| | 15:30 15:45 | A Data-Driven Approach to Estimating the Number of Clusters in Hierarchical Clustering - Antoine Emil Zambelli |
| | 15:45 16:00 | A novel approach for highly-diverse multi-omics data fusion applied to tomato germ plasm selection - Georgina Stegmayer |
| | 16:00 16:15 | Pasteur_galaxy: An open and sustainable Galaxy instance for NGS data analysis - Oussama Souiai |
| | 16:15 16:30 | 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<br>**Emilio Kropff, PhD**, Researcher at the National Research Council (CONICET), Leloir Institute IIBBA, Buenos Aires, Argentina |
| 18:00 19:30 | | **Networking and Posters Presentations, Odd numbered posters being presented, view poster abstracts at**<br>https://www.iscb.org/cms_addon/conferences/la2016/posterlist.php |

# Schedule at a Glance

## TUESDAY – 22 November

| | | | |
|---|---|---|---|
| 08:30 19:30 | | | Registration |
| 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<br>**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 10.50 | | Tech-Talk, CITES, Latin American Business Incubator located in Sunchales, Santa Fe, Starting UP Bioinformatics |
| | 10:50 11:10 | | Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers - Søren Brunak |
| | 11:10 11:30 | | Advanced data mining reveals a non-canonical mode of interaction for MHC class II ligands - Morten Nielsen |
| | 11:30 11:50 | | Novel microRNA discovery from genome-wide data: a computational pipeline with unsupervised machine learning<br>Georgina Stegmayer |
| | 11:50 12:03 | | NetPhosPan: a pan specific predictor for phosphorylation site predictions - Emilio Fenoy |
| | 12:03 12:16 | | Machine Learning Tools to Computationally Identify Genomic Elements - Melissa Woghiren |
| | 12:16 12:30 | | TAXOFOR: Taxonomic Assignment of 16S rDNA sequences using Fourier Analysis - Guillerm Luque y Guzman Saenz |
| 12:30 14:30 | | | **Lunch on Own** |

## *TUESDAY, 22 November Cont.*

14:30 16:30 **Disease Session**

- 14:30 14:50 Multi-Cohort Analysis Identifies Cross-Tissue Gene Signature to Predict Lung Function and TFS in Patients with Idiopathic Pulmonary Fibrosis - Scott Madeleine

- 14:50 15:10 Differential network analysis for the identification of common and specific regulatory mechanisms between idiopathic dilated cardiomyopathy and ischemic cardiomyopathy
  Mariana Recamonde-Mendoza

- 15:10 15:30 A bioinformatics approach shows significant overlap of molecular pathology in early preeclampsia with endometrial diseases - Maria Rabaglino

- 15:30 15:45 Diagno: an online Clinical Genomics Diagnosis tool
  Patricio Yankilevich

- 15:45 16:00 MultiOmics: an R package to infer genomics and epigenomics mechanisms involved with cancer disease progression
  Martin Abba

- 16:00 16:15 In silico prediction of biological targets of small molecules by a chemical similarity approach - Andreas Schüller

- 16:15 16:30 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**
https://www.iscb.org/cms_addon/conferences/la2016/posterlist.php

# Schedule at a Glance

## WEDNESDAY – 23 November

| | | |
|---|---|---|
| 08:00 12:30 | | Registration |
| 08:45 09:00 | | Morning Welcome and Announcements |
| 09:00 10:00 | | **Keynote Presentation**: Data Visualization in Bioinformatics: Exploring the 'Dark' Proteome<br>**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 10:50 | Tech Talk: Heritas, Bioinformatics for clinical diagnostics |
| | 10:50 11:15 | Extreme learning machines for discovering gene regulatory networks from temporal profiles of expression<br>Mariano Rubiolo |
| | 11:15 11:40 | Dynamics of tRNA fragments and their targets in aging mammalian brain - Andrey Grigoriev |
| | 11:40 12:05 | Exploring the human virome, new tools, new insights<br>Alejandro Reyes |
| | | Seeking informative regions in viral genomes<br>Jaime Leonardo Moreno |
| | 12:05 12:17 | Bioinformatic sequence analysis tools for the search for new short peptide in "non-coding" sequences - Luciana Ines Escobar |
| | 12:17 12:30 | Prediction of microRNA targets in Echinococcus<br>Natalia Macchiaroli |
| 12:30 14:30 | | **Lunch on Own** |

***WEDNESDAY - 23 November Cont.***

14:30 16:30 **Systems Session**

| | |
|---|---|
| 14:30 - 14:53 | Bioinformatic mapping of microRNAs related with cervical cancer on Human Latinoamerican Genomic Variants - Milena Guerrero Flórez |
| 14:53 - 15:15 | An integrative method to unravel the host-parasite interactome: an orthology based approach - Yesid Cuesta Astroz |
| 15:15 - 15:30 | Universal attenuators and their interactions with feedback loops in gene regulatory networks - Dianbo Liu |
| 15:30 - 15:45 | Combining miRNA and their regulators to understand the formation of diapause as transgenerational defense against pathogens in C. elegant<br>Alberto Jesus Martin |
| 15:45 - 16:00 | Cellular Information Processing: pre-equilibrium signalling, cooperatively effects and membrane receptor trafficking<br>Federico Sevlever |
| 16:00 - 16:15 | Evaluation of Anti-biofilm activity of synthetic peptides analogous to human cathelicidin LL-37 in clinical isolates of Staphylococcus app<br>Fredy Alexander Guevara Agudelo |
| 16:15 - 16:30 | 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**

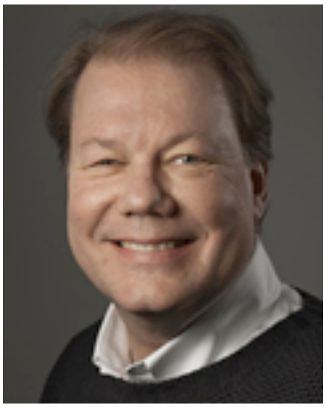
# Keynote Speakers

**Ana Amador, PhD**
Dept. of Physics
University of Buenos Aires and IFIBA
National Research Council (CONICET)
Buenos Aires, Argentina

*Birdsong to study neural control and biomechanics in a learned sensorimotor task*

Birdsong is a complex motor activity that emerges from the interaction between the peripheral system, the central nervous system and the environment. The similarities to human speech, both in production and learning, have positioned songbirds as unique animal models for studying this learned motor skill.

In this talk I will present a low dimensional dynamical system model of the vocal apparatus in which inputs could be related to physiological variables, being the output a synthetic song (SYN) that is a copy of the recorded birdsong (BOS). To go beyond sound comparison, we measured neural activity highly tuned to BOS and found that the patterns of response to BOS and SYN were remarkable similar. This work allowed to relate motor gestures and neural activity, making specific predictions on the timing of the neural activity. To study the dynamical emergence of this feature, we developed a neural model in which the variables were the average activities of different neural populations within the nuclei of the song system. This model was capable of reproducing the measured respiratory patterns and the specific timing of the neural activity. These results suggest that vocal production is controlled by a distributed recurrent network rather than by a top-down architecture.



**Søren Brunak, PhD**
Professor, Research Director
Novo Nordisk Foundation Center for Protein Research
University of Copenhagen

EMBO Lecture
*Systematic Patterns in Millions of 20 Yearlong Individual Patient Disease Trajectories*

Compared to the initial expectation human beings are gene-poor organisms. Many genes and pathways are likely to play a role in more than one disease, and numerous examples of gene pleiotropy and protein multi-functionality presumably await discovery. This situation contributes to the recent interest in clinical healthcare sector data and their accounts of fine-grained multi-morbidities. Patient record data remain a rather unexplored, but potentially rich data source for discovering correlations between diseases, drugs and genetic information in individual patients. A fundamental question in establishing biomarker-phenotype relationships is the basic definition of phenotypic categories. As an alternative to the conventional case-control, single disease model the talk will describe attempts to create phenotyoic categories and patient stratification based on longitudinal data covering long periods of time. We carry out temporal analysis of clinical data in a more life-course oriented fashion. We use data covering 6-7 million patients from Denmark collected over a 20 year period and use them to “condense” millions of individual trajectories into a smaller set of recurrent ones. This set of trajectories can be interpreted as re-defined phenotypes representing a temporal diseaseome as opposed to a static one computed from non-directional comorbidities only. A special case is represented by disease co-occurrences which are treatment provoked, e.g. adverse drug reactions. An important issue is to resolve whether specific adverse drug reactions relate to variation in the individual genome of a patient, to drug/environment cocktail effects, or both. From patient records ADR profiles of approved drugs can be constructed using drug-ADR networks, or alternatively patients can be stratified from their ADR profiles and compared. This type of work can potentially gain importance in projects involving population-wide genome sequencing in the future.

**Emilio Kropff, PhD**
Researcher at the National Research Council (CONICET)
Leloir Institute IIBBA
Buenos Aires, Argentina
Associate Researcher
Abdus Salam International Centre for Theoretical Physics (ICTP)
Triest, Italy

*Coding for running speed and computing displacement in the mammalian brain's GPS*

The last decades have witnessed major discoveries concerning the brain mechanisms through which mammals compute their own location and orient in space. Hippocampal place cells provide maps that describe the position of the animal within a known environment, including a rich contextual description. Entorhinal grid cells provide instead a spatial map that is applied to all environments and is not altered by contextual variations. For this reason grid cells have been proposed to be the framework for an egocentric representation of location, where position is computed independently of contextual cues and based only on the animal's knowledge of its own movements. To achieve this, grid cells should receive information about orientation and speed of instantaneous movements. While neurons coding for the head orientation have been described in the entorhinal cortex, the entorhinal speed code has remained elusive for almost a decade. We present the Flintstone car, a new behavioral paradigm that allows the precise control of rat running speed. Using this device we have discovered a new functional entorhinal cell type: the speed cell. These neurons code for running speed in an instantaneous and linear way. The code is context-independent, allowing running speed to be decoded from the activity of a handful of speed cells even across environments. In addition, we found speed cells to be slightly ahead in time with respect to the actual running speed (~80 ms on average) and, consistently, we found grid cells to be ahead in time with respect to the actual position. Taken together, these observations point to entorhinal speed cells as a key component in the dynamic representation of self-location.

**Ruth Nussinov, PhD**
Center for Cancer Research
National Cancer Institute
Maryland, United States

*A Mechanistic View of Oncogenic K-Ras Biology*

Ras proteins are small GTPases that act as signal transducers between cell surface receptors and several intracellular signaling cascades. KRAS is among the most frequently mutated oncogenes in human tumors. Ras proteins consist of highly homologous catalytic domains, and flexible C-terminal hypervariable regions (HVRs) that differ significantly across Ras isoforms. We have been focusing on key mechanistic questions in oncogenic Ras biology from the structural and signaling standpoints. These include whether Ras' disordered hypervariable region (HVR) has a role beyond membrane anchoring; Does Ras form dimers, and if so what is their structural landscape and how they help in activating Raf; What are Ras' redundant pathways and importantly how to identify redundant pathways in cancer; What are the mechanisms of oncogenic mutations; Is RASSF5 - which links Ras and the MAPK pathway to the Hippo pathway - a tumor suppressor or activator as some experiments suggest, and what is the mechanism through which it works, and more. We believe that structural biology - computations and experiment – is uniquely able to tackle these fascinating and important questions.

**Sean I. O’Donoghue, PhD**
CSIRO & Garvan Institute of Medical Research
Sydney, Australia

*Data Visualization in Bioinformatics: Exploring the 'Dark' Proteome*

The rapidly increasing volume and complexity of biological data calls for new approaches to help life scientists gain insight from these data, rather than being overwhelmed. To address this, the application of modern data visualization principles and methods will be critical, in combination with improved data management, machine learning, and statistics. I will illustrate the power of this 'BioVis' approach by presenting several bioinformatics resources that empower biologists by making complex data easier to access and use. This includes Aquaria (http://aquaria.ws), Minardo (http://minardo.org/snapshot), and Rondo (http://rondo.ws). I will showcase how these resources are being used to explore the known and unknown ('dark') proteome, generating new insights into human biology and health. I will also discuss VIZBI, an international initiative aimed at raising the global standard of bioinformatics software (http://vizbi.org/). Finally, I’ll discuss the use of visualization to create molecular and cellular-scale animations aimed at educating and inspiring the public about cutting-edge biomedical research (http://vizbi.org/plus).

# Thank You Sponsors

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# Technology Talks

**Monday, 21 November**
**14:30 - 14:50**
**EMBL-EBI: freely available data and bioinformatics services**
Dominick A Clark, European Molecular Biology Laboratory-European Bioinformatics Institute

The primary mission of EMBL-EBI is to provide freely available data and bioinformatics services to all facets of the scientific community. The first part of the presentation will provide a high level overview of the core data, bioinformatics and cheminformatics services that are freely available from EMBL-EBI. The presentation will describe how we collaborate internationally and employ standards, integration tools and semantic technologies to make these data and services available to the global scientific community. The second part of the presentation will illustrate use cases with a pharmaceutical industry focus arising from some of our interactions with industry and illustrate how working with industry is important in the continual development of our services.

**Tuesday, 22 November**
**10:30 - 10: 50**
**Cites, The First High Tech Incubator in Latam**

Starting Up in bioinformatics.

We will explore the experiences of a scientist turned entrepreneur who started a European technology company. The most important features will be considered and how to overcome common bottlenecks. We will contrast this situation with the existing opportunities for starting a technology based company with Cites in the “wild” Latin American Start Up ecosystem.

**Wednesday, 23 November**
**10:30 - 10:50**
**Heritas: a model for translation of clinical genomics information into diagnostics for patient management in Argentina**
Martin P Vazquez, INDEAR-Heritas Ocampo 210 bis, Rosario, Argentina, CONICET, Argentina

Heritas is a technology start-up aiming to translate clinical genomics into diagnostics for improved therapies and patient management in human health. Heritas is the result of a joint venture between the R&D Biotech company INDEAR and the clinical diagnostics lab CIBIC, both based in Rosario, Argentina. Heritas model is based on building an ecosystem with three key components: 1) Develop and produce high quality metrics of genomic raw data with Illumina systems, 2) Develop clinical genomic applications with key opinion leaders of the medical community, 3) Develop our own genetic counsellors group to assist medical doctors and patients to translate clinic genomic information into actionable results. Heritas is developing this ecosystem in three major areas: 1) clinical genomics for hereditary or acquired genetic diseases 2) clinical genomics for reproductive health, and 3) Human microbiome dysbiosis based diseases. A major challenge in clinical genomics is to translate genotype to phenotype correlations, and this premise escalates to a serious problem when dealing with intronic variants, one of the dark sides of the human genome. We will present our approaches in dealing with these major challenges in clinical genomics and our vision to translate this information into clinical actionable results.

*Supported by: PROFIET – Programa de Fomento a la inversión Emprendedora en Tecnologia, MINCyT*

# Posters

**Odd numbered posters will be presented on MONDAY - 21 November.**
**Even numbered posters will be presented on TUESDAY - 22 November.**

To view the poster abstracts visit
https://www.iscb.org/cms_addon/conferences/la2016/posterlist.php

**P001** Pasteur_galaxy: An open and sustainable Galaxy instance for NGS data analysis
Oussama Souiai

**P002** Evaluation of Anti-biofilm activity of synthetic peptides analogous to human cathelicidin LL-37 in clinical isolates of Staphylococcus spp. - Fredy Guevara Agudelo

**P004** An Exhaustive Feature Selection Approach for Blastocyst Differentiation
Elmer Fernandez

**P006** In silico prediction of the thermolysin inhibition as antihypertensive model using artificial intelligent tools. - Yudith Cañizares Carmenate

**P007** Fuzzy Clustering: Identification of Similar Compounds for Virtual Screening in Rational Drug Design - Ignacio Ponzoni

**P008** On testing genetic covariance with the R package biotools - Anderson Silva

**P010** Discovery of novel pre-miRNAs: unsupervised versus supervised machine learning
Georgina Stegmayer

**P012** Computational Study of Bromopyrrole Alkaloids with Antimalarial Activity. A QSAR Approach - Edgar Brazon

**P013** Parallel Bootstrap Consensus Clustering - Macarena Saenz

**P014** Unsupervised Learning Based on Deep Learning Applied to the Identification of Applicability Domain of QSAR Models - Ignacio Ponzoni

**P015** Prototype of deductive computing using deoxyribonucleic acid - Nelson Rivera

**P016** Optimal threshold estimation in binary classifiers using game theory
Ignacio Sanchez

**P017** Graphing genomes in 2D, applications of multivariate statistics on the genomic composition - Maria Martinez

**P018** Novel microRNA discovery from genome-wide data: a computational pipeline with unsupervised machine learning - Georgina Stegmayer

**P019** Drug targets prioritization for neglected diseases - Santiago Videla

**P020** A novel approach for highly-diverse multi-omics data fusion applied to tomato germplasm selection - Georgina Stegmayer

**P021** Development of analytic and visualization tools for linear B cell epitope mapping from peptide-arrays - Carolina Barra

**P022** The impact of RNA-Seq differential expression algorithms on Over-Representation Analysis of Gene Sets. - Juan Rodriguez

**P023** Bioinformatics workflow and assessment of software to seek secondary metabolites in Bacteria - Jose Alzate Ocampo

**P024** FastqCleaner: a Shiny web application for cleaning Illumina FASTQ files with R
Leandro Roser

**P026** UTRme: a tool to annotate UTRs in Trypanosoma cruzi - Santiago Radío

**P028** StructRNAfinder: Predicting RNA families from 3'UTR regions of Zika and related viruses through an automated tool - Raul Arias-Carrasco

**P027** Analysis of alternative splicing in timecourse experiments using Aspli R/Bioconductor package - Javier Iserte

**P029** Identification of multi-resistant bacteria through a machine learning approach using the whole genome - Harold Ballén Mejía

**P030** A platform for integration, data acquisition and data analysis in electronical medical records - Fernanda Almeida

**P032** Metagenomic binning of the uncultured fraction of the gut microbiome reveals neutral signature of rare taxa - Patricio Jeraldo

**P033** Analysis of a soil metagenome from the Argentine Northwest Monte and Thistle of the Prepuna region of the Province of Salta - Jorgelina Moreiras Clemente

**P034** Updates to the TDR Targets chemogenomics database - Lionel Uran Landaburu

**P035** Highly resolved phylogeny for Corynebacteriales - Nilson Da Rocha COimbra

**P036** Assessing bioinformatics strategies for de-novo transcriptome assembly
Sergio Gonzalez

**P037** Landscape of non-coding RNAs in Archaea: diversity, conservation and functional characterization. - Victor Aliaga-Tobar

**P038** TNSim: Simulating tumor-tissue sequencing data with wide-spectrum of somatic variant allelic fractions - Jiayin Wang

**P039** A bioinformatics approach shows significant overlap of molecular pathology in early preeclampsia with endometrial diseases - Maria Rabaglino

**P040** Differential network analysis for the identification of common and specific regulatory mechanisms between idiopathic dilated cardiomyopathy and ischemic cardiomyopathy
Mariana Recamonde-Mendoza

**P041** Transcriptomic analysis of drug resistant isolates of the parasitic trematode Fasciola hepatica - Jose Tort

**P042** In silico prediction of biological targets of small molecules by a chemical similarity approach - Andreas Schüller

**P043** multiOmics: an R package to infer genomics and epigenomics mechanisms involved with cancer disease progression - Martin Abba

**P044** Diagno an online Clinical Genomics Diagnosis tool - Patricio Yankilevich

**P045** Identification, organization, and record of rhomboid proteases of Babesia and Theileria hemoprotozoans - Romina Gallenti

**P048** Metagenomics in the identification of infectious agents - Liliane Conteville

**P049** Towards a better cancer classification: mutational patterns of loci and cancer types
Soledad Ochoa

**P050** Homology Modeling of T. cruzi Squalene Epoxidase. Estimation of Ligand-Binding Affinities by MM-PSBA - Guido Noguera

**P051** Computational Study On Flavonoids With Anti-Hiv-1 Activity Employing The Density Fuctional Theory - José Malavé Guerra

**P052** Bond-based Bilinear Indices in QSAR: Computational Discovery of Novel Trypanosomicidals Drug-Like Compounds - Juan Castillo-Garit

**P054** Interactions of OHMLINE, a new lipid-antimetastatic agent, with different lipid membrane components. A molecular dynamics study - Natalia Piñeiro

**P056** Glycosylated Flavonoids as Potential HIV-1 Reverse Transcriptase Inhibitors
Joseph Ortega

**P057** Design and discovery of prodrugs of Zidovudine with high affinity to human serum albumin. - Esteban Schenfeld

**P058** Regulatory molecular circuits in leukocytes of Juvenile Idiopathic Arthritis patients
César Prada-Medina

**P059** Genome-Wide Prioritization Of Candidate Diagnostic Antigenic Markers In Human Pathogens - Diego Ramoa

**P060** Metagenomic Analysis for identification of Viruses Associated with Neonatal Calf Diarrhea - Laura Avellaneda

**P061** Identification of Potential Pancreatic Lipase Inhibitors by Structure-Based Repurposing - Irvyng Patrick Lanchero Barrios

**P063** Scaling the Andean Compound: a new neuro anti-inflammatory agent in the treatment of Alzheimer’s disease. - Víctor Andrade

**P064** Differential TP73 exon usage in breast cancer molecular subtypes - Martin Guerrero

**P065** Computational design of a Dengue virus sensor - Franco Tavella

**P066** A Computational Methodology to Overcome Challenges Associated with the Search for Specific Targets to Develop Drugs against Leishmania major - Larissa Costa

**P067** A comparative approach to identify discriminative DNA sequences. Case study: MTB Complex and Genus Mycobacterium - Iván Duque Aldana

**P068** Inexpensive Mobile Diagnosis of Diabetic Retinopathy using Deep Learning Kavya Kopparapu

**P071** Non alcoholic fatty liver disease in Octodon degus. - Francisco Altimiras

**P072** Dengue virus serotype 2 intra-host diversity in patients with different clinical outcomes - Maria Torres

**P073** Exploring biological patterns in Anopheles associated microbiota: Is there a core bacterial assembly shared between African and American anophelines? - Luis Martínez

**P074** Association of Tandem repeats to the pathogenicity of Gardnerella vaginalis in bacterial vaginosis - Fabian Tobar-Tosse

**P075** Identification of unique nucleotide patterns between mucosal and cutaneous Human papillomaviruses using KM-Finder - Luciana Montera

**P076** Perl for Biologists - An online tutorial - Huseyin Kocak

**P078** Extreme learning machines for discovering gene regulatory networks from temporal profiles of expression - Mariano Rubiolo

**P079** TAXOFOR: Taxonomic Assignment of 16S rDNA sequences using Fourier Analysis - Guillermo Luque y Guzman Saenz

**P080** Bioinformatic sequence analysis tools for the search for new short peptide in "non-coding" sequences. - Luciana Escobar

**P081** Machine Learning Tools to Computationally Identify Genomic Elements Melissa Woghiren

**P082** Prediction of microRNA targets in Echinococcus - Natalia Macchiaroli

**P083** Seeking informative regions in viral genomes. - Jaime Moreno

**P084** Impact of the Different Discretization Methods on Gene Expression Biclustering: Alzheimer Disease Progression Data as a Case Study - Ignacio Ponzoni

**P085** Evaluation of the interaction networks of important Genes and microRNAs in HCV - Mohammad Navaderi

**P086** Predicting Breast Cancer Drug Response via an Level-wise Gene Selection Approach - Dr. Alioune Ngom

**P088** Improving the Uncertainty Estimation in PAM50: Impact on Subtype Assignment and ROR - Elmer A Fernandez

**P090** Evolution of Proboscidea genomes illustrated by structural variant analysis

Andrey Grigoriev

**P091** Evolution of Two Uncharacterized Non-catalytic Carboxylesterase Subfamilies Involved with Early Development of the Sensory Organs and Tracheal System in Insects André Luiz Torres

**P092** Comparative genomics of Acinetobacter baumannii international clone 1 reveals a high degree of synteny and gene sequence conservation - Verónica Álvarez

**P093** Comparative genomics of miRNAs in Cestodes - Santiago Fontenla

**P094** Loss and gain of genes in flatworms: adaptation of parasites to their way of life. - Santiago Fontenla

**P095** The antimicrobial resistance determinants harbored in mobile elements collaborate with the genomic adaptation of P. aeruginosa during chronic infections - Maria Rapisardi

**P096** The microsynteny of genes functionally related with the fruit ripening process in Solanaceae species - Paolo Cacchiarelli

**P097** Transcriptomics of sensory stimuli detection in a Chagas disease vector
Jose Manuel Latorre Estivalis

**P098** Preliminary data on UTR prediction procedure of Piaractus mesopotamicus (pacu) aiming muscle development analysis. - Bruno Fantinatti

**P099** HLA-MAPPER: an application to optimize the mapping of hla-related sequences produced by massively parallel sequencing procedures - Michelle Paz

**P100** Variant Caller Assigner Comparison for Ion Torrent Data - Yanina Murua

**P101** Whole genome SNPs analyses unravel Echinococcus species phylogeny
Lucas Maldonado

**P102** Non-negative matrix factorization for prediction of gene annotations
Georgina Stegmayer

**P103** Characterization of ABC-transporters, a detoxification-related gene family in the Chagas' disease vector Rhodnius prolixus - Lucila Traverso

**P104** Using transcriptomic data to improve the annotation of Mesocestoides corti genome - Alicia Costábile

**P105** Metatranscriptomic and transcriptomic analyses of the digestive tract of Spodoptera frugiperda larvae captured in the province of Tucumán - Gastón Rozadilla

**P106** Elucidating gut microbiota of captive and wild Andean bears using comparative analysis of the 16S rDNA gene. - Andrea Borbon

**P107** Analysis of the Microbial Community of Wastewater Stabilization Ponds from Small Dairy Industries using Whole Genome Shotgun Sequencing - José Irazoqui

**P108** Identification of Bacteriophage crAssphage Through Hidden Markov Models - Laura Forero

**P109** Using Oxford Nanopore MinION technology to deeply explore metagenome functions in the Argentine Human microbiome dataset characterised by Illumina 16s metagenomics pipeline - Cristian Rohr

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The Argentine Association for Bioinformatics and Computational Biology (A2B2C) is a non-profit organization established in 2009 that seeks to promote the development of research in Biology by means of computational methods. The Association connects researchers and professionals from different areas in Biology, Mathematics and Computer Science to advance the knowledge of living things and the emergence of productive computational tools. Besides, we are interested in promoting new generations of Bioinformaticians and Computational Biologists in Argentina. To that end, the Association organizes scientific meetings and courses, and interacts with public and private organizations to foster necessary changes in education and science policies.

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Heritas model is based on building an ecosystem with three key components: 1) Develop and produce high quality metrics of genomic raw data with Illumina systems, 2) Develop clinical genomic applications with key opinion leaders of the medical community , 3) Develop our own genetic counsellors group to assist medical doctors and patients to translate clinic genomic information into actionable results. Heritas is developing this ecosystem in three major areas: 1) clinical genomics for hereditary or acquired genetic diseases 2) clinical genomics for reproductive health, and 3) Human microbiome dysbiosis based diseases.

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