ISCB-LA
SOIBIO
EMBnet
2018

NOVEMBER
5-9

Universidad Andrés Bello
Vina Del Mar Campus
Viña del Mar
Valparaiso Region, Chile

CONFERENCE PROGRAMME

http://www.iscb.org/iscb-latinamerica2018

Pre-Conference Workshops, Tutorials, and Mini-courses

Schedule at a Glance

Ticket Required

START TIME	END TIME	
8:00 am	**5:00 pm**	**REGISTRATION**
9:00 am	6:00 pm	Human genomic analysis for precision medicine with GATK4 Best Practices and FireCloud
9:00 am	6:00 pm	Analyzing large datasets with Apache Spark
9:00 am	6:00 pm	Designing, delivering and evaluating bioinformatics training
9:00 am	6:00 pm	Introduction to python with application on genomic data
1:00 pm	2:00 pm	**Lunch**, provided with registration, separate ticket for tutorials

Tuesday, 6 November

START TIME	END TIME	
8:00 am	**5:00 pm**	**REGISTRATION**
9:00 am	6:00 pm	ISCB Student Council Latin America Symposium
9:00 am	6:00 pm	Human genomic analysis for precision medicine with GATK4 Best Practices and FireCloud
9:00 am	6:00 pm	Analyzing large datasets with Apache Spark
9:00 am	6:00 pm	Open data and tools for bioinformatics research
1:00 pm	2:00 pm	**Lunch**, provided with registration, separate ticket for tutorials

Main Conference Programme
Schedule at a Glance

Wednesday, 7 November

8:00 am	**5:00 pm**	**REGISTRATION**
8:45 am	9:00 am	Welcome
9:00 am	10:00 am	Keynote - David Holmes - Are We Alone in the Universe?
10:00 am	10:30 am	Presentation of organisations: ISCB-LA, SolBio, EMBnet: Celebrating the 30° Anniversary (1988-2018)
10:30 am	11:00 am	**Coffee Break**
11:00 am	12:00 pm	Scientific Sessions I
11:00 am	11:15 am	Structural aspects of antibody recognition: a moments-based approach to shape and electrostatics - Lorenzo Di Rienzo - Sapienza University of Rome
11:15 am	11:30 am	Computational prediction of disease-causing variants from the molecular to the interactome scale - Marianne Rooman, Université Libre de Bruxelles
11:30 am	11:45 am	Pharmacophore-based virtual screening of Peroxizome (Pex)14 inhibitors to combat Trypanosomiasis - Bruno Alejandro Del Carpio Martinez, Centro de Investigación en Ingeniería Molecular - Universidad Católica de Santa Maria
11:45 am	12:00 pm	New robust Bayesian methods detecting Allelic Specific Expression (ASE) and associating it with external phenotypes - Inti Pedroso, Universidad Mayor
12:00 pm	12:15 pm	Ubiome Technology Talk
12:15 pm	12:30 pm	Genoma Mayor Technology Talk
12:30 pm	2:30 pm	Lunch on own, vendors available onsite
12:30 pm	2:30 pm	**Poster Presentations, Group A - Odd Numbers**
2:30 pm	4:00 pm	Scientific Sessions II
2:30 pm	3:00 pm	Genome-scale analysis of Wolbachia metabolism - Natalia Jimenez, CeBiB, CMM, University of Chile
3:00 pm	3:15 pm	The site-specific amino acid preferences of homologous proteins depend on sequence divergence - Evandro Ferrada, Universidad Mayor
3:15 pm	3:30 pm	Implications of the Recent Explosion In Police Use Of Genealogy Databases To Open Cold Cases By Identifying Suspects From DNA Voluntarily Contributed By Their Distant Relatives - Howard Cash, Gene Codes Forensics
3:30 pm	3:45 pm	Analysis of variations among Mycobacterium tuberculosis isolates with the MinHash algorithm - Leonardo Lucianna, Universidad de Buenos Aires. Maestría en Explotación de Datos y Descubrimiento de Conocimiento
3:45 pm	4:00 pm	Insights on protein thermal stability: a graph representation of molecular interactions - Eduardo Milanetti, Sapienza University of Rome
4:00 pm	4:30 pm	**Coffee Break**
4:30 pm	5:30 pm	Keynote - Ana Tereza Ribeiro de Vasconcelos - From Virus to Human Genome Through Bioinformatics
5:30 pm	7:00 pm	Welcome Reception

Main Conference Programme
Schedule at a Glance

Thursday, 8 November

8:00 am	**5:00 pm**	**REGISTRATION**
8:45 am	9:00 am	Welcome
9:00 am	10:00 am	Keynote - Nikos C Krypdides - Microbiome Research: from Products to Data
10:00 am	10:45 am	**Coffee Break**
10:45 am	12:30 pm	Scientific Sessions III
10:45 am	11:00 am	Using large-scale shotgun proteomics and R Bioconductor packages to understand host-parasite interactions - Miguel De Jesús Cosenza Contreras, Federal University of Ouro Preto
11:00 am	11:15 am	Distinct Microbes, Metabolites, and Ecologies Define the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers - Patricio Jeraldo, Mayo Clinic
11:15 am	11:30 am	Copaifera langsdorffi novel putative lncRNA conservational analysis in adaptive response to different ecosystems - Monica Danilevicz, Universidade Federal do Rio de Janeir
11:30 am	11:45 am	Systems immunology to predict regulation factors on skin cutaneous melanoma - Mindy Muñoz, USP
11:45 am	12:00 pm	Host-microbe interaction analysis of the Crohn's disease metaproteome reveals potential differences in the microbiome-mediated autophagy modulation - Tahila Andrighetti, UNESP / Earlham Institute
12:00 pm	12:30 pm	Mathematical Modeling of the Relocation of the Divalent Metal Transporter DMT1 in the Intestinal Iron Absorption Process - Layimar Cegarra, University of Chile
12:30 pm	2:30 pm	Lunch on own, vendors will be available
12:30 pm	2:30 pm	**Poster Presentation Group B - Even Numbers**
2:30 pm	4:00 pm	Scientific Sessions IV
2:30 pm	3:00 pm	A Radiogenomic Approach for Decoding Molecular Mechanisms Underlying Tumor Progression in Prostate Cancer - Sarah Fischer, Rostock university medical Center
3:00 pm	3:15 pm	Modelling the regulatory network controlling dendritic cell differentiation from human monocytes - Karen J. Nuñez-Reza, International Laboratory for Human Genome Research
3:15 pm	3:30 pm	Generalizing experimental evidence through Hidden Markovian Models for a transcriptome de novo assembly selection criteria - Patricia Carvajal-Lopez, Centro de Investigaciones Biológicas del Noroeste, S.C.
3:30 pm	3:45 pm	The structure of a giant. Bioinformatics meets experimental techniques - Marta Bunster, Universidad de Concepción
3:45 pm	4:00 pm	The use of metagenomics for environmental monitoring of altitude savannas in the Amazon - Guilherme Oliveira, Instituto Tecnológico Vale
4:00 pm	4:30 pm	**Coffee Break**
4:30 pm	5:30 pm	Keynote - Wendy Gonzales - From the atoms to the disease: a way modelled by the study of ion channels
7:30 pm		Conference Dinner (*ticketed event)*

Main Conference Programme
Schedule at a Glance

Friday, 9 November

8:45 am	9:00 am	Welcome
9:00 am	10:00 am	Keynote - Morten Sogaard
10:00 am	10:30 am	**Coffee Break**
10:30 am	12:30 pm	Scientific Sessions V
10:30 am	10:45 am	Tumor phenotype precedes metabolic reprograming in chemically induced hepatocellular carcinoma - Noé García-Chávez, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional
10:45 am	11:00 am	Knowledge networks reveal novel drug candidates and genetic mechanisms for Psychiatric Diseases - Thomaz Luscher Dias, Universidade Federal de Minas Gerais
11:00am	11:15 am	Defining non-coding genetic variants contributing to Autism Spectrum Disorder severity using Elastic-Net regression - Leandro Roser, Elson S. Floyd College of Medicine, Washington State University
11:15 am	11:30 am	Automatic Reconstruction of Rule-Based Gene Regulatory Network Models and its Calibration - Rodrigo Santibáñez, NetBioLab, Centro de Genómica y Bioinformática, Universidad Mayor
11:30 am	11:45 am	Defining a Core Genome for the Herpesvirales and Exploring their Evolutionary Relationship with the Caudovirales - Juan Sebastián Andrade Martínez, Universidad de los Andes
11:45 am	12:00 pm	Active Site Flexibility as a Hallmark for Efficient PET Degradation by I. sakaiensis PETase - Pablo Galaz-Davison, Institute for Biological and Medical Engineering, Pontificia Universidad Catolica de Chile
12:00 pm	12:15 pm	Insights into the genome and variability of Phytophthora palmivora, the causal agent of the bud rot disease in oil palm - Juanita Gil, Cenipalma & Universidad de Los Andes
12:15 pm	12:50 pm	Special Session: Research Highlights from Universidad Andrés Bello
12:15 pm	12:20 pm	Conducting Research at Universidad Andrés Bello - Fernando Danilo Gonzalez Nilo
12:20 pm	12:35 pm	Deciphering the lifestyle of the plant pathogen Pseudomonas syringae under various nutrient-limiting conditions via genome-scale flux and proteomic analysis - Ignacio Poblete-Castr, Center for Bioinformatics and Integrative Biology (CBIB), Universidad Andres Bello, Chile
12:35 pm	12:50 pm	Fighting antimicrobial resistance with computational and experimental biophysics - Daniel Aguayo V., Center for Bioinformatics and Integrative Biology, Universidad Andres Bello, Santiago, Chile
12:50 pm	2:30 pm	**Lunch** and Open Networking
2:30 pm	4:15pm	Scientific Sessions VI
2:30 pm	2:45 pm	The COST Action CHARME: a European initiative for the harmonisation of standards for life-science research - Domenica D'Elia, Institute for Biomedical Technologies -CNR
2:45 pm	3:15 pm	MassComp, a Lossless Compressor for Mass Spectrometry Data - Ruochen Yang, University of Southern California
3:15 am	3:30 pm	**Stretch/Bio Break**
3:30 pm	4:30 pm	Special Session: on Bioinformatics Research and Education in Latin America
4:35 pm	5:35 pm	Keynote - Janet Thornton

Poster Presentation

Odd posters will present on Wednesday; Even posters will present on Thursday

01 Computational prediction of disease-causing variants from the molecular to the interactome scale, Marianne Rooman, Université Libre de Bruxelles, Belgium

02 Limits and potential of in silico target prediction by chemical similarity, Mauricio Ruiz, Pontificia Universidad Católica de Chile, Chile

03 VHL-Hunter, web service for classification of clinical relevance in single point mutations in Von Hippel-Lindau disease, David Medina, CeBiB, Chile

04 Complex data structure discovery and analysis of large biological datasets via ElPiGraph, Luca Albergante, Institut Curie, France

05 Gene expression and dynamics in simulated cell populations, Ignacio Medina, Pontificia Universidad Catolica de Chile, Chile

06 Generalizing experimental evidence through Hidden Markovian Models for a transcriptome de novo assembly selection criteria., Patricia Carvajal-Lopez, Centro de Investigaciones Biológicas del Noroeste, S.C., Mexico

07 A Benchmarking of machine learning algorithms in the coding potential prediction and functional assignation of non-coding RNAs, Thaís Ramos, Núcleo Multidisciplinar de Bioinformática, IMD, Universidade Federal do Rio Grande do Norte, Natal, Brazil, Brazil

08 In silico study of tools that predict SNPs impact in protein functionality, Elizabeth Tapia, UNR; CIFASIS-CONICET, Argentina

09 Defining non-coding genetic variants contributing to Autism Spectrum Disorder severity using Elastic-Net regression, Leandro Roser, Elson S. Floyd College of Medicine, Washington State University, United States

10 Implementation of a Bioinformatic pipeline to study HTLV-1 integration sites in NGS data, Maximiliano Distefano, Laboratorio de Biología Celular y Retrovirus, Hospital de Pediatría "Dr. J. P. Garrahan", Argentina

11 Collaborative DNA Databases For Combatting Child and Adult Human Trafficking and Disappeared Persons In the Americas, Howard Cash, Gene Codes Forensics, United States

12 Computational modelling sources of variability in transcription-translation cell-free reactions, Anibal Arce, Pontificia Universidad Católica de Chile, Chile

13 PISKaS: a Parallel Implementation of Spatial Kappa Simulator, Ignacio Fuenzalida, Computational Biology Lab. Fundación Ciencia para la Vida, Chile

14 A machine learning approach for antibody binding affinity prediction based on Structural Interaction Fingerprints, Victor Fica-León, University of Concepción, Chile

15 Association of variants with clinical data in a sample of the Colombian population using the Apriori algorithm, Jennifer Vélez Segura, Universidad Nacional de Colombia, Colombia

16 Bio-inspired deep learning model to replicate retinal encoding, Jeronimo Barrios, Computational Biology Lab (DLab), Fundación Ciencia & Vida, Chile

17 The COST Action CHARME: a European initiative for the harmonisation of standards for life-science research, Domenica D'Elia, Institute for Biomedical Technologies -CNR, Italy

18 Analysis of gene expression in esophageal cancer of the TCGA data portal, Diana Cubas Montecino, Universidad Nacional Mayor de San Marcos, Peru

19 Simple scalable data storage and analysis for systems and synthetic biology, Timothy Rudge, universidad católica de chile, Chile

20 Art v 4 protein structure as a representative template for allergen profilins: Homology modeling and Molecular Dynamic, Haruna L. Barazorda-Ccahuana, Centro de Investigación en Ingeniería Molecular - Universidad Católica de Santa María, Peru

21 Mango: Distributed Visualization for Genomic Analysis, Alyssa Morrow, Department of Computer Science, University of California-Berkeley, United States

Poster Presentation

Odd posters will present on Wednesday; Even posters will present on Thursday

22 Disease related and neutral variants in human proteins in ordered, disordered and order-disorder transition regions, Martin Salas, Departamento de Ciencias y tecnologia, Universidad Nacional de Quilmes, Argentina

23 Assembly and characterization of transposable elements in the genome of two annual killifishes, Felipe Gajardo, Centro de regulación del Genoma, Chile

24 MYB transcription factors in the transcriptome in response to low temperature of Eucalyptus spp, Myriam Solís, University of Concepción, Chile

25 ProtMiscuity: Promiscuous Proteins Database, Ana Julia Velez Rueda, UNQ, Argentina

26 High resolution profiling of microbial communities through novel approach of taxonomic mapping, Joaquín Gutiérrez, uBiome, Chile

27 Consistent Cross-Ontology Prediction of GO proteins in Glycine max, Flavio Spetale, Cifasis-Conicet, Argentina

28 Genomic analyses of clinical isolates of Aspergillus fumigatus showing different sensitivity to the antifungal drug caspofungin, Renato Augusto Corrêa Dos Santos, Department of Pharmaceutical Sciences, Faculty of Pharmaceutical Sciences of Ribeirão Preto - University of São Paulo, Brazil

29 Knowledge networks reveal novel drug candidates and genetic mechanisms for Psychiatric Diseases, Thomaz Luscher Dias, Universidade Federal de Minas Gerais, Brazil

30 Possible relationship between diet, gut microbiota and Health in the Colombian population, Angela Garcia, Universidad de los Andes, Colombia

31 Using RNA-seq to determine cancer-specific therapeutic targets, Mainá Bitar, QIMR Berghofer, Australia

32 Bacterial taxa and enzyme function abundances in the human gut correlate with lactose tolerance, Rodrigo Ortiz, UNAB - uBIome, Chile

33 Application of genomic and bioinformatic tools for the study of CADASIL disease, Verónica Latapiat, Laboratorio de Genómica Avanzada, Centro de Genómica y Bioinformática, Universidad Mayor., Chile

34 GenIO: a phenotype-genotype analysis web server for clinical genomics of rare diseases, Daniel Koile, Instituto de Investigación en Biomedicina de Buenos Aires (IBioBA), Argentina

35 Extension and evaluation of SGLT2 inhibitors with a refined ensemble of models conformations, Jose Lema, Department of Pharmacology, Faculty of Biological Sciences, University of Concepcion., Chile

36 Improving the prediction of loops and drug binding in GPCR structure models, Bhumika Arora, Indian Institute of Technology Bombay, India, Monash University, Australia and IITB-Monash Research Academy, India

37 EVALUATION in silico OF INHIBITORY MOLECULES OF FIMH FROM Escherichia coli ISOLATES RESPONSIBLE OF UROPATHOGENIC INFECTIONS IN CARTAGENA-COLOMBIA, Alfredo Montes Robledo, Grupo Microbiología Clínica y Ambiental. Facultad de Ciencias Exactas y Naturales. Universidad de Cartagena., Colombia

38 SNPs within miRNA Binding Sites of Inflammatory Genes in Multiple sclerosis: an in silico study, Mina Zafarpiran, Department of Genetics, Animal Biology Group, Faculty of Natural Science, Tabriz University, Tabriz, Iran

39 A comprehensive variant filtering and annotation strategy for tumor sequencing targeted NGS assays, Alejandro Blanco, Pfizer Chile S.A., Chile

40 Identification of new druggable sites based on the conformational analysis of the IDO1 enzyme for the rational design of new pharmacological inhibitors, Patricio Chinestrad, UNQ, Argentina

Poster Presentation

Odd posters will present on Wednesday; Even posters will present on Thursday

41 Target-based sequencing panel and copy-number variant mutation screening for Tuberous Sclerosis Complex diagnosis in Brazilian patients, Topic: Disease Models & Molecular Medicine, Michele Araújo Pereira, Instituto Hermes Pardini / Universidade Federal de Minas Gerais, Brazil

42 Mechanisms of diabetes mellitus and dengue fever co-morbidity revealed by integrated omics analysis, Nikhil Pathak, Acedemia Sinica, Taipei, Taiwan, Taiwan

43 IN-SILICO APPROACH TO PRIMER DESIGN IN REGIONS ASSOCIATED WITH MICROSATELLITES IN FLATFISHES, Johnny Davila-Sandoval, Universidad Nacional Mayor de San Marcos, Peru

44 In silico dd-RAD Seq as a possible tool for ancestry determination in H. pylori, Cindy P. Ulloa-Guerrero, Universidad de los Andes, Colombia

45 Comparative analysis of genes of the mycolic acid synthesis route between strains of Mycobacterium tuberculosis, Andrea Monserrat Negrete Paz, Universidad Michoacana de San Nicolás de Hidalgo, Mexico

46 In silico evaluation of the Echinococcus granulosus Thioredoxin Glutathione Reductase (TGR) as a target for Gold (I) drugs, Enrico Bruno-Riscarolli, Universidade Federal do Estado Rio do Janeiro, Brazil

47 Pharmacophore-based virtual screening of Peroxizome (Pex)14 inhibitors to combat Trypanosomiasis, Bruno Alejandro Del Carpio Martinez, Centro de Investigación en Ingeniería Molecular - Universidad Católica de Santa Maria, Peru

48 CARACTERIZATION AND MOLECULAR DOCKING OF A TRIMERIC AUTOTRANSPORTER BRP ADHESIN PROTEIN FROM Bartonella bacilliformis WITH COLLAGEN OF ENDOTHELIAL HUMAN CELLS, Cleidy Mirela Osorio Mogollón, Grupo de Investigación en Bioinformatica y Biologia Estructural. Universidad Nacional Mayor de San Marcos., Peru

49 IN SILICO ANALYSIS OF N-ACYL-HOMOSERINE LACTONE ACYLASE OF Pseudomonas aeruginosa AND STUDY OF POSSIBLE INHIBITORS USING MOLECULAR DOCKING, Malú Chávez-Gamarra, Grupo de Investigación en Bioinformatica y Biologia Estructural. Universidad Nacional Mayor de San Marcos., Peru

50 The LTR Retrotransposon Copia Superfamily is frequently involved in Horizontal Transfers in Angiosperms, Simon Orozco-Arias, Department of Electronics and Automatization, Universidad Autónoma de Manizales, Colombia

51 Analysis of variations among Mycobacterium tuberculosis isolates with the MinHash algorithm, Marcelo Soria, Universidad de Buenos Aires. Facultad de Agronomía, Argentina

52 Defining a Core Genome for the Herpesvirales and Exploring their Evolutionary Relationship with the Caudovirales, Juan Sebastián Andrade Martínez, Universidad de los Andes, Colombia

53 Copaifera langsdorffi novel putative lncRNA conservational analysis in adaptive response to different ecosystems, Monica Danilevicz, Universidade Federal do Rio de Janeiro, Brazil

54 The draft genome of the parasitic nematode, Setaria digitata, Kanchana Senanayake, Institute of Biochemistry, Molecular Biology and Biotechnology, University of Colombo, Sri Lanka

55 Fine-scale human genetic structure reveals a Central-Patagonic and a Northern-Andean ancestry components throughout Argentina, Juan Manuel Berros, Biocódices S.A. - CONICET, Argentina

56 Pan-genome Analysis of Mycobacterium tuberculosis Lineage 4 Isolates and their Association with Prevalence of the Disease in Northeastern Area of Medellin - Colombia, Uriel Hurtado, Corporación para Investigaciones Biológicas, Universidad Nacional de Colombia, Colombia

57 Phylogenomic and comparative genomic analyses shed light on the evolution of acidophilic traits in the Phylum Verrucomicrobia, Gonzalo Neira, Universidad de Chile, Fundación Ciencia & Vida, Chile

58 Analysis of metabolic pathways based on the genome of the annual killifish Austrolebias charrua, Cristina Muñoz, Universidad de Chile, Chile

Poster Presentation

Odd posters will present on Wednesday; Even posters will present on Thursday

59 High quality genomic resources to understand independent domestication processes in Lima bean, Tatiana Garcia, Universidad Nacional de Colombia, Colombia

60 FORCES SHAPING MICROBIAL SPECIATION IN EXTREMELY ACIDIC ENVIRONMENTS, Carolina González, Center for Bioinformatics and Genome Biology, Fundación Ciencia y Vida, Chile

61 Bulk and single-cell transcriptomics allow the characterization and identification of blood cell types in Halicryptus spinulosus and Priapulus caudatus (Ecdysozoa: Scalidophora), Felipe Aguilear, Universidad de Concepción, Chile

62 Development of a software solution for genome alignment, Daniel Tello, Universidad de Los Andes, Colombia

63 The emergence and evolution of post-translational modifications associated to proteostatic regulation in Yeast., Carolina Valdivia, Universidad Mayor, Chile

64 Phylogenomics and Accessory Genome Analysis of Pasteurela multocida Reveals Disease Specialization in Different Hosts, Dennis Carhuaricra, Universidad Nacional Mayor de San Marcos, Peru

65 Phylogenetic analysis reveals the taxonomically diverse distribution of the Piscirickettsia salmonis group, Pedro Sepúlveda.,Bioinformatic Engineer, Universidad Mayor

66 Insights into the genome and variability of Phytophthora palmivora, the causal agent of the bud rot disease in oil palm, Juanita Gil, Cenipalma; Universidad de Los Andes, Colombia

67 Evolutionary and functional genomic analysis of â€˜caleosin/peroxygenaseâ€™ gene family in the Viridiplantae and Fungi, Farzana Rahman, University of South Wales, United Kingdom

68 In silico analysis of gene copy number of small heat shock proteins in tomato wild species, Paolo Cacchiarelli, IICAR-CONICET/UNR, Argentina

69 BAYESIAN INFERENCE FOR THE DETERMINATION OF EVOLUTIONARY HISTORY AND RECONSTRUCTION OF A FILOGENETIC TREE OF CYCLONE PRECURSORS OF DIFFERENT FAMILIES,, Paula Catacora Padilla, Centro de Investigación en Ingeniería Molecular, Peru

70 Computational search of UV radiation resistance strategies in Deinococcus swuensis, isolated from Paramo ecosystems, Jorge Diaz-Riaño, Universidad de Los Andes, Colombia

71 Functional network and regulation of the human small heat shock protein (sHSP) family, Debora Pamela Arce, UTN-Facultad Regional San Nicolás (FRSN-UTN), CONICET- Instituto de Investigaciones Agrarias (IICAR), Argentina

72 Coding and non-coding transcriptional modulation induced by IPN virus on Salmo salar, Estefanía Tarifeño-Saldivia, Laboratory of Gene Expression and Regulation, Faculty of Biological Science, University of Concepcion, Chile, Chile

73 A-to-I UTR editing at 3â€™UTR by ADAR1 is associated with breast cancer, Eduardo A. Sagredo, Pfizer Chile, Chile

74 Modelling the regulatory network controlling dendritic cell differentiation from human monocytes, Karen J. Nuñez-Reza, International Laboratory for Human Genome Research, Mexico

75 Development of a method for inferring regulatory networks of genes time and specific location, Leandro Murgas-Saavedra, Centro de Genómica y Bioinformática, Facultad de Ciencias, Universidad Mayor, Chile

76 Modelling non-equilibrium polysome dynamics with totally asymmetric simple exclusion process (TASEP), Gonzalo Andrés Vidal Peña, Pontificia Universidad Católica de Chile, Chile

77 Role of Transposable Elements in small RNA regulation of genes in spinal cord regeneration in the frog Xenopus laevis, Braulio Valdebenito Maturana, Universidad de Talca, Chile

Poster Presentation

Odd posters will present on Wednesday; Even posters will present on Thursday

78 Occurrence of differential alternative splicing in the transcriptome of mice hearts infected with two strains of Trypanosoma cruzi by a proteogenomics approach, Glória Regina Franco, Universidade Federal de Minas Gerais, Brazil

79 Ezh1 (a member of Polycomb Repressive Complex 2) associated transcription in the hippocampus, Mauricio Saez, Universidad Mayor, Chile

80 Transcriptomic analysis of nephrotoxicity induced by cisplatin: the role of noncoding RNAs, Stellamaris Soares, Universidade Federal de Minas Gerais, Brazil

81 Differential expression of genes involved in response to freezing stress in Solanum tuberosum spp. Andigena, Diana Susana Martinez Corcino, Universidad Peruana Cayetano Heredia, Peru

82 Automatic Reconstruction of Rule-Based Gene Regulatory Network Models and its Calibration, Rodrigo Santibáñez, NetBioLab, Centro de Genómica y Bioinformática, Facultad de Ciencias, Universidad Mayor, Chile

83 Comparison of de novo transcriptome assembly methods using larvae and juveniles of the fine flounder Paralichthys adspersus, Marcos Espinel, Laboratorio de Genética Molecular. Area Funcional de Investigaciones en Acuicultura, Instituto del Mar del Perú, Peru

84 The pangenome of Leishmania spp: a comparative genomic study, J. Eduardo Martinez, Programa de Doctorado en Genomica Integrativa, Vicerrectoria de Invesitigacion , Universidad Mayor, Chile

85 Genome analysis of biodegradative routes for furanic compounds in novel isolates having the ability to use furan aldehydes as carbon source, Favián González-Toro, Universidad Tecnológica Metropolitana, Chile

86 Assembly, annotation and comparative genomics of Phytophtora betacei and Phytophthora infestans, David Andrés Ayala Usma, Universidad de los Andes, Colombia

87 Codon adaptation biases among sylvatic and urban genotypes of Dengue virus type 2, Ayda Susana Ortiz Baez, Univerdidade de São Paulo, Brazil

88 Analysis of hydrogen bonds in alpha helix 5 of Ras oncoprotein reveals an allosteric effect of mutations at catalytic pocket, Nikita Poddar, BANARAS HINDU UNIVERSITY, India

89 Sequence to structure and immunological analysis of MOMP from Chlamydiae, Francis O Atanu, Department of Biochemistry, Kogi State University, P.M.B. 1008, Nigeria., Nigeria

90 Structural aspects of antibody recognition: a moments-based approach to shape and electrostatics, Lorenzo Di Rienzo, Sapienza University of Rome, Italy

91 Structure-function relationships of human Cx50 hemichannels, Claudia Pareja-Barrueto, Dlab, Fundación Ciencia para la Vida & CINV, Universidad de Valparaíso, Chile, Chile

92 Water dynamics and electrostatic interaction network in human Cx26 hemichannels: structure and dynamics upon mutations in the IC-pocket, Joaquin Jensen Flores, Computational Biology Lab, Fundacion Ciencia y Vida, Chile

93 COMPARATIVE STUDY OF ALLOPHYCOCYANIN-LINKER CORE COMPLEX IN RHODOPHYTA AND CYANOBACTERIA, Diego Ortiz López, Laboratorio de Biofísica Molecular, Universidad de Concepción., Chile

94 Oleanolic acid as a potential Pfn2 inhibitor: In silico approach, Diego J. Paz Caya, Universidad Católica de Santa Maria, Peru

95 Tracing the evolutionary history of protein thermal stability in a thermophilic bacterial lineage, Pablo Cea, Universidad de Chile, Chile

96 A role for the electrostatic potential in the human Cx26 hemichannel calcium blockade, Jorge Carrasco Alarcon, Computational Biology Lab, Chile

97 Bioinformatic characterization and structural modeling of the complex (αβ)6γ31of Gracilaria chilensis, Topic: Structural Bioinformatics, Juan Ignacio Cisternas Ramos, Universidad de Concepción, Chile

Poster Presentation

Odd posters will present on Wednesday; Even posters will present on Thursday

98 A Comprehensive Analysis of Alpha/Beta-Hydrolases and a PASS2 Perspective, Sridhar Hariharaputran, National Centre for Biological Sciences AND Indian Institute of Science,Bangalore AND Bharathidasan University,India, India

99 Design of agonists TLR2 peptides derived from the gut microbiota to be used as new therapeutics drugs, Melissa Alegría-Arcos, Centro Interdisciplinario de Neurociencias de Valparaíso (CINV), Universidad de Valparaíso, Chile

100 Structure-based Discovery of novel Two-Pore-Domain Potassium Channel TASK-3 (K2P9.1) modulators, Wendy Gonzalez, Universidad de Talca, Chile

101 Computational Methods to Assess the Correspondence Between Protein Structural, Functional Changes and Evolutionary Divergence, Sridhar Hariharaputran, National Centre for Biological Sciences, TIFR, Bangalore, Bharathidasan University, Trichy, India, India

102 An efficient use of X-Ray information, Homology Modeling, Molecular Dynamics and Knowledge based Docking techniques to predict Protein-Carbohydrate complexes, Carlos Modenutti, University of Buenos Aires, Argentina

103 ENANTIOMERS OF BMMA CARBAMATES BIND AS GLUTAMATE AT ACTIVE SITE OF TWO AMPA RECEPTORS: A DOCKING APPROACH, Marco Peña-García, Grupo de Investigación en Bioinformática y Biología estructural. Universidad Nacional Mayor de San Marcos., Peru

104 RELEVANCE OF EXTRACELLULAR PORTALS IN THE POTASSIUM K2P ION CHANNEL CONDUCTION MECHANISM, Mauricio Bedoya, Universidad de Talca, Chile

105 Hotspot characterization from a 3D structural model of resveratrol O-methyltransferase (VvROMT), Daniela Herrera, Department of Chemical and Bioprocesses Engineering, Schools of Engineering, Pontificia Universidad Católica de Chile, Chile

106 Molecular dynamics study of the amyloid-beta peptide of Alzheimer's disease and its behaviour towards different suggested drugs, Diego Ernesto Valencia, Research Center for Molecular Engineering, Universidad Católica de Santa María, Peru

107 Structural exploration of the C-terminus in the activation mechanism of connexin 43 hemichannels, Jonathan Canan, CBIB, Facultad de Ciencias de la Vida, Universidad Andrés Bello, Santiago, Chile, Chile

108 Three dimensional structures of pannexin1-based channels, Maximiliano J. I. Rojas-Reyes, CINV, Universidad de Valparaíso, Valparaíso - CBIB, Facultad Ciencias de la Vida, Universidad Andrés Bello, Santiago, Chile

109 Computational assessment of the PET degradation activity of Oleispira antarctica cutinase, Felipe Engelberger, Institute for Biological and Medical Engineering, Pontificia Universidad Católica de Chile, Santiago, Chile, Chile

110 Study of the translocation mechanism of octopamine in the dopamine transporter. New insights from molecular simulation studies, Sandra Arancibia-Opazo, Universidad Mayor - Pontificia Universidad Católica de Chile, Chile

111 Nilson Da Rocha Coimbra, Aristoteles Goes, Vasco Azevedo and Aida Ouangraoua, Georcki Ropon Palacios, UNIVERSIDAD NACIONAL DE SAN ANTONIO ABAD DEL CUSCO, Peru

112 Comparison of the microbiota of salmonids resistance and susceptible to Flavobacterium psychrophilum and characterization of antimicrobial activity, Natalia Valdes, USACH, Chile

113 Host-microbe interaction analysis of the Crohn?s disease metaproteome reveals potential differences in the microbiome-mediated autophagy modulation, Tahila Andrighetti, UNESP / Earlham Institute, Brazil

114 Unravelling the evolution of the extremely acidophilic (pH1) Leptospirillum genus, Eva Vergara, Fundación Ciencia & Vida, Chile

115 Microbiota structure analyses among asthma patients in Santiago and Washington reveals key shared and exclusive microorganisms, Ignacio Ramos-Tapia, Microbial Genomics Lab, Center of Bioinformatics and Integrative Biology, Universidad Andrés Bello, Chile

Poster Presentation

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116 Challenges and approaches on the 16S annotation, a big picture of uBiome Explorer database, Felipe Melis, uBiome, Chile

117 Distinct Microbes, Metabolites, and Ecologies Define the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers, Patricio Jeraldo, Mayo Clinic, United States

118 Bacterial meta-analyis of chicken cecal microbiome, Luis Chica, Universidad de los Andes, Colombia

119 Virus-like particles from fecal samples of healthy and undernourished children can facilitate the colonization of a probiotic consortium of growth-promoting bacteria, Laura Avellaneda-Franco, Universidad de los Andes, Colombia

120 Structural and functional changes in the gut microbiome of Andean bears in captivity, Andrea Borbon, Universidad de los Andes, Colombia

121 Metagenome-associated genomes from Antarctic rhizosphere microbial communities reveal patterns of taxonomic and functional diversity, Florence Gutzwiller, Universidad Andrés Bello, Chile

122 A first insight into the metagenome and virome of a unique human-impacted ecosystem in Patagonia, Katterinne Mendez, Universidad Andrés Bello, Chile

123 Microbial ecology of the Comau Fjord (42oS): drivers of community structure and potential anthropogenic impact, Eduardo Castro-Nallar, Universidad Andres Bello, Chile

124 Microbiome analysis of the Fragile X syndrome mouse model using 16S rRNA amplicon sequencing, Francisco Altimiras, Center for Research and Development, Telefonica, Chile

125 Functional subnetworks involving sHSPs during tomato fruit ripening, Debora Pamela Arce, IICAR-CONICET, FRSN-UTN, Argentina

126 Insights on protein thermal stability: a graph representation of molecular interactions, Edoardo Milanetti, Sapienza University of Rome, Italy

127 A gap filling solution for the reconciliation between experimental data and in silico whole-genome metabolic network reconstructions, Rodrigo Amarante Colpo, Laboratorio Nacional de Computação Científica, Brazil

128 Systems immunology to predict regulation factors on skin cutaneous melanoma, Mindy Muñoz, USP, Brazil

129 Genome-scale metabolic model of Phytophthora betacei: A key tool for the understanding and control of the phytopathogen, Maria Juliana Rodriguez Cubillos, Universidad de los Andes, Colombia

130 Panpulmonate transcriptomes reveal candidate genes involved in the transition to terrestrial realms in gastropods, Pedro Romero, Universidad Peruana Cayetano Heredia, Peru

131 Molecular characterization of Rhinovirus species and types in the infant population of Santa Fe using bioinformatic methods, Rodrigo Peralta, Facultad de Ingeniería, Universidad Nacional de Entre Ríos, Argentina

132 Evolutionary constraints determine the three-dimensional domain swapping of the DNA? binding domain of FoxP transcription factors, Pablo Villalobos, Universidad de Chile, Chile

133 Taxogenomics of "Difficult-to-Identify" Emerging Pathogenic Corynebacterium Species, Luis Pacheco, Federal University of Bahia, Brazil

134 Prediction of protein protein interactions between humans and Plasmodium falciparum via Short Linear Motifs (SLIMs), Fatoumata Fofana, African Center of Excellence in Bioinformatics, Mali

135 Bioinformatics back to school: A way to rethink the teaching of biology, Ana Julia Velez Rueda, UNQ, Argentina

136 Activation study of TRPV1 channel through external electric field, Fernanda Maldonado-Biermann, CBIB, Facultad de Ciencias de la Vida, UNAB-Departamento de Física, UNAB-CINV, Universidad de Valparaíso, Chile

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137 De novo genome sequencing by secondary school students in the classroom: a collaborative experience with Oxford Nanopore technology, Jonathan Maldonado, Lab. de Bioinfo. y Expr. Génica, Instituto de Nutrición y Tecnología de los Alimentos (INTA), Universidad de Chile, Chile

138 Unveiling the thermal diffusion pathway of TRPV1 using non-equilibrium molecular dynamics methods, Felipe A. Gomez-Becerra, Center for Bioinformatics and Integrative Biology, Universidad Andres Bello, Santiago, Chile, Chile

139 Probiotic specialized database and identification of probiotic genes from de novo genomic assembly of Lactobacillus brevis, Brian Gatica, Universidad de Concepción, Chile

140 MOLECULAR DOCKING AND ANAYLISIS OF P55 VacA DOMAIN of HELICOBATER PYLORI AND POTENCIAL LIGAND, Alicia Arica Sosa, Universidad Ricardo Palma, Peru

141 Benchmark of metagenomics sequence classification tools using in silico generated mock communities, Felipe Sepúlveda, uBiome, Chile

142 A big data pipeline for the discovery of gene regulatory networks from time course GEO data, Juan Camilo Ramírez, Universidad Antonio Nariño, Colombia

143 Genome and transcriptome analysis of xylose-fermenting industrial yeast for second generation bioethanol

144 Genetic diversity of Clavibacter michiganensis subsp. michiganensis from Mexico, Marco Aurelio Aragón Magadán, Colegio de Postgraduados, Mexico

145 Inner core phosphate groups interaction of the LPS layer contributes to stabilize the bacterial outer membrane hydrophobic core: A computational Calorimetry Study, Simón Correa, Center for Bioinformatics & Integrative Biology, Universidad Andres Bello, Santiago, Chile., Chile

146 Pipeline design for viral metagenomic analysis, Laura Forero, Universidad de los Andes, Colombia

147 A heuristic-based strategy to reconstruct viral sequences from metagenomic data, Eric Roberto Guimarães Rocha Aguiar, UFBA, Brazil

148 MITE Tracker: An accurate approach to identify miniature inverted-repeat transposable elements in large genomes, Juan Manuel Crescente, CONICET, Argentina

149 Genome-wide identification of salt and drought stress related non coding RNAs in Eugenia uniflora

150 LABioinfo.org: an integrated web portal for user-friendly bioinformatics tools and genomic information on organisms of interest in Latin America, Bruno Correia, Laboratory of Integrative Bioinformatics - LIB, Advanced Center for Chronic Diseases - ACCDiS, Brazil

151 The landscape of non-coding RNAs in the archaeon Sulfolobus genus, Victor Aliaga-Tobar, Universidad Mayor; Laboratory of Integrative Bioinformatics (LIB), Chile

152 Kinetic model of Clostridium beijerinckii based on superposition of its phenotypic states, Marcelo Rivas-Astroza, Pontificia Universidad Catolica de Valparaiso, Chile

153 MinBar: An automated pipeline to design mini-barcode primers for traceability and detection of marine species, Ulises Rosas-Puchuri, Center for Conservation and Sustainability, Smithsonian Conservation Biology Institute, Peru

154 3D-PP: a tool for discovering conserved three-dimensional protein patterns, Alejandro Valdés-Jiménez, Universidad de Talca, Chile

155 Mining and structural analysis on the antibody V-domains, Louis Papageorgiou, Dep. of Biotechnology, Agricultural University of Athens; Dep. of Informatics and Telecommunications, UOA, Greece

156 Computational approaches for the identification of potential disease associated site in APTX, Hilda Torres Ulate, Universidad de Costa Rica, Costa Rica

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157 Loss of trans regulation in breast cancer molecular subtypes, Diana García-Cortés, National Institute of Genomic Medicine, Mexico

158 Reconstructing the phylogeny of Corynebacteriales while accounting for Horizontal Gene Transfer, Nilson Da Rocha Coimbra, Universidade Federal de Minas Gerais, Brazil

159 Bioinformatics Modeling of HCV proteins with mutations of resistance to antivirals, Arturo Trigo, Research Group in Applied Genetics (GIGA)-IBS-CONICET-UNaM, Jujuy 1745, Posadas, Misiones, Argentina., Argentina

160 A computational method for internal repeats detection in protein structure, Claudia Alvarez-Carreño, IFC, Universidad Nacional Autónoma de México, Mexico

161 Application of genomic and bioinformatics tools for the study of CADASIL, Verónica Latapiat, Laboratorio de Genómica Avanzada, Centro de Genómica y Bioinformática, Universidad Mayor, Santiago, Chile, Chile

162 A novel enolase from Taenia solium metacestodes and its evaluation as an immunodiagnostic antigen for porcine cysticercosis, Reynaldo Ponce Almeri, Universidad Peruana Cayetano Heredia, Peru

163 STRUCTURAL MODELLING AND MOLECULAR DOCKING ANALYSIS OF THE MAJOR ROYAL JELLY PROTEIN 1 (MRJP1) FROM Apis mellifera REVEALS POSSIBLE ALLERGENIC SITES FOR HUMANS, Eduardo Apari, Grupo de Investigación en Bioinformatica y Biologia Estructural. Universidad Nacional Mayor de San Marcos, Peru

164 PsalmonisDB: a database of genomic information of Piscirickettsia salmonis, Guillermo Nourdin-Galindo, Programa de Magister en Ciencias, mención Microbiología, Facultad de Ciencias, Universidad Austral de Chile., Chile

165 Identification of metabolic pathways and candidate genes associated to leaf senescence process in sunflower by integration of transcriptomic, metabolomic and phenomics data and functional validation in model species, Paula Fernandez, INTA, Argentina

166 DESIGN OF A MULTIEPITOPIC PROTEIN AGAINST THE PULMONARY SYNDROME CAUSED BY HANTAVIRUS THROUGH AN IMMUNOINFORMATICS APPROACH, Stacy Kelly Bendezú Sayas, Grupo de Investigacion de Bioinformatica y Biologia Estructural. Universidad Nacional Mayor de San Marcos, Peru

167 Crowdsourcing for Curating Small Molecule Arsenal against Nipah Virus: NIDB. Nishi Kumari, University Institute of Engineering and Technology, Panjab University, India

168 Discovery of novel Cx43 hemichannel blocker by Structure-Based Virtual Screening, Yorley Andrea Duarte, Center for bioinformatics an integrative biology, Universidad Andres Bello

We ask all poster presenters to place their posters on their assigned boards by 12:30 PM on Wednesday, 7 November, and leave them up through the end of the day on Thursday, 8 November.

Abstracts are available to online at https://www.iscb.org/cms_addon/conferences/la2018/posters.php

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CABANA is a capacity strengthening project for bioinformatics in Latin America. It aims to accelerate the implementation of data-driven biology in the region by creating a sustainable capacity-building programme. CABANA is orchestrated by an international consortium of ten organisations - nine in Latin America and one in the UK.

- CABANA will help to accelerate data-driven biology in Latin America by introducing a sustainable programme for building capacity in the region

- CABANA's international and uniquely broad range of activities will address the training needs of Latin America's diverse biological and biomedical sciences communities

- CABANA will accelerate the use of bioinformatics in lead institutions in the region, which will become hubs in a pan-Latin-American bioinformatics network.

URL: http://www.cabana.online/

Center for Bioinformatics and Integrative Biology (CBIB)

The Center for Bioinformatics and Integrative Biology (CBIB), hosted at the Faculty of Biological Sciences at University Andres Bello in Santiago, Chile, is composed by an interdisciplinary team, and its main objective is to develop research strategies that combine the benefits of theoretical estimations and experimental validation. It was born in 2012, after an important effort by the University to install a first-rate applied research center.

Currently, CBIB develops state-of-the-art research in the areas of Molecular Simulation, Computational Genomics, Bionanotechnology, Drug Discovery & Drug Delivery, Bioengineering, Biophysical Characterization and Software Development.

Through this integrated approach, CBIB generates an iterative cycle of research, based on observation, modeling, simulation and experimental validation, to finally contribute to the development of solutions to biological, medical and biotecnological problems that affect everyday life.
CBIB is directed by Fernando Danilo González-Nilo, PhD. has 7 Principal Investigators and more than 90 members of several fields such as bioinformatics, biochemistry, chemistry, biology and physics. Currently has 20 R&D projects in execution, some of them in collaboration with prestigious national and international partners.

URL: http://www.cbib.cl/cbib/

EMBnet

EMBnet is a group of collaborating organisations and individuals across the world. It is organised as a foundation called ‘The EMBnet Stichting’, registered in The Netherlands.

The Annual General Meeting (AGM), in which each representative has an equal vote, is the main decision-making body of EMBnet.

EMBnet’s mission is:

- to provide education and training in bioinformatics
- to assist biotechnology- and bioinformatics-related research
- bridging between commercial and academic sectors
- promoting global cooperation through its community networks

URL: https://www.embnet.org/wp/

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EMBO stands for excellence in the life sciences.

EMBO is an organization of more than 1800 leading researchers that promotes excellence in the life sciences. The major goals of the organization are to support talented researchers at all stages of their careers, stimulate the exchange of scientific information, and help build a European research environment where scientists can achieve their best work.

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EMBO supports talented researchers, selected through impartial evaluation processes, to allow them to do great science. The wide scientific scope across the full range of life science research coupled with the broad geographical reach of more than 1800 members and associate members – some of the best researchers in Europe and around the world – positions EMBO optimally to serve Europe's life science community.

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The Center for Genomics and Bioinformatics at Universidad Mayor (CGB-UM) is the first research center of its kind in Chile and was established on 2010 in order to address key challenges in science, technology and innovation in this field. The CGB-UM is fostered by Universidad Mayor, an open and independent higher education institution, committed to the training of professionals and entrepreneurs, as well as the preservation and dissemination of knowledge.

The CGB-UM works in an associative and synergistic manner with Chilean and international research organizations to generate interdisciplinary high-impact fundamental and applied research. Our Center also provides consulting services in genomics and bioinformatics to a wide array of public and private institutions in Chile and overseas.

Our Center integrates the latest technologies available from molecular biology, ecology, physiology and cell biology with high-throughput technologies (genomics, proteomics, metabolomics) using bioinformatics and computer science. Our main goal is to improve Chile’s environmental sustainability, life quality and economic competitiveness in order to become a national and international reference center for science, technology and innovation. The CGB-UM is composed by 16 researchers of recognized national and international trajectory, working in diverse areas of science, including Plant Genomics, Biotechnology, Environmental Microbiology, Human and Animal Health, Genetics, Genomics, theoretical biology and Bioinformatics. Our research programs and the interaction with national and international partners promote the development of high impact interdisciplinary research.

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SoIBio (Iberoamerican Society for Bioinformatics) is an international scientific society, founded in 2009 following the previous work and experience of the RIB (Iberoamerican Network for Bioinformatics) which was, from 2002 to 2008, a joint collaborative project of several research groups from Iberoamerica working in the new field of Bioinformatics and Computational Biology.

SoIBio aims to promote research and development on Bioinformatics in the large international region of Iberoamerica. As such it looks to help either individuals or national societies or groups that want to work in this field, both at academic and professional level. To do so, SoIBio facilitates transnational exchange, collaboration, formation and development for issues and topics related to Bioinformatics and Computational Biology. It is also a platform to interact and collaborate with other international societies and networks that work in the same field: European Molecular Biology Network (EMBnet); Asian-Pacific Bioinformatics Network (APBioNet); International Society for Computational Biology (ISCB).

URL: http://www.soibio.org/

International Society for Computational Biology (ISCB)

Since its founding in 1997, the International Society for Computational Biology, Inc. (ISCB) has emerged as the leading professional society for participants in the field of computational biology and bioinformatics. This global, diverse group includes researchers, practitioners, technicians, students, and suppliers. ISCB serves its global membership community by:

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- Promoting, representing, and advocating for the field using its influential voice in conversations with governments and the agencies responsible for scientific funding

URL: www.iscb.org

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The Pontificia Universidad Católica de Chile (UC) is one of the main higher education institutions in the country. It was created on June 21, 1888 and is organized into 4 campuses located in Santiago and 1 campus located in Villarrica (Southern Chile). Its mission is "to reach excellence in the creation and transference of knowledge and educational training of people, inspired by Catholic values and always at the service of the Church and society". The Institution has accomplished this by creating some of the best academic programs in Latin America in the areas of agriculture, astronomy, architecture, art, sciences, business, education, history, and engineering among many others. This University has been ranked #1 in Latin America according to the OS Latin America University Rankings 2018.

The University aims to achieve a solid education, founded on the sciences, arts, and humanities. It plans to continue its growth and quality of education by preparing its students to be technically and scientifically ready, as much as, to be open to different human realities and to the social and personal responsibilities involved in the complete development of the society.

URL: http://www.uc.cl/

uBiome

uBiome, the leader in microbial genomics, was founded in 2012 by Stanford-, Oxford-,and UCSF-educated researchers, Dr. Jessica Richman, PhD, and Dr. Zachary Apte, PhD, with a mission to advance the science of the microbiome and make useful products to improve human life. The company's technology platform is based on the largest microbial dataset in the world (over 250,000 samples), covered by six issued patents (and over 180 patent assets), and used in over 20 peer-reviewed publications and presentations. Over 200 research institutions around the world, including the US Centers for Disease Control (CDC), US National Institutes of Health (NIH), Harvard University, Stanford University, University of California, San Francisco, University College London, and University of Sydney, have used this platform.

uBiome is funded by Y Combinator, Andreessen Horowitz, and 8VC, as well as other leading investors. Since its launch, the company has received widespread recognition including CNN 10: Startups to Watch, the IVY Technology Award, CNN Future 30, was a Medtech Innovator Finalist, and was named one of Fast Company's Most Innovative Companies in Healthcare in 2016 and in Data Science in 2018. Most recently, uBiome was selected as a 2018 Technology Pioneer by the World Economic Forum.

URL: www.ubiome.com

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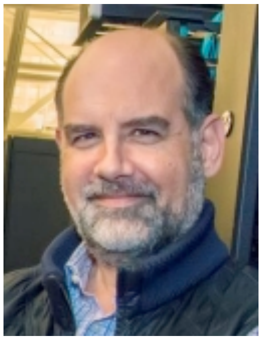

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