Advances in Computational Biology

Fostering collaboration among women scientists

Thursday, 28th November

Oral presentations

BioMed01	Claudia Arnedo-Pac	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers
BioMed02	Eva G Alvarez	Detecting aberrant integrations of viral DNA that promote major restructuring of cancer genome architecture.
BioMed03	Frances Pearl	Predicting synthetic lethal interactions using conserved patterns in protein interaction networks
BioMed04	Inmaculada Álamo-Álvarez	Mechanistic approach for optimal model selection in cancer research
BioMed05	Renée Beekman	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics
BioSeq01	Aida Ripoll-Cladellas	Characterization of Selenoprotein Gene Expression across Tissues and Individuals
BioSeq02	Ana Conesa	Tools for transforming multiomics data into disease models
BioSeq03	Elena Bernabeu	Widespread sexual dimorphism in genetic architecture in UK Biobank
BioSeq04	Erola Pairo-Castineira	Fine-mapping UK Biobank traits GWAS using bayesian algorithms and chromatin annotation data
BioSeq05	Irene Unterman	Genomic based drug repurposing screen for Rett syndrome
BioSeq06	Vivian Link	Go low with ATLAS: a tool for maximizing insight from minimal sequencing depth
Compute01	Arezou Rahimi	Discriminating Early- and Late-Stage Cancers Using Multiple Kernel Learning on Gene Sets
Compute02	Divya Sitani	An RPCA (Robust Principal Component Analysis) based approach for protein-protein interaction hot-spot prediction.
Compute03	Jessica Nye	Automated extraction of color pattern and anatomical characteristics in dairy cows
Compute04	Marta Garcia-Gasulla	The human heart seen by the eyes of a computer scientist
Compute05	Sarra Itidal Abbou	DLMF: Deep Logistic Matrix Factorization with multiple information integration for drug-target interaction prediction

Poster presentations

BioMed06	Aina Jene Cortada	File QC Portal: first insight of the sequencing samples deposited at EGA
BioMed07	Angela Sofia García Vega	Dietary patterns by food groups are important shapers of the gut microbiota.
BioMed08	Ania Alay	Multi-omics profiling as an approach to precision oncology in a rare CRC tumor: a case report
BioMed11	Claudia Vasallo	Lighting an Evidence Beacon to support disease exploration using the DisGeNET platform
BioMed12	Coral Fustero-Torre	In silico prescription of anticancer drugs in single-cell RNA-seq.
BioMed13	Effrosyni Karakitsou	Combining GSMMs with machine learning: a new tool in the development of personalised medicine
BioMed14	Fatma Cankara	Prediction of the Effects of Single Amino Acid Variations on Protein Functionality with Annotation Centric Modeling
BioMed15	Gerda Cristal Villalba Silva	Differential expression analysis of lysosomal storage related genes in gliomas
BioMed16	Hanna Kranas	Genomic segments with different DNA repair dynamics
BioMed17	Judith Pérez Granado	ResMarkerDB: a database of biomarkers of response to antibody therapy in breast and colorectal cancer
BioMed18	Judith Pérez Granado	Exploring the genetic architecture of Major Depression: low agreement between the results of candidate gene studies and GWAS
BioMed19	Laia Bassaganyas	Immunogenomic characterization of renal cell carcinomas
BioMed20	María José Jiménez-Santos	Targeting Intratumoral Heterogeneity with in silico Drug Prescription Tools
BioMed37	Rosario Carmona	Functional variant prioritization in rare diseases using a mechanistic approach
BioSeq07	Aileen Ferraro	A large-scale RNA-seq screen reveals novel transcriptional regulators in Neurospora crassa
BioSeq08	Amandine R. Bertrand	Impact of the sequencing coverage in metagenetic and metagenomic studies
BioSeq09	Ana Conesa	The Functional Iso-Transcriptomics analysis framework to assess the functional impact of alternative isoform usage
BioSeq10	Ángeles Arzalluz-Luque	Measuring isoform co-expression in single-cell RNAseq successfully decodes splicing coordination as a key determinant of neural cell-type identity
BioSeq11	Anja Fullgrabe	Single Cell Expression Atlas: Systematic Analysis and Visualisation of Single Cell RNA-Seq
BioSeq12	Annika Gable	A new functional gene annotation system based on STRING protein interaction network clusters for gene set enrichment analysis
BioSeq13	Babita Singh	Future of Sharing Genomics Data: Glimpse of EGA’s initiatives
BioSeq14	Dimitra Karagkouni	Exploring the coding and non-coding miRNA targetome
BioSeq15	Elisheva Heilbrun	High throughput sequencing uncovers patterns of UV damage formation
BioSeq16	Ester Vilaprinyo	Quantitative Operating Principles of Yeast Metabolism during Adaptation to Heat Stress
BioSeq17	Hafida Bouziane	Multi-Label Learning with Heterogeneous Label-Specific Features for Human Protein Subcellular Localization Sites Prediction
BioSeq18	Hagit Philip	Specific T-cell clones are associated with mammary tumor development
BioSeq19	Heather Stever	Genomic analysis of an insect-microbial symbiosis on the summit of a Hawaiian volcano
BioSeq20	Isabel Birds	Understanding the translation potential and evolution of cytoplasmic long non-coding RNA
BioSeq21	Kathryn Asalone	Annotation of the Mysterious Germline-Restricted Chromosome in Zebra Finch (Taeniopygia guttata)
BioSeq22	Klaudia Walter	Whole genome sequencing to study the contribution of structural variation to human complex traits
BioSeq23	Laura Martínez Gómez	Importance of exon duplications in alternative splicing
BioSeq24	Mar González-Ramírez	Meta-analysis of NGS data to study poised enhancers in ESCs along differentiation
BioSeq25	Marie Leleu	Chlamydiales implication in the evolution of Archaeplastida
BioSeq31	Alejandra Medina-Rivera	Characterization of regulatory variants in promoters with enhancer activity and their relation with human diseases
BioSeq35	Sapir Peled	Function Prediction: Predicting whether a proteins binds DNA from sequence
Compute06	Aleksandra Swiercz	GRASShopPER - a tool for de novo assembly
Compute07	Amita Barik	Prediction of small RNAs in bacteria and deciphering their interactions with proteins
Compute08	Ana Jokanovic	Enabling job scheduling flexibility in heterogeneous modular supercomputing systems
Compute09	Beatriz Eguzkitza	Drug delivery simulations inside human body with a parallel high performance simulation platform, Alya.
Compute10	Beatriz García-Jiménez	Condensed Microbiome representation using Transfer and Deep Learning to Promote Microbial Composition Prediction
Compute11	Burcu Bakir-Gungor	Use of Machine Learning to Diagnose Inflammatory Bowel Disease using Associated Metagenomics Dataset
Compute12	Claudia Llinas del Torrent	Mechanisms Underlying Allosteric Molecular Switches of Metabotropic Glutamate Receptor 5
Compute13	Claudia Rosas	Evaluation of Natural Language Processing and Machine Learning modules for High-Performance Computing: Experiences with Tumor classification
Compute14	Heval Atas	How to Best Represent Target Proteins for Artificial Learning Based Drug Discovery and Repurposing

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Oral presentations

BioMed21	Alice Ledda	Computational challenges associated to plasmid mediated AMR spread
BioMed22	Julia Puig	Cell-intrinsic core-regulatory circuits driving tumor-related phenotypes with the I3-OncoNet cycle
BioSeq26	Ilana Buchumenski	Dynamic hyper editing underlines temperature adaptation in Drosophila
BioSeq27	Jennifer Mitchell	Comparative epigenomics determines the enhancer sequence code of pluripotent embryonic stem cells and facilitates the creation of synthetic enhancers
BioSeq28	Mireya Plass	Single-cell transcriptomics analysis reveals the dynamics of alternative polyadenylation during cell cycle progression
BioSeq29	Rocio Rama Ballesteros	Benchmarking coevolution methods
Compute15	Antonia Vyrkou	An atomistic molecular dynamics simulations approach to the study of h-LDHA inhibition

Poster presentations

BioMed09	Benedetta Bolognesi	The Mutational Landscape of a Prion-like Domain.
BioMed10	Burcu Bakir-Gungor	The Identification of Affected Pathway Subnetworks and Pathway Clusters in Colon Cancer
BioMed23	Marta Cascante	Model-driven discovery of metabolic reprogramming associated to metastatic cancer and cisplatin resistance
BioMed24	Elva María Novoa del Toro	A Multi-Objective Genetic Algorithm to Find Active Modules in Multiplex Biological Networks
BioMed25	Laura Cantini	Benchmarking of multi-omics joint Dimensionality Reduction approaches for cancer studies
BioMed26	Laura Judith Marcos-Zambrano	Targeting colorectal cancer: microbiome modulation and effect over tumour metabolism signalling pathways
BioMed27	Teresa Laguna	Applying human metabolic inter-variability for effective personalized nutrition strategies
BioMed28	Victoria Ruiz-Serra	Deciphering the interactions between the immune system and cancer cells
BioMed29	Marielena Georgaki	Systematic integration of somatic mutation calling algorithms for reliable identification of cancer mutations
BioMed30	Marina Esteban Medina	Expanding the scope of drug repositioning in Juvenile Idiopathic Arthritis: A mechanistic approach using machine learning methodologies.
BioMed31	Orly Weissberg	Exploration of unique chimeras as biomarkers in Alzheimer's disease
BioMed32	Qingyao Huang	Interpreting copy number variation pattern in cancer with protein interaction network
BioMed33	Rosa Barcelona	Genomics tools in the cloud: The new frontier in omics data analysis
BioMed34	Sonsoles Martín-Santamaría	Innate immunity receptors: computational approaches to their modulation
BioMed35	Ute Roehrig	Quantum methods for structure-based drug design
BioMed36	Nicia Rosário-Ferreira	Non-Structural Protein 1 (NS1) – A Hub Protein Essential for Influenza Infection – Using a Molecular Dynamics Approach to Understand its Behavior
BioSeq30	Agnieszka Rybarczyk	Selected aspects of essential hypertension and cardiovascular disease - modeled and analyzed using Petri nets
BioSeq32	Nazeefa Fatima	Evaluation of Single-Molecule Long-Read Sequencing Technologies for Structural Variant Detection in Human Genomes
BioSeq33	Ruchishree Konhar	The whole genome de novo sequence assembly of Nepenthes khasiana, a rare and endemic tropical pitcher plant of Meghalaya, North-east India
BioSeq34	Ruchishree Konhar	Next generation sequencing (NGS)-based de novo assembly of expressed transcripts and genome information of Dendrobium nobile, an endangered medicinal orchid from North-east India
BioSeq36	Sarah Wooller	Deciphering the Influence of the Exome on Mutations
BioSeq37	Yulia M. Suvorova	Alignment-free evolutionary events prediction.
BioSeq38	Marina Garrote-López	The positive part of phylogenetic varieties
BioSeq39	Martiela Freitas	CRISPR/Cas9 in silico off-targets prediction for Mucopolysaccharidosis Type I through comparative analysis
BioSeq40	Morgane Thomas-Chollier	RSAT: Regulatory Sequence Analysis Tools
BioSeq41	Noelia Ferruz	Fragment-based protein design guided by evolutionary relationships
BioSeq42	Raquel Garcia Perez	The anatomy of the human transcriptome in health and disease
BioSeq43	Sara Guirao-Rico	A benchmarking study of the performance of SNP callers for pool-seq data with an application for genomics analyses of multiple populations
BioSeq44	Tazin Rahman	A Survey on Different Approaches to Construct Phylogenetic Tree from SNP Data
BioSeq45	Tehila Atlan	influence of function in bacteria concerning cancer
BioSeq46	Vera Pancaldi	Chromatin 3D organization principles revealed by chromatin networks: gene-regulation, replication, and beyond
BioSeq47	Virginia Díez-Obrero	Gene expression and splicing regulation in the colon helps to explain the genetic heritability of inflammatory and metabolic complex traits and diseases
Compute16	Beatriz García	From tech to bench: Deep learning pipeline for image segmentation of High-Throughput High-Content microscopy data
Compute17	Katya Rodriguez Vazquez	Bioinspired Algorithms in Bioinformatics
Compute18	Laura M Zingaretti	Link-HD: a tool to multiple- microbial communities integration
Compute19	Heval Atas	Deep and Shallow Chemogenomic Modelling for Compound-Target Binding Affinity Prediction Using Pairwise Input Neural Networks & Random Forests
Compute20	Hilal Kazan	MEXCOWalk: Mutual Exclusion and Coverage Based Random Walk to Identify Cancer Modules
Compute21	Judit Planas	Filling the gap between computing and I/O performance in Brain Tissue Simulations
Compute22	Laura Carolina Camelo Valera	Phage-Host interaction prediction
Compute23	M. Isabel Agea Lorente	Classification model with Conformal Prediction applied to Glucocorticoid Receptor virtual library.
Compute24	Marta Szachniuk	ElTetrado captures topological features of nucleic acid quadruplexes
Compute25	Miriam Elbaz	NeuroConstruct-based implementation of Retinal Circuitry
Compute26	Rosa M. Badia	Managing failures in Computational Biology Workflows with PyCOMPSs