



21st European Conference on Computational Biology

Planetary Health and Biodiversity

FINAL PROGRAMME

12-21 September 2022
Sitges, Barcelona



Barcelona
Supercomputing
Center
Centro Nacional de Supercomputación



eccb2022.org

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Welcome

Dear colleague,

We are delighted to welcome you to the **21st European Conference on Computational Biology (ECCB2022)** under the motto **Planetary Health and Biodiversity**, which will take place in Sitges (Barcelona, Spain) from the 12th to the 21st of September, 2022.

We are excited to announce that the **ECCB2022 main conference** will run again as an **in person event** from the **18th to the 21st of September**. Computational biology has been a key instrument to help our societies in finding solutions to the current health crisis and emerge stronger from it. Spaces like the ECCB2022 are essential to promote the scientific debates and collaborations that contribute to moving the field forward.

The four-day conference will offer a number of top keynote speakers, insightful talks selected from delegates submissions, onsite poster sessions and an exhibition for institutions and companies. The programme will feature a new track on “Climate Crisis and Health”, which complements the traditional themed tracks. In the week prior to the main conference, delegates will be invited to join the New Trends in Bioinformatics by ECCB, a program to host a selection of virtual and face-to-face workshops and tutorials.

ECCB2022 welcomes scientists working in a variety of disciplines, including bioinformatics, computational biology, systems biology, artificial intelligence, biology, medicine and environmental sciences. Participating in ECCB2022 will be a unique opportunity to keep pace with cutting edge research while interacting with a diverse and broad representation of the research community across many domains in Life Sciences and beyond. We are sure that the conference will facilitate knowledge dissemination of great interest and vivid scientific discussions, as well as stimulating a creative exchange of ideas.

We look forward to meeting you in person again in the unique scenery of Sitges!

With best regards,

Alfonso Valencia & Salvador Capella-Gutiérrez on behalf of the ECCB2022

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Programme at a glance

	SUNDAY, 18 September
08:15 - 08:30	Registration desk open all day from 08:15h
18:00 - 18:30	Conference opening (18:00h) Speakers: Alfonso Valencia and Niklas Blomberg
18:30 - 19:00	Conference opening Keynote talk César Hidalgo (University of Toulouse, France) How humans judge machines Chair: Alfonso Valencia
19:00 - 19:30	
19:30 - 20:00	
20:00 - 20:30	
20:30 - 21:00	<i>Welcome cocktail</i>
21:00 - 21:30	
21:30 - 22:00	
22:00 - 22:30	

	MONDAY, 19 September		
08:00 - 08:30	Registration desk open all day		
08:30 - 09:00	Welcome and announcements (08:45h)		
09:00 - 09:30	Keynote talk Raúl Rabadán (Columbia University, USA) Some mysteries about microbes and cancer Chair: Niklas Blomberg		
09:30 - 10:00			
	Auditorium Anna Tramontano Room Margaret O. Dayhoff Room Rosalind Franklin		
	ELIXIR (Session #01) Chair: Katharina Heil	GENOMES (Session #02) Chair: Toni Gabaldón	SYSTEMS (Session #03) Chair: Patrick Aloy
10:00 - 11:00	ELIXIR talk Identifying resources and exploring synergies between the ELIXIR 3D-Bioinfo, proteomics and IDP communities • Authors: Emmanuel Levy, Christine Orengo, Nathalie Reuter, Sameer Velankar, Shoshana Wodak, Norman Davey, Zsuzsa Dosztányi, Damiano Piovesan, Silvio Tosatto, Eva Csosz, Julien Marcoux, Lennart Martens, Pathmanaban Ramasamy, Juan Antonio Vizcaino, Massimiliano Bonomi, Wim Vranken	Proceeding talk SALAI-Net: Species-Agnostic Local Ancestry Inference Network • Authors: Benet Oriol Sabat, Daniel Mas Montserrat, Xavier Giro-i-Nieto and Alexander Ioannidis	Proceeding talk MERRIN: MEtabolic Regulation Rule INFERENCE from time series data • Authors: Kieran Thullier, Caroline Baroukh, Alexander Bockmair, Ludovic Cottret, Loïc Paulev� and Anne Siegel
	ELIXIR talk Using the IDP-KG to enable IDPcentral information on submission • Authors: Alasdair Gray, Ivan Mi�eti�, Alexander Monzon and Damiano Piovesan	Proceeding talk Improving Bacterial Genome Assembly Using a Test of Strand Orientation • Authors: Grant Greenberg and Ilan Shomrony	Proceeding talk Small compound-based direct cell conversion with combinatorial optimization of pathway regulations • Authors: Toru Nakamura, Michio Iwata, Momoko Hamano, Ryohi Eguchi, Jun-Ichi Takeshita and Yoshihiro Yamanishi
	ELIXIR talk AHoJ: rapid, tailored search and retrieval of apo and holo protein structures • Authors: Christos P. Feidakis, Radoslav Krivak, David Hoksza and Marian Novotn�	Highlight talk plotsr: Visualising structural similarities and rearrangements between multiple genomes • Authors: Manish Goel and Korbinian Schneeberger	Proceeding talk Design centering enables robustness screening of pattern formation models • Authors: Anastasia Solomatina, Alice Cezanne, Yannis Kalaidzidis, Marino Zerial and Ivo F. Sbalzarini
11:00 - 11:30	Coffee break and Exhibition		
	Auditorium Anna Tramontano Room Margaret O. Dayhoff Room Rosalind Franklin		
	ELIXIR (Session #04) Chair: Katharina Heil	DATA (Session #05) Chair: Peter Maccallum	PROTEINS (Session #06) Chair: Mark Wass
11:30 - 12:30	ELIXIR talk Open source genome-scale metabolic models: why and how • Authors: Mihai Anton, Barbara Szomolay and Vitor A P Martins dos Santos	Proceeding talk Linking cells across single-cell modalities by synergistic matching of neighborhood structure • Authors: Borislav Hristov, Jeffrey Bilmes and William Noble	Highlight talk TITAN: T-cell receptor specificity prediction with bimodal attention networks • Authors: Anna Weber, Jannis Born and Maria Rodriguez Martinez
	ELIXIR talk Genome-wide metabolic annotation for Methanocaldococcus (Methanococcus) jannaschii, the first member of the Archaea to be sequenced a quarter of a century ago • Authors: Ismini Baltasv�, George Stamoulis, Konstantinos Tziavar�, Alexandros Dermaris, Ioannis Iliopoulos, Ron Caspi, Peter D. Karp, Nikos C. Kyriides, Christos A. Ouzounis	Highlight talk Marker-based annotation and integration of large scale single-cell transcriptomics data on a laptop • Authors: Sikander Hayat, Yang Xu, Simon Baumgart, Christian Stegmann, Rafael Kramann and Rachel Patton McCord	Highlight talk Online predictions for protein biophysical features and their conservation • Authors: Wim Vranken, Luciano Kagami and Adrian Diaz
	ELIXIR talk Rare disease specific FAIR Maturity Indicators • Authors: Nuria Queralt Rosinach, Rajaram Kaliyaperumal, Annika Jacobsen, Mark Wilkinson, Marc Hanauer, Marco Roos	Highlight talk Polympect: exploring functional relations among common human genetic variants • Authors: Samuel Valentini, Francesco Gandolfi, Mattia Carolo, Davide Dalfovo, Lara Pozza and Alessandro Romanel	Proceeding talk Group-walk, a rigorous approach to group-wise false discovery rate analysis by target-decoy competition • Authors: Jack Freestone, Temana Short, William Stafford Noble and Uri Keich
12:30 - 13:00	Lunch, Exhibition and Poster viewing		
13:00 - 13:30			
13:30 - 14:00			
	Auditorium Anna Tramontano Room Margaret O. Dayhoff Room Rosalind Franklin		
	SYSTEMS (Session #07) Chair: Patrick Aloy	GENES (Session #08) Chair: Artemis Hatzigeorgiou	APPLICATIONS (Session #09) Chair: Javier De Las Rivas

Programme at a glance

14:00 - 15:00	Proceeding talk PiSL: pairwise interaction learning-based graph neural network for synthetic lethality prediction in human cancers • Authors: Xin Liu , Jiale Yu, Siyu Tao, Beiyuan Yang, Shike Wang, Lin Wang, Fang Bai and Jie Zheng	Proceeding talk NSF4SL: negative-sample-free contrastive learning for ranking synthetic lethal partner genes in human cancers • Authors: Shike Wang , Yimiao Feng, Xin Liu, Yong Liu, Min Wu and Jie Zheng	Applications talk A cloud based resource to manage, access and explore omics datasets in multiuser environments • Authors: Mario Looso , Philipp Goymann, Franz Ziegeneck, Carsten Kuenne, Daniel Spothelfer, Noah Knoppik and Jasmin Walter
	Highlight talk Interpretable systems biomarkers predict response to immune-checkpoint inhibitors • Authors: Óscar Lapuente-Santana , Maisa van Genderen , Peter Hilbers , Francesca Finotello and Federica Eduati	Proceeding talk Efficient Permutation-based Genome-wide Association Studies for Normal and Skewed Phenotypic Distributions • Authors: Maura John , Markus Ankenbrand, Carolin Artmann, Jan Freudenthal, Arthur Korte and Dominik Grimm	Applications talk Introducing X-Omics, the central multi-omics data integration and AI modeling platform for biomarker data at Merck • Author: Sven-Eric Schelhorn
	Highlight talk Comprehensive prediction of robust synthetic lethality between paralog pairs in cancer cell lines • Authors: Barbara De Kegel , Niall Quinn , Nicola Thompson , David Adams and Colm Ryan	Highlight talk Analysis of eukaryotic lincRNA sequences indicates signatures of hindered translation linked to selection pressure • Authors: Anneke Bruemmer , Rene Dreos , Ana Claudia Marques and Sven Bergmann	Applications talk Global biodata resources: challenges to long-term sustainability of a crucial data infrastructure • Authors: Guy Cochrane and Chuck Cook
15:00 - 15:30			
15:30 - 16:30	Auditorium Anna Tramontano	Coffee break and Exhibition	Room Rosalind Franklin
	PROTEINS (Session #10) Chair: Mark Wass	Room Margaret O. Dayhoff	GENOMES (Session #11) Chair: Toni Gabaldón
	Highlight talk PDBe-KB: collaboratively defining the biological context of structural data • Author: Preeti Choudhary	Proceeding talk 3CAC: improving the classification of phages and plasmids in metagenomic assemblies using assembly graphs • Authors: Lianrong Pu and Ron Shamir	APPLICATIONS (Session #12) Chair: Javier De Las Rivas
16:30 - 17:00			
17:00 - 17:30			
17:30 - 18:00			
18:00 - 18:30			
18:30 - 19:00			
19:00 - 19:30			

TUESDAY, 20 September			
08:00 - 08:30	Registration desk open all day		
08:30 - 09:00	Welcome and announcements (08:45h)		
09:00 - 09:30			
	Keynote talk		
	Ana T. Freitas (INESC-ID/IST Technical University of Lisbon, Portugal) Personalized medicine in the era of artificial intelligence		
09:30 - 10:00	Chair: Fátima Sánchez-Cabo		
10:00 - 11:00			
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	ELIXIR (Session #13) Chair: Katharina Heil	PROTEINS (2) + GENES (1) (Session #14) Chair: Mark Wass	SYSTEMS (2) + DATA (1) (Session #15) Chair: Anais Baudot
	From integrated COVID-19 data to integrated pathogen data analysis Title: Setting the scene: Beyond COVID-19 - European preparedness for infectious disease outbreaks • Speaker: Katharina Lauer (ELIXIR)	Proceeding talk Genes: Improved NSGA-II algorithms for multi-objective biomarker discovery • Authors: Luca Cattelan and Vittorio Fortino	Highlight talk Data: The AIMe registry for artificial intelligence in biomedical research • Authors: Julian Matschinski, Nicolas Alcaraz, Arriel Benis, Gerda Cristal Villalba Silva, Martin Golebiowski, Dominik G. Grimm, Lukas Heumos, Tim Kacprowski, Olga Lazareva, Markus List, Zakaria Louadi, Josch Pauling, Nico Pfeifer, Richard Rötger, Veit Schwämmele, Kristel Van Steen, Gregor Sturm, Alberto Traverso, Martiela Vaz de Freitas, Leonard Wee, Nina Wenke, Massimiliano Zanin, Olga Zolotareva, Jan Baumbach and David B. Blumenthal
	Title: Pathogen Data Sharing and Workflows at the ENA • Speaker: Colman O'Cathail (EBI/COVID19 Data Portal)	Proceeding talk Proteins: DistilProtBert: A distilled protein language model used to distinguish between real proteins and their randomly shuffled counterparts • Authors: Yaron Geffen , Yanay Ofran and Ron Unger	Proceeding talk Systems: DrDimont: Explainable drug response prediction from differential analysis of multi-omics networks • Authors: Pauline Hiort , Julian Hugo, Justus Zeinert, Nataniel Müller, Spoorthi Kashyap, Jagath C. Rajapakse, Francisco Azuaje, Bernhard Y. Renard and Katharina Baum
	Title: Using COVID-19 data genomics and sharing to set a new future standard • Speaker: Bas Oude Munnink (Erasmus MC/VEO)		
	Title: Fully transparent viral genomics data analysis and sharing for everyone using public infrastructure		

Programme at a glance

	<p>Sharing for everyone using public infrastructure • Speaker: Wolfgang Maier (Universität Freiburg/Galaxy) > Discussion</p>	<p>Highlight talk Proteins: The clinical importance of tandem exon duplication-derived substitutions • Authors: Laura Martinez Gomez, Fernando Pozo Ocampo, Thomas Walsh, Federico Abascal and Michael Tress</p>	<p>Proceeding talk Systems: GNN-SubNet: disease subnetwork detection with explainable Graph Neural Networks • Authors: Bastian Pfeifer, Anna Saranti and Andreas Holzinger</p>
11:00 - 11:30	Coffee break and Exhibition		
	<p>Auditorium Anna Tramontano</p> <p>ELIXIR (Session #16) Chair: Katharina Heil</p> <p>ELIXIR talk The ELIXIR Machine Learning Focus Group: achievements and the road ahead • Speakers: Silvio Tosatto, Fotis Psomopoulos</p> <p>ELIXIR talk The ELIXIR Biodiversity Community - "Biodiversity data" aims and challenges • Speakers: Toni Gabaldón, Josephine Burgin, Robert Waterhouse</p> <p>ELIXIR talk Federated EGA (title TBC) • Speaker: Jordi Rambla</p>	<p>Room Margaret O. Dayhoff</p> <p>DATA (Session #17) Chair: Josep Lluís Gelpí</p> <p>Proceeding talk SimBu: Bias-aware simulation of bulk RNA-seq data with variable cell type composition • Authors: Alexander Dietrich, Gregor Sturm, Lorenzo Merotto, Federico Marini, Francesca Finotello and Markus List</p> <p>Proceeding talk Detecting DNA of novel fungal pathogens using ResNets and a curated fungi-hosts data collection • Authors: Jakub M Bartoszewicz, Ferdous Nasri, Melania Nowicka and Bernhard Y Renard</p> <p>Highlight talk Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data • Authors: Akram Vasighizaker, Saiteja Danda and Luis Rueda</p>	<p>Room Rosalind Franklin</p> <p>PROTEINS (Session #18) Chair: Mark Wass</p> <p>Proceeding talk Insights into performance evaluation of compound-protein interaction prediction methods • Authors: Adiba Yaseen, Imran Amin, Naeem Akhter, Asa Ben-Hur and Fayyaz Ul Amir Afzar Minhas</p> <p>Proceeding talk Cross-Modality and Self-Supervised Protein Embedding for Compound-Protein Affinity and Contact Prediction • Authors: Yuning You and Yang Shen</p> <p>Highlight talk Missense variants in human ACE2 strongly affect binding to SARS-CoV-2 Spike providing a mechanism for ACE2 mediated genetic risk in Covid-19: A case study in affinity predictions of interface variants • Authors: Stuart A. MacGowan, Michael I. Barton, Mikhail Kutuzov, Omer Dushek, P. Anton van der Merwe and Geoffrey J. Barton</p>
11:30 - 12:30			
12:30 - 13:00	Lunch, Exhibition and Poster viewing		
13:00 - 13:30	<p>Birds of a Feather [12:45h - 13:45h, Margaret O. Dayhoff] Sex and Gender Biases in Technology and Artificial Intelligence Organised by Bioinfo4Women: Chair: R. Gonzalo Parra</p>		
13:30 - 14:00			
	<p>Auditorium Anna Tramontano</p> <p>ELIXIR meets Latin America (Session #19) Chair: José María Carazo</p> <p>Welcome and Introduction • Speakers: José María Carazo and Andrew Smith</p> <p>ELIXIR Europe: overview and opportunities • Author: Andrew Smith</p> <p>Development and evolution of Bioinformatics Societies in Latin America: A2B2C (Argentina), AB3C (Brasil), BIOCANET (Costa Rica & Panama), BioNetMX (Mexico), SC2B2 (Colombia), SCB (Chile), SPB2C (Peru) and SOIBIO (Iberoamerica) • Author: Javier De Las Rivas and Consortium Representatives Of Seven Bioinformatics National Societies From Latin-America And Soibio</p> <p>AB3C • Author: Marcelo Brandão</p> <p>Creating paths for the development and application of bioinformatics in Mexico • Authors: Irma Martínez-Flores, Shirley Alquicira-Hernández and Alejandra Eugenia Medina-Rivera</p> <p>Bioinformatics in Argentina: The first 10+3 years of A2B2C • Authors: Nicolas Palopoli, Lucia Chemes, Georgina Stegmayer, Elin Teppa, Diego Bustos, Cristina Marino-Buslje, Flavio Spetale and Sebastián Fernández Alberti</p>	<p>Room Margaret O. Dayhoff</p> <p>GENOMES (Session #20) Chair: Toni Gabaldón</p> <p>Proceeding talk Discovering Significant Evolutionary Trajectories in Cancer Phylogenies • Authors: Leonardo Pellegrina and Fabio Vandin</p> <p>Highlight talk Towards a metagenomics machine learning interpretable model for understanding the transition from adenoma to colorectal cancer • Authors: Carlos Sánchez Casimiro-Soriguer, Carlos Loucera, María Peña-chilet and Joaquín Dopazo</p> <p>Highlight talk Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers • Authors: Solip Park, Fran Supek and Ben Lehner</p>	<p>Room Rosalind Franklin</p> <p>Institutional talks (Session #21) Chair: Salvador Capella-Gutierrez</p> <p>Institutional talk The Spanish Supercomputing Network (RES): HPC and Data Resources for a scientific revolution • Authors: Infrastructure Access Policy Unit - Barcelona Supercomputing Center. Oriol Pineda and Alberto A. Gómez</p> <p>Institutional talk Ersilia, a hub of open-source AI/ML models for drug discovery and global health • Authors: Gemma Turon and Miquel Duran-Frigola</p> <p>Institutional talk The Bioinfo4Women Programme: towards gender equity and diversity in science • Authors: Alba Jene-Sanz, María José Rementeria, Eva Alloza and Álvia Cortés</p>
14:00 - 15:00			
15:00 - 15:30	Coffee break and Exhibition		
	<p>Auditorium Anna Tramontano</p> <p>ELIXIR meets Latin America (Session #22) Chair: José María Carazo</p> <p>Research data management (RDM) in ELIXIR and insight into the RDM Toolkit • Authors: Frederik Coppens and Carole Goble</p> <p>ELIXIR Training activities and opportunities for engagement • Author: Katharina Heil, Jessica Lindvall and Fotis E Psomopoulos</p>	<p>Room Margaret O. Dayhoff</p> <p>DATA (Session #23) Chair: Josep Lluís Gelpí</p> <p>Proceeding talk Exploiting Pretrained Biochemical Language Models for Targeted Drug Design • Authors: Gökçe Uludoğan, Arzucan Özgür, Elif Özkinmli, Kultu Ülgen and Nilgün Karali</p> <p>Highlight talk Scaling up oligogenic diseases research with OLIDA: the Oligogenic Diseases Database • Authors: Barbara Gravel, Charlotte Nachtegael, Arnau Dillen, Guillaume Smits, Ann Nowé, Sofia Papadimitriou and Tom Lenaerts</p>	<p>Room Rosalind Franklin</p> <p>APPLICATIONS (Session #24) Chair: Jaime Huerta-Cepas</p> <p>Applications talk Bioinformatics methods for the analysis of rare-disease patient data – applications for target discovery and obtaining phenotype associations • Authors: Elena Rojano, James Perkins, Fernando Moreno Jabato, José Córdoba-Caballero, Elena Diaz-Santiago, Federico García-Criado, Florencio Pazos, Pedro Seoane and Juan Ranea</p> <p>Applications talk AI microbiome-based recommendation system for improving soil health with bio-stimulants • Authors: Beatriz García-Jiménez, Sam Röttgers, Diego Rodríguez-de-Prado and Alberto Acedo</p>
15:30 - 16:30			

Programme at a glance

	> Open discussion	<p>Highlight talk Pharmacogenomics analysis 2.0: improving scalability and transparency of in vitro pharmacogenomics analysis</p> <ul style="list-style-type: none"> • Authors: Nikta Feizi, Sisira Kadambat Nair, Petr Smirnov, Gangesh Beri, Christopher Eeles, Parinaz Nasr Esfahani, Minoru Nakano, Denis Tkachuk, Anthony Mammootti, Evgeniya Gorobets, Arvind Singh Mer, Eva Lin, Yihong Yu, Scott Martin, Marc Hafner and Benjamin Haibe-Kains 	<p>Applications talk Whole-genome sequencing analysis of food enzyme products reveals contaminations with genetically modified microorganisms of related origin</p> <ul style="list-style-type: none"> • Authors: Jolien D'Aes, Marie-Alice Fraiture, Bert Bogaerts, Sigrid C.J. De Keersmaecker, Nancy H.C. Roosens and Kevin Vanneste
16:30 - 17:00		Keynote talk	
17:00 - 17:30		Graciela Gonzalez-Hernandez (Cedars-Sinai Medical Center (USA)) Mining for Digital Epidemiology: Overcoming the Challenges of Real World Data Chair: Salvador Capella-Gutierrez	
17:30 - 18:00			
18:00 - 18:30			
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23:00 - 23:30			
23:30 - 00:00			

WEDNESDAY, 21 September			
08:00 - 08:30	Registration desk open all day from 8:00h		
08:30 - 09:00	Welcome and announcements 8:45h		
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	CLIMATE CRISIS AND HEALTH (Session #25) Chair: Ana Conesa	DATA (Session #26) Chair: Josep Lluís Gelpí	APPLICATIONS (Session #27) Chair: Anais Baudot
09:00 - 10:00	<p>Invited talk Infectious disease decision-support tools to enhance resilience in climate change hotspots</p> <ul style="list-style-type: none"> • Speaker: Rachel Lowe 	<p>Highlight talk Flimma: Federated and privacy-aware medical differential gene expression analysis</p> <ul style="list-style-type: none"> • Authors: Olga Zolotareva, Reza Nasirigerdeh, Julian Matschinski, Reihaneh Torkzadehmahani, Mohammad Bakhtiari, Tobias Frisch, Julian Alexander Späth, David B. Blumenthal, Amir Abbasinejad, Paolo Tieri, Georgios Kaassis, Daniel Rückert, Nina Wenke, Markus List and Jan Baumbach <p>Proceeding talk This is GlycoQL</p> <ul style="list-style-type: none"> • Authors: Catherine Hayes, Vincenzo Daponte, Julien Mariethoz and Frédérique Lisacek <p>Highlight talk Orchestrating and sharing large multimodal data for transparent and reproducible research</p> <ul style="list-style-type: none"> • Authors: Anthony Mammootti, Petr Smirnov, Minoru Nakano, Zhaleh Safikhani, Christopher Eeles, Heewon Seo, Sisira Kadambat Nair, Arvind S Mer, Ian Smith, Chantal Ho, Gangesh Beri, Rebecca Kusko, Eva Lin, Yihong Yu, Scott Martin, Marc Hafner and Benjamin Haibe-Kains 	<p>Applications talk METALoci, identification of spatial enhancer hubs</p> <ul style="list-style-type: none"> • Authors: Marc A. Martí-Renom, Irene Mota Gomez-Argente, Juan Antonio Rodriguez Perez and Dario Lupiañez <p>Applications talk Power analysis of cell-type deconvolution across human tissues</p> <ul style="list-style-type: none"> • Author: Anna Vathrakokoli Pournara, Zhichao Miao and Irene Papathoerodou <p>Applications talk ChiTaH: a fast and accurate tool for identifying known human chimeric sequences from high-throughput sequencing data</p> <ul style="list-style-type: none"> • Authors: Milana Frenkel-Morgenstern, Rajesh Detroja and Sumit Mukherjee
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	CLIMATE CRISIS AND HEALTH (Session #28) Chair: Ana Conesa	GENOMES (Session #29) Chair: Alba Jené-Sanz	APPLICATIONS (Session #30) Chair: Anais Baudot
10:00 - 11:00	<p>Invited talk Synergies between climate variation and environmental degradation on malaria in southern Venezuela</p> <ul style="list-style-type: none"> • Speaker: Isabel Fletcher <p>Invited talk Real-time Genomics for One Health</p> <ul style="list-style-type: none"> • Speaker: Lara Urban <p>Invited talk Climate-sensitive disease outbreaks in the aftermath of extreme climatic events</p> <ul style="list-style-type: none"> • Speaker: Tilly Alcyona 	<p>Proceeding talk DeepZF: Improved DNA-binding prediction of C2H2-zinc-finger proteins by deep transfer learning</p> <ul style="list-style-type: none"> • Authors: Sofia Aizenstein-Gazit and Yaron Orenstein <p>Proceeding talk CRISPRtracrRNA: Robust approach for CRISPR tracrRNA detection</p> <ul style="list-style-type: none"> • Authors: Alexander Mitrofanov, Marcus Ziemann, Omer Alkhnashi, Wolfgang Hess and Rolf Backofen <p>Highlight talk Revisiting genetic artifacts on DNA methylation microarrays exposes novel biological implications</p> <ul style="list-style-type: none"> • Authors: Benjamin Planterose Jiménez, Manfred Kayser and Athina Vidaki 	<p>Applications talk A near-full compression of SARS-CoV-2 peptidome using UNIQmin</p> <ul style="list-style-type: none"> • Authors: Li-Chuin Chong and Asif M. Khan <p>Applications talk Cancer patient stratification and molecular mechanism identification using patient clinotypes and transcriptomics embeddings</p> <ul style="list-style-type: none"> • Author: Zongliang Yue, Samuel Bharti, Eric Gong, Radomir Siominski, Thanh Nguyen, Lara Lanov, Christopher Willey and Jake Chen <p>Applications talk Evaluation of machine learning strategies for imaging confirmed prostate cancer recurrence prediction on electronic health records</p> <ul style="list-style-type: none"> • Authors: Jacqueline Beinecke, Patrick Anders, Tino Schurrat, Dominik Heider, Markus Luster, Damiano Librizzi and Anne-Christin Hauschild
11:00 - 11:30	Coffee break and Exhibition		
11:30 - 12:00	Conference closing Keynote talk Mar Albà (ICREA-IMIM, Spain)		

Programme at a glance

12:00 - 12:30	The emerging small proteome Chair: Ana Conesa
12:30 - 13:00	Conference closing ceremony Presentation of ECCB/ISMB2023 Awards Final remarks
13:00 - 13:30 13:30 - 14:00	Lunch and Exhibition

Scientific Programme

Sunday, 18 Sept., 2022

18:00 - 18:30 | **Conference Opening**

Auditorium Anna Tramontano

18:00 - 18:15 Alfonso Valencia

Barcelona Supercomputing Center (BSC), Catalan Institution for Research and Advanced Studies (ICREA), INB/ELIXIR-ES, Spain

18:15 - 18:30 Niklas Blomberg

ELIXIR, United Kingdom

18:30 - 19:30 | **Conference Opening Keynote talk**

Auditorium Anna Tramontano

How humans judge machines

César Hidalgo

University of Toulouse, France

Chaired by: Alfonso Valencia

Barcelona Supercomputing Center (BSC), Catalan Institution for Research and Advanced Studies (ICREA), INB/ELIXIR-ES, Spain

Monday, 19 Sept., 2022

08:45 - 09:00 | Welcome and announcements

09:00 - 10:00 | Keynote talk

Auditorium Anna Tramontano

Some mysteries about microbes and cancer

Raúl Rabadán

Columbia University, United States

Chaired by: Niklas Blomberg

ELIXIR, United Kingdom

10:00 -11:00 | Session #01 | ELIXIR

Auditorium Anna Tramontano

Chaired by: Katharina Heil

ELIXIR, United Kingdom

10:00 - 10:20 ELIXIR talk | Identifying resources and exploring synergies between the ELIXIR 3D-Bioinfo, proteomics and IDP communities

Wim Vranken

Vrije Universiteit Brussel, Belgium

10:20 - 10:40 ELIXIR talk | Using the IDP-KG to enable IDPcentral information on submission

Alexander Monzón

University of Padova, Italy

10:40 - 11:00 ELIXIR talk | AHoJ: rapid, tailored search and retrieval of apo and holo protein structures

Christos Feidakis

Charles University, Czech Republic

10:00 - 11:00 | Session #02 | GENOMES

Room Margaret O. Dayhoff

Chaired by: Toni Gabaldón

Barcelona Supercomputing Center (BSC), ICREA, INB/ELIXIR-ES, Spain

10:00 - 10:20 Proceeding talk | SALAI-Net: Species-Agnostic Local Ancestry Inference Network

Benet Oriol Sabat

University of California, Los Angeles, United States

10:20 - 10:40 Proceeding talk | Improving Bacterial Genome Assembly Using a Test of Strand Orientation

Grant Greenberg

University of Illinois, United States

10:40 - 11:00 Highlight talk | plotsr: Visualising structural similarities and rearrangements between multiple genomes

Manish Goel

Ludwig-Maximilians-Universität München, Germany

10:00 -11:00 | Session #03 | SYSTEMS

Room Rosalind Franklin

Chaired by: Patrick Aloy

Institute for Research in Biomedicine (IRB Barcelona), Catalan Institution for Research and Advanced Studies (ICREA), INB/ELIXIR-ES, Spain

10:00 - 10:20 Proceeding talk | MERRIN: MEtabolic Regulation Rule INference from time series data

Kerian Thuillier

CNRS, IRISA, France

10:20 - 10:40 Proceeding talk | Small compound-based direct cell conversion with combinatorial optimization of pathway regulations

Michio Iwata

Kyushu Institute of Technology, Japan

10:40 - 11:00 Proceeding talk | Design centering enables robustness screening of pattern formation models

Anastasia Solomatina

Max Planck Institute of Molecular Cell Biology and Genetics, Germany

11:00 - 11:30 | Coffee Break and Exhibition

11:30 - 12:30 | Session #04 | ELIXIR

Auditorium Anna Tramontano

Chaired by: Katharina Heil

ELIXIR, United Kingdom

11:30 - 11:50 ELIXIR talk | Open source genome-scale metabolic models: why and how

Mihail Anton

Chalmers University of Technology, Sweden

11:50 - 12:10 ELIXIR talk | Genome-wide metabolic annotation for Methanocaldococcus (Methanococcus) jannaschii, the first member of the Archaea to be sequenced a quarter of a century ago

Ismini Baltsavia

University of Crete, Greece

12:10 - 12:30 ELIXIR talk | Rare disease specific FAIR Maturity Indicators

Núria Queralt Rosinach

Leiden University, Netherlands

11:30 - 12:30 | Session #05 | DATA

Room Margaret O. Dayhoff

Chaired by: Peter MacCallum

ELIXIR, United Kingdom

- 11:30 - 11:50 **Proceeding talk | Linking cells across single-cell modalities by synergistic matching of neighborhood structure**
Borislav Hristov
University of Washington, United States
- 11:50 - 12:10 **Highlight talk | Marker-based annotation and integration of large scale single-cell transcriptomics data on a laptop**
Sikander Hayat
Uniklinik RWTH Aachen, Germany
- 12:10 - 12:30 **Highlight talk | PolymPact: exploring functional relations among common human genetic variants**
Samuel Valentini
University of Trento, CIBIO, Italy

11:30 - 12:30 | Session #06 | PROTEINS

Room Rosalind Franklin

Chaired by: Mark Wass

University of Kent, United Kingdom

- 11:30 - 11:50 **Highlight talk | TITAN: T-cell receptor specificity prediction with bimodal attention networks**
Anna Weber
IBM Research, Switzerland
- 11:50 - 12:10 **Highlight talk | Online predictions for protein biophysical features and their conservation**
Wim Vranken
Vrije Universiteit Brussel, Belgium
- 12:10 - 12:30 **Proceeding talk | Group-walk, a rigorous approach to group-wise false discovery rate analysis by target-decoy competition**
Jack Freestone
University of Sydney, Australia

12:30 - 14:00 | Lunch, Exhibition, Birds of a Feather and Poster viewing

14:00 - 15:00 | Session #07 | SYSTEMS

Auditorium Anna Tramontano

Chaired by: Patrick Aloy

Institute for Research in Biomedicine (IRB Barcelona), Catalan Institution for Research and Advanced Studies (ICREA), INB/ELIXIR-ES, Spain

- 14:00 - 14:20 **Proceeding talk | PiSL: pairwise interaction learning-based graph neural network for synthetic lethality prediction in human cancers**
Xin Liu
ShanghaiTech University, China
- 14:20 - 14:40 **Highlight talk | Interpretable systems biomarkers predict response to immune-checkpoint inhibitors**
Federica Eduati
Eindhoven University of Technology, Netherlands
- 14:40 - 15:00 **Highlight talk | Comprehensive prediction of robust synthetic lethality between paralog pairs in cancer cell lines**
Colm Ryan
University College Dublin, Ireland

14:00 - 15:00 | Session #08 | GENES

Room Margaret O. Dayhoff
Chaired by: Artemis Hatzigeorgiou
University of Thessaly, Greece

- 14:00 - 14:20 **Proceeding talk | NSF4SL: negative-sample-free contrastive learning for ranking synthetic lethal partner genes in human cancers**
Shike Wang
ShanghaiTech University, China
- 14:20 - 14:40 **Proceeding talk | Efficient Permutation-based Genome-wide Association Studies for Normal and Skewed Phenotypic Distributions**
Maura John
TUM Campus Straubing for Biotechnology and Sustainability, Germany
- 14:40 - 15:00 **Highlight talk | Analysis of eukaryotic lincRNA sequences indicates signatures of hindered translation linked to selection pressure**
Anneke Brümmer
University of Lausanne, Switzerland

14:00 - 15:00 | Session #09 | APPLICATIONS

Room Rosalind Franklin
Chaired by: Javier De Las Rivas
Cancer Research Center (CiC-IBMCC), University of Salamanca (USAL-CSIC), INB/ELIXIR-ES Spain

- 14:00 - 14:20 **Applications talk | A cloud based resource to manage, access and explore omics datasets in multiuser environments**
Mario Looso
Max Planck Institute for Heart and Lung Research, Germany

14:20 - 14:40 Applications talk | Introducing X-Omics, the central multi-omics data integration and AI modeling platform for biomarker data at Merck

Sven-Eric Schelhorn

Merck, Germany

14:40 - 15:00 Applications talk | Global biodata resources: challenges to long-term sustainability of a crucial data infrastructure

Guy Cochrane

Global Biodata Coalition, France

15:30 - 16:30 | Session #10 | PROTEINS

Auditorium Anna Tramontano

Chaired by: Mark Wass

University of Kent, United Kingdom

15:30 - 15:50 Highlight talk | PDBe-KB: collaboratively defining the biological context of structural data

Preeti Choudhary

EMBL-EBI, United Kingdom

15:50 - 16:10 Proceeding talk | APPRIS Principal Isoforms and MANE Select Transcripts Define Reference Splice Variants

Michael Tress

Spanish National Cancer Research Centre (CNIO), Spain

16:10 - 16:30 Highlight talk | AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models

Mihaly Varadi

EMBL-EBI, United Kingdom

15:30 - 16:30 | Session #11 | GENOMES

Room Margaret O. Dayhoff

Chaired by: Toni Gabaldón

Barcelona Supercomputing Center (BSC), ICREA, INB/ELIXIR-ES, Spain

15:30 - 15:50 Proceeding talk | 3CAC: improving the classification of phages and plasmids in metagenomic assemblies using assembly graphs

Lianrong Pu

Tel Aviv University, Israel

15:50 - 16:10 Highlight talk | A global metagenomic map of urban microbiomes and antimicrobial resistance

Alina Frolova

Institute of molecular biology and genetics, Ukraine

16:10 - 16:30 **Highlight talk | Unlocking capacities of genomics for the COVID-19 response and future pandemics**
Karishma Chhugani
University of Southern California, United States

15:30 - 16:30 | **Session #12 | APPLICATIONS**

Room Rosalind Franklin
Chaired by: Javier De Las Rivas
Cancer Research Center (CiC-IBMCC), University of Salamanca (USAL-CSIC), INB/ELIXIR-ES, Spain

15:30 - 15:50 **Applications talk | Open Targets: A Platform for Biological Data Integration**

Irene Lopez Santiago
Open Targets, United Kingdom

15:50 - 16:10 **Sponsored talk by Vaticle | Building Biomedical Knowledge Graphs for In-Silico Drug Discovery**

Tomas Sabat and Wejdan Ismail

16:10 - 16:30 **Applications talk | Scalable In-memory paradigm for genomics data processing**

Ritesh Krishna

16:30 - 17:30 | **Keynote talk**

Auditorium Anna Tramontano

Personalized medicine in the era of artificial intelligence

Ana T. Freitas
Technical University of Lisbon, Portugal

Chaired by: Fátima Al-Shahrour

Spanish National Centre for Cardiovascular Research (CNIC), Spain

17:30 - 18:30 | **Monday Poster Session [from P001-M to P265-M] and Exhibition**

Poster Area Rita Levi-Montalcini

Tuesday, 20 Sept. 2022

09:00 - 10:00 | **Keynote talk**

Auditorium Anna Tramontano

Interpretable AI for cancer personalized medicine

Maria Rodríguez-Martínez

IBM Research Europe, Switzerland

Chaired by: Fátima Al-Shahrour

Spanish National Cancer Research Centre (CNIO),

INB/ELIXIR-ES, Spain

10:00 - 11:00 | **Session #13 | ELIXIR**

Auditorium Anna Tramontano

Chaired by: Katharina Heil

ELIXIR, United Kingdom

10:00 - 10:15 **ELIXIR talk | Setting the scene: Beyond COVID-19 - European preparedness for infectious disease outbreaks**

Katharina Lauer

ELIXIR, United Kingdom

10:15 - 10:30 **ELIXIR talk | Pathogen Data Sharing and Workflows at the ENA**

Colman Ocatail

EMBL-EBI, United Kingdom

10:30 - 10:45 **ELIXIR talk | Using COVID-19 data genomics and sharing to set a new future standard**

Bas Oude Munnink

Erasmus MC/VEO

10:45 - 11:00 **ELIXIR talk | Fully transparent viral genomics data analysis and sharing for everyone using public infrastructure**

Wolfgang Maier

University of Freiburg, Germany

Discussion

10:00 - 11:00 | **Session #14 | GENES (1) + PROTEINS (2)**

Room Margaret O. Dayhoff

Chaired by: Mark Wass

University of Kent, United Kingdom

10:00 - 10:20 **Proceeding talk | Genes: Improved NSGA-II algorithms for multi-objective biomarker discovery**

Luca Cattelani

University of Eastern Finland, Finland

- 10:20 - 10:40 **Proceeding talk | Proteins: DistilProtBert: A distilled protein language model used to distinguish between real proteins and their randomly shuffled counterparts**
Yaron Geffen
Bar-Ilan University, Israel
- 10:40 - 11:00 **Highlight talk | Proteins: The clinical importance of tandem exon duplication-derived substitutions**
Michael Tress
Spanish National Cancer Research Centre (CNIO), Spain

10:00 - 11:00 | Session #15 | SYSTEMS (2) + DATA (1)

Room Rosalind Franklin
Chaired by: Anaïs Baudot
Aix-Marseille University, France

- 10:00 - 10:20 **Highlight talk | Data: The AIMe registry for artificial intelligence in biomedical research**
David B. Blumenthal
Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany
- 10:20 - 10:40 **Proceeding talk | DrDimont: Explainable drug response prediction from differential analysis of multi-omics networks**
Katharina Baum
Hasso Plattner Institute, University of Potsdam, Germany
- 10:40 - 11:00 **Proceeding talk | GNN-SubNet: disease subnetwork detection with explainable Graph Neural Networks**
Bastian Pfeifer
Medical University of Graz, Austria

11:00 - 11:30 | Coffee Break and Exhibition

11:30 - 12:30 | Session #16 | ELIXIR

Auditorium Anna Tramontano
Chaired by: Katharina Heil
ELIXIR, United Kingdom

- 11:30 - 11:50 **ELIXIR talk | The ELIXIR Machine Learning Focus Group: achievements and the road ahead**
Fotis Psomopoulos
Centre for Research and Technology Hellas, Greece
- 12:10 - 12:30 **ELIXIR talk | The ELIXIR Biodiversity Community - "Biodiversity data" aims and challenges**
Toni Gabaldón
Barcelona Supercomputing Center (BSC), ICREA, INB/ELIXIR-ES, Spain
- 12:10 - 12:30 **ELIXIR talk | Federated EGA**
Jordi Rambla
Center for Genomic Regulation (CRG), INB/ELIXIR-ES, Spain

11:30 - 12:30 | Session #17 | DATA

Room Margaret O. Dayhoff

Chaired by: Josep Lluís Gelpí

*University of Barcelona, Barcelona Supercomputing Center (BSC), INB/
ELIXIR-ES, Spain*

- 11:30 - 11:50 **Proceeding talk | SimBu: Bias-aware simulation of bulk RNA-seq data with variable cell type composition**
Alexander Dietrich
Technical University of Munich, Germany
- 11:50 - 12:10 **Proceeding talk | Detecting DNA of novel fungal pathogens using ResNets and a curated fungi-hosts data collection**
Jakub Bartoszewicz
Hasso Plattner Institute, Germany
- 12:10 - 12:30 **Highlight talk | Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data**
Luis Rueda
University of Windsor, Canada

11:30 - 12:30 | Session #18 | PROTEINS

Room Rosalind Franklin

Chaired by: Mark Wass

University of Kent, United Kingdom

- 11:30 - 11:50 **Proceeding talk | Insights into performance evaluation of compound-protein interaction prediction methods**
Fayyaz Minhas
University of Warwick, United Kingdom
- 11:50 - 12:10 **Proceeding talk | Cross-Modality and Self-Supervised Protein Embedding for Compound-Protein Affinity and Contact Prediction**
Yang Shen
Texas A&M University, United States
- 12:10 - 12:30 **Highlight talk | Missense variants in human ACE2 strongly affect binding to SARS-CoV-2 Spike providing a mechanism for ACE2 mediated genetic risk in Covid-19: A case study in affinity predictions of interface variants**
Stuart Macgowan
University of Dundee, United Kingdom

12:30 - 14:00 | Lunch, Exhibition, Birds of a Feather and Poster Viewing

12:45h - 13:45h | Birds of a feather session at ECCB2022: Sex and Gender Biases in Technology and Artificial Intelligence

Room Margaret O. Dayhoff

Chaired by: R. Gonzalo Parra

Organised by Bioinfo4Women

Speakers:

Strategies towards sex and gender equality and to increase diversity
Maria Jose Rementeria

What happens if we don't make our biases conscious?

R. Gonzalo Parra

The gender dimension at the 7th European Student Council Symposium (ESCS)

Monica Cabrera

Presentation of the book "Sex and Gender Biases in Technology and Artificial Intelligence"

Davide Cirillo

14:00 - 15:00 | Session #19 | ELIXIR meets Latin America

Auditorium Anna Tramontano

Chaired by: José María Carazo

Spanish National Center for Biotechnology (CNB-CSIC), INB/ELIXIR-ES, Spain

14:00 - 14:05 Welcome and Introduction

José María Carazo

Spanish National Center for Biotechnology (CNB-CSIC), INB/ELIXIR-ES, Spain

Andrew Smith

ELIXIR, United Kingdom

14:05 - 14:20 ELIXIR Europe: overview and opportunities

Andrew Smith

ELIXIR, United Kingdom

14:20 - 14:35 Development and evolution of Bioinformatics Societies in Latin America: A2B2C (Argentina), AB3C (Brasil), BIOCANE (Costa Rica & Panama), BioNetMX (Mexico), SC2B2 (Colombia), SCB (Chile), SPB2C (Peru) and SOIBIO (Iberoamerica)

Javier De Las Rivas

Cancer Research Center (CiC-IBMCC), University of Salamanca (USAL-CSIC), INB/ELIXIR-ES, Spain

14:35 - 14:45 18 years after foundation it is time to divide and conquer

Marcelo Brandão

State University of Campinas, Brazil

14:45 - 14:55 Creating paths for the development and application of bioinformatics in Mexico

Shirley Alquicira-Hernández,

Center for Genomic Sciences

14:55 - 15:05 Bioinformatics in Argentina: The first 10+3 years of A2B2C

Nicolás Palopoli

National Scientific and Technical Research Council

14:00 - 15:00 | Session #20 | GENOMES

Room Margaret O. Dayhoff

Chaired by: Toni Gabaldón

Barcelona Supercomputing Center (BSC), ICREA, INB/ELIXIR-ES, Spain

14:00 - 14:20 Proceeding talk | Discovering Significant Evolutionary Trajectories in Cancer Phylogenies

Leonardo Pellegrina

University of Padova, Italy

14:20 - 14:40 Highlight talk | Towards a metagenomics machine learning interpretable model for understanding the transition from adenoma to colorectal cancer

Carlos S. Casimiro-Soriguer

Fundación Andaluza Progreso y Salud, Spain

14:40 - 15:00 Highlight talk | Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers

Solip Park

Spanish National Cancer Research Centre (CNIO), Spain

14:00 - 15:00 | Session #21 | Institutional talks

Room Rosalind Franklin

Chaired by: Salvador Capella-Gutierrez

Barcelona Supercomputing Center (BSC), INB/ELIXIR-ES, Spain

14:00 - 14:20 Institutional talk | The Spanish Supercomputing Network (RES): HPC and Data Resources for a scientific revolution

Alberto Antonio Gómez Martínez

Barcelona Supercomputing Center (BSC), Spain

14:20 - 14:40 Institutional talk | Ersilia, a hub of open-source AI/ML models for drug discovery and global health

Miquel Duran-Frigola

Ersilia Open Source Initiative, Spain

14:40 - 15:00 Institutional talk | The Bioinfo4Women Programme: towards gender equity and diversity in science

Alba Jené-Sanz

Barcelona Supercomputing Center (BSC), Spain

15:30 - 16:30 | Session #22 | ELIXIR meets Latin America

Auditorium Anna Tramontano

Chaired by: José María Carazo

Spanish National Center for Biotechnology (CNB-CSIC), INB/ELIXIR-ES, Spain

15:30 - 15:45 Research data management (RDM) in ELIXIR and insight into the RDM Toolkit

Frederik Coppens

ELIXIR Belgium

15:45 - 16:00 ELIXIR Training activities and opportunities for engagement

Katharina Heil

ELIXIR Communities and Training platform Coordinator

16:00 - 16:30 Open discussion

15:30 - 16:30 | Session #23 | DATA

Room Margaret O. Dayhoff

Chaired by: Josep Lluís Gelpí

*University of Barcelona, Barcelona Supercomputing Center (BSC), INB/
ELIXIR-ES, Spain*

- 15:30 - 15:50 **Proceeding talk | Exploiting pretrained biochemical language models for targeted drug design**
Gökçe Uludogan
Bogazici University, Turkey
- 15:50 - 16:10 **Highlight talk | Scaling up oligogenic diseases research with OLIDA: the Oligogenic Diseases Database**
Barbara Gravel
Interuniversity Institute of Bioinformatics in Brussels, Belgium
- 16:10 - 16:30 **Highlight talk | PharmacoDB 2.0: improving scalability and transparency of in vitro pharmacogenomics analysis**
Petr Smirnov
University of Toronto, Canada

15:30 - 16:30 | Session #24 | APPLICATIONS

Room Rosalind Franklin

Chaired by: Fátima Sánchez-Cabo

Centre for Plant Genomics and Biotechnology (CBGP, UPM-INIA), Spain

- 15:30 - 15:50 **Applications talk | Bioinformatics methods for the analysis of rare-disease patient data – applications for target discovery and obtaining phenotype associations**
Elena Rojano
University of Málaga, Spain
- 15:50 - 16:10 **Applications talk | AI microbiome-based recommendation system for improving soil health with bio-stimulants**
Beatriz Garcia-Jimenez
Biome Makers Inc., United States
- 16:10 - 16:30 **Applications talk | Whole-genome sequencing analysis of food enzyme products reveals contaminations with genetically modified microorganism of related origin**
Jolien D'Aes
Sciensano, Belgium

16:30 - 17:30 | Keynote talk

Auditorium Anna Tramontano

Text Mining for Digital Epidemiology: Overcoming the Challenges of Real World Data

Graciela Gonzalez-Hernandez

Cedars-Sinai Medical Center, United States

Chaired by: Salvador Capella-Gutierrez

Barcelona Supercomputing Center (BSC), INB/ELIXIR-ES, Spain

17:30 - 18:30 | Tuesday Poster Session [from P001-T to P265-T] and Exhibition

Poster Area Rita Levi-Montalcini

Wednesday, 21 Sept., 2022

09:00 - 10:00 | Session #25 | CLIMATE CRISIS AND HEALTH

Auditorium Anna Tramontano

Chaired by: Ana Conesa

Institute for Integrative Systems Biology (I2SysBio), Spain

09:00 - 09:30 Invited talk | Infectious disease decision-support tools to enhance resilience in climate change hotspots

Rachel Lowe

Barcelona Supercomputing Center (BSC), Catalan Institution for Research and Advanced Studies (ICREA), Spain

09:30 - 10:00 Invited talk | The Catalan Initiative for the Earth Biogenome Project

Montserrat Corominas

University of Barcelona, Spain

09:00 - 10:00 | Session #26 | DATA

Room Margaret O. Dayhoff

Chaired by: Josep Lluís Gelpí

University of Barcelona, Barcelona Supercomputing Center (BSC), INB/ELIXIR-ES, Spain

09:00 - 09:20 Highlight talk | Flimma: Federated and privacy-aware medical differential gene expression analysis

Mohammad Bakhtiari

University of Hamburg, Germany

09:20 - 09:40 Proceeding talk | This is GlycoQL

Catherine Hayes

University of Geneva, France

09:40 - 10:00 Highlight talk | Orchestrating and sharing large multimodal data for transparent and reproducible research

Petr Smirnov

University of Toronto, Canada

09:00 - 10:00 | Session #27 | APPLICATIONS

Room Rosalind Franklin

Chaired by: Anaïs Baudot

Aix-Marseille University, France

09:00 - 09:20 Applications talk | METALoci, identification of spatial enhancer hubs

Marc Marti-Renom

CNAG-CRG, Spain

09:20 - 09:40 Applications talk | Power analysis of cell-type deconvolution across human tissues

Anna Vathrakokoili Pournara

EMBL-EBI, United Kingdom

09:40 - 10:00 **Applications talk | ChiTaH: a fast and accurate tool for identifying known human chimeric sequences from high-throughput sequencing data**
Milana Frenkel-Morgenstern
Bar Ilan University, Israel

10:00 - 11:00 | **Session #28 | CLIMATE CRISIS AND HEALTH**

Auditorium Anna Tramontano

Chaired by: Ana Conesa

Institute for Integrative Systems Biology (I2SysBio), Spain

10:00 - 10:20 **Invited talk | Synergies between climate variation and environmental degradation on malaria in southern Venezuela**
Isabel Fletcher
Wellcome Trust, United Kingdom

10:20 - 10:40 **Invited talk | Real-time Genomics for One Health**
Lara Urban
Helmholtz Munich, Germany

10:40 - 11:00 **Invited talk | Climate-sensitive disease outbreaks in the aftermath of extreme climatic events**
Tilly Alcayna
London School of Hygiene and Tropical Medicine, United Kingdom

10:00 - 11:00 | **Session #29 | GENOMES**

Room Margaret O. Dayhoff

Chaired by: Toni Gabaldón

Barcelona Supercomputing Center (BSC), Spain.

10:00 - 10:20 **Proceeding talk | DeepZF: Improved DNA-binding prediction of C2H2-zinc-finger proteins by deep transfer learning**
Sofia Aizenshtain-Gazit
Ben Gurion University of the Negev, Israel

10:20 - 10:40 **Proceeding talk | CRISPRtracrRNA: Robust approach for CRISPR tracrRNA detection**
Alexander Mitrofanov
Albert-Ludwigs-Universität Freiburg, Germany

10:40 - 11:00 **Highlight talk | Revisiting genetic artifacts on DNA methylation microarrays exposes novel biological implications**
Benjamin Planterose Jiménez
Erasmus MC, University Medical Center Rotterdam, Netherlands

10:00 - 11:00 | Session #30 | APPLICATIONS

Room Rosalind Franklin

Chaired by: Anaïs Baudot

Aix-Marseille University, France

10:00 - 10:20 Applications talk | A near-full compression of SARS-CoV-2 peptidome using UNIQmin

Li Chuin Chong

Hannover Medical School/TWINCORE GmbH, Germany

10:20 - 10:40 Applications talk | Cancer patient stratification and molecular mechanism identification using patient clinotypes and transcriptomics embeddings

Jake Chen

University of Alabama at Birmingham, United States

10:40 - 11:00 Applications talk | Evaluation of Machine Learning Strategies for Imaging Confirmed Prostate Cancer Recurrence Prediction on Electronic Health Records

Jacqueline Beinecke

University Medical Center Göttingen, Germany

11:00 - 11:30 | Coffee Break and Exhibition

11:30 - 12:30 | Conference closing Keynote talk

Auditorium Anna Tramontano

The emerging small proteome

Mar Albà

Hospital del Mar Medical Research Institute (IMIM), Catalan Institution for Research and Advanced Studies (ICREA), Spain

Chaired by: Ana Conesa

Institute for Integrative Systems Biology (I2SysBio), Spain

12:30 - 13:00 | Conference closing ceremony

Auditorium Anna Tramontano

Presentation of ECCB/ISMB2023

Awards

Final remarks

13:00 - 14:00 | Lunch and Exhibition

New Trends in Bioinformatics by ECCB



eccb2022.org

New Trends in Bioinformatics by ECCB

12th – 18th September 2022
Sitges, Barcelona



New Trends in Bioinformatics by ECCB is the programme of workshops and tutorials organised within the frame of ECCB2022. The sessions will provide participants with a space to learn and discuss on technical issues, exchange research ideas, and share practical experiences on emerging topics in bioinformatics. The programme will run virtually from the 12th to the 16th of September and will host sessions in face-to-face format on the 18th of September from the venue of the ECCB2022 main conference in Sitges (Barcelona, Spain).

New Trends in Bioinformatics by ECCB – VIRTUAL

MON, 12 SEPT

Code	Time	Title
NTB-W01	13:30 – 16:30	Machine Learning good practices–DOME recommendations for better Machine Learning in Computational Biology
NTB-W02	17:00 – 20:00	FAIRification of multi-omics metadata

TUE, 13 SEPT

Code	Time	Title
NTB-W03	13:30 – 16:30	Simulating cellular behaviours: advancing HPC-enabled Computational Biology
NTB-W04	17:00 – 20:00	Spatial transcriptomics and cell-cell communication modeling: new opportunities to study the cellular dynamics of biological systems

New Trends in Bioinformatics by ECCB

WED, 14 SEPT

Code	Time	Title
NTB-W05	13:30 – 16:30	<u>Building high-quality reference genome assemblies of eukaryotes</u>
NTB-W08	17:00 – 20:00	<u>Integration of large-scale data for reference genome development in biodiversity</u>

THU, 15 SEPT

Code	Time	Title
NTB-W06	13:30 – 16:30	<u>Tools and techniques to make sensitive data discoverable (Use-cases, hands-on session of Beacon implementation)</u>
NTB-T02	17:00 – 20:00	<u>To rarefy or not to rarefy microbiome data? What are the alpha diversity metrics?</u>

FRI, 16 SEPT

Code	Time	Title
NTB-W07	13:30 – 16:30	<u>Sex and Gender Dimension in Biomedical Research</u>

New Trends in Bioinformatics by ECCB

New Trends in Bioinformatics by ECCB – Face to face in the venue

SUN, 18 SEPT

Code	Time	Title
NTB-T03	09:00 – 13:00	Deep Learning For Biological Sequence Data: From Convolutional Neural Networks To Transformers
NTB-T04	09:00 – 13:00	Functional analysis of single-cell transcriptomics data
NTB-T05	09:00 – 13:00	Guidelines for the assessment and analysis of lRNA-seq data for transcript identification and quantification (LRGASP challenge)
NTB-W09	09:00 – 13:00	Annual European Bioinformatics Core Community (AEBC2) Workshop 2022
NTB-EW01	09:00 – 13:00	FAIR applied: a practical FAIRification guide for life science data from FAIRplus This workshop session is sponsored by ELIXIR
	13:00 – 14:00	Lunch break
NTB-T01	14:00 – 18:00	Computational Challenges in Phospho-Proteomics and Systems Biology of Cellular Signaling
NTB-T06	14:00 – 18:00	Boost your Data Management Planning
NTB-W10	14:00 – 18:00	Computational modelling of immunological mechanisms: From statistical approaches to interpretable machine learning
NTB-T07	14:00 – 18:00	Software containerization in bioinformatics: how to make reproducible, portable and reusable bioinformatics software&pipelines
NTB-W11	14:00 – 18:00	Novel challenges in the quest for orthologs

Satellite Meetings



ESCS2022

7th European Student Council Symposium 2022

Sun, 18 September, 2022

[More info](#)



ELIXIR Innovation and SME Forum

Data driven innovation in healthcare diagnostics

Thu, 22 September, 2022

[More info](#)



Global Alliance for Genomics and Health (GA4GH)

10th Plenary Meeting

22-23 September, 2022

[More info](#)

Quest-for-Orthologs

Novel Challenges in the Quest for Orthologs

17-18 September, 2022

[More info](#)

Keynote speakers



CÉSAR HIDALGO

Center for Collective Learning, University of Toulouse (France)

How humans judge machines

Sunday, 18 Sept
18:30 - 19:30h

Chaired by **Alfonso Valencia**

Barcelona Supercomputing Center (BSC), Catalan Institution for Research and Advanced Studies (ICREA), INB/ELIXIR-ES, Spain

Abstract

How would you feel about losing your job to a machine? How about a tsunami alert system that fails? Would you react differently to acts of discrimination performed by a machine or a human? How about public surveillance? *How Humans Judge Machines* compares people's reactions to actions performed by humans and machines. Using data collected in dozens of experiments, this book reveals the biases that permeate human-machine interactions. Are there conditions in which we judge machines unfairly? Is our judgment of machines affected by the moral dimensions of a scenario? Is our judgment of machines correlated with demographic factors, such as education or gender?

Hidalgo and colleagues use hard science to take on these pressing technological questions. Using randomized experiments, they create revealing counterfactuals and build statistical models to explain how people judge A.I. and whether we do it fairly or not. Through original research, they bring us one step closer to understanding the ethical consequences of artificial intelligence. *How Humans Judge Machines* can be read for free at [How Humans Judge Machines](#) (in print with MIT Press).

Biography

Cesar Hidalgo directs the Center for Collective Learning at ANITI, University of Toulouse. He directed the Collective Learning group at MIT, holds a PhD in Physics from the University of Notre Dame, and is the author of dozens of papers & three books.

Keynote speakers



RAÚL RABADÁN

Departments of Systems Biology, Biomedical Informatics, and Surgery at Columbia University (USA)

Some mysteries about microbes and cancer

Monday, 19 Sept
09:00 - 10:00h

Chaired by **Niklas Blomberg**

ELIXIR, United Kingdom

Abstract

At least 20% of all tumors in the world are linked to pathogens. Viral-related tumors present very unique characteristics including unusual age, sex and geographical distributions. For instance, some of these tumors like Burkitt Lymphomas occur commonly in young kids in Africa but not in other parts of the world. Others in some populations in South America and Japan. As more genomic studies illuminate the distinct mutational spectrum of these tumors some common patterns are emerging.

Biography

Raúl Rabadán is the Gerald and Janet Carrus Professor in the Departments of Systems Biology, Biomedical Informatics and Surgery at Columbia University. He is the director of the Program for Mathematical Genomics at Columbia University and he was the Director of the NCI Center for Topology of Cancer Evolution and Heterogeneity at Columbia University (2015-2021). From 2001 to 2003, Dr. Rabadán was a fellow at the Theoretical Physics Division at CERN, the European Organization for Nuclear Research, in Geneva, Switzerland. In 2003 he joined the Physics Group of the School of Natural Sciences at the Institute for Advanced Study. Previously, Dr. Rabadán was the Martin A. and Helen Chooljian Member at The Simons Center for Systems Biology at the Institute for Advanced Study in Princeton, New Jersey. He has been named one of Popular Science's Brilliant 10 (2010), a Stewart Trust Fellow (2013), and he received the Harold and Golden Lamport Award at Columbia University (2014) and the Diz Pintado award (2018). Dr. Rabadán's current interest focuses on uncovering patterns of evolution in biological systems through the lens of genomics. His recent interests include the development of mathematical approaches to uncover the evolution of cancer and infectious diseases, including topological data analysis and Random Matrix Theory, among others.

Keynote speakers



ANA TERESA FREITAS

INESC-ID/IST Technical University of Lisbon (Portugal)

Personalized medicine in the era of artificial intelligence

Monday, 19 Sept

16:30 - 17:30h

Chaired by **Fátima Sánchez-Cabo**

Spanish National Centre for Cardiovascular Research (CNIC), Spain

Abstract

Like in many other industries, the healthcare sector routinely generates vast amounts of data from many different sources ranging from biochemical exams, electronic medical records, vital signs, patient-reported outcomes, health surveys, clinical trials, insurance claims, administrative data, and more recently omics. These days, large volumes of data associated with the new technologies of artificial intelligence are promising to create the foundations for a new paradigm of medicine focused on the individuality of each person.

In this talk I will discuss different approaches that are being tested in EU hospitals with the goal to transform healthcare from reactive disease care to care that is patient or person-centered and focused on disease prevention. A special focus will be given to the use of polygenic risk scoring models in the implementation of genetic panels that can support health professionals in disease prevention. Additionally, I will discuss how the field of pharmacogenomics is being able to make its way from research to clinical practice, which could become, in the short term, the first pillar of the democratization of preventive and personalized medicine.

Since artificial intelligence is becoming a disruptive technology in the healthcare sector, it is also crucial to address the ethical and legal challenges imposed by this new technological advance.

Biography

Ana Teresa Freitas is a Full Professor at the Department of Computer Science and Engineering at Instituto Superior Técnico, University of Lisbon, and a Senior Researcher at INESC-ID.

Keynote speakers



MARÍA RODRÍGUEZ MARTÍNEZ

IBM Research Europe

Interpretable AI for cancer personalized medicine

Tuesday, 20 Sept
09:00 - 10:00h

Chaired by **Fátima Al-Shahrour**

Spanish National Cancer Research Centre (CNIO), INB/ELIXIR-ES, Spain

Abstract

In recent years, deep learning models have resulted in outstanding breakthrough performances. However, many models behave as black boxes that can hide data biases, incorrect hypotheses or even software errors. In this talk, I will illustrate how interpretable deep learning models can achieve both high prediction accuracy and transparency.

First, I will introduce multi-modal deep learning models that predict drug response while highlighting the genetic and chemical patterns that were more informative to make a prediction. I will also discuss how reinforcement learning approaches can facilitate the early phases of drug discovery and support the personalised design of new candidate compounds.

Focusing next on T cell-based immunotherapies, I will present a model to predict the binding of T cell receptors and epitopes. This model can be coupled with an easy-to-use interpretable pipeline to extract the binding rules governing the T cell binding. These approaches are a first step towards the design and engineering of receptors of improved affinity.

Finally, I will discuss how the integration of AI and mechanistic models is necessary to tackle many current computational challenges and enable the personalized design of new therapeutic interventions.

Biography

Technical Leader of Systems Biology at IBM Research Europe (Switzerland), associated member of the Department of Biology at ETH and editor for Immunoinformatics and Frontiers in Systems Biology.

Keynote speakers



GRACIELA GONZÁLEZ HERNÁNDEZ

Vice Chair of Research and Education, Department of Computational Biomedicine at Cedars-Sinai Medical Center (USA)

Mining for Digital Epidemiology: Overcoming the Challenges of Real World Data

Tuesday, 20 Sept

16:30 - 17:30h

Chaired by **Salvador Capella-Gutierrez**

Barcelona Supercomputing Center (BSC), INB/ELIXIR-ES, Spain

Abstract

The use of Real World Data (RWD) such as social media or electronic health record data for large-scale epidemiological studies presents many challenges. From identifying the right cohort and reducing bias to finding key patterns or unique data points, RWD can be very valuable but is sometimes misused and frowned upon for “serious” studies. Systematic methods and validated approaches are necessary to turn ‘real world data’ into ‘real world evidence.’

Biography

Dr Graciela González-Hernández is Vice Chair for Research and Education in the new Department of Computational Biomedicine at Cedars-Sinai Medical Center. Cedars-Sinai is a research hospital in Beverly Hills, California ranked #1 in California and #2 in the nation by US News and World Reports in 2022. Prior to joining Cedars-Sinai in May 2022, Dr González-Hernández was an Associate Professor of Informatics in the Department of Biostatistics, Epidemiology and Informatics (DBEI) of the Perelman School of Medicine, University of Pennsylvania. She transferred her Health Language Processing (HLP) Lab to Cedars-Sinai, which focuses on natural language processing (NLP) and machine learning for knowledge discovery, extracting unstructured information from clinical records, journal articles, and social media postings to elucidate data patterns, trends, and relationships that can aid the discovery process in areas such as pharmacoepidemiology, clinical research, or public health monitoring and surveillance.

Keynote speakers



MAR ALBÀ

ICREA-IMIM, Barcelona, ICREA Research Professor

The emerging small proteome

Wednesday, 21 Sept

16:30 - 17:30h

Chaired by **Ana Conesa**

Institute for Integrative Systems Biology (I2SysBio), Spain

Abstract

Research in recent years has uncovered the existence of a large non-canonical proteome that mostly consists of proteins smaller than 100 amino acids. In humans alone, thousands of non-canonical proteins have been discovered using ribosome profiling and proteomics techniques. These proteins are translated from alternative open reading frames or from regions previously believed to be non-coding, such as long non-coding RNAs (lncRNAs) and untranslated regions (UTRs). A subset of the small proteins show strong phylogenetic conservation and are involved in fundamental cellular functions. Another large fraction is species- or lineage-specific, and represents a much more rapidly evolving part of the proteome than remains poorly characterized. Using studies in yeast, we provide evidence that these proteins are important for short evolutionary time scale adaptations.

We also show that they can provide plenty of raw material for de novo gene birth, a process by which proteins with completely new sequences emerge from previously non-coding parts of the genome.

Biography

Mar Albà is ICREA Research Professor since 2005 and leads the Evolutionary Genomics Group at Hospital del Mar Medical Research Institute (IMIM-PRBB, Barcelona). Her team is working on different projects related to comparative transcriptomics, the evolution of non-canonical small proteins and the formation of neoantigens in cancer cells. The group has pioneered research on de novo gene birth as an important mechanism of evolutionary innovation. The techniques employed in the group include short and long read RNA-Seq and ribosome profiling data. The work focuses on different biological systems, including yeast and humans. The research of the group is supported by several public and private national grants and by an ERC Advanced Grant.

Technical Secretariat



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