

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	Welcome cocktail
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	<p><b>ELIXIR talk</b>   Identifying resources and exploring synergies between the ELIXIR 3D-Bioinfo, proteomics and IDP communities • <b>Authors:</b> Emmanuel Levy, Christine Orengo, Nathalie Reuter, Sameer Velankar, Shoshana Wodak, Norman Davey, Zsuzsa Dosztanyi, Damiano Piovesan, Silvio Tosatto, Eva Csoz, Julien Marcoux, Lennart Martens, Pathmanaban Ramasamy, Juan Antonio Vizcaino, Massimiliano Bonomi, Wim Vranken</p> <p><b>ELIXIR talk</b>   Using the IDP-KG to enable IDPcentral information on submission • <b>Authors:</b> Alasdair Gray, Ivan Mičetić, Alexander Monzon and Damiano Piovesan</p> <p><b>ELIXIR talk</b>   AHOJ: rapid, tailored search and retrieval of apo and holo protein structures • <b>Authors:</b> Christos P. Feidakis, Radoslav Krivak, David Hoksza and Marian Novotný</p>	<p><b>Proceeding talk</b>   SALAI-Net: Species-Agnostic Local Ancestry Inference Network • <b>Authors:</b> Benet Oriol Sabat, Daniel Mas Montserrat, Xavier Giro-i-Nieto and Alexander Ioannidis</p> <p><b>Proceeding talk</b>   Improving Bacterial Genome Assembly Using a Test of Strand Orientation • <b>Authors:</b> Grant Greenberg and Ilan Shomrony</p> <p><b>Highlight talk</b>   plots: Visualising structural similarities and rearrangements between multiple genomes • <b>Authors:</b> Manish Goel and Korbinian Schneeberger</p>	<p><b>Proceeding talk</b>   MERRIN: METabolic Regulation Rule INference from time series data • <b>Authors:</b> Kerian Thuillier, Caroline Baroukh, Alexander Bockmayr, Ludovic Cottret, Loïc Paulevé and Anne Siegel</p> <p><b>Proceeding talk</b>   Small compound-based direct cell conversion with combinatorial optimization of pathway regulations • <b>Authors:</b> Toru Nakamura, Michio Iwata, Momoko Hamano, Ryohhei Eguchi, Jun-Ichi Takeshita and Yoshihiro Yamanishi</p> <p><b>Proceeding talk</b>   Design centering enables robustness screening of pattern formation models • <b>Authors:</b> Anastasia Solomatina, Alice Cezanne, Yannis Kalaidzidis, Marino Zerial and Ivo F. Sbalzarini</p>

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 Maccallaum	PROTEINS (Session #06) Chair: Mark Wass
11:30 - 12:30	<p><b>ELIXIR talk</b>   Open source genome-scale metabolic models: why and how • <b>Authors:</b> Mihail Anton, Barbara Szomolay and Vitor A P Martins dos Santos</p> <p><b>ELIXIR talk</b>   Genome-wide metabolic annotation for Methanocaldococcus (Methanococcus) jannaschii, the first member of the Archaea to be sequenced a quarter of a century ago • <b>Authors:</b> Ismini Baltasavia, George Stamoulos, Konstantinos Tziavara, Alexandros Dermanis, Ioannis Iliopoulos, Ron Caspi, Peter D. Karp, Nikos C. Kyrpides, Christos A. Ouzounis</p> <p><b>ELIXIR talk</b>   Rare disease specific FAIR Maturity Indicators • <b>Authors:</b> Núria Queralt Rosinach, Rajaram Kaliyaperumal, Annika Jacobsen, Mark Wilkinson, Marc Hanauer, Marco Roos</p>	<p><b>Proceeding talk</b>   Linking cells across single-cell modalities by synergistic matching of neighborhood structure • <b>Authors:</b> Borislav Hristov, Jeffrey Bilmes and William Noble</p> <p><b>Highlight talk</b>   Marker-based annotation and integration of large scale single-cell transcriptomics data on a laptop • <b>Authors:</b> Sikander Hayat, Yang Xu, Simon Baumgart, Christian Stegmann, Rafael Kramann and Rachel Patton McCord</p> <p><b>Highlight talk</b>   Polympact: exploring functional relations among common human genetic variants • <b>Authors:</b> Samuel Valentini, Francesco Gandolfi, Mattia Carolo, Davide Dalfovo, Lara Pozza and Alessandro Romanel</p>	<p><b>Highlight talk</b>   TITAN: T-cell receptor specificity prediction with bimodal attention networks • <b>Authors:</b> Anna Weber, Jannis Born and Maria Rodriguez Martínez</p> <p><b>Highlight talk</b>   Online predictions for protein biophysical features and their conservation • <b>Authors:</b> Wim Vranken, Luciano Kagami and Adrian Diaz</p> <p><b>Proceeding talk</b>   Group-walk, a rigorous approach to group-wise false discovery rate analysis by target-decoy competition • <b>Authors:</b> Jack Freestone, Temana Short, William Stafford Noble and Uri Keich</p>

12:30 - 13:00	
Lunch, Exhibition and Poster viewing	

	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

14:00 - 15:00	<p><b>Proceeding talk</b>   PILSL: pairwise interaction learning-based graph neural network for synthetic lethality prediction in human cancers  <b>Authors:</b> <a href="#">Xin Liu</a>, Jiale Yu, Siyu Tao, Beiyuan Yang, Shike Wang, Lin Wang, Fang Bai and Jie Zheng</p> <p><b>Highlight talk</b>   Interpretable systems biomarkers predict response to immune-checkpoint inhibitors  <b>Authors:</b> <a href="#">Óscar Lapuente-Santana</a>, Maisa van Genderen, Peter Hilbers, Francesca Finotello and <a href="#">Federica Eduati</a></p> <p><b>Highlight talk</b>   Comprehensive prediction of robust synthetic lethality between paralog pairs in cancer cell lines  <b>Authors:</b> <a href="#">Barbara De Kegel</a>, Niall Quinn, Nicola Thompson, David Adams and <a href="#">Colm Ryan</a></p>	<p><b>Proceeding talk</b>   NSF4SL: negative-sample-free contrastive learning for ranking synthetic lethal partner genes in human cancers  <b>Authors:</b> <a href="#">Shike Wang</a>, Yimiao Feng, Xin Liu, Yong Liu, Min Wu and Jie Zheng</p> <p><b>Proceeding talk</b>   Efficient Permutation-based Genome-wide Association Studies for Normal and Skewed Phenotypic Distributions  <b>Authors:</b> <a href="#">Maura John</a>, Markus Ankenbrand, Carolin Artmann, Jan Freudenthal, Arthur Korte and Dominik Grimm</p> <p><b>Highlight talk</b>   Analysis of eukaryotic lincRNA sequences indicates signatures of hindered translation linked to selection pressure  <b>Authors:</b> <a href="#">Anneke Bruemmer</a>, Rene Dreos, Ana Claudia Marques and Sven Bergmann</p>	<p><b>Applications talk</b>   A cloud based resource to manage, access and explore omics datasets in multiuser environments  <b>Authors:</b> <a href="#">Mario Looso</a>, Philipp Goymann, Franz Ziegengest, Carsten Kuenne, Daniel Spothelfer, Noah Knoppik and Jasmin Walter</p> <p><b>Applications talk</b>   Introducing X-Omics, the central multi-omics data integration and AI modeling platform for biomarker data at Merck  <b>Author:</b> <a href="#">Sven-Eric Schelhorn</a></p> <p><b>Applications talk</b>   Global biodata resources: challenges to long-term sustainability of a crucial data infrastructure  <b>Authors:</b> <a href="#">Guy Cochrane</a> and Chuck Cook</p>
15:00 - 15:30	<b>Coffee break and Exhibition</b>		
15:30 - 16:30	<b>Auditorium Anna Tramontano</b>	<b>Room Margaret O. Dayhoff</b>	<b>Room Rosalind Franklin</b>
	<b>PROTEINS</b> (Session #10) Chair: <a href="#">Mark Wass</a>	<b>GENOMES</b> (Session #11) Chair: <a href="#">Toni Gabaldón</a>	<b>APPLICATIONS</b> (Session #12) Chair: <a href="#">Javier De Las Rivas</a>
	<p><b>Highlight talk</b>   PDBe-KB: collaboratively defining the biological context of structural data  <b>Author:</b> <a href="#">Preeti Choudhary</a></p> <p><b>Proceeding talk</b>   APPRIS Principal Isoforms and MANE Select Transcripts Define Reference Splice Variants  <b>Authors:</b> <a href="#">Fernando Pozo Ocampo</a>, <a href="#">Laura Martínez Gomez</a>, <a href="#">Jose Manuel Rodriguez</a>, <a href="#">Jesús Vázquez</a> and <a href="#">Michael Tress</a></p> <p><b>Highlight talk</b>   AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models  <b>Authors:</b> <a href="#">Mihaly Varadi</a>, Sameer Velankar, Stephen Anyango, Mandar Deshpande, Sreenath Nair, Cindy Natassia, Galabina Yordanova, David Yuan, Oana Stroe, Gemma Wood, Agata Laydon, Augustin Zidek, Tim Green, Kathryn Tunyasuvunakool, Stig Petersen, John Jumper, Ellen Clancy, Richard Green, Ankur Vora, Mira Lutfi, Michael Figurnov, Andrew Cowie, Nicole Hobbs, Pushmeet Kohli, Gerard Kleywegt, Ewan Birney and Demis Hassabis</p>	<p><b>Proceeding talk</b>   3CAC: improving the classification of phages and plasmids in metagenomic assemblies using assembly graphs  <b>Authors:</b> <a href="#">Lianrong Pu</a> and Ron Shamir</p> <p><b>Highlight talk</b>   A global metagenomic map of urban microbiomes and antimicrobial resistance  <b>Authors:</b> <a href="#">Alina Frolova</a>, David Danko, Daniela Bezdán, Christopher E. Mason and The International Consortium Metasub</p> <p><b>Highlight talk</b>   Unlocking capacities of genomics for the COVID-19 response and future pandemics  <b>Authors:</b> <a href="#">Sergei Mangul</a>, <a href="#">Karishma Chhugani</a>, <a href="#">Sergey Knyazev</a>, <a href="#">Varuni Sarwal</a>, <a href="#">Ram Ayyala</a>, <a href="#">Angela Lu</a> and <a href="#">Adam Smith</a></p>	<p><b>Applications talk</b>   Open Targets: A Platform for Biological Data Integration  <b>Author:</b> <a href="#">Irene Lopez Santiago</a></p> <p><b>Sponsored talk by Vaticle</b>   Building Biomedical Knowledge Graphs for In-Silico Drug Discovery  <b>Authors:</b> <a href="#">Tomás Sabat</a></p> <p><b>Applications talk</b>   Scalable In-memory paradigm for genomics data processing  <b>Authors:</b> <a href="#">Ritesh Krishna</a>, <a href="#">Vadim Elisseev</a> and <a href="#">Laura-Jayne Gardiner</a></p>
16:30 - 17:00	<b>Keynote talk</b>		
17:00 - 17:30	<p><b>Ana T. Freitas (INESC-ID/IST Technical University of Lisbon, Portugal)</b>  Personalized medicine in the era of artificial intelligence</p> <p>Chair: <a href="#">Fátima Sánchez-Cabo</a></p>		
17:30 - 18:00	<b>Monday Poster session and Exhibition</b>		
18:00 - 18:30			
18:30 - 19:00			
19:00 - 19:30			

<b>TUESDAY, 20 September</b>			
08:00 - 08:30	<b>Registration desk open all day</b>		
08:30 - 09:00	<b>Welcome and announcements (08:45h)</b>		
09:00 - 09:30	<b>Keynote talk</b>		
09:30 - 10:00	<p><b>Maria Rodriguez-Martínez (IBM Research Europe, Switzerland)</b>  Interpretable deep learning for cancer personalized medicine</p> <p>Chair: <a href="#">Fátima Al-Shahrour</a></p>		
10:00 - 11:00	<b>Auditorium Anna Tramontano</b>	<b>Room Margaret O. Dayhoff</b>	<b>Room Rosalind Franklin</b>
	<b>ELIXIR</b> (Session #13) Chair: <a href="#">Katharina Heil</a>	<b>PROTEINS (2) + GENES (1)</b> (Session #14) Chair: <a href="#">Mark Wass</a>	<b>SYSTEMS (2) + DATA (1)</b> (Session #15) Chair: <a href="#">Anaïs Baudot</a>
	<p><b>From integrated COVID-19 data to integrated pathogen data analysis</b></p> <p><b>Title:</b> Setting the scene: Beyond COVID-19 - European preparedness for infectious disease outbreaks  <b>Speaker:</b> <a href="#">Katharina Lauer</a> (ELIXIR)</p> <p><b>Title:</b> Pathogen Data Sharing and Workflows at the ENA  <b>Speaker:</b> <a href="#">Colman O'Cathail</a> (EBI/COVID19 Data Portal)</p> <p><b>Title:</b> Using COVID-19 data genomics and sharing to set a new future standard  <b>Speaker:</b> <a href="#">Bas Oude Munnink</a> (Erasmus MC/VEO)</p> <p><b>Title:</b> Fully transparent viral genomics data analysis and sharing for everyone using public infrastructure</p>	<p><b>Proceeding talk</b>   <b>Genes:</b> Improved NSGA-II algorithms for multi-objective biomarker discovery  <b>Authors:</b> <a href="#">Luca Cattelan</a> and <a href="#">Vittorio Fortino</a></p> <p><b>Proceeding talk</b>   <b>Proteins:</b> DistilProtBert: A distilled protein language model used to distinguish between real proteins and their randomly shuffled counterparts  <b>Authors:</b> <a href="#">Yaron Geffen</a>, <a href="#">Yanay Ofra</a> and <a href="#">Ron Unger</a></p>	<p><b>Highlight talk</b>   <b>Data:</b> The AIMe registry for artificial intelligence in biomedical research  <b>Authors:</b> <a href="#">Julian Matschinske</a>, <a href="#">Nicolas Alcaraz</a>, <a href="#">Arriel Benis</a>, <a href="#">Gerda Cristal Villalba Silva</a>, <a href="#">Martin Golebiewski</a>, <a href="#">Dominik G. Grimm</a>, <a href="#">Lukas Heumos</a>, <a href="#">Tim Kacprowski</a>, <a href="#">Olga Lazareva</a>, <a href="#">Markus List</a>, <a href="#">Zakaria Louadi</a>, <a href="#">Josch Pauling</a>, <a href="#">Nico Pfeifer</a>, <a href="#">Richard Röttger</a>, <a href="#">Veit Schwämmle</a>, <a href="#">Kristel Van Steen</a>, <a href="#">Gregor Sturm</a>, <a href="#">Alberto Traverso</a>, <a href="#">Martíela Vaz de Freitas</a>, <a href="#">Leonard Wee</a>, <a href="#">Nina Wenke</a>, <a href="#">Massimiliano Zanin</a>, <a href="#">Olga Zolotareva</a>, <a href="#">Jan Baumbach</a> and <a href="#">David B. Blumenthal</a></p> <p><b>Proceeding talk</b>   <b>Systems:</b> DrDimont: Explainable drug response prediction from differential analysis of multi-omics networks  <b>Authors:</b> <a href="#">Pauline Hiort</a>, <a href="#">Julian Hugo</a>, <a href="#">Justus Zeinert</a>, <a href="#">Nataníel Müller</a>, <a href="#">Spoorthi Kashyap</a>, <a href="#">Jagath C. Rajapakse</a>, <a href="#">Francisco Azuaje</a>, <a href="#">Bernhard Y. Renard</a> and <a href="#">Katharina Baum</a></p>

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

	> Open discussion	<b>Highlight talk</b>   PharmacDB 2.0: improving scalability and transparency of in vitro pharmacogenomics analysis <b>• Authors:</b> Nikta Feizi, Sisira Kadambat Nair, <a href="#">Petr Smirnov</a> , Gangesh Beri, Christopher Eeles, Parinaz Nasr Esfahani, Minoru Nakano, Denis Tkachuk, Anthony Mammoliti, Evgeniya Goroberts, Arvind Singh Mer, Eva Lin, Yihong Yu, Scott Martin, Marc Hafner and Benjamin Haibe-Kains	<b>Applications talk</b>   Whole-genome sequencing analysis of food enzyme products reveals contaminations with genetically modified microorganism of related origin <b>• Authors:</b> <a href="#">Jolien D'Aes</a> , 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	<b>Graciela Gonzalez-Hernandez (Cedars-Sinai Medical Center (USA))</b> Mining for Digital Epidemiology: Overcoming the Challenges of Real World Data Chair: <a href="#">Salvador Capella-Gutierrez</a>		
17:30 - 18:00	Tuesday Poster session and Exhibition		
18:00 - 18:30			
18:30 - 19:00			
19:00 - 19:30			
19:30 - 20:00			
20:00 - 20:30	Conference dinner		
20:30 - 21:00			
21:00 - 21:30			
21:30 - 22:00			
22:00 - 22:30			
22:30 - 23:00			
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
	<b>CLIMATE CRISIS AND HEALTH</b> (Session #25) Chair: <a href="#">Ana Conesa</a>	<b>DATA</b> (Session #26) Chair: <a href="#">Josep Lluis Gelpí</a>	<b>APPLICATIONS</b> (Session #27) Chair: <a href="#">Anaïs Baudot</a>
09:00 - 10:00	<b>Invited talk</b>   Infectious disease decision-support tools to enhance resilience in climate change hotspots <b>• Speaker:</b> Rachel Lowe  <b>Invited talk</b>   The Catalan Initiative for the Earth Biogenome Project <b>• Speaker:</b> Montserrat Corominas	<b>Highlight talk</b>   Flimma: Federated and privacy-aware medical differential gene expression analysis <b>• Authors:</b> Olga Zolotareva, Reza Nasirigerdeh, Julian Matschinske, Reihaneh Torzadehmahani, <a href="#">Mohammad Bakhtiari</a> , Tobias Frisch, Julian Alexander Späth, David B. Blumenthal, Amir Abbasinejad, Paolo Tieri, Georgios Kaissis, Daniel Rückert, Nina Wenke, Markus List and Jan Baumbach  <b>Proceeding talk</b>   This is GlycoQL <b>• Authors:</b> <a href="#">Catherine Hayes</a> , Vincenzo Daponte, Julien Mariethoz and Frederique Lisacek  <b>Highlight talk</b>   Orchestrating and sharing large multimodal data for transparent and reproducible research <b>• Authors:</b> Anthony Mammoliti, <a href="#">Petr Smirnov</a> , 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	<b>Applications talk</b>   METALoci, identification of spatial enhancer hubs <b>• Authors:</b> <a href="#">Marc A. Marti-Renom</a> , Irene Mota Gomez-Argente, Juan Antonio Rodriguez Perez and Dario Lupiañez  <b>Applications talk</b>   Power analysis of cell-type deconvolution across human tissues <b>• Author:</b> <a href="#">Anna Vathrakokouli Pournara</a> , Zhichao Miao and Irene Papatheodorou  <b>Applications talk</b>   ChiTAH: a fast and accurate tool for identifying known human chimeric sequences from high-throughput sequencing data <b>• Authors:</b> <a href="#">Milana Frenkel-Morgenstern</a> , Rajesh Detroja and Sumit Mukherjee
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	<b>CLIMATE CRISIS AND HEALTH</b> (Session #28) Chair: <a href="#">Ana Conesa</a>	<b>GENOMES</b> (Session #29) Chair: <a href="#">Toni Gabaldón</a>	<b>APPLICATIONS</b> (Session #30) Chair: <a href="#">Anaïs Baudot</a>
10:00 - 11:00	<b>Invited talk</b>   Synergies between climate variation and environmental degradation on malaria in southern Venezuela <b>• Speaker:</b> Isabel Fletcher  <b>Invited talk</b>   Real-time Genomics for One Health <b>• Speaker:</b> Lara Urban  <b>Invited talk</b>   Climate-sensitive disease outbreaks in the aftermath of extreme climatic events <b>• Speaker:</b> Tilly Alcayna	<b>Proceeding talk</b>   DeepZF: Improved DNA-binding prediction of C2H2-zinc-finger proteins by deep transfer learning <b>• Authors:</b> <a href="#">Sofia Aizenshtein-Gazit</a> and Yaron Orenstein  <b>Proceeding talk</b>   CRISPRtracrRNA: Robust approach for CRISPR tracrRNA detection <b>• Authors:</b> <a href="#">Alexander Mitrofanov</a> , Marcus Ziemann, Omer Alkhnbashi, Wolfgang Hess and Rolf Backofen  <b>Highlight talk</b>   Revisiting genetic artifacts on DNA methylation microarrays exposes novel biological implications <b>• Authors:</b> <a href="#">Benjamin Planterose Jiménez</a> , Manfred Kayser and Athina Vidaki	<b>Applications talk</b>   A near-full compression of SARS-CoV-2 peptidome using UNIQmin <b>• Authors:</b> <a href="#">Li Chuin Chong</a> and Asif M. Khan  <b>Applications talk</b>   Cancer patient stratification and molecular mechanism identification using patient clintypes and transcriptomics embeddings <b>• Author:</b> Zongliang Yue, Samuel Bharti, Eric Gong, Radomir Slominski, Thanh Nguyen, Lara Lanov, Christopher Willey and <a href="#">Jake Chen</a>  <b>Applications talk</b>   Evaluation of machine learning strategies for imaging confirmed prostate cancer recurrence prediction on electronic health records <b>• Authors:</b> <a href="#">Jacqueline Beinecke</a> , 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 <b>Mar Albà (ICREA-IMIM, Spain)</b>		

12:00 - 12:30	The emerging small proteome Chair: <a href="#">Ana Conesa</a>
12:30 - 13:00	Conference closing ceremony Presentation of ECCB/ISMB2023 Awards Final remarks
13:00 - 13:30	<b>Lunch and Exhibition</b>
13:30 - 14:00	