Thursday, 28th November 2019

8:00 - 9:00	REGISTRATION
9:00 - 9:25	 WELCOME - Chair: Rosa M. Badia Janet Kelso, Group leader, Max Planck Institute for Evolutionary Anthropology Alison Kennedy, Director, STFC Hartree Centre Núria López Bigas, ICREA Research Professor and Group leader, Institute for Research in Biomedicine Barcelona Carla Conejo, Scientific Projects Leader, Area of Knowledge, Education and Research at Fundació Catalunya La Pedrera Ångels Chacón, Minister of Business and Knowledge, Government of Catalonia
9:25 - 10:10	KEYNOTE TALK - Chair: Janet Kelso Christine Orengo (UCL). CATH Functional families - insights into impacts of genetic variations.
10:10 - 11:10	Plenary session 1 - Chair Janet Kelso - Compute02: An RPCA (Robust Principal Component Analysis) based approach for protein-protein interaction hot-spot prediction, Divya Sitani - BioMed03: Predicting synthetic lethal interactions using conserved patterns in protein interaction networks, Frances Pearl - BioSeq01: Characterization of Selenoprotein Gene Expression across Tissues and Individuals, Aida Ripoll-Cladellas
11:10 - 11:40	Coffee break
11:40 - 13.00	 Plenary session 2 - Chair: Alison Kennedy BioSeq06: Go low with ATLAS: a tool for maximizing insight from minimal sequencing depth, Vivian Link BioSeq02: Tools for transforming multiomics data into disease models, Ana Conesa BioSeq05: Genomic based drug repurposing screen for Rett syndrome, Irene Unterman Compute05: DLMF: Deep Logistic Matrix Factorization with multiple information integration for drug-target interaction prediction, Sarra Itidal Abbou
13:00 - 14:00	Lunch + Poster session I
14:00 - 14:45	KEYNOTE TALK - Chair: Alison Kennedy Marie-Christine Sawley (Intel). Data centric large scale computing, a powerful scientific instrument for life and science.
14:45 - 16:05	 Plenary sessions 3 - Chair: Rosa M. Badia BioSeq03: Widespread sexual dimorphism in genetic architecture in UK Biobank, Elena Bernabeu BioSeq04: Fine-mapping UK Biobank traits GWAS using bayesian algorithms and chromatin annotation data, Erola Pairo-Castineira Compute03: Automated extraction of color pattern and anatomical characteristics in dairy cows, Jessica Nye Compute04: The human heart seen by the eyes of a computer scientist, Marta Garcia-Gasulla
	Group Picture
16:10 - 17:10	Coffee Break + Meeting with Women Leaders (prior confirmed registration) + Poster session I



Advances in Computational Biology Fostering collaboration among women scientists

17:10 - 18:50	 Plenary session 4 - Chair: Núria López-Bigas BioMed05: Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics, Renée Beekman BioMed01: OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers, Claudia Arnedo-Pac BioMed02: Detecting aberrant integrations of viral DNA that promote major restructuring of cancer genome architecture, Eva G Alvarez Compute01: Discriminating Early- and Late-Stage Cancers Using Multiple Kernel Learning on Gene Sets, Arezou Rahimi BioMed04: Mechanistic approach for optimal model selection in cancer research, Inmaculada Álamo-Álvarez
18:50 - 19:20	Theatre Performance
20:30	Networking Conference Dinner (prior registration, 7 Portes Restaurant)

Friday, 29th November 2019

9:00 - 9:45	KEYNOTE TALK - Chair: Núria López-Bigas Natasa Przulj (BSC, ICREA). Towards Data-Integrated Medicine.
9:45 - 10:45	Plenary session 5 - Chair: Mar Albà - BioSeq26: Dynamic hyper editing underlines temperature adaptation in Drosophila, Ilana Buchumenski - BioSeq29: Benchmarking coevolution methods, Rocío Rama Ballesteros - BioMed21: Computational challenges associated to plasmid mediated AMR spread, Alice Ledda
10:45 - 11:15	Coffee Break
11:15 - 12:35	 Plenary session 6 - Chair: Marta Melé BioMed22: Cell-intrinsic core-regulatory circuits driving tumor-related phenotypes with the I3-OncoNet cycle, Julia Puig BioSeq28: Single-cell transcriptomics analysis reveals the dynamics of alternative polyadenylation during cell cycle progression, Mireya Plass Compute15: An atomistic molecular dynamics simulations approach to the study of h-LDHA inhibition, Antonia Vyrkou BioSeq27: Comparative epigenomics determines the enhancer sequence code of pluripotent embryonic stem cells and facilitates the creation of synthetic enhancers, Jennifer Mitchell
12:35 - 14:45	Lunch + Poster session II
14:45 - 15:45	Panel discussion: Challenges of Artificial Intelligence in Biomedical Research (ACM-WE & RSG-Spain)
15:45 - 16:10	Closing remarks and Best Poster and Oral presentation awards - Chairs: Janet Kelso, Alison Kennedy and Núria López-Bigas
16:10 - 17:00	Guided visit to La Pedrera (prior registration)
16:10 - 17:30	Networking activity (RSG-Spain)

