

# BBCC2021

Bioinformatics and Computational Biology Conference

December 1-3, 2021

Virtual Conference  
Program  
*(Central Europe Time)*

## Day 1<sup>st</sup> - December 1<sup>st</sup>

15:00-15:10	<i>Time for Connection to the Virtual Conference Room and Registration</i>
15:10-15:30	<b>Conference Opening</b> Angelo Facchiano and Margherita Mutarelli – Chairs of BBCC2021
15:30-16:15	<i>Invited Lecture</i>
	<b>Vera Pancaldi</b> <i>INSERM, Centre de Recherches en Cancérologie de Toulouse, France</i> <b>Network approaches to explore the epigenomic bases of heterogeneity and plasticity in immune cells</b>
	<b>Session – Transcriptomics</b> <i>Chair: Mario Rosario Guarracino</i>
16:15-16:30	<u>Douglas Meyer</u> , Jacob Kames, Haim Bar, Anton Komar, Aikaterini Alexaki, Juan Ibla, Ryan Hunt, Luis Santana-Quintero, Anton Golikov, Michael DiCuccio and Chava Kimchi-Sarfaty <b>Changes in synonymous codon preferences in tumorigenesis are tumor-type specific and predictive of patient survival</b>
16:30-16:45	<u>Chiara Lauritano</u> <b>Transcriptomic approach to study marine microalgae as source of bioactive secondary metabolites</b>
16:45-17:00	<u>Mattia Furlan</u> , Stefano de Pretis and Mattia Pelizzola <b>Inference of transcriptional and post-transcriptional dynamics from sequencing experiments</b>
17:00-17:45	<i>Invited lecture</i>
	<b>Alice Eunjung Lee</b> <i>Division of Genetics and Genomics at Boston Children's Hospital and Harvard Medical School, Boston, MA, USA</i> <b>Transposon genomics: progress and challenges</b>
17:45-18:00	<b>Poster Session Group A</b>

## Day 2<sup>nd</sup> – December 2<sup>nd</sup>

	<p><b>Session – Metagenomics and microbiome</b> <i>Chair: Claudia Angelini</i></p>
9:30-9:45	<p>Marco Cappellato, <u>Francesca Longhin</u>, Claudia Del Vecchio, Giuseppina Brancaccio, Massimo Bellato, Anna Maria Cattelan, Paola Brun, Claudio Salaris, Ignazio Castagliuolo and Barbara Di Camillo</p> <p><b>Uncover a microbiota signature of upper respiratory tract in patients with SARS-CoV-2+</b></p>
9:45-10:00	<p><u>Yunxiao Ren</u> and Dominik Heider</p> <p><b>Prediction of antimicrobial resistance based on whole-genome sequencing and machine learning</b></p>
10:00-10:15	<p><u>Marco Cappellato</u>, Giacomo Baruzzo and Barbara Di Camillo</p> <p><b>Comprehensive assessment of microbiome differential abundance tools</b></p>
	<p><b>Session – Computational methods, omics and multiomics</b> <i>Chair: Annamaria Carissimo</i></p>
10:15-10:30	<p><u>Pietro Hiram Guzzi</u>, Giuseppe Tradigo and Pierangelo Veltri</p> <p><b>A Novel Local Alignment Algorithm based on Network Embedding</b></p>
10:30-10:45	<p><u>Valeria Policastro</u>, Dario Righelli, Annamaria Carissimo, Luisa Cutillo and Italia De Feis</p> <p><b>ROBustness In Network (robin) for Single Cell clustering</b></p>
10:45-11:00	<p><u>Giacomo Baruzzo</u>, Giulia Cesaro and Barbara Di Camillo</p> <p><b>Analyze cellular communication from single cell RNA sequencing data with scSeqComm</b></p>
11:00-11:15	Break
	<p><b>Session – Computational methods, omics and multiomics <i>continued</i></b> <i>Chair: Michele Pinelli</i></p>
11:15-11:30	<p><u>Eugenio Del Prete</u>, Ana Margarida Campos, Fabio Della Rocca, Genoveffa Nuzzo and Claudia Angelini</p> <p><b>A workflow for the analysis of lipidomic data</b></p>
11:30-11:45	<p><u>Giulia De Riso</u>, Daniele Vitale, Piero Pignataro, Simona Blanco, Gerarda Cappuccio, Andrea Chiariello, Lucio Nitsch, Mario Nicodemi, Rita Genesisio, Nicola Brunetti-Pierri and Michele Pinelli</p> <p><b>Systematic analysis of CNV positional effect implicates enhancer mediated SHH dysregulation in a patient with multiple congenital malformations</b></p>
11:45-12:00	<p><u>Giulio Spinozzi</u>, Valentina Tini, Alessio Ferrari, Ilaria Gionfriddo, Francesca Milano, Federica Mezzasoma, Brunangelo Falini and Maria Paola Martelli</p> <p><b>SiCoDEA: a simple, fast and complete app for analyzing the effect of individual drugs and their combinations</b></p>
12:00-12:45	<i>Invited lecture</i>
	<p><b>Mario Nicodemi</b> <i>Physics Department, University of Naples “Federico II”, Naples, Italy</i></p> <p><b>Chromatin 3D architecture: mechanisms and function</b></p>
12:45-13:00	<b>Poster Session Group B</b>
13:00-14:00	Lunch break

14:00-14:15	<b>Poster Session Group C</b>
	<i>Invited lecture</i>
14:15-15:00	<b>Tiina Salminen</b> <i>Abo Akademi University, Turku, Finland</i> <b>Siglec-9 - A gold mine of targeted therapies and diagnostics for inflammation and cancer</b>
	<b>Session: Molecular simulations (1)</b> <i>Chair: Anna Marabotti</i>
15:00-15:15	<u>Domenico Loreto</u> , Giarita Ferraro and Antonello Merlino <b>Protein metalation by Au-, Pt- and Ru-based complexes: a systematic analysis of metal/protein adducts in the Protein Data Bank</b>
15:15-15:30	<u>Tommaso Palomba</u> , Carmine Vacca, Jenny Desantis, Massimo Baroni, Matteo Bartalucci, Gabriele Cruciani and Lydia Siragusa <b>From E3 ligase Platform to scaffold-repurposing opportunities: the TRIM24-TRIM33 case study</b>
15:30-15:45	<u>Sohayb Bekkal Brikci</u> , Abdelli Imane, Faïçal Hassani, Amina Belhadji and Mimouna Mostari <b>In silico study the control of Citrus nematode Tylenchulus semipenetrans by natural components</b>
15:45-16:00	Break
16:00-16:15	<u>Magnus Kinder</u> and Christof Seiler <b>ascc: Conformalized Classifiers for Efficient Cell-Type Predictions</b>
16:30-16:45	<u>Sugunakar Vuree</u> <b>Phytochemicals: Remerging Tools as Epigenetic Therapeutics for Cervical Cancer Prevention</b>
16:45-17:00	Alexandr Svidlov, Mikhail Drobotenko, Anna Elkina and <u>Stepan Dzhimak</u> . <b>Numerical simulation of DNA dynamics under periodic force effects</b>
17:00-17:45	<i>Invited lecture</i>
	<b>Francesco Iorio</b> <i>Wellcome Sanger Institute, Hixton, UK, and Human Technopole, Milan, Italy</i> <b>Genome-editing screens and (big) data integration for Cancer Pharmacogenomics and therapeutic target discovery</b>
17:45-18:00	<b>Poster Session Group D</b>

<b>Day 3 – December 3rd</b>	
	<b>Session – System Biology and System Medicine</b> <i>Chair: Dominik Heider</i>
9:30-9:45	Maurizio Giordano, Lucia Maddalena, <u>Mario Manzo</u> and Mario Rosario Guarracino <b>Adversarial attacks on graph embedding: applications in computational biology and bioinformatics</b>
9:45-10:00	<u>Massimo Bellato</u> , Hsih-Ho Huang, Yili Qian, Pablo Cardenas, Lorenzo Pasotti, Paolo Magni and Domitilla Del Vecchio <b>Engineering of a dCas9 feedback regulator to neutralize competition effects in CRISPRi-based genetic circuits</b>
10:00-10:45	<i>Invited lecture</i>
	<b>Richard Röttger</b> <i>University of Southern Denmark (SDU), Odense, Denmark</i> <b>Towards systems medical analysis of complex biomedical data</b>
10:45-11:00	Break
	<b>Session: Molecular simulations (2)</b> <i>Chair: Angelo Facchiano</i>
11:00-11:15	<u>Sandhya Karakkadparambil Sankaran</u> and Achuthsankar S Nair <b>Active phytochemical compounds for inhibiting SARSCOV2 Mprotease: Molecular docking and Molecular dynamics study</b>
11:15-11:30	<u>Valerio Marino</u> , Alberto Borsatto, Gianfranco Abrusci, Gianluca Lattanzi and Daniele Dell'Orco <b>The structural and allosteric properties of Recoverin are influenced by membrane and its biological target</b>
11:30-11:45	<u>Stefano Motta</u> , Lara Callea, Laura Bonati and Alessandro Pandini <b>A Neural Network Approach for the Identification of Pathways in Molecular Dynamics Simulations of Ligand Binding</b>
11:45-12:00	Bernardina Scafuri, <u>Nancy D'Arminio</u> , Sara Alfieri, Mauro Petrillo, Maddalena Querci, Guy Van den Eede, Angelo Facchiano and Anna Marabotti <b>Mutations in the SARS-CoV-2 Spike protein and antibody interactions</b>
12:00-12:15	Olivier Sheik Amamuddy and <u>Ozlem Tastan Bishop</u> <b>Dynamic Residue Networks to Identify Allosteric Paths in (Homodimeric) Proteins with Mutations and Ligands</b>
12:15-13:00	<i>Invited lecture</i>
	<b>Franca Fraternali</b> <i>King's College London, UK</i> <b>Mutations and Variations in Health and Disease: Protein Interaction Networks and 3D Structure Information</b>
13:00-13:10	<b>Angelo Facchiano and Margherita Mutarelli – Chairs of BBCC2021</b> <i>Meeting announcements and closing remarks</i>