

BITS2016 and associated activities: Program

June 14, 2016

9.00-9.30	Registration (for participants to satellite workshop)
9.30-18.00	Satellite Workshop: "Uses and Applications of Crystallographic Data in Structural Chemistry and Drug Discovery"

June 15, 2016

9.00-9.30	Registration (for participants to tutorials and ELIXIR Workshop)
9.30-13.00	BITS Tutorials and Satellite ELIXIR Workshop

13.00-14.30	Registration and poster hang-up
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13.00-14.00	Light lunch (in the Aula Magna Building)
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BITS2016 Meeting Opening

14.30-15.00	Opening remarks
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Session 1: Genomics and Transcriptomics (Chairs: Manuela Helmer-Citterich and Paolo Romano)

15.00 – 15.45	<u>Preparata Lecture – Invited Speaker:</u> <i>Janusz M. Bujnicki</i> Computational modeling and design of RNA 3D structure and protein-RNA complexes
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15.45-16.00	<i>Chawla M, Oliva R, Bujnicki JM, Cavallo L</i> Impact of modified nucleobases on base pairing in RNA experimental structures
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16.00-16.15	<i>Dal Molin A, Lorenzi P, Romanelli MG, Malerba G</i> Searching for sequence motifs that affect splicing of exons regulated by RBM20
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16.15-16.30	<i>Ambrosino L, Bostan H, Ruggieri V, Chiusano ML</i> An integrated multi-level comparison highlights common aspects and specific features between distantly-related species Tomato and Grapevine
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16.30-17.00	Coffee break and poster hang-up
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17.00-17.15	Assemblea Straordinaria BITS
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17.15-20.00	Assemblea Ordinaria BITS
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June 16, 2016

Session 2: Special Session: Big Data Management, Modeling and Computing (Chairs: Marco Masseroli and Giancarlo Mauri)

9.00-9.30	<u>Highlight lecture</u> <i>Stefano Ceri</i> Data-Driven Genomic Computing: Making Sense of the Signals from the Genome
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9.30-9.45	<i>Prezza N, Policriti A</i> Algorithms and data structures for the compression and indexing of genomic big data
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9.45-10.00	<i>Cumbo F, Fiscon G, Ceri S, Masseroli M, Weitschek E</i> TCGA2BED: converting and querying The Cancer Genome Atlas
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10.00-10.15	<i>Montanari P, Ceol A, Bartolini I, Ciaccia P, Patella M, Ceri S, Masseroli M</i> Discovering similar (epi)genomics feature patterns in multiple genome browser tracks
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10.15-10.30	<i>Bosotti R, Melloni GM, Ukmar G, D'aiuto F, Vescovi M, Rossi P, Pirchio MR, Callari M, Leone A, Somaschini A, Cesarini M, Radrizzani L, Della Vedova G, Dugo M, Canevari S, Zambon A, Corrao G, Nepa G, Daidone MG, Pettenella M, Isacchi A</i>
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10.30-10.45	<i>PATRI: an integrated platform for genomics data analysis</i> <i>Cordero F, Beccuti M, Genuardi E, Romano G, Calogero RA, Ladetto M, Ferrero S</i>
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Hash Clone: a new tool to quantify the minimal residual disease during patient follow-up

10.45-11.30 **Coffee break and Poster Session**

Session 3: Next-Generation Sequencing (Chairs: Luciano Milanese and Alessandro Weisz)

11.30-12.15	<u>Invited Speaker:</u> <i>Susanna-Assunta Sansone</i> On community-standards, data curation and scholarly communication
12.15-12.30	<i>Picardi E, D'Erchia AM, Pesole G</i> Single Cell RNAseq reveals RNA editing heterogeneity in human brain
12.30-12.45	<i>Geraci F, Manzini G, Genovese LM, D'Aurizio R, Pellegrini M</i> A tool for genotyping variable length tandem repeats in high throughput sequencing data
12.45-13.00	<i>Granata I, Sangiovanni M, Guarracino MR</i> Var2GO: a web-based tool for gene variants annotation and selection
13.00-13.15	<i>Via A</i> Elixir Workshop results: Ten simple rules to make your teaching (more) effective

13.15-14.30 **Lunch (in the poster room)**

Session 4: Protein Structure and Function (Chairs: Francesca Cordero and Anna Marabotti)

14.30-15.15	<u>Invited Speaker:</u> <i>Alexandre Bonvin</i> Structure, affinity and specificity riddles in biomolecular interactions
15.15-15.30	<i>Scafuri B, Marabotti A, Carbone V, Minasi P, Dotolo S, Facchiano A</i> Computational screening and bioinformatics functional analysis for the investigation of apple polyphenols chemopreventive effects in cancer
15.30-15.45	<i>Corrada D, Bonati L</i> Modelling the intertwined network of PPIs along the AhR:ARNT dimer.
15.45-16.00	<i>Balasco N, Barone D, Sandomenico A, Iaccarino E, Ruvo M, Vitagliano L</i> Structural characterization of the Hepatitis C Virus E2 protein: computational and experimental approaches
16.00-16.15	<i>Paladin L, Richard F, Kajava AV, Tosatto SCE</i> Tandem Repeat proteins at a glance: function, disease and role in protein-protein interaction networks

16.15-23.00 **Social activities**

June 17, 2016

Session 5: Special Session: Clinical Bioinformatics: from computational models to clinical answers (Chairs: Roberta Bosotti and Davide Cangelosi)

9.00-9.30	<u>Highlight lecture:</u> <i>Tommaso Mazza</i> Multilayered transcriptional crosstalks are sustained by cooperating micro-societies in human colorectal cancer
9.30-9.45	<i>Spinozzi G, Calabria A, Caravagna G, Graudenzi A, Ramazzotti D, Antoniotti M, Mauri G, Montini E</i> Confirming and investigating the role of breast cancer <i>PIK3CA-ERBB2</i> genes in anti-cancer drug-resistance with a new framework for the inference of cancer progression graphs using vector integration sites data
9.45-10.00	<i>Izzo M, Cangelosi D, Pezzolo A, Morini M, Varesio L</i> XTENS: a neuroblastoma copy number variation repository at the BIT-Gaslini biobank
10.00-10.15	<i>Paladin L, Necci M, Babbi G, Fiscon G, Russo F</i> RSG Italy
10.15-10.30	<i>Pesole G</i> ELIXIR-ITA
10.30-10.45	<i>Armano G</i> Presentation of BITS2017

10.45-11.30 **Coffee break and Poster Session**

Session 6: Algorithms for Bioinformatics and Systems Biology (Chairs: Giuliano Armano and Roberto Tagliaferri)

11.30-12.15	<u>Invited Speaker:</u> <i>Michael M. Hoffman</i> Modeling methyl-sensitive transcription factor motifs with an expanded epigenetic alphabet
12.15-12.30	<i>Marini S, Demartini A, Vitali F, Bellazzi R, Akutsu T</i> Data Fusion for cleavage target prediction
12.30-12.45	<i>Colaprico A, Silva TC, Olsen C, Garofano L, Cava C, Garolini D, Sabedot T, Malta TM, Pagnotta SM, Castiglioni I, Ceccarelli M, Bontempi G, Noushmehr H</i> TCGAbiolinks: An R/Bioconductor package for integrative analysis with TCGA data
12.45-13.00	<i>Tomasi F, Squillario M, Bagnara D, Verri A, Barla A</i> A graph-based method to evaluate clonally related Immunoglobulins
13.00-13.15	<i>Pagliarini R, Castello R, Napolitano F, Borzone R, Annunziata P, Mandrile G, De Marchi M, Brunetti-Pierri N, di Bernardo D</i> A computational systems-level approach to decipher inborn errors of metabolism
13.15-14.00	Lunch (in the poster room)
14.00-15.30	Round Table: Teaching Bioinformatics (Chairs: Roberto Marangoni and Allegra Via)
15.30-15.45	Conclusions