

Scientific Programme

16 March	COST Conference “NGS: a look into the future”
08:30-09:00	<i>Registration and Coffee</i>
09:00-09:20	Welcome from organisers
	NGS Technologies and their Applications
09:20-10:00	Keynote Lecture <i>Session Chair: Erik Bongcam-Rudloff</i> Power and Limitations of RNA-Seq: Findings from the SEQC (MAQC-III) consortium <u>Paweł Łabaj</u> <i>Chair of Bioinformatics Research Group, Boku University Vienna, Austria</i>
10:00-10:30	<i>Coffee Break & posters set-up</i>
10:30-12:00	Oral Presentations
	Reproducible Research in the era of Next Generation Sequencing: current approaches, examples and future perspectives <u>Claudia Angelini</u> , <u>Dario Righelli</u> , <u>Francesco Russo</u> Current status of nanopore sequencing using the minION device – from full length cDNA sequencing to genome assembly improvements <u>Ola Wallerman</u> Deep insights into Mecp2-driven transcriptional (de)regulation at embryonic developmental stage through RNA-Seq data analysis <u>Kumar Parijat Tripathi</u> , <u>Maurizio D'Esposito</u> , <u>Mario R Guarracino</u> , <u>Marcella Vacca</u> Exploring the activity of microorganisms in the forest soil using metatranscriptomics <u>Petr Baldrian</u>
12:00-13:00	<i>Lunch</i>
	Storage and Analysis Systems
13:00-13:40	Keynote Lecture <i>Session Chair: Ralf Herwig</i> Population-Scale Genomics with BiobankCloud and Hops/Hadoop <u>Jim Dowling</u> <i>KTH - Royal Institute of Technology, Stockholm, Sweden</i>
13:40- 15:00	Oral Presentations
	Creating a successful facility for large-scale extraction of DNA, an example from the Swedish biobank initiative BBMRI.se <u>James Thompson</u> Using neural networks to filter predicted errors in NGS Data <u>Dimitar Vassilev</u> , <u>Milko Krachunov</u> DIANA-TarBase v7: indexing thousands experimentally supported miRNA:mRNA interactions <u>Dimitra Karagkouni</u> Biobanking for the future, how to prepare for the next generation of next generation sequencing <u>Tomas Klingström</u>
15:00-15:30	<i>Coffee Break</i>
15:30-16:10	Keynote Lecture <i>Session Chair: Claudia Angelini</i> Data deluge demands training tsunami <u>Eija Korpelainen</u> <i>CSC, Espo, Finland</i>

16:10-17:10	Oral Presentations
	<p>Introducing Meta²genomics: the search for the “micro-bee” <u>Jose R Valverde</u></p> <p>Information-theoretic approach for detection of differential splicing from RNA-seq data <u>Ralf Herwig</u></p> <p>iMir: An innovative and complete pipeline for smallRNA-Seq data analysis <u>Giorgio Giurato</u>, Antonio Rinaldi, Adnan Hashim, Giovanni Nassa, Maria Ravo, Francesca Rizzo, Roberta Tarallo, Angela Cordella, Giovanna Marchese, Domenico Memoli, Alessandro Weisz</p>
17:10-17:20	Closing remarks
17:20-18:00	Poster session
19:30	<i>Dinner</i>

17 March	SeqAhead Management Committee Meeting
08:30-09:00	<i>Morning Coffee</i>
09:00-09:15	Welcome and introduction
09:15-10:00	Business meeting
10:00-10:30	<i>Coffee Break</i>
10:30-12:00	Business meeting
12:00	<i>Lunch</i>

Chairs and Conference Committees

Scientific Committee

Prof. Teresa Attwood (University of Manchester, Manchester, United Kingdom)
 Dr. Claudia Angelini (CNR, Naples, Italy)
 Dr. Erik Bongcam-rudloff (SLU, Uppsala, Sweden)
 Dr. Laurent Falquet (University of Fribourg, Fribourg, Switzerland)
 Prof. Jacques van Helden (AMU, Marseille, France)
 Mr. Oliver Hunewald (CRP-Sante, Luxembourg, Luxembourg)
 Dr. Lubos Klucar (IMB SAS, Bratislava, Slovakia)
 Prof. Claude Muller (CRP-Sante, Luxembourg, Luxembourg)
 Dr. Guy Perriere (Université Claude Bernard, Lyon, France)
 Dr. Jose Ramon Valverde (CNB/CSIC, Madrid, Spain)
 Dr. Dimitar Vassilev (Agro Bio Institute, Sofia, Bulgaria)
 Dr. Vicky Schneider (TGAC, Norwich, United Kingdom)

Scientific Organisers

Prof. Teresa Attwood (University of Manchester, Manchester, United Kingdom)
 Dr. Erik Bongcam-Rudloff (SLU, Uppsala, Sweden)
 Dr. Lubos Klucar (IMB SAS, Bratislava, Slovakia)

Session Chairs

Dr. Erik Bongcam-Rudloff (SLU, Uppsala, Sweden)
 Dr. Ralf Herwig (Max-Planck-Institute for Molecular Genetics, Berlin, Germany)
 Dr. Claudia Angelini (CNR, Naples, Italy)