

RNA Informatics 2019

Wellcome Genome Campus Conference Centre,
Hinxton, Cambridge

9 – 11 September

Lectures to be held in the Rosalind Franklin Pavilion

Lunch and dinner to be held in the Hall Restaurant

Poster sessions to be held in the Conference Centre

Spoken presentations - If you are an invited speaker, or your abstract has been selected for a spoken presentation, please give an electronic version of your talk to the AV technician.

Poster presentations – If your abstract has been selected for a poster, please display this in the Conference Centre on arrival.

Conference programme

Monday, 9 September

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| 11:30-12:45 | Registration |
| 12:45-13:00 | Welcome and Introductions
<i>Programme Committee</i> |
| 13:00-14:00 | Keynote Lecture
Co-transcriptional splicing
<i>Maria Carmo-Fonseca</i>
<i>Instituto de Medicina Molecular Lisbon, Portugal</i>
<i>Chair: Mihaela Zavolan</i> |
| 14:00-15:30 | Session I: Regulatory RNA's
<i>Chair: Mihaela Zavolan</i> |
| 14:00 | The role of microRNA-mediated circuits in the control of gene expression fluctuations
<i>Michele Caselle</i>
<i>University of Turin, Italy</i> |
| 14:30 | Low structure bias expression profiling of human transcripts reveals new snoRNAs as well as annotated snoRNAs with canonical and non-canonical functional capacity
<i>Michelle Scott</i>
<i>University of Sherbrooke, Canada</i> |
| 15:00 | A graph-based approach for identifying conserved element combinations in long noncoding RNAs
<i>Caroline Jane Ross</i>
<i>Weizmann Institute of Science, Israel</i> |

15:15 PAREfirst: a tool for PARE assisted miRNA prediction from high-throughput sequencing data
Salma Alzahrani
University of East Anglia, UK

15:30-16:00

Afternoon Tea

16:00-17:30

Session 2: Translational Control

Chair: Alex Bateman

16:00 Computational modelling of novel gene expression rules encoded in the mRNA
Tamir Tuller
Tel Aviv University, Israel

16:30 A Landscape of RNA splicing and translation in the mammalian heart
Christoph Dieterich
University Hospital Heidelberg, Germany

17:00 Identification and characterisation of ribosome-associated lncRNAs in human and mouse
Chao Zeng
National Institute of Advanced Industrial Science and Technology (AIST), Japan

17:15 Functional annotation of human microRNAs using the Gene Ontology
Ruth Lovering
University College London, UK

17:30-17:45

Lightning talks

17:45-19:15

Poster Session I (odd numbers) with drinks reception

19:15

Dinner

Tuesday, 10 September

09:00-10:30

Session 3: RNA Sequence and Structure

Chair: Alex Bateman

09:00 Understanding the mechanistic basis of non-coding RNA through molecular dynamics simulations
Giulia Palermo
University of California, USA

09:30 Co-transcriptional RNA folding kinetics
Ivo Hofacker
University of Vienna, Austria

10:00 Estimating the power of sequence covariation for detecting conserved RNA structure and predicting their complete structures
Elena Rivas
Harvard University, USA

10:30-11:00

Morning Coffee

11:00-12:30

Session 4: RNA Processing

Chair: Yoseph Barash

11:00 Deciphering functional genetic variants in RNA processing and expression
Xinshu Grace Xiao
University of California, Los Angeles, USA

11:30 Investigating the deep evolutionary roots of tissue-specific alternative splicing
Manuel Irimia
Centre for Genomic Regulation, Spain

12:00 Androgen-regulated transcription of ESRP2 drives alternative splicing patterns in prostate cancer
David Elliott
Newcastle University, UK

12:15 RNA splicing analysis for large heterogeneous datasets
Matthew Gazzara
University of Pennsylvania, USA

12:30-14:00

Lunch

14:00-15:15

Session 5: RNA Complexes

Chair: Manja Marz

14:00 A computational framework to predict protein-RNA interactions
Gian Gaetano Tartaglia
Centre for Genomic Regulation, Spain

14:30 Using network clustering to investigate the evolution of RNA gene regulators
Michelle Meyer
Boston College, USA

15:00 A network of poison exons controls splicing factor expression during neurogenesis
Carlos Fernando Buen Abad Najar
University of California Berkeley, USA

15:15-15:45

Afternoon Tea

15:45-17:30

Session 6: RNA Biology and Disease

Chair: Yoseph Barash

- 15:45 The RNA-binding ubiquitin ligase MKRN1 functions in ribosome-associated quality control of poly(A) translation
Kathi Zarnack
Buchmann Institute, Germany
- 16:15 Full-length transcript isoforms associated with SF3B1 mutation in chronic lymphocytic leukemia
Angela Brooks
University of California Santa Cruz, USA
- 16:45 Defining the regulatory landscape of cancer through de novo splicing archetype discovery
Nathan Salomonis
Cincinnati Children's Hospital, USA
- 17:00 Predicting clinical significance of intronic variation in disease-causing genes
Pedro Barbosa
Instituto de Medicina Molecular João Lobo Antunes, Portugal
- 17:15 Cancer transcriptome at nucleotide resolution
Daniel Gautheret
Université Paris-Sud, CNRS, France

17:30-17:45

Lightning talks

17:45-19:15

Poster Session 2 (even numbers) with drinks reception

19:15

Conference Dinner

Wednesday, 11 September

09:00-10:30

Session 7: Technology

Chair: Manja Marz

- 09:00 Annotation of human lncRNAs through multi-omics data integration and analysis
Lina Ma
Beijing Institute of Genomics, China
- 09:30 Single-cell isoform RNA sequencing characterizes isoforms in thousands of cerebellar cells
Hagen Tilgner
Weill Cornell Medicine, USA
- 10:00 How long-read transcriptomic data is transforming the GENCODE lncRNA catalogue
Adam Frankish
EMBL-EBI, UK

10.15 RNA 2D/3D structure prediction with a consensus of contact methods
Russell Hamilton
University of Cambridge, UK

10:30-11:00

Morning Coffee

11:00-12:00

Keynote Lecture

Assessing the specificity of protein-RNA binding sites identified with CLIP technologies

Jernej Ule

The Francis Crick Institute, UK

Chair: Alex Bateman

12:15-12:30

Closing remarks:

Programme Committee

12:30-13:30

Lunch

13:30

**Coaches depart to Cambridge City Centre and Train Station,
Stansted Airport via Heathrow Airport**