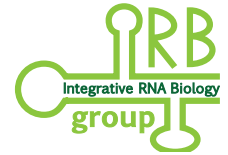


RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS

SATURDAY, JULY 7 • ROOM: GRAND BALLROOM B

https://www.iscb.org/cms_addon/conferences/ismb2018/rna.php



- 10:15 AM-10:20 AM **Introduction**
- 10:20 AM-11:00 AM **Michael Seiler**, H3 Biomedicine, United States
Invited Talk I
- 11:00 AM-11:20 AM **Ammar Naqvi**, Children's Hospital of Philadelphia, United States
Aberrant splicing in B-cell acute lymphoblastic leukemia
- 11:20 AM-11:40 AM **Marina Reixachs**, Universitat Pompeu Fabra, Spain
Measuring ribosome profiling at isoform level: towards unveiling the functional impact of alternative splicing
- 11:40 AM-12:00 PM **Auinash Kalsotra**, University of Illinois at Urbana-Champaign, United States
Overexpression of a non-muscle Rbfox2 splice isoform drives cardiac dysfunctions in Myotonic Dystrophy type I
- 12:00 PM-12:10 PM **Pooja Sethiya**, University Of Macau, Macao
Integrating different transcription profiling data to determine mRNA stability upon host-pathogen interaction
- 12:10 PM-12:20 PM **Weizhong Li**, Sun Yat-sen University, China
ncRPheDB: identify and prioritize associations between noncoding RNAs and disease phenotypes based on novel evidential metrics
- 12:20 PM-12:30 PM **Vanessa Aguiar-Pulido**, Cornell University, United States
High-throughput single-cell transcriptomics profiling interneuron specification during brain development
- 12:30 PM-12:40 PM **Zhen Tan**, University of Rochester, United States
TurboFold II: RNA Structural Alignment and Secondary Structure Prediction Informed by Multiple Homologs
- 12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
- 2:00 PM-2:20 PM **Jean-Pierre Glouzon**, University of Sherbrooke, Canada
Proceedings Presentation: aliFreeFold: an alignment-free approach to predict secondary structure from homologous RNA sequences
- 2:20 PM-2:40 PM **Dezhong Deng**, School of EECS, Oregon State University, United States
LinearFold: Linear-Time Prediction of RNA Secondary Structures
- 2:40 PM-3:00 PM **Anton Petrov**, EMBL-EBI, United Kingdom
Rfam: The transition to a genome-centric sequence database
- 3:00 PM-3:20 PM **Jan Gorodkin**, University of Copenhagen, Denmark
Enhanced prediction of CRISPR-Cas9 off-targets through modeling of nucleic acid duplex interactions
- 3:20 PM-3:40 PM **Lucia Lorenzi**, Ghent University, Belgium
RNA atlas: a nucleotide resolution map of the human transcriptome
- 3:40 PM-4:00 PM **Vincent Boivin**, Université de Sherbrooke, Canada
Uncovering new non-coding RNA genes in human with TGIRT-Seq.
- 4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
- 4:40 PM-5:00 PM **Yasubumi Sakakibara**, Keio University, Japan
Proceedings Presentation: Convolutional neural networks for classification of alignments of non-coding RNA sequences
- 5:00 PM-5:20 PM **Jean-Michel Garant**, Université de Sherbrooke, Canada
RNA G-quadruplex prediction to investigate a novel RNA regulation model.
- 5:20 PM-6:00 PM **Stirling Churchman**, Harvard University, United States
Exploring the nascent transcriptome with direct RNA nanopore sequencing

RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • ROOM: GRAND BALLROOM B

https://www.iscb.org/cms_addon/conferences/ismb2018/rna.php



- 10:15 AM-10:20 AM **Introduction**
- 10:20 AM-11:00 AM **Gene Yeo**, UCSD University, United States
Large-scale studies of RNA binding proteins by eCLIP and proximity labeling
- 11:00 AM-11:20 AM **Mark Gerstein**, Yale University, United States
RADAR: Annotation and prioritization of variants in the post-transcriptional regulome for RNA-binding proteins
- 11:20 AM-11:40 AM **Reazur Rahman**, Brandeis University, United States
Identification of RNA-Binding Protein Targets with HyperTRIBE
- 11:40 AM-12:00 PM **Carla Mann**, Iowa State University, United States
RPIDisorder: A machine learning method for improved prediction of RNA-Protein interaction partners
- 12:00 PM-12:10 PM **Bojan Losic**, Icahn School of Medicine at Mount Sinai Hospital, United States
Using co-expression networks and predictive models to infer circular RNA regulatory function in colitis models
- 12:10 PM-12:20 PM **Hendrik Weisser**, STORM Therapeutics Limited, United Kingdom
New tools for RNA epigenetics: an open-source approach to RNA modification analysis
- 12:20 PM-12:30 PM **Renana Sabi**, Tel Aviv University, Israel
Novel Insights into Gene Expression Regulation during Meiosis Revealed by Translation Elongation Dynamics
- 12:30 PM-12:40 PM **Dimitra Karagkouni**, University of Thessaly, Hellenic Pasteur Institute, Greece
Ushering in a new era of CLIP-guided detection of miRNA targets
- 12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
- 2:00 PM-2:10 PM **Dana Wyman**, University of California, Irvine, Center for Complex
Generating full-length, high quality human transcriptomes from PacBio Iso-seq data
- 2:10 PM-2:20 PM **TBD**
Long noncoding RNA (lncRNA)-Protein coding gene (PCG) regulatory networks responsive to diverse xenobiotics in rat liver
- 2:20 PM-2:40 PM **Tilgner Hagen**, Cornell University, United States
A deep long-read sequencing technology reveals coordination of distant exons on RNA molecules to be widespread.
- 2:40 PM-3:00 PM **Mingfu Shao**, Carnegie Mellon University, United States
Accurate assembly of transcripts through phase-preserving graph decomposition
- 3:00 PM-3:20 PM **Christopher Jürges**, Institut für Virologie und Immunbiologie, Julius-Maximilians-Universität Würzburg, Germany
Proceedings Presentation: Dissecting newly transcribed and old RNA using GRAND-SLAM
- 3:20 PM-3:40 PM **Andrew Thurman**, University of Iowa, United States
Gene isoform abundance quantification with third generation transcriptome sequencing
- 3:40 PM-4:00 PM **Steven E. Brenner**, University of California, Berkeley, United States
Revealing the hidden transcriptome: Analysis of nonsense-mediated mRNA decay target reveals mechanistic insights
- 4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
- 4:40 PM-5:00 PM **Donny Licatalosi**, Case Western Reserve University, United States
Stage-specific mRNA regulatory programs drive mammalian gametogenesis
- 5:00 PM-5:20 PM **Namshik Han**, University of Cambridge, United Kingdom
Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci
- 5:20 PM-6:00 PM **Chaolin Zhang**, Columbia University, United States
Modeling RNA-binding protein specificity using single-nucleotide-resolution binding maps: a case study of LIN28 and two subclasses of let-7 microRNAs