RiboClub 2018
September 23-27
RNomics: Big data, analysis and mechanism of action.
Hotel et Villégiature Chéribourg
2603 Chemin du Parc
Orford (Magog) Quebec, Canada

Sunday, September 23\textsuperscript{th}

15:00 – 18:00  Registration for early arrivals
18:00 – 19:30  Welcome reception
19:30 – 21:30  Opening dinner
Monday, September 24th

08:00 – 08:45 Registration

08:45 – 08:55 Opening Notes (Sherif Abou Elela)

08:55 – 09:00 Presentation of Keynote speaker (Benoit Chabot)

09:00 – 10:00 **Keynote presentation**
Hidden treasures of the RNA world: RBPs from moonlighting to riboregulation
Matthias W. Hentze, EMBL Heidelberg, Heidelberg

10:00 – 10:30 Coffee break

Session 1: Transcription and RNA synthesis

Chair: Shona Murphy

10:30 – 10:35 **Introduction by Shona Murphy**

10:35 – 10:55 Photo-dependent control of transcription elongation
Jean-François Nadon, Université de Sherbrooke, Sherbrooke

10:55 – 11:15 Nus factors prevent Rho-dependent transcription termination of CRISPR arrays in diverse bacterial species
Joseph Wade, University at Albany-SUNY, Albany

11:15 – 11:35 Influenza A virus cap-snatching profiling reveals inhibition of the cellular response at the earliest steps of infection
Martin Pelchat, University of Ottawa, Ottawa

11:35 – 11:55 Common mechanism of transcription termination at coding and noncoding RNA genes in fission yeast
François Bachand, Université de Sherbrooke, Sherbrooke

11:55 – 12:15 The mysterious world of pol II CTD kinases
Shona Murphy, University of Oxford, UK

12:15 – 14:00 Networking Lunch
Session 2:
RNP Maturation and Function

Chair: Benoit Chabot

14:00 – 14:05 Introduction by Benoit Chabot

14:05 – 14:25 Early Recognition in the spliceosome
Andrew MacMillan, University of Alberta, Edmonton

14:25 – 14:45 Investigating the biological function of an extremely reduced splicing system
Stephen Rader, University of Northern British Columbia, Prince George

14:45 – 15:05 Alternative splicing in apoptotic resistance associated with senescence
Mathieu Deschênes, Université de Sherbrooke, Sherbrooke

15:05 – 15:25 The exon junction complex undergoes a compositional switch that alters overall mRNP structure and nonsense-mediated mRNA decay activity
Guramrit Singh, The Ohio State University, Ohio

15:25 – 15:45 Genome-wide CRISPR-Cas9 interrogation of splicing networks reveals a mechanism for recognition of autism-misregulated neuronal microexons
Thomas Gonatopoulos-Pournatzis, University of Toronto, Toronto

15:45 – 16:10 Coffee break

Session 3:
Trancriptomics and Bioinformatics of Splicing

Chair: Jernej Ule

16:10 – 16:15 Introduction by Jernej Ule

16:15 – 16:35 Big RNA splicing data - challenges and advancements
Mathieu Quesnel-Vallières, University of Pennsylvania, Philadelphia

16:35 – 16:55 Multiple spliced alignment and visualization of gene structure alignment
Aïda Ouangraoua, Université de Sherbrooke, Sherbrooke

16:55 – 17:15 The exon junction complex shapes the transcriptome by repressing recursive splicing
Jernej Ule, Institute of Neurology, London
17:15 – 17:35  Proteome remodeling by neuronal microexons across bilaterian animals 
Manuel Irimia, Centre for Genomic Regulation (CRG), Barcelona

17:35 – 17:55  What transcriptomes tell us about disease 
Nuno L. Barbosa Morais, iMM Lisboa, Lisbon

18:00 – 19:30  Dinner

19:30 – 20:30  Gairdner event - After Dinner Speaker 
Introduction by Brendan Bell, Université de Sherbrooke 
Davor Solter, 2018 Gairdner Award winner

20:30 – 21:30  Poster competition IA: (Odd numbers)
21:30 – 22:30  Poster competition IB: (Even numbers)
22:30 – 24:00  Get Together (Bistro)
Tuesday, September 25th

07:00 – 08:30
Breakfast

Session 4:
Ribosome Profiling and transcriptomics

Chair: Alan G. Hinnebusch

08:30 – 08:35
Introduction by Alan G. Hinnebusch

08:35 – 08:55
Identifying translated isoforms from ribosome profiling data
Uwe Ohler, Max Delbruck Center for Molecular Medicine, Berlin

08:55 – 09:15
Dissecting the roles of eIF2 and eIF3 during translation using TCP-seq
Thomas Preiss, The John Curtin School of Medical Research, Canberra

09:15 – 09:35
Reconstituting distinct functions of DEAD-box RNA helicases Ded1, Dbp1, and eIF4A in stimulating translation initiation of structured native yeast mRNAs
Alan G. Hinnebusch, NIH, Bethesda

09:35 – 9:55
Translating the cancer genome one codon at a time and its therapeutic implications
Davide Ruggero, UCSF, San Francisco

09:55 – 10:15
Endogenous rRNA sequence variation can regulate gene expression and phenotype
Scott Blanchard, Weill Cornell Medical College, New York

10:15 – 10:45
Coffee break

Session 5:
Translation Mechanisms and Function

Chair: Neva Caliskan

10:45 – 10:50
Introduction by Neva Caliskan

10:50 – 11:10
eIF2α Methylation by PRMT7 is Required for S51 Phosphorylation and Subsequent Stress Granule Formation
Jocelyn Côté, University of Ottawa, Ottawa
Eukaryotic initiation factor 5B (eIF5B) is a regulatory hub for non-canonical translation initiation in glioblastoma progression

Joseph A. Ross, University of Lethbridge, Lethbridge

The conserved translational ATPase YchF interacts with tRNA and the ribosomal A-site for ribosome quality control

Harland E. Brandon, University of Lethbridge, Lethbridge

Small synthetic molecule-stabilized RNA pseudoknot as an activator for – 1 ribosomal frameshifting

Neva Caliskan, Helmholtz Institute for RNA-based Infectious Research (HIRI/HZI), Würzburg

Group Photo

Lunch

Virtual computational RNA community meeting

Session 6: Translation Regulation

Chair: Christine Clayton

Introduction by Christine Clayton

Human La binds the poly(A) tail to promote cap-independent translation

Mark Bayfield, York University, Toronto

The suppressive cap-binding-complex factor 4EIP is required for normal differentiation

Christine Clayton, University (ZMBH), Heidelberg

Investigating nPABP, a mammalian neural poly(A) binding protein that represses mRNA translation

Sahil Sharma, Lady Davis Institute for Medical Research, Montréal

Translation activation by mRNA secondary structures revealed by small RNA regulation

Maude Guillier, CNRS, Paris

Elucidating the interplay between RNA structure and translation during vertebrate embryogenesis

Jean-Denis Beaudoin, Yale University School of Medicine, New Haven
15:35 – 16:00 Coffee Break

**Session 7:**
**RNA Degradation**

Chair: **Joel G. Belasco**

16:00 – 16:05 Introduction by **Joel G. Belasco**

16:05 – 16:25 Mechanisms of bacterial mRNA degradation
**Joel G. Belasco**, New York University School of Medicine, New York

16:25 – 16:45 Posttranscriptional feedback regulation of S-adenosylmethionine production
**Nicholas K. Conrad**, University of Texas Southwestern Medical Center, Dallas

16:45 – 17:05 Deconvolving the RNA life cycle from high-resolution time-resolved protein-RNA interaction data
**Sander Granneman**, University of Edinburgh, Edinburgh

17:05 – 17:25 Human antigen R (HuR) mediates cancer-induced muscle wasting by regulating PGC1a-dependent muscle fiber type specification
**Imed Gallouzi**, McGill University, Montreal

17:25 – 17:30 Students’ Award Introduction (students’ representatives)

17:30 – 17:45 Best Talk Award of the RiboWest (introduced by Students’ Representative)

17:45 – 18:00 Best Seminar Award (introduced by Students' Representative)

18:00 – 19:00 Poster competition IIA (Even numbers), Cocktail and light snacks

19:00 – 20:00 Poster competition IIB: (Odd numbers), Cocktail and light snacks

20:00 – 21:30 Dinner

21:30 – 24:00 Get Together (Bistro)
Wednesday, September 26th

07:00 – 08:30 Breakfast

Session 8:
Eukaryotic Non-Coding RNA

Chair: René F. Ketting

08:30 – 08:35 Introduction by René F. Ketting

08:35 – 08:55 Tissue-based map of the snoRNome
Michelle Scott, Université de Sherbrooke, Sherbrooke

08:55 – 09:15 A nested 2-level cross-validation ensemble learning pipeline suggests a negative pressure against crosstalk snoRNA-mRNA interactions in Saccharomyces Cerevisae
Antoine Paul Soulé, McGill University, Montreal

09:15 – 09:35 Molecular mechanisms driving small RNA pathways in germ cells
René F. Ketting, Institute of Molecular Biology gGmbH, Mainz

09:35 – 09:55 Evf2 ultraconserved enhancer (UCE) IncRNA regulates UCE target gene selection and activity through cohesin recruitment and cis and trans mechanisms
Jhumku D. Kohtz, Northwestern University & Stanley Manne Children’s Research Institute, Chicago

09:55 – 10:15 Mechanisms regulating dyskerin SUMOylation and effects of X-linked dyskeratosis congenita mutations on dyskerin function
Chantal Autexier, McGill University, Montreal

10:15 – 10:35 ADAR1 RNA editing mediated dsRNA sensing in innate immunity
Jin Billy Li, Stanford University, Stanford

10:35 – 11:05 Coffee Break
Session 9:
Bacterial Non-Coding RNA

Chair: Cari Vanderpool

11:05 – 11:10 Introduction by Cari Vanderpool

11:10 – 11:30 Determinants of target prioritization and regulatory hierarchy for the bacterial small RNA SgrS
Cari Vanderpool, University of Illinois at Urbana-Champaign, Champaign

11:30 – 11:50 A systems approach to bacterial cell stress and small non-coding RNAs
Eric D. Brown, McMaster University, Hamilton, Canada

11:50 – 12:10 Real-time Imaging of Cotranscriptional Folding During Transcription Elongation
Jonathan Grondin, Université de Sherbrooke, Sherbrooke

12:10 – 14:00 Lunch

13:15 – 14:00 Business meeting

Session 10:
RNA-Seq, System Biology and Networks

Chair: Jack D. Keene

14:00 – 14:05 Introduction by Jack D. Keene

14:05 – 14:25 Efficient regulatory circuits by a protein and a small RNA encoded in a single gene
Hanah Margalit, The Hebrew University of Jerusalem, Jerusalem

14:25 – 14:45 Post-transcriptional Regulation in RAS-induced malignant cells
Jack D. Keene, Duke University Medical Center, Durham

14:45 – 15:05 Dissecting the role of SINE non-coding RNAs in aging and amyloid pathology: An integrative RNA genomics approach
Athanasios Zovoilis, University of Lethbridge, Lethbridge

15:05 – 15:25 Widespread & functional RNA circularization in localized prostate cancer
Sujun Chen, Princess Margaret Cancer Center, Toronto

15:25 – 15:55 Coffee Break
Session 11: New Methods for Bioinformatics and Transcriptomics

Chair: Lydia L. Sohn

15:55 – 16:00  Introduction by Lydia L. Sohn
16:00 – 16:20  Inferring the targets of RNA-binding proteins
               Quaid Morris, University of Toronto, Toronto
16:20 – 16:40  Mechano-NPS: An electronic method to mechanically phenotype cells
               Lydia L. Sohn, University of California, Berkeley
16:40 – 17:00  Cataloguing recurrent long-range interactions in RNA structures exhibits embedded hierarchies in network families
               Vladimir Reinharz, Institute of Basic Science, Ulju-gun
17:00 – 17:20  Fission yeast transcriptional heterogeneity surveyed by single cell RNA sequencing
               Samuel Marguerat, MRC London Institute of Medical Sciences, London
17:20 – 18:20  Students’ Choice Seminar
               Ribosome heterogeneity in translating the genetic code
               Introduction by student representatives
               Maria Barna, Stanford University, Stanford
18:20 – 20:30  Banquet
20:30 – 20:35  Presentations of the travel awards
               Éric Massé, Université de Sherbrooke
20:35 – 20:40  Poster prizes
               Michelle Scott, Université de Sherbrooke
20:40 – 20:45  Blue Jacket Award
               Benoit Chabot, Université de Sherbrooke
20:45 – 20:55  RNA Group Notes and Progress
               François Bachand, Université de Sherbrooke
21:00 – ..  Special Presentation of Quebec Folk Music and Dance
Thursday, September 27th

07:00 – 09:30  Breakfast and Departure.