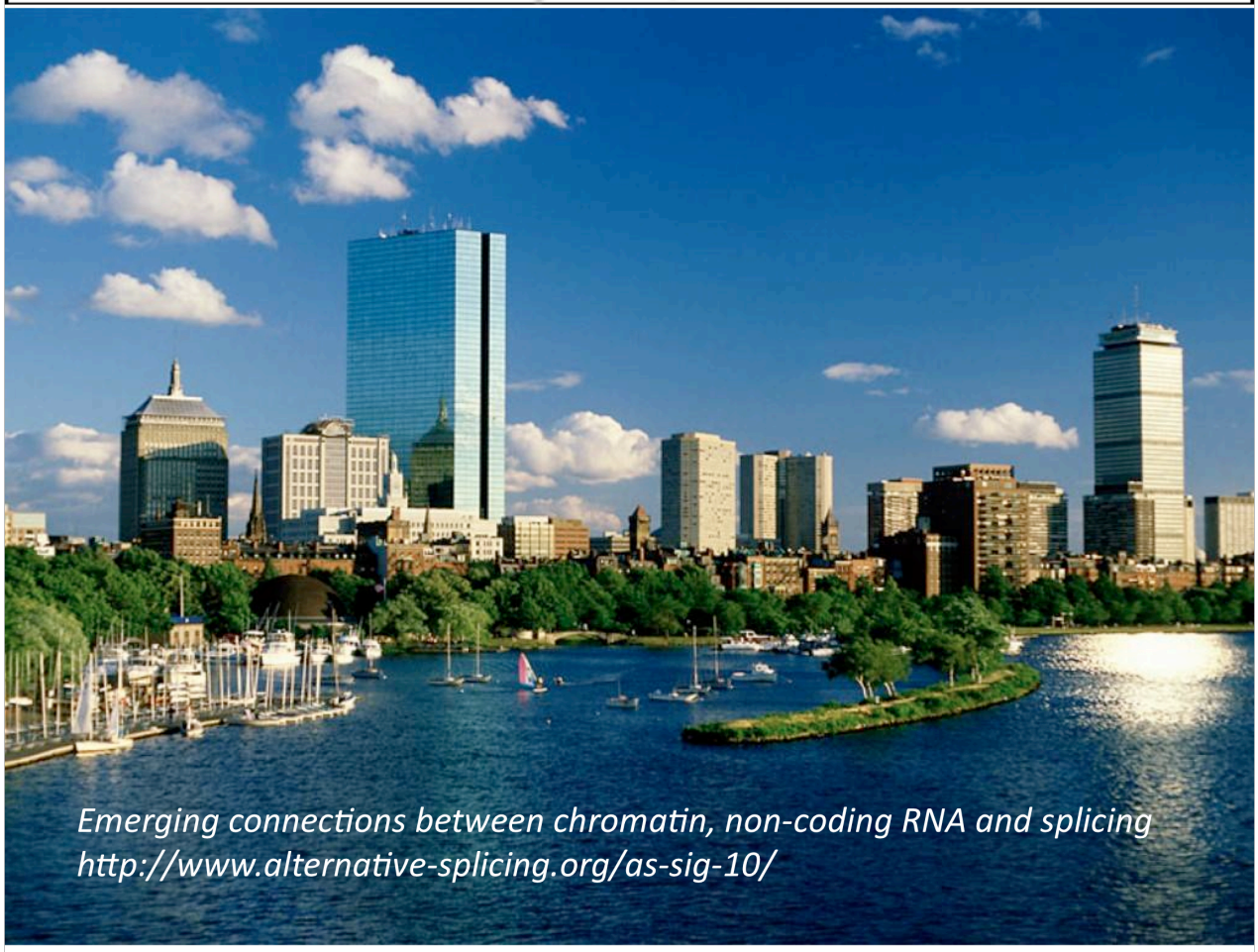
AS-SIG @ ISMB

Alternative Splicing - Special Interest Group meeting

July 9-10, 2010



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Program, July 9th

07.30 - 08.30 Registration

09.00 - 09.05 Opening

THE SPLICING CODE

9.05 – 9.25 **Yoseph Barash**. *Deriving the Code for Alternative Splicing.*

9.25 – 10.10 **Reini Luco.** *A role for epigenetic modifications in alternative splicing.*

10.15 – 10.45 *Coffee break*

CHROMATIN AND RNA REGULATION I

10.45 – 11.05 **Jason Huff**. *A novel organizing principle of the human epigenome: reciprocal intronic and exonic histone marks.*

11.05 – 11.25 **Alexandra Rapoport**. *Exons, amphipathic alpha-helices, and nucleosomes.*

11.25 – 11.45 **Ekaterina Khrameeva**. *Spatial proximity and similarity of functional states of genome domains.*

11.45 – 12.30 **Kevin Morris.** *Endogenous long non-coding RNAs: transcriptional modulators of gene expression in human cells.*

12.30 – 13.40 *Lunch break*

CHROMATIN AND RNA REGULATION II

13.40 – 14.00 **Christian Muchardt**. *Histone H3 lysine 9 tri-methylation and HP1γ favor inclusion of alternative exons.*

14.00 – 14.20 **Eneritz Agirre**. *Small RNAs that regulate splicing: ChIP-Seq analysis of AGO proteins and Histone modifications.*

14.20 – 14.40 **Hagen Tilgner**. *ChIP- and RNAseq in two tissues for a combined vision of chromatin, transcription and splicing changes.*

14.40 – 15.25 **Mariano Allo**. *Search for endogenous small RNAs affecting alternative splicing by TGS*

15.30 – 16.00 *Coffee break*

HIGHLIGHT

16.00 – 16.45 **Chris Burge.** *High-throughput mapping of the nucleic acid binding specificity of proteins*

17.00 - 18.30 Poster session

followed by Conference dinner (invited speakers and pre-booked attendees)

Program, July 10th

Protein and RNA Regulatory Networks

09.00 – 09.20 **Quaid Morris**. *RNAcontext: a motif finding algorithm for learning the sequence and structural binding preferences of RNA-binding proteins.*

09.20 – 10.05 **John Rinn.** *Chromatin Associated Large Intergenic Non-Coding RNAs (lincRNAs) in Cancer*

10.15 – 10.45 *Coffee break*

10.45 – 11.05 **Yael Mandel-Gutfreund**. *Unraveling the transcription-splicing co-regulatory network.*

11.05 – 11.25 **Adam Frankish**. *Assessing the utility of new data sources for the identification and validation of alternative splicing.*

11.25 – 11.45 **Angela N. Brooks**. *Using RNAi and RNA-Seq to Identify Alternative Exons Regulated by Individual RNA Binding Proteins and their Associated Regulatory Motifs.*

11.45 – 12.30 **Jean Beggs**. *Coupling of transcription and splicing in yeast.*

12.30 - 14.00 *Lunch break*

Splicing and Disease

14.00 – 14.20 **Smita Agrawal**. *RNA splicing affected in Spinocerebellar Ataxia type I.*

14.20 – 14.40 **Ahmet D. Arslan**. *Splicing Factor Polypyrimidine tract-binding protein (PTB) plays a role in tumorigenesis.*

14.40 – 15.00 **Xinchen Wang**. *An RNA-Seq analysis of mis-regulated alternative splicing in Alzheimer's Disease.*

15.00 – 15.20 **Claes Wadelius**. *Assessment of association between chromatin and splicing*

15.30 – 16.00 *Coffee break*

16.00 – 16.20 **Yi Xing**. *Evolution of alternative splicing in primate brain transcriptomes.*

Splicing Regulation

16.20 – 16.45 **Philipp Drewe**. *Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts.*

16.45 – 17.00 **Rileen Sinha**. *Tissue-specific subtle alternative splicing: the devil's in the details.*

17.05 – 17.25 **Klemens Hertel**. *Getting Close to Splice Sites: The Proximity Rule Revisited.*

Highlight

17.30 – 18.15 **Roderic Guigo.** *Uncovering and understanding splicing through massively parallel sequencing.*

18.15 *Conclusion*