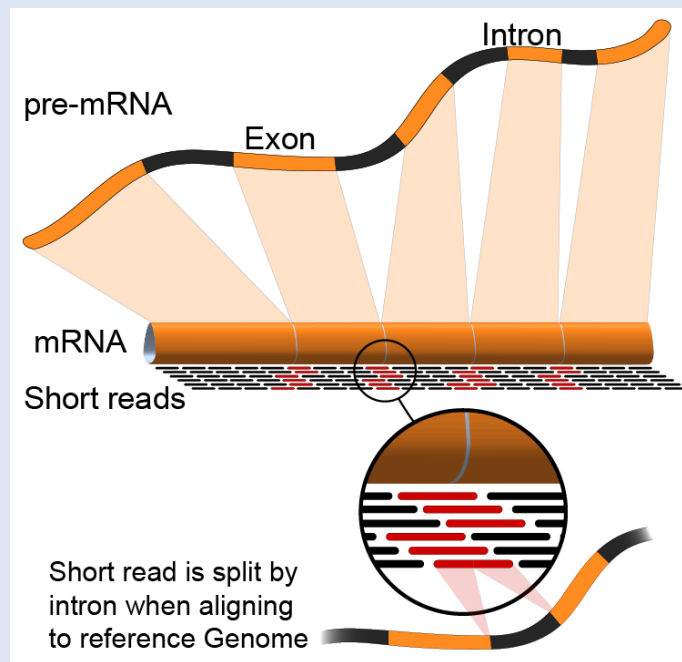
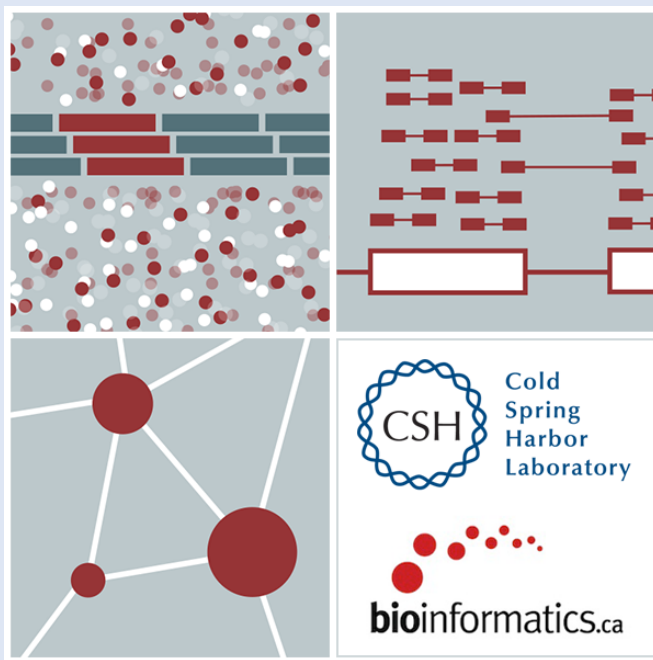




Cold
Spring
Harbor
Laboratory

RNA-Seq Module 5: Alternative Splicing Analysis

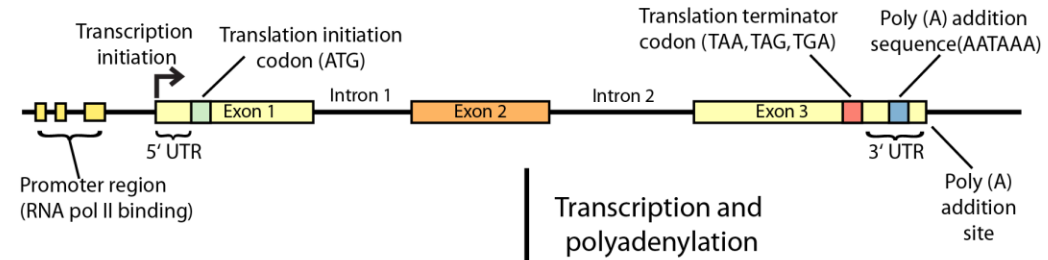
Felicia Gomez, Charlz Jerold, Obi Griffith, Malachi Griffith,
My Hoang, Mariam Khanfar, Chris Miller, Kartik Singhal, Jennie Yao
Advanced Sequencing Technologies & Bioinformatics Analysis November 10-21, 2025



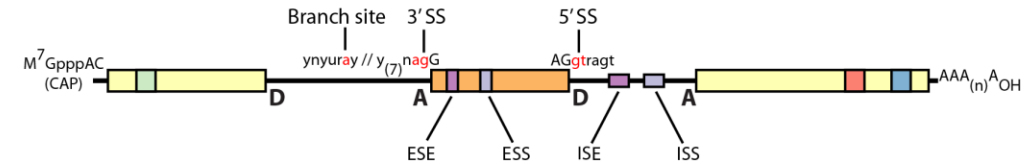
Washington University in St. Louis
SCHOOL OF MEDICINE

Review of gene expression

Double-stranded genomic DNA template

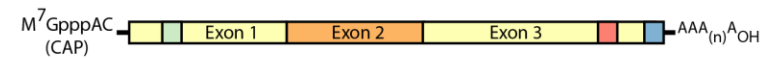


Single-stranded pre-mRNA (nuclear RNA)



RNA processing

Mature mRNA

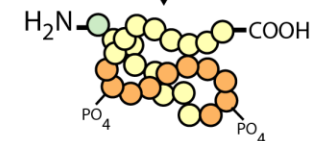


Export to cytoplasm and translation

Protein (amino acid sequence)

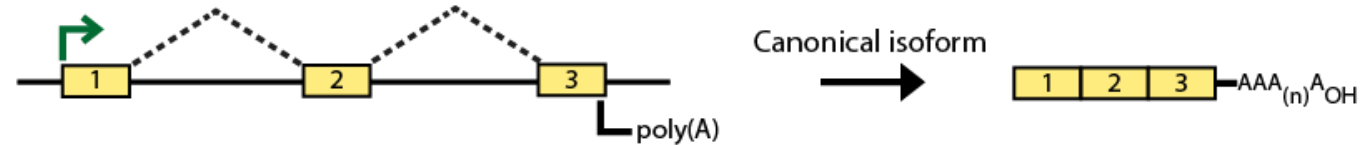


Folding, posttranslational modification, subcellular localization, etc.

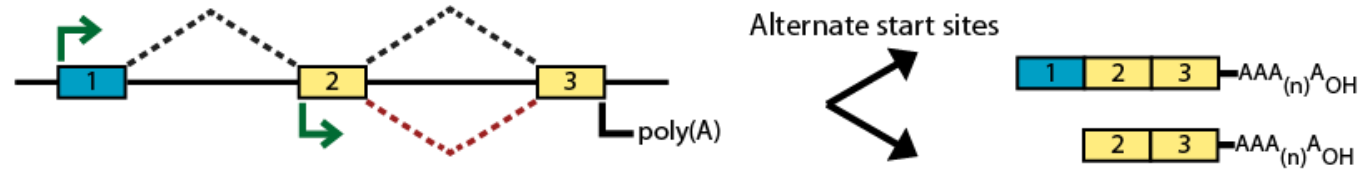


Types of alternative expression - part 1

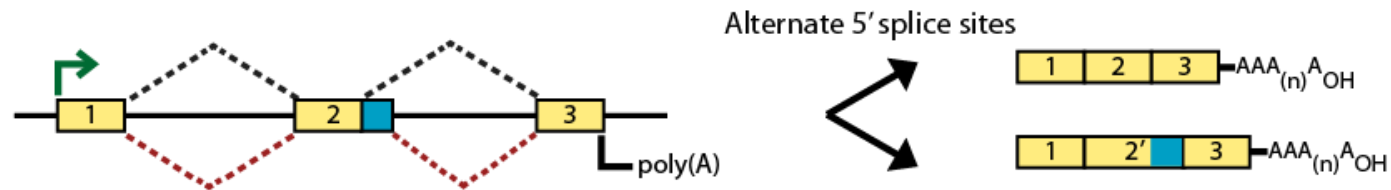
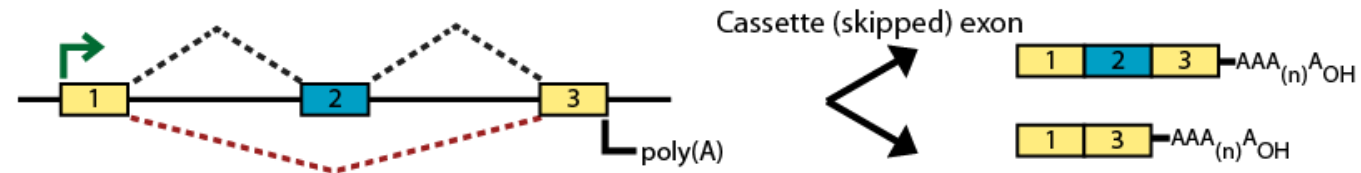
Simple transcription



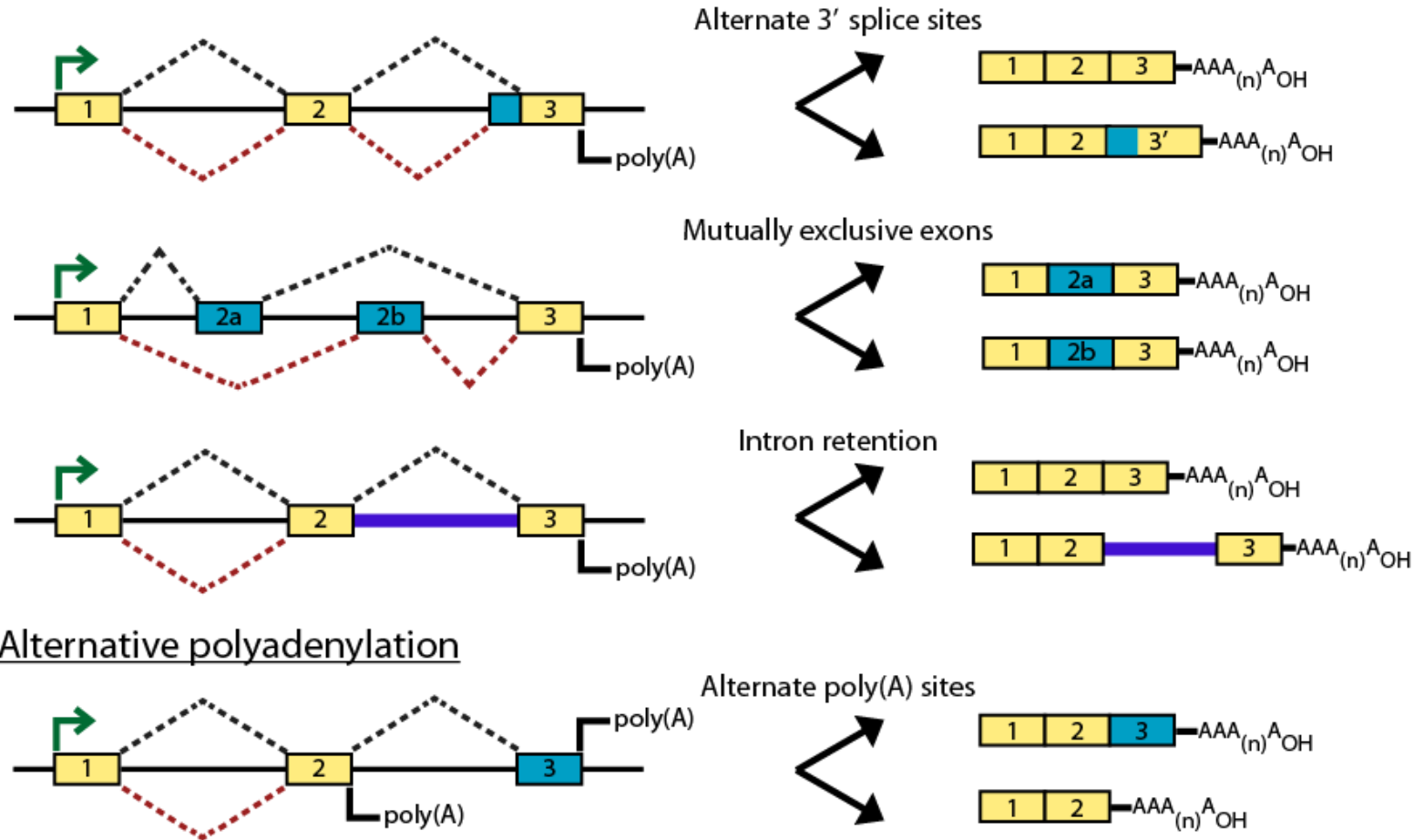
Alternative transcript initiation



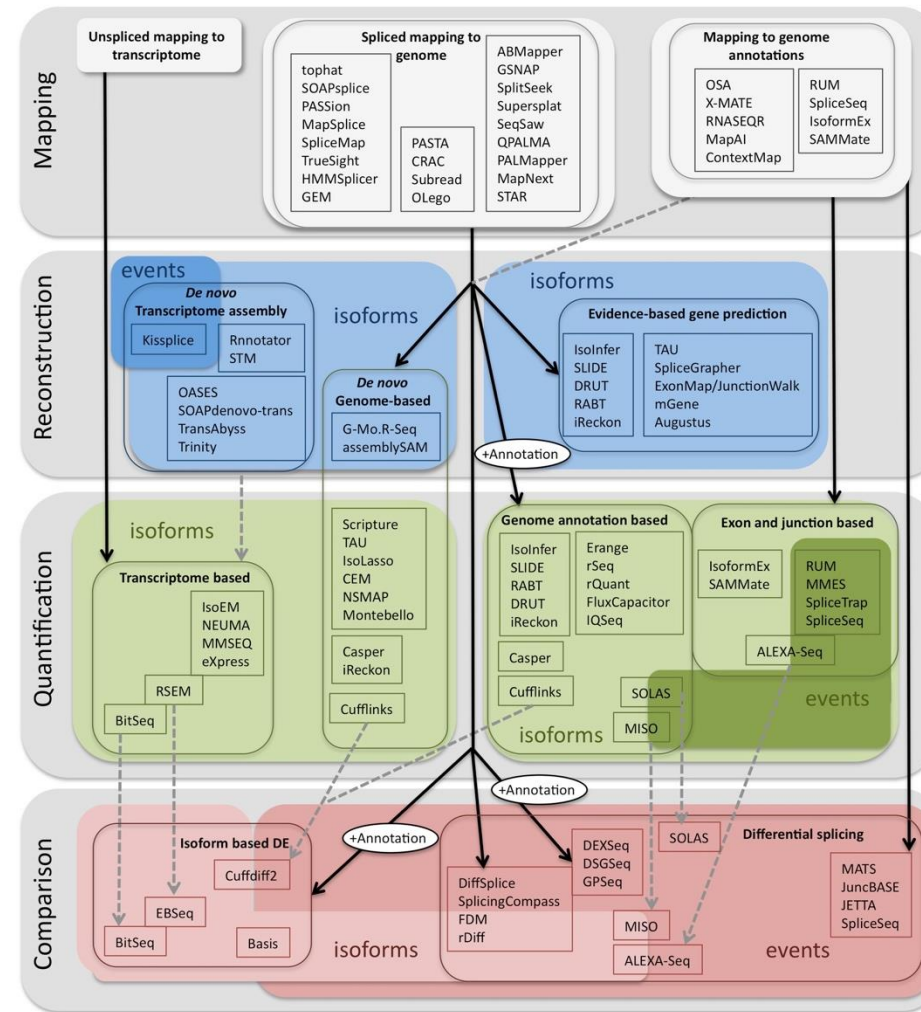
Alternative splicing



Types of alternative expression – part 2

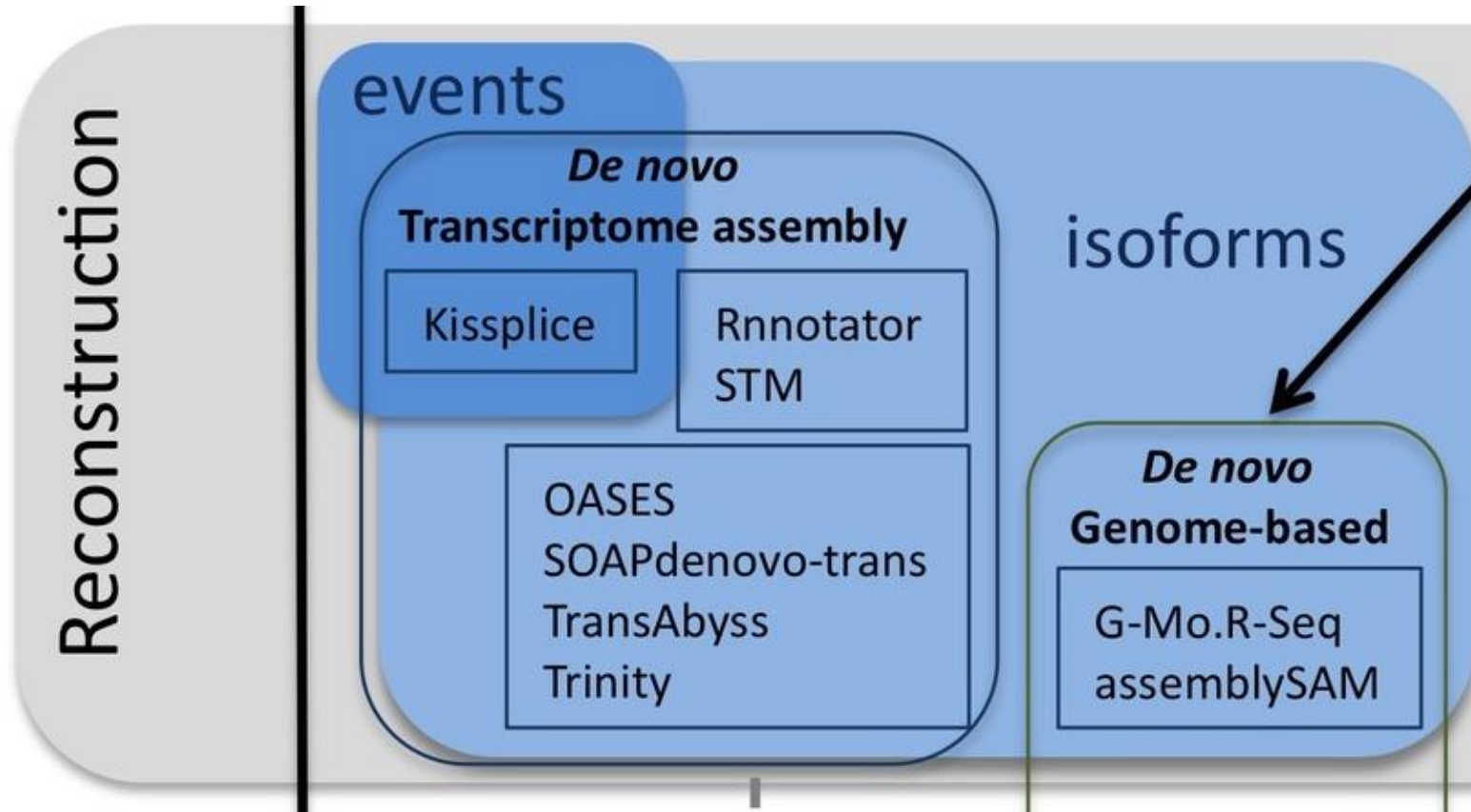


Methods to study splicing by RNA-seq



<http://www.rna-seqblog.com/data-analysis/splicing-junction/methods-to-study-splicing-from-rna-seq/>
<http://arxiv.org/ftp/arxiv/papers/1304/1304.5952.pdf>

Methods to study splicing by RNA-seq

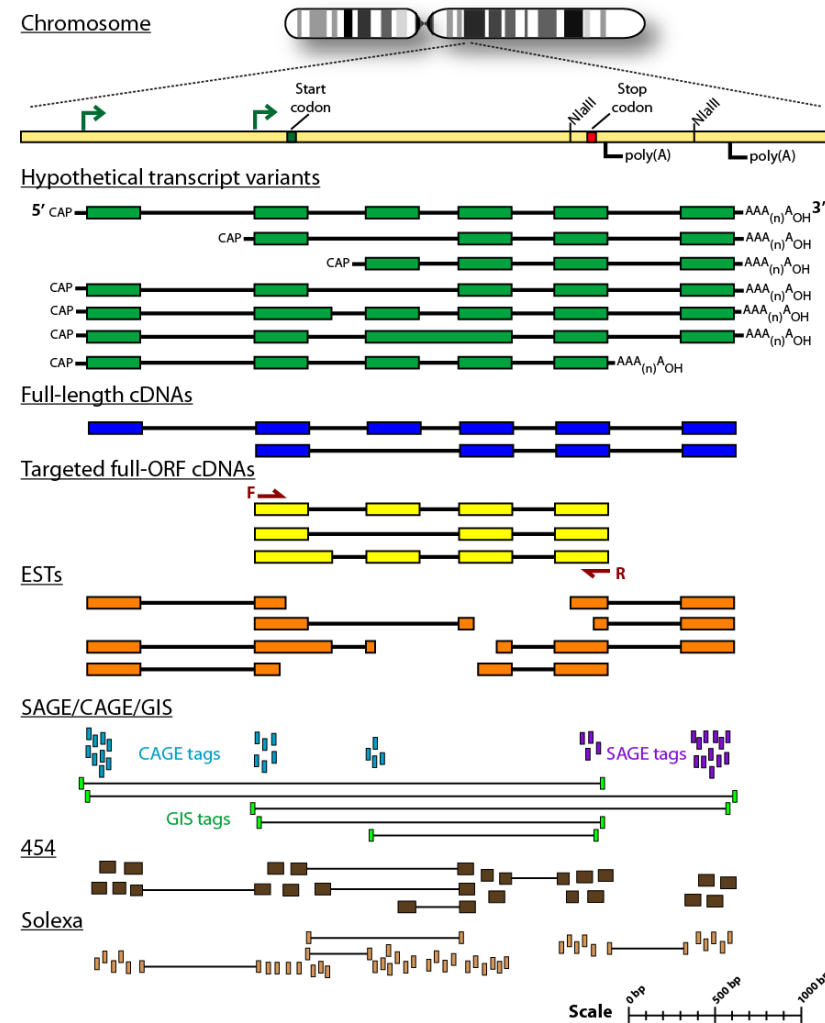


<http://www.rna-seqblog.com/data-analysis/splicing-junction/methods-to-study-splicing-from-rna-seq/>
<http://arxiv.org/ftp/arxiv/papers/1304/1304.5952.pdf>

Useful resources and discussion

- Best approach to predict novel and alternative splicing events from RNA-seq data
 - <http://www.biostars.org/p/68966/>
 - <http://www.biostars.org/p/62728/>
- Alternative splicing detection
 - <http://www.biostars.org/p/65617/>
 - <http://www.biostars.org/p/11695/>
- Identifying genes that express different isoforms in cancer vs normal RNA-seq data
 - <http://www.biostars.org/p/50365/>
- Cufflinks / Cuffdiff Output - How are tests different?
 - <http://www.biostars.org/p/13525/>
- Visualization of alternative splicing events using RNA-seq data
 - <http://www.biostars.org/p/8979/>

Sequencing methods for studying alternative isoforms



We are on a Coffee Break & Networking
Session