



RNA-RNA long range interactions in human introns

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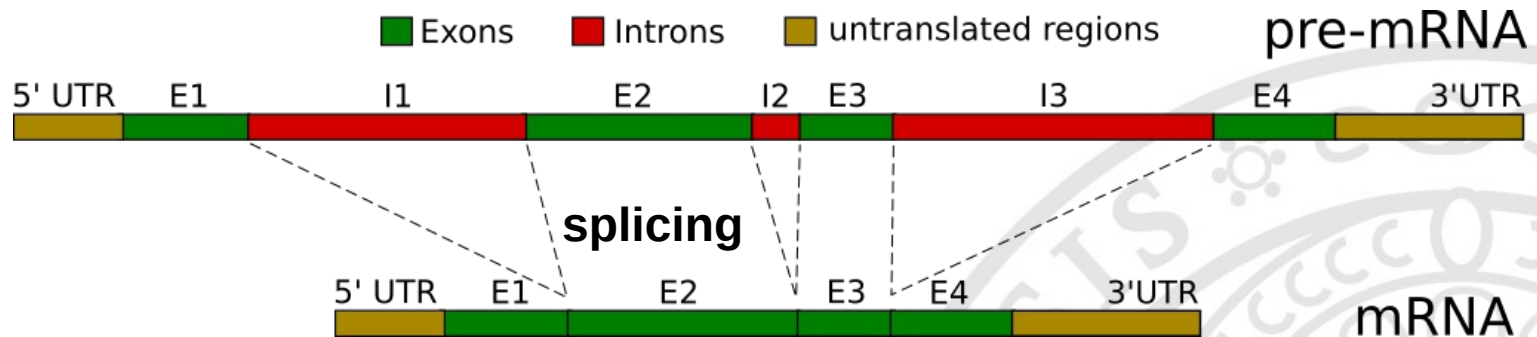


Overview

- Biological Background - Introns
- Biological Background - Splicing
- Questions
- Project Workflow
- Outlook



Biological Background - Introns

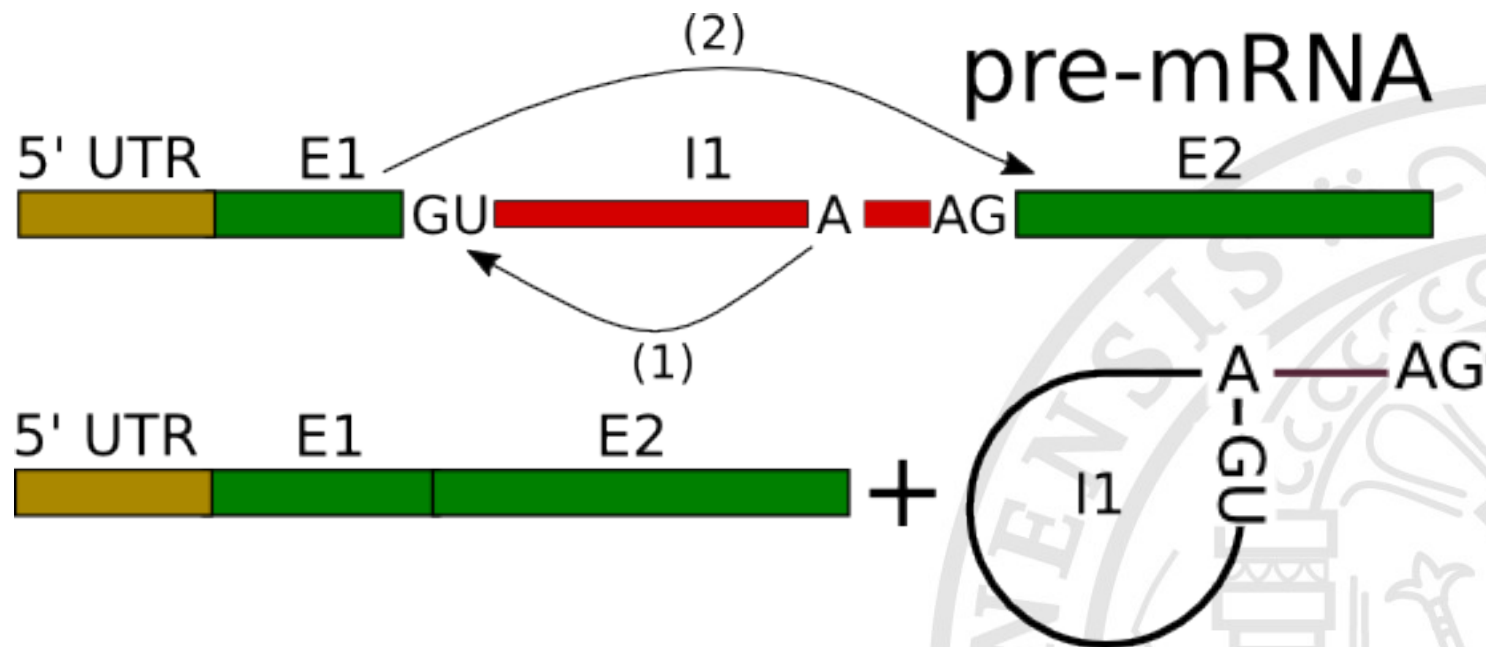


~85 % of exons < 200bp - low stdev

avg. intron length ~5500bp - high stdev

avg. human gene: 6-9 introns (nebulin2 ~150 introns)

Biological Background - splicing



spliceosome (5snRNAs + ~150 proteins)

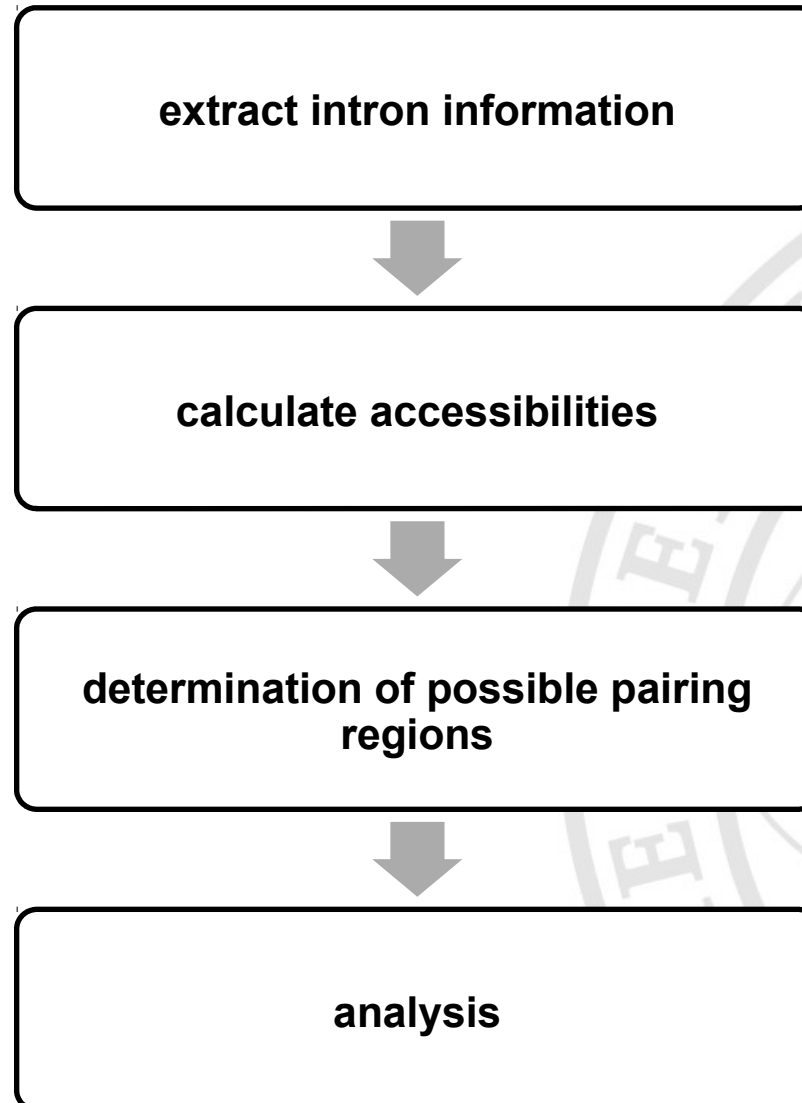


Question

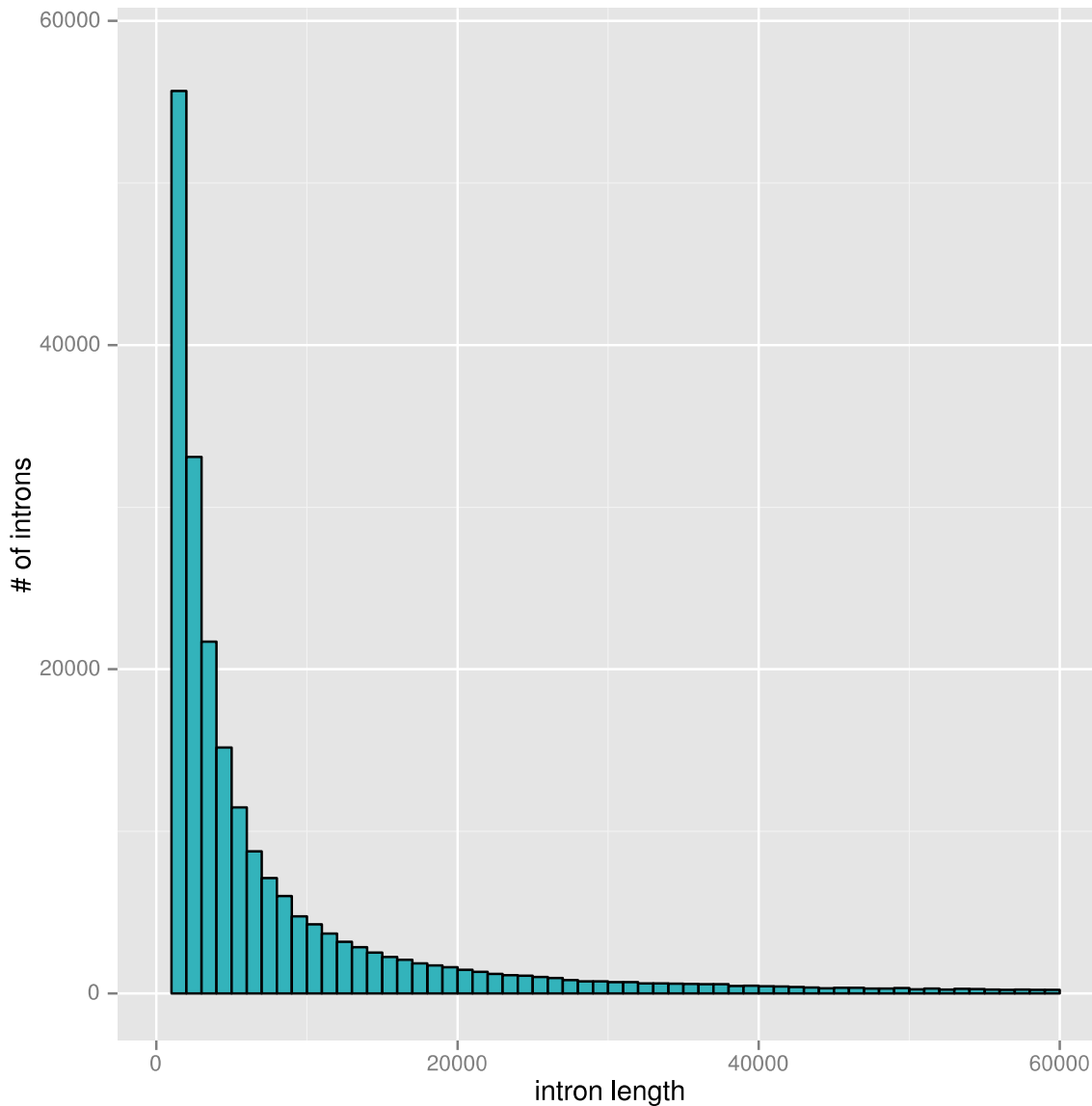
Are there secondary structures supporting the splicing mechanism of long intronic sequences?



Project Workflow



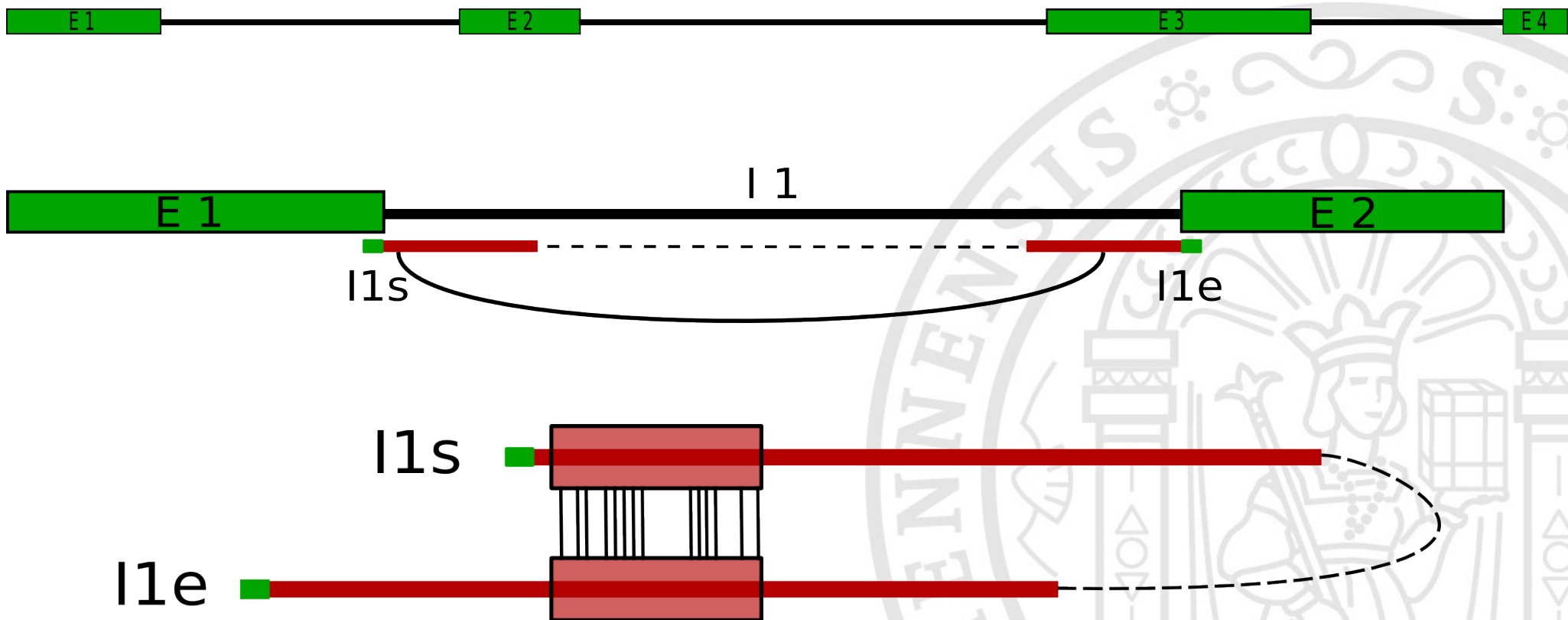
Intron distribution dataset



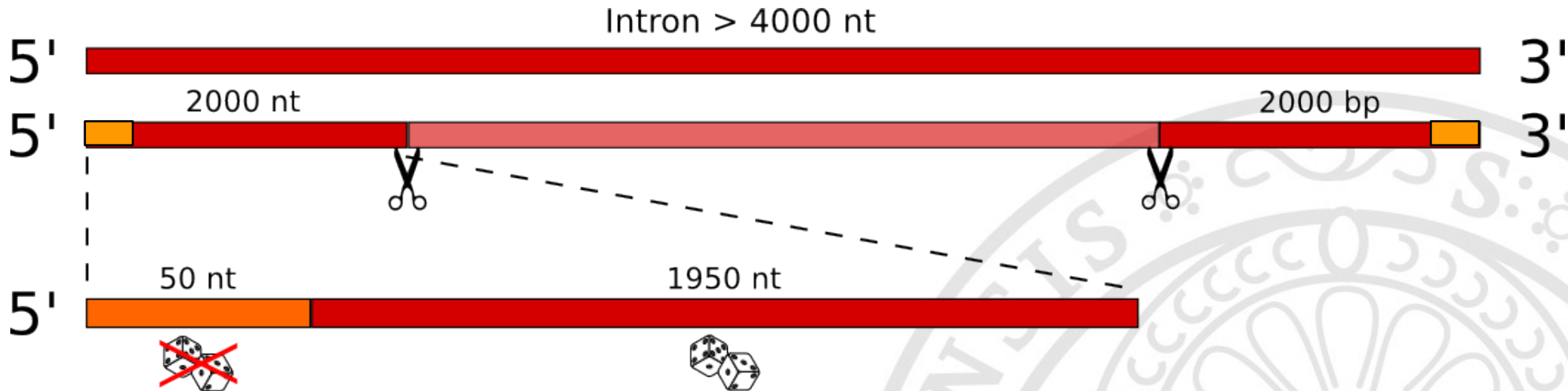
Introns:

- Total:
~280.000 > 400bp
- 220.000 < 10.000 bp
- 3 % longer than 60k bp
- 1% longer than 120k bp

Interaction scheme



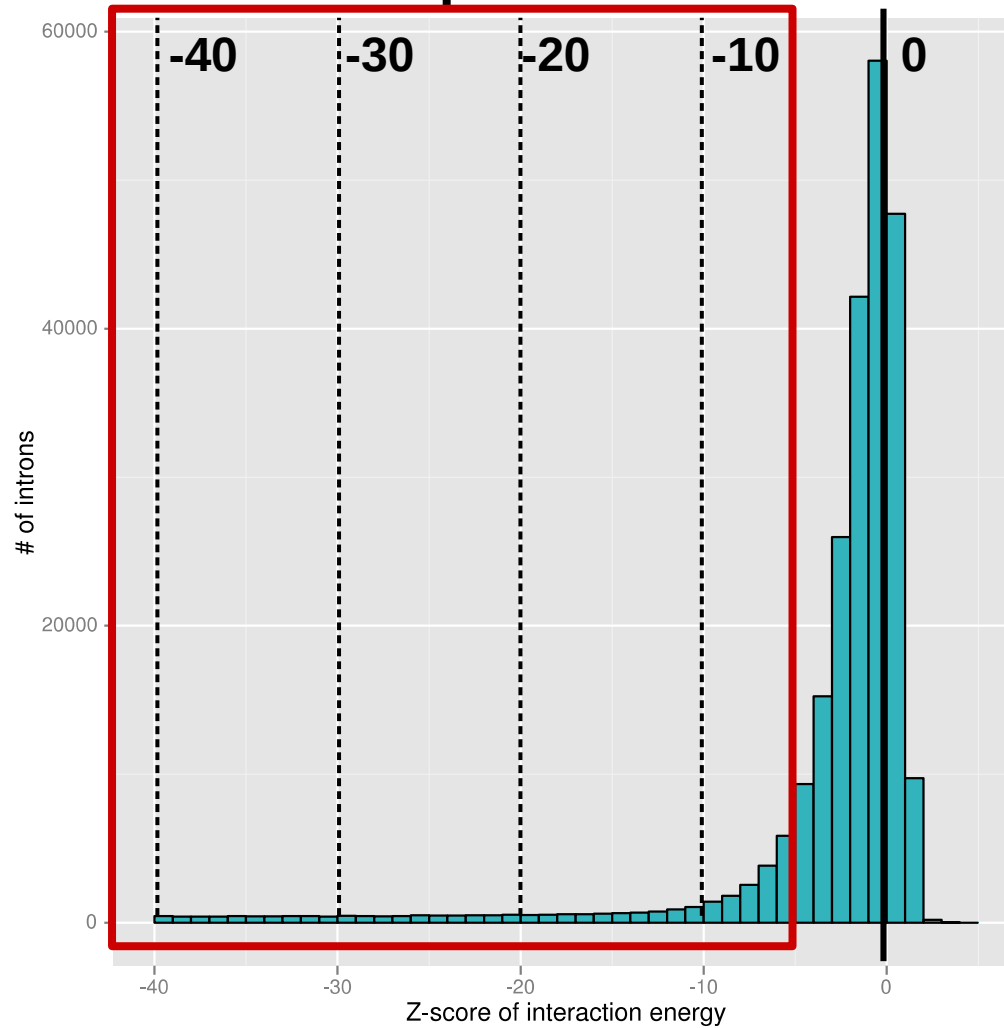
Flanking Regions



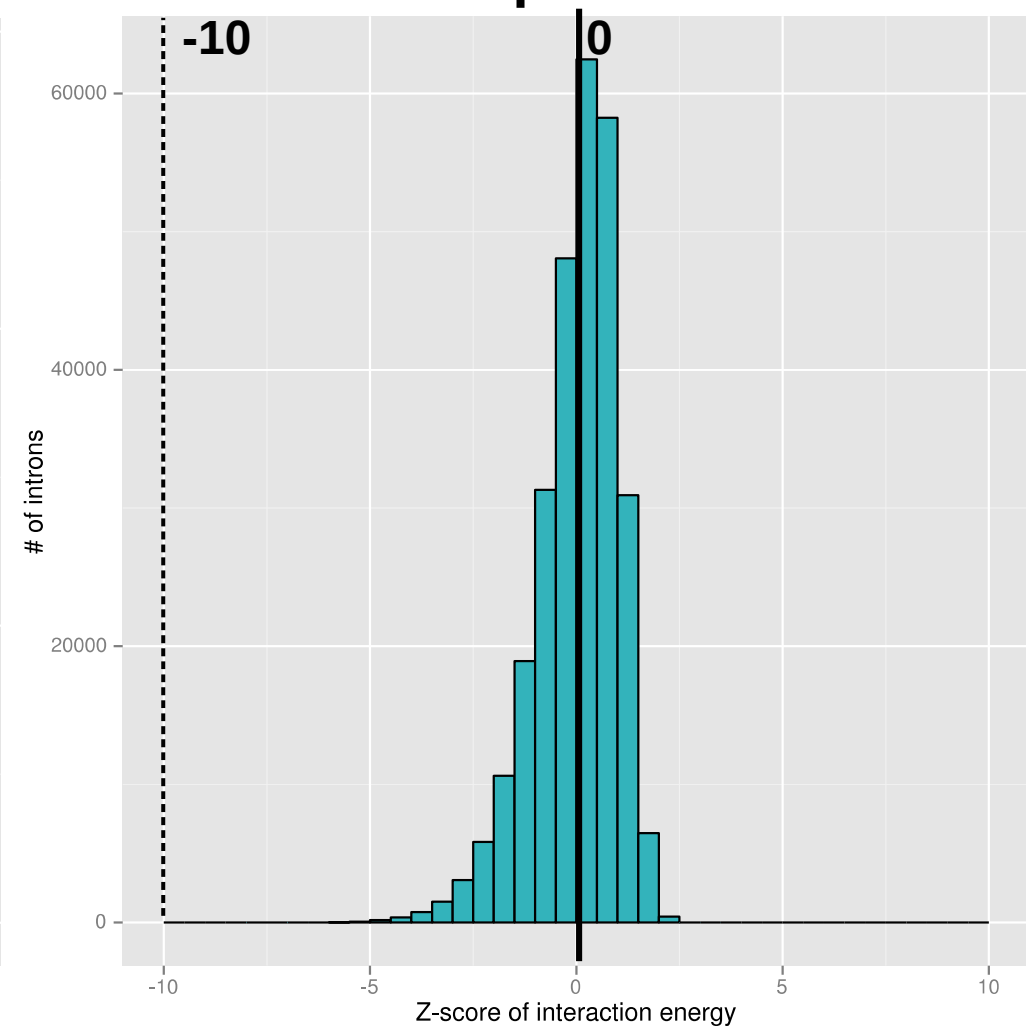
- Possible splicing motifs
e.g. Polypyrimidin tract (3' end)

Z-scores: native vs random

native Sequences



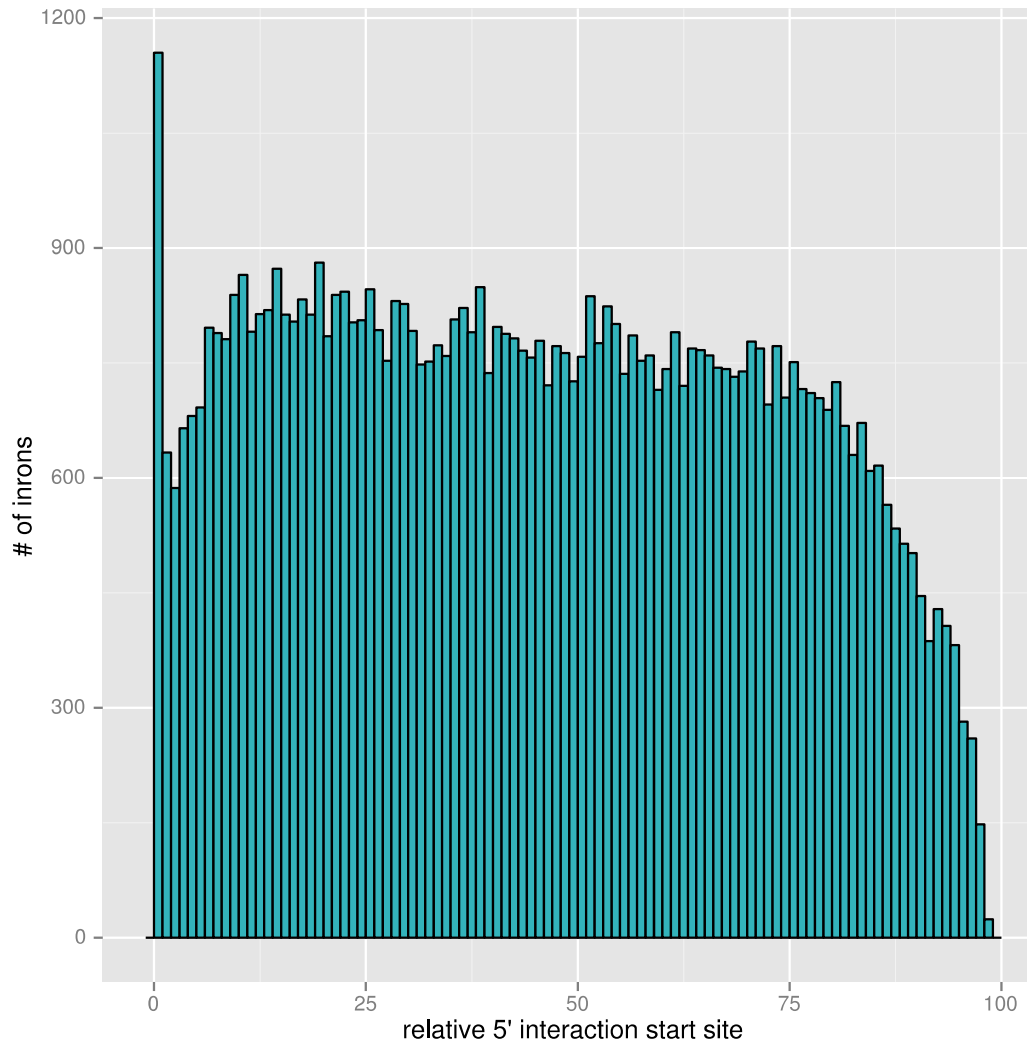
random Sequences



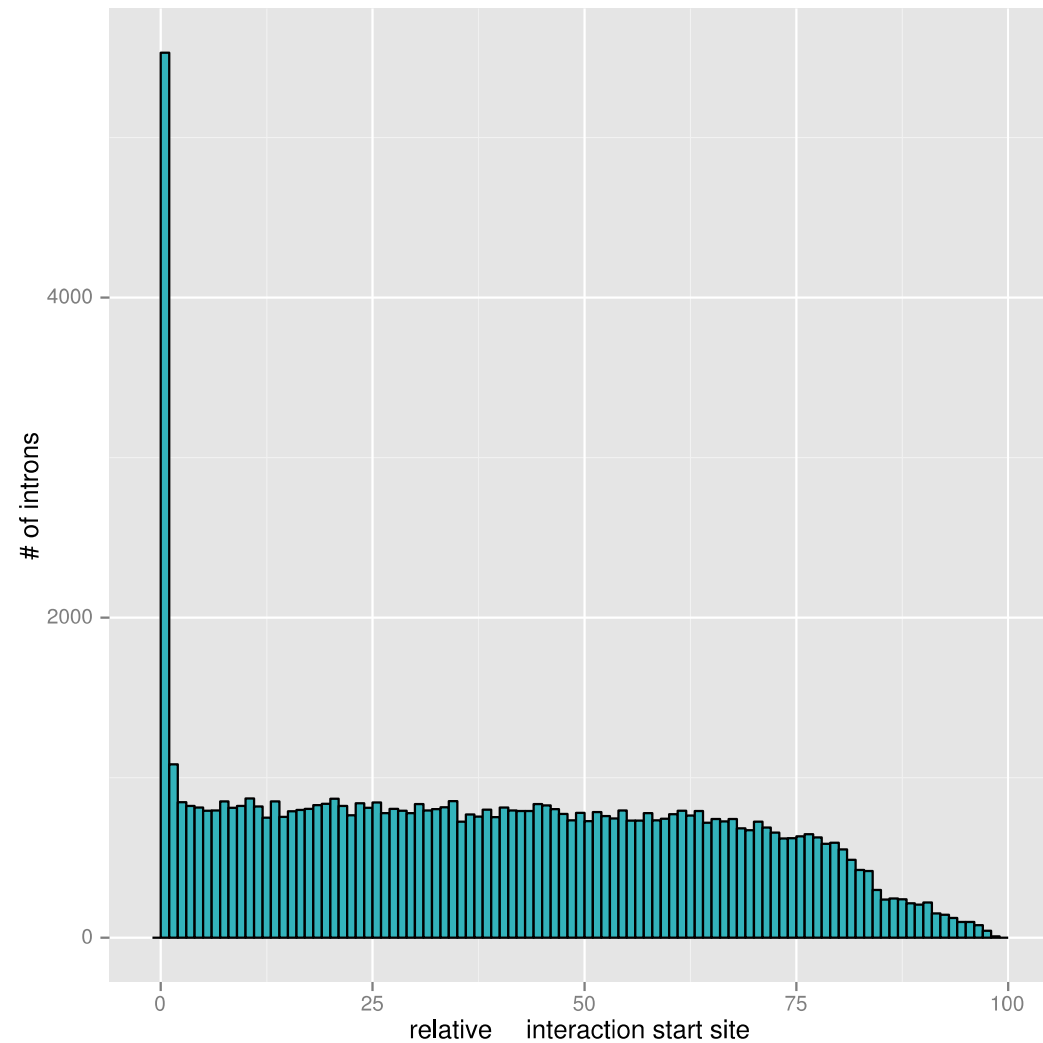


Relative interaction start

5' region



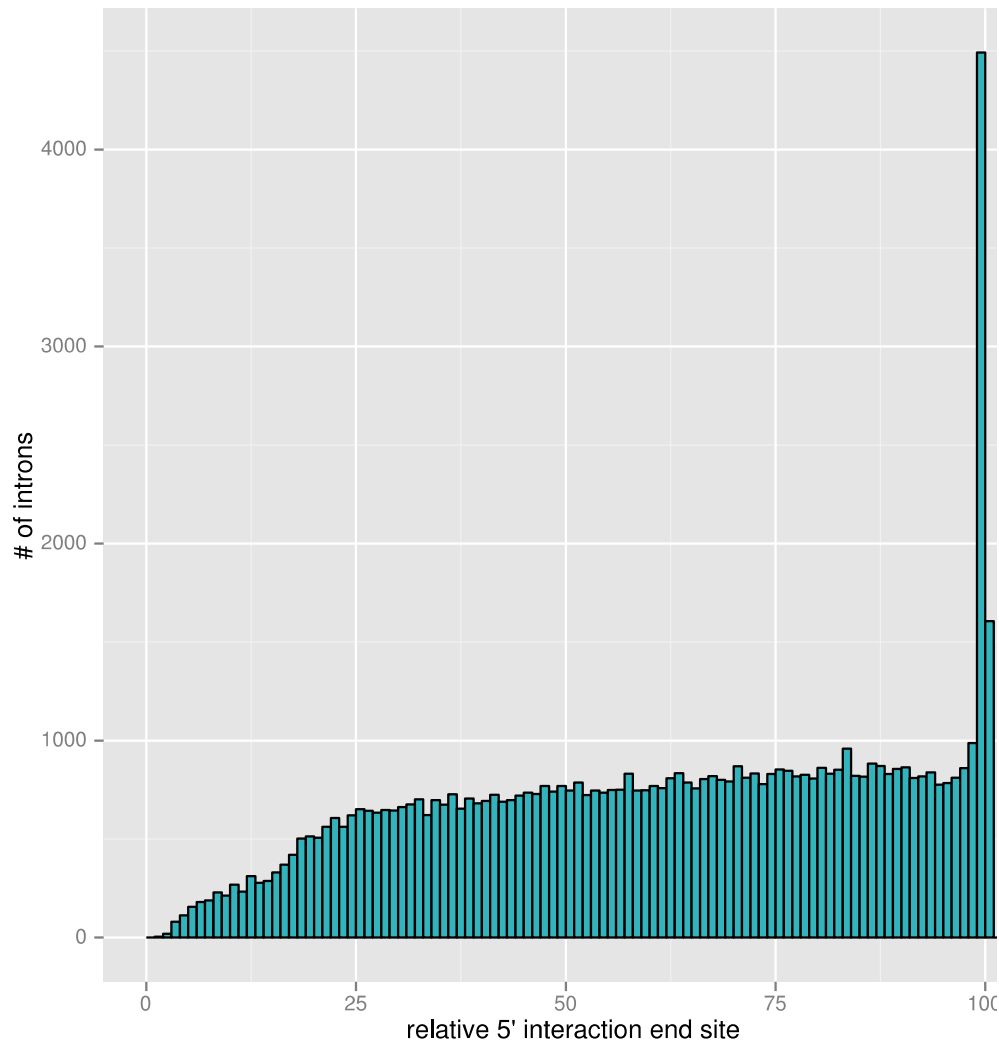
3' region



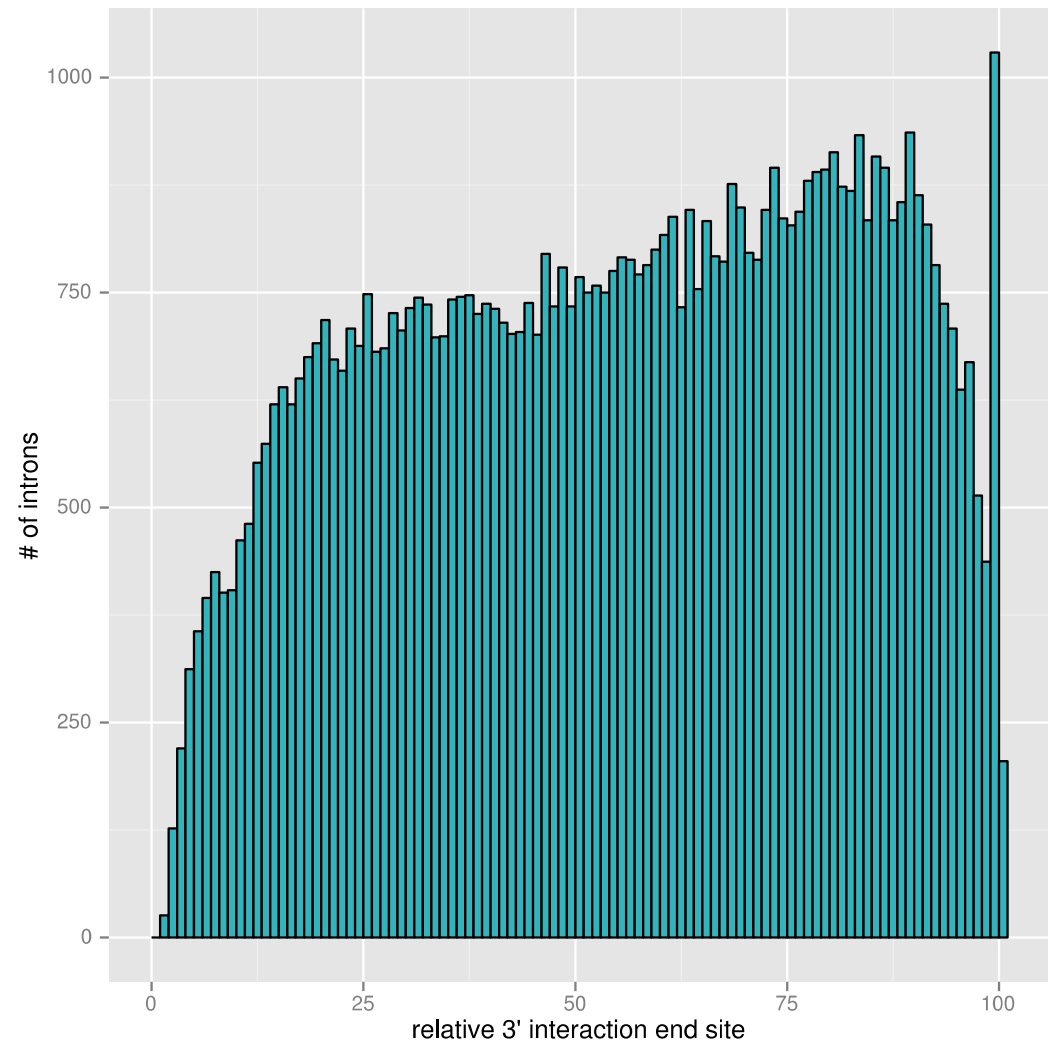


Relative interaction end

5' region



3' region





Outlook

- get rid of border effects
- clustering of introns
- examine nice examples
- more detailed analysis of good interactions
- pattern search



Thanks for your attention!

