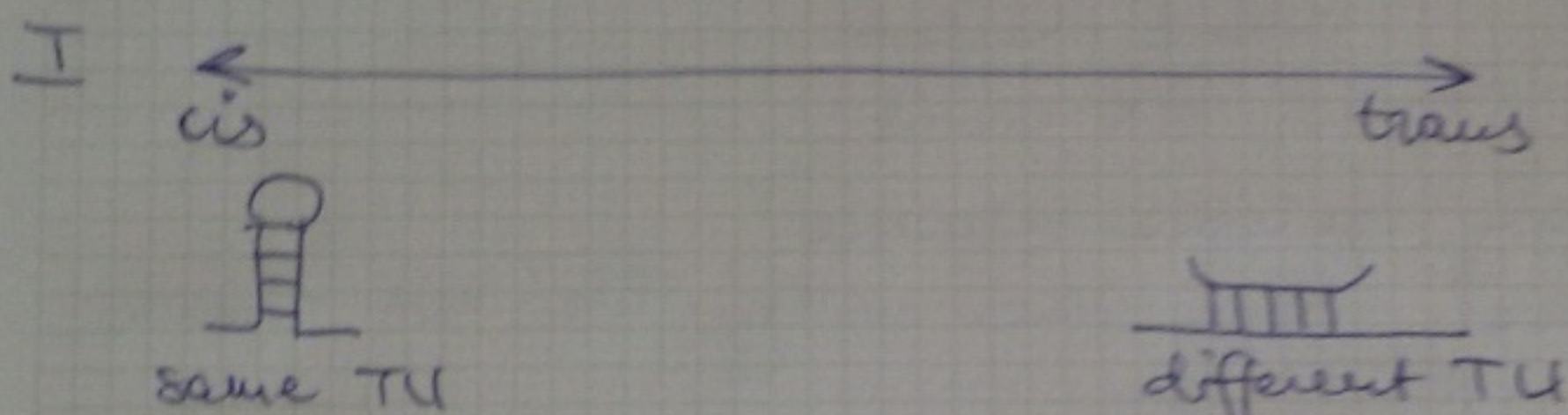
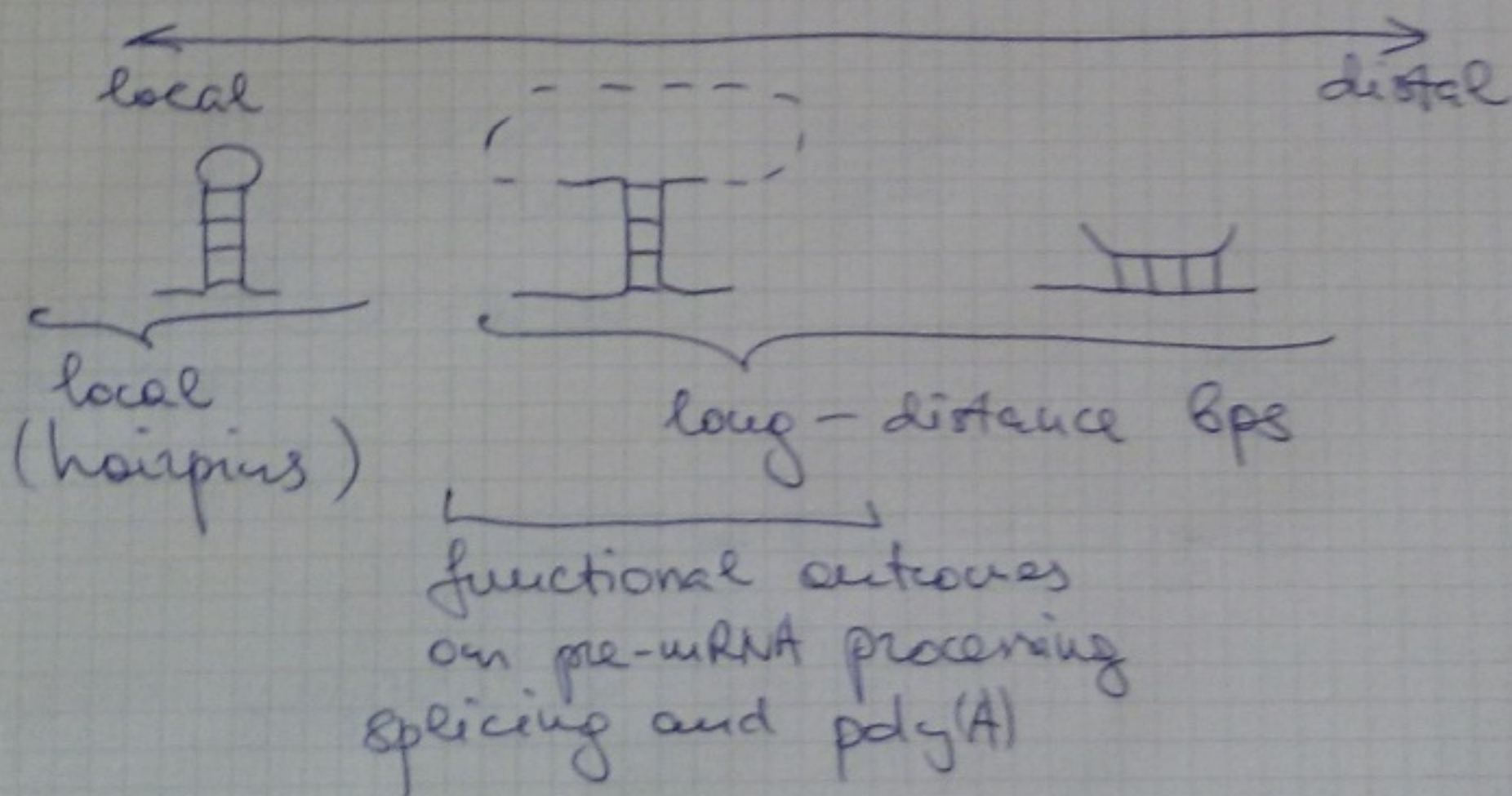


Old and new hypotheses about eukaryotic RNA-RNA interactions

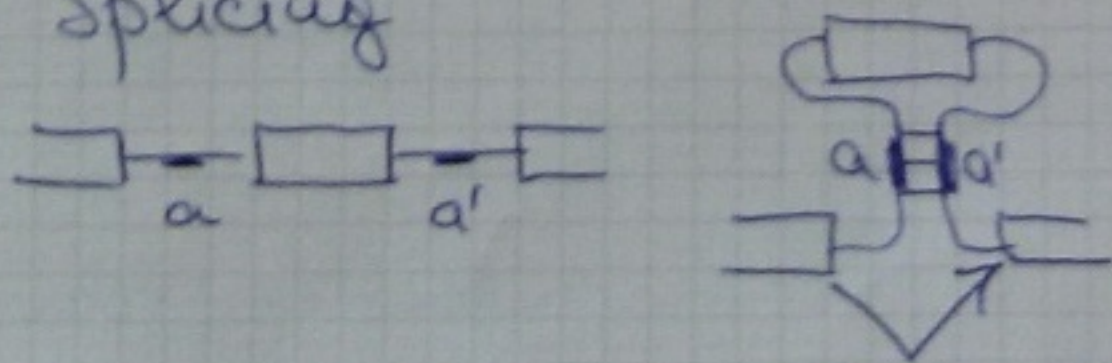


prok. upregulators
 euk. miRNA/target 3'UTR
 HBI-S2/SH2(2C)R

Functionality: interference with some important regulatory element in the target sequence

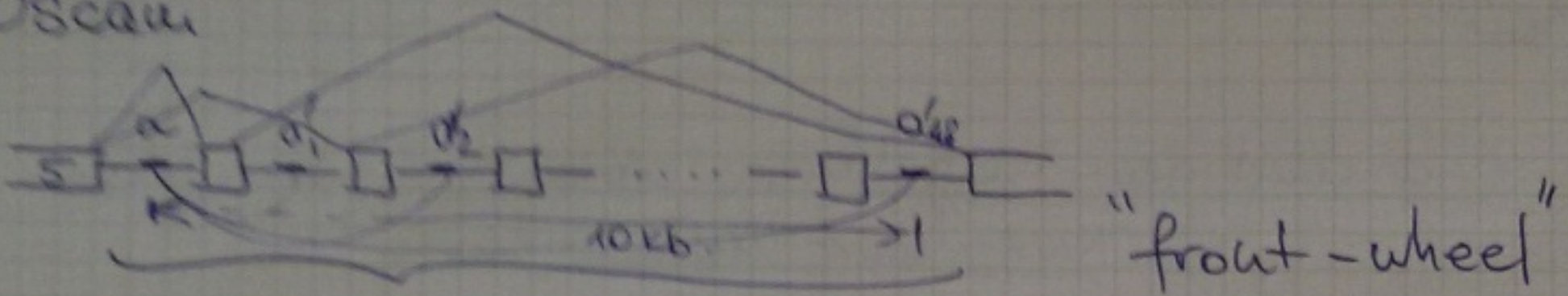


II Splicing



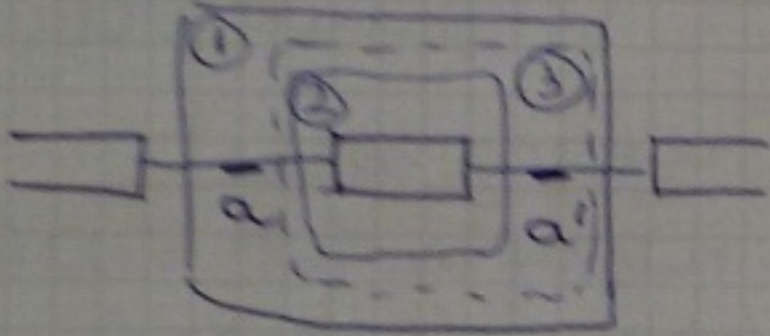
looping-out, conformation

1. Dscam

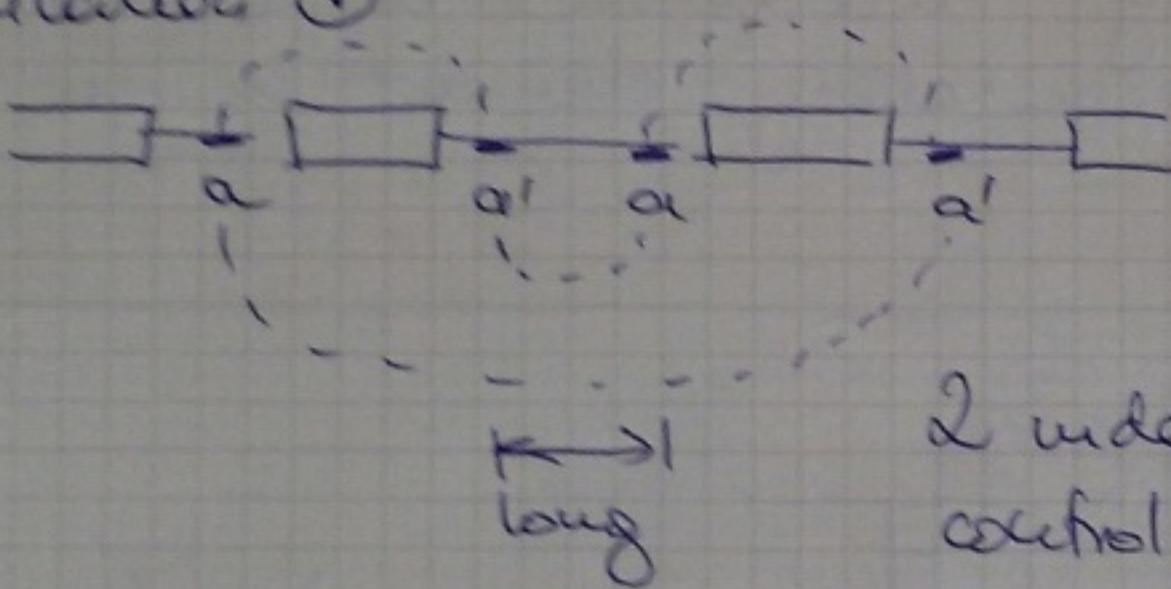


exon 6 cluster
48 HEX exons.

highly repetitive sequence
Evolve? Some genes really "like" RNA structure



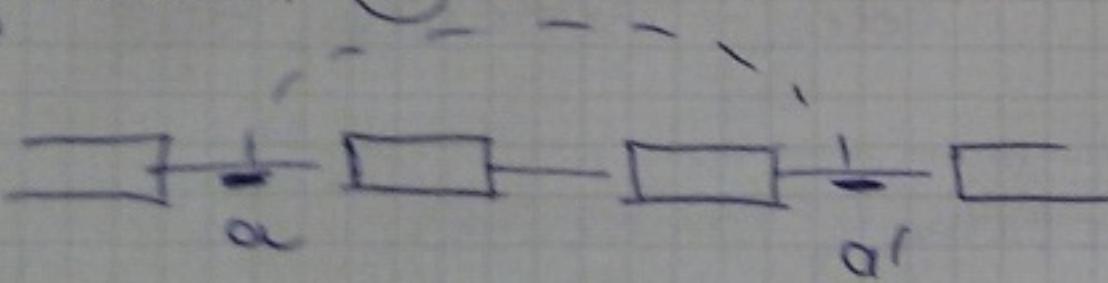
Duplication ①



2 independent
control elements

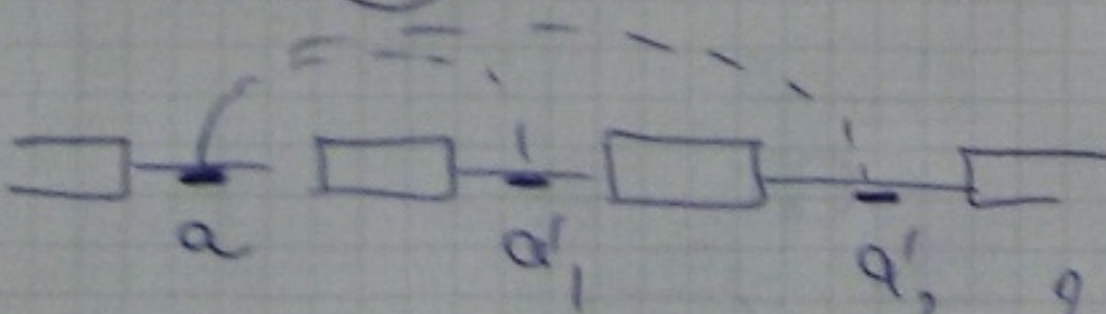
Ca-d-10 [Pervouchine
RNA, 2014]

Duplication ②



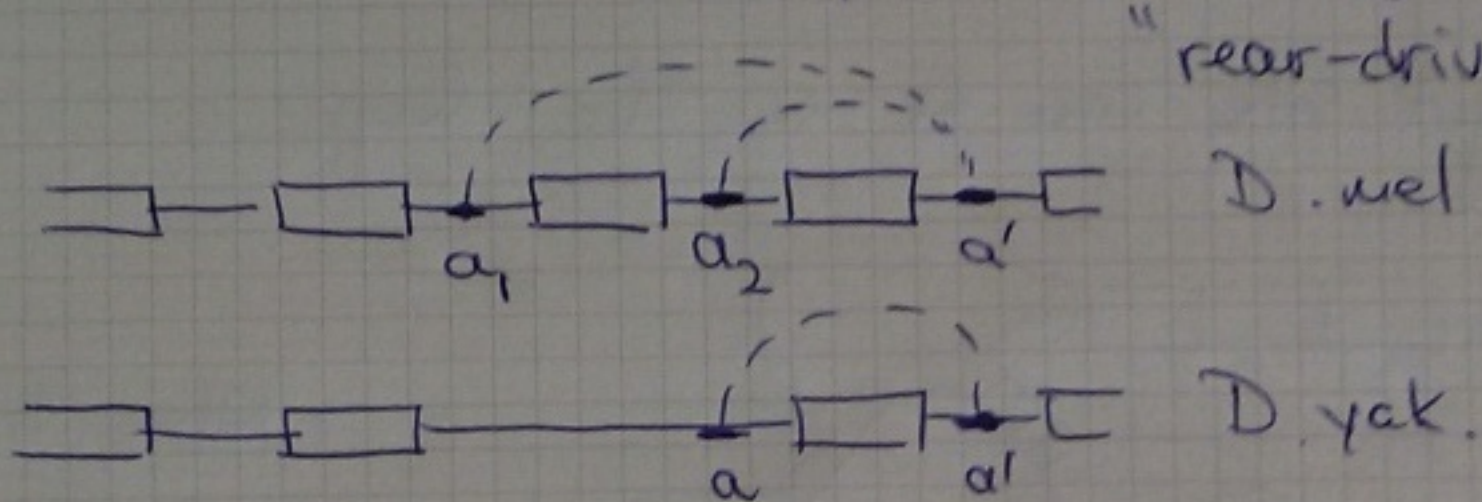
2 overlapping exons

Duplication ③



2 mutually-exclusive
exons

2. Gene 14-3-3 ζ *Drosophila* [Yang et al, 2010]

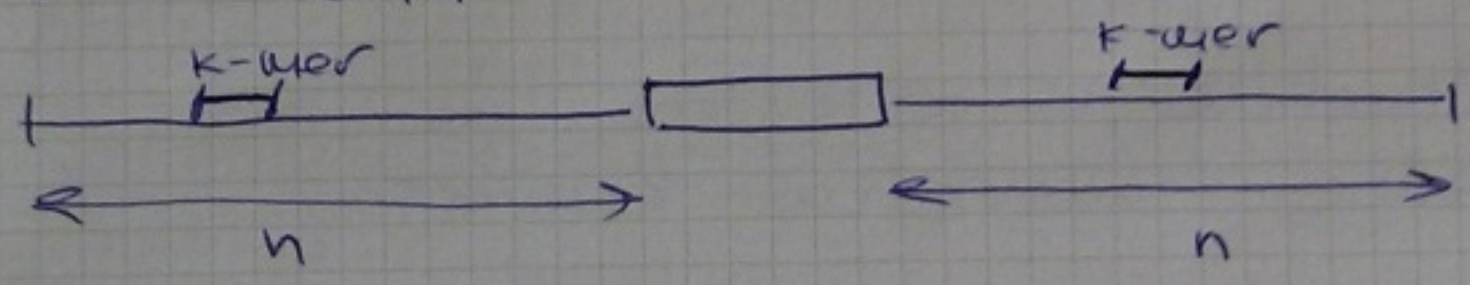


MHC gene *Drosophila*

3. MRP gene in *Drosophila* [in progress]

- 9 mex exons in *D. mel*.
- 4 mex exons in *C. elegans*

4. How frequently do these structures occur on random?



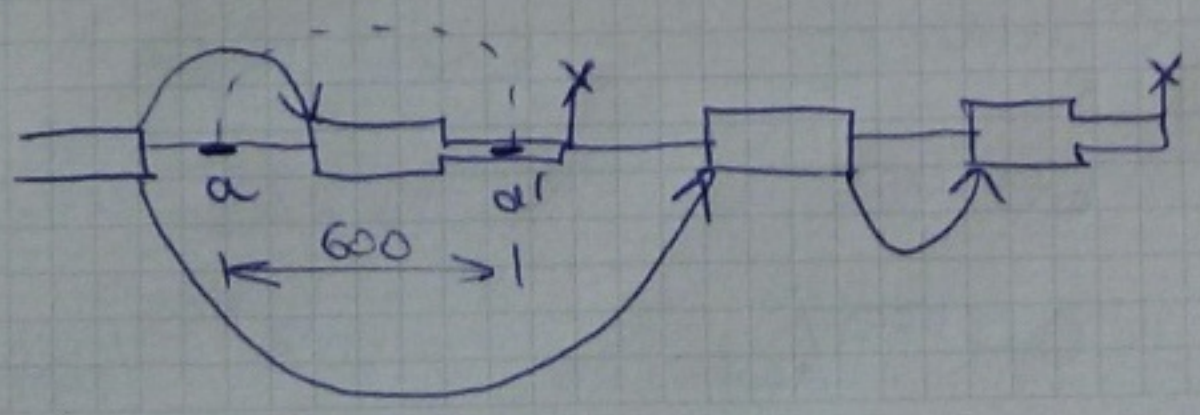
$$k \ll n$$

$$E[\# \text{ of compl. } k\text{-mers}] = \frac{1}{4^k} \cdot n^2 \approx 1.$$

$$n^2 = 4^k \quad n = 2^k$$

$$k = 10 \quad n \approx 2^{10} = 1024$$

III Splicing, Cleavage, and Polyadenylation



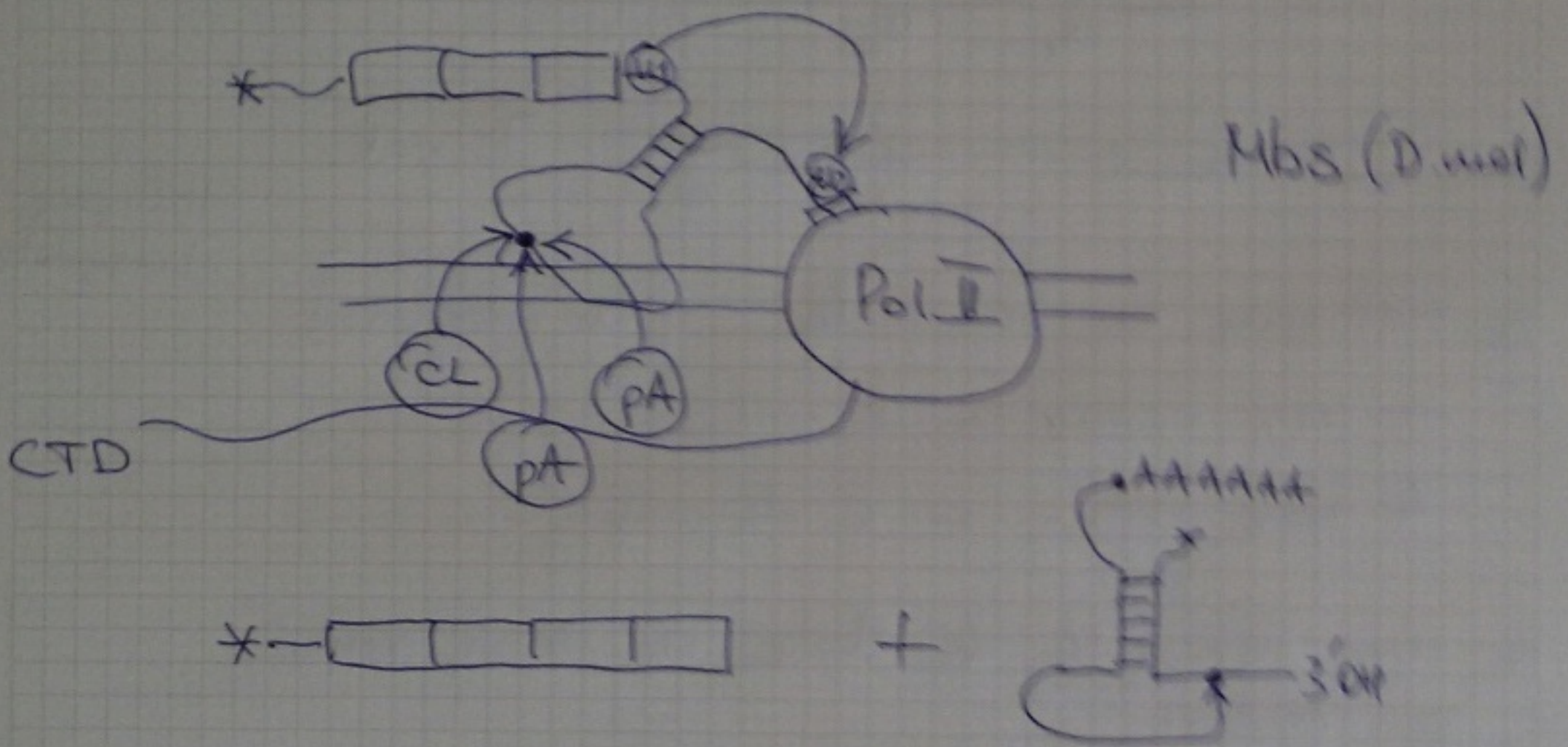
Nmnet
[Raker, 2009]

RNA structure \rightarrow poly A?

1. cleavage/pA senses



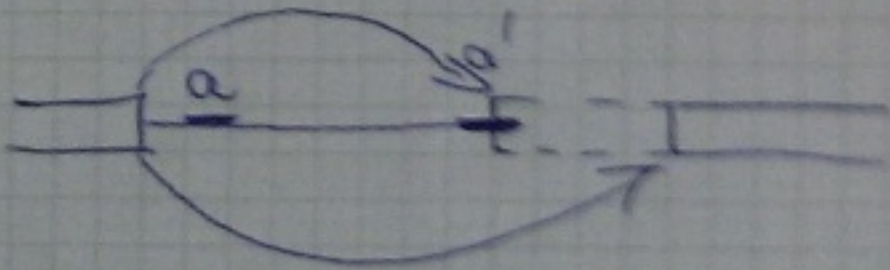
2. pA site can be in the loop



RNA structure is a rescue for pre-mature transcription termination

IV Constitutive vs alt. splicing

1. Atrophin (Gug)



CAAUCG
GUUAGC

50:50

6AAACC
CUUUCG

60:40

-0.4 kcal/mol

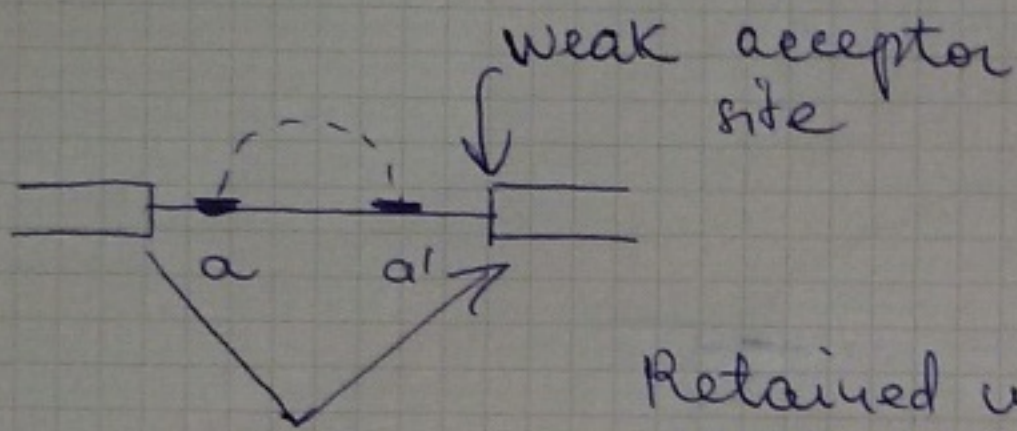
GAGACC
CUCUGG

75:25

-0.8 kcal/mol

tee-2 in *C. elegans*

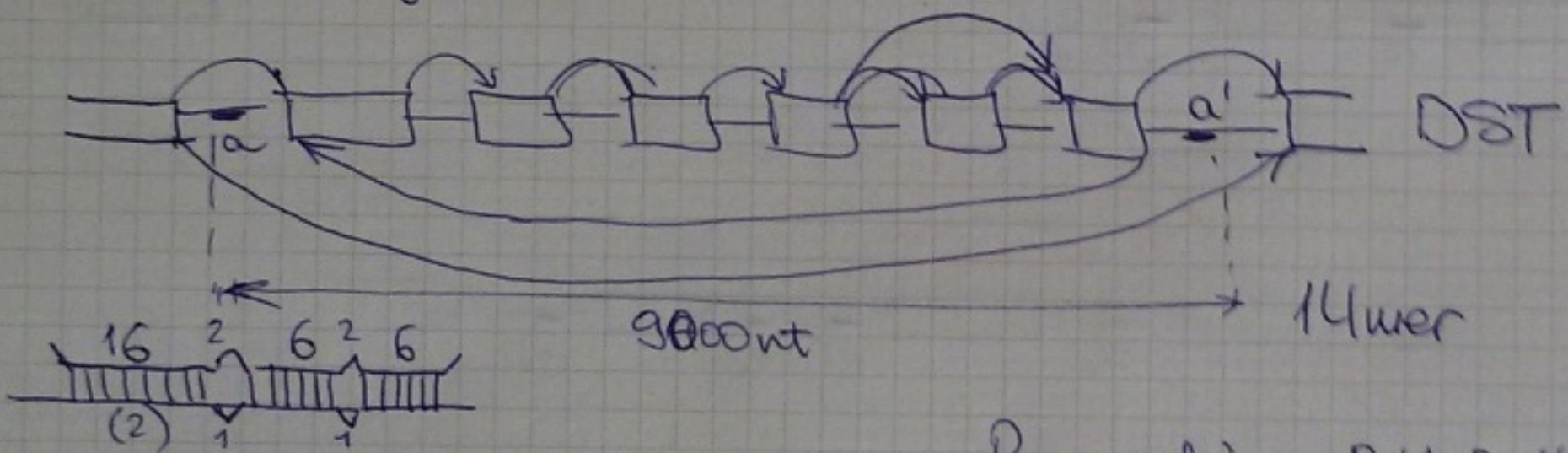
2. SF1



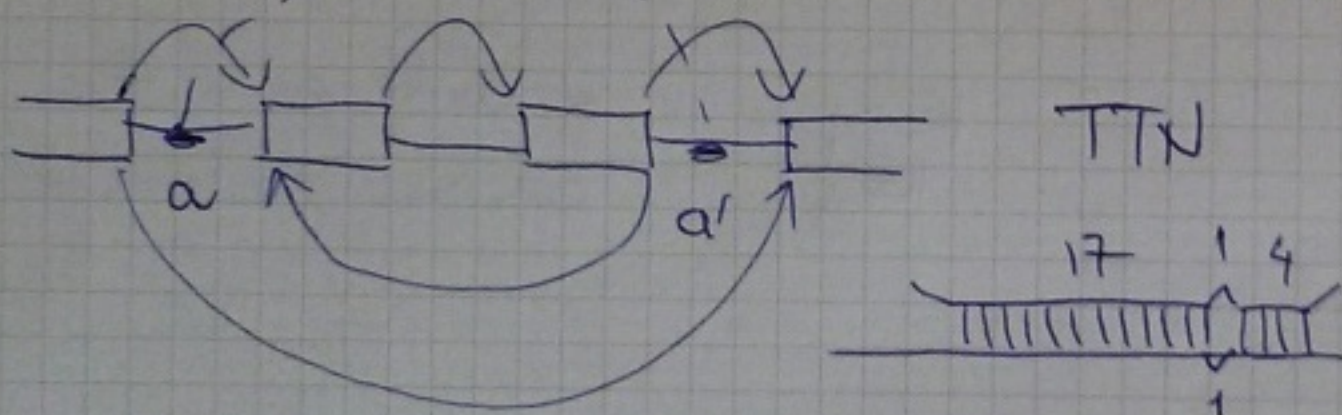
Retained intron \rightarrow PTC \rightarrow NMD

Most of the RNA structural elements are associated with constitutive splicing events.

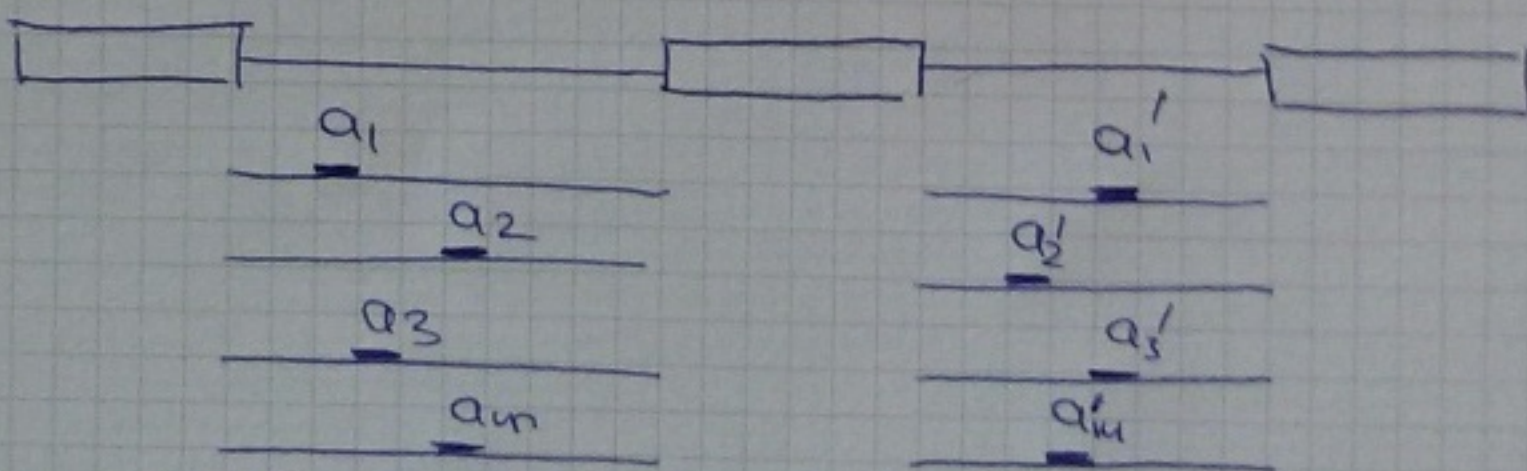
V. Circularization



Pervouchine, RNA 2014



VI. Technology to discover these structures



a_i is complementary to a'_i

$a_1 \sim a_2 \sim$

$a'_1 \sim a'_2 \sim$

$\sim a_n$ are similar

$\sim a'_n$ are similar