3. Gene prediction

- All genes end on a stop codon
- A simple algorithm for gene prediction
- Searching for start and stop codons
- Predicting all the genes in a sequence
- Making the predictions more reliable
- Boyer-Moore algorithm
- Index and suffix trees
- Probabilistic methods
- Benchmarking the prediction methods
- **Gene prediction in eukaryotic genomes**

Eukaryotic genomes

- Very long intergenic regions
  - Genes: less than 5% of a human genome

- Genes are interrupted by non-coding introns


exon
intron
exon
intron
exon
intron
exon
RNA

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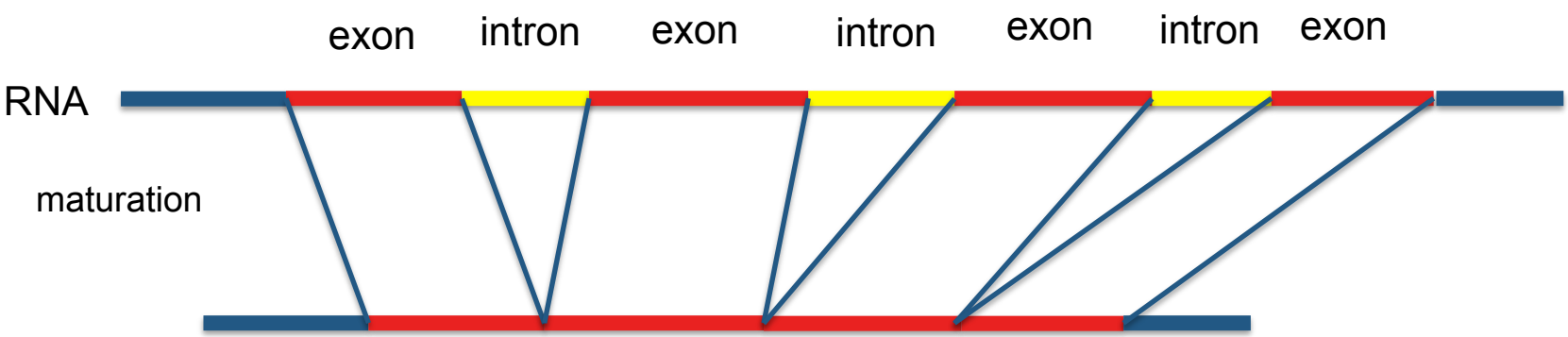
  - Less then 2.5% of a human genome is made up of coding regions
- Introns are removed (spliced) during mRNA maturation


exon
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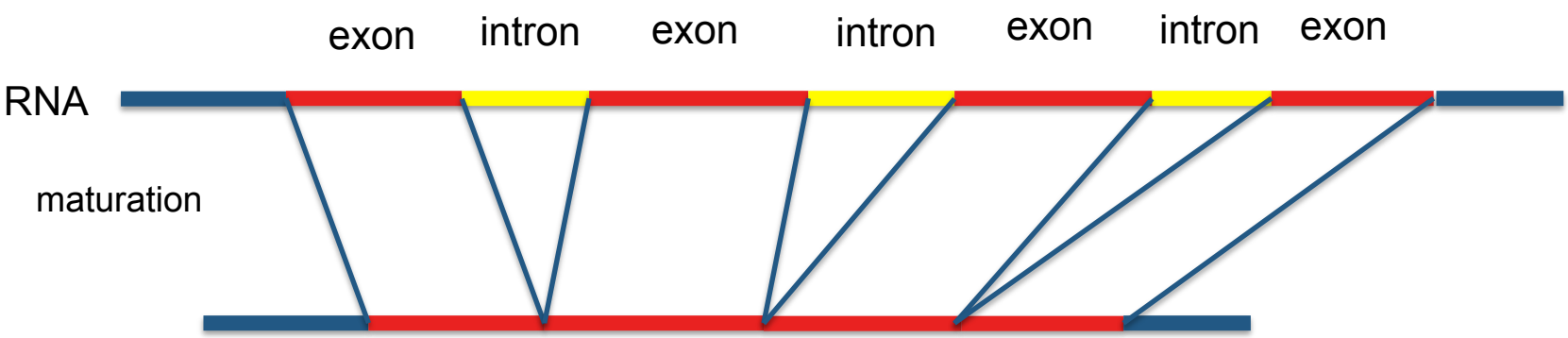
intron
exon
RNA
maturation


exon
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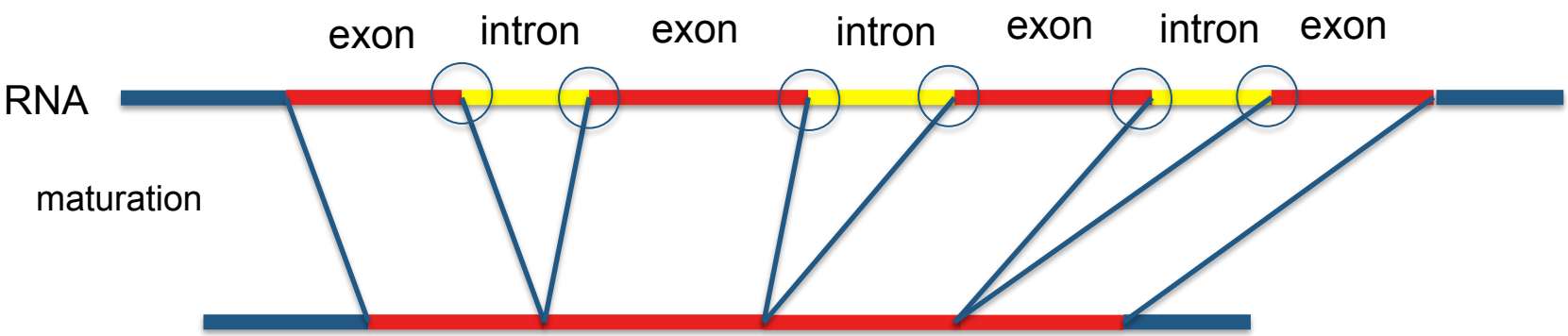
exon
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RNA
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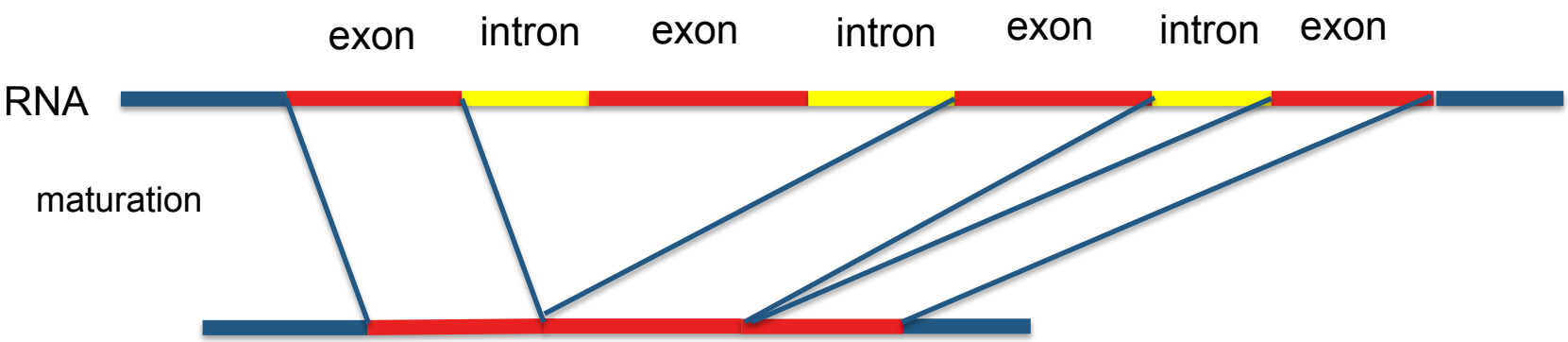
- Alternative splicing
  - One gene, several proteins


exon
intron
exon
intron
exon
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exon
RNA
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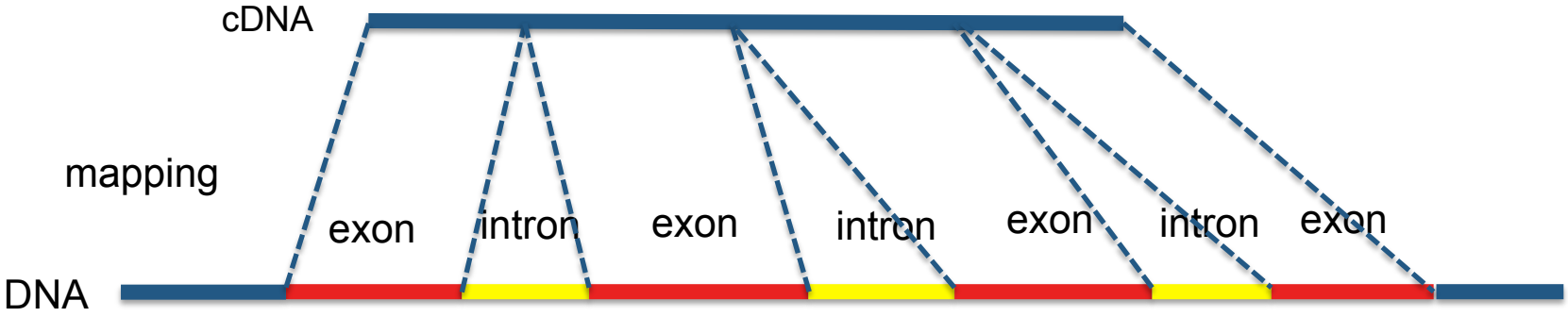
Use every source of knowledge

- Hidden Markov Models (HMM)
  - As many connected models as types of regions:

    coding, non coding, intergenic, etc.
- Patterns for exon/intron junctions
- Experimental data
  - complementary DNA (cDNA)


cDNA
mapping
exon
intron
exon
intron
exon
intron
exon
DNA

Still an open problem

- Eukaryotic gene prediction is still an open problem
- Gene predictors do not attempt to mimick the cellular processes
- Bioinformatic gene predictions are predictions