



Markovovy modely v Bioinformatice

Outline

- Markovovy modely obecně
- Profilové HMM
- Další použití HMM v Bioinformatice

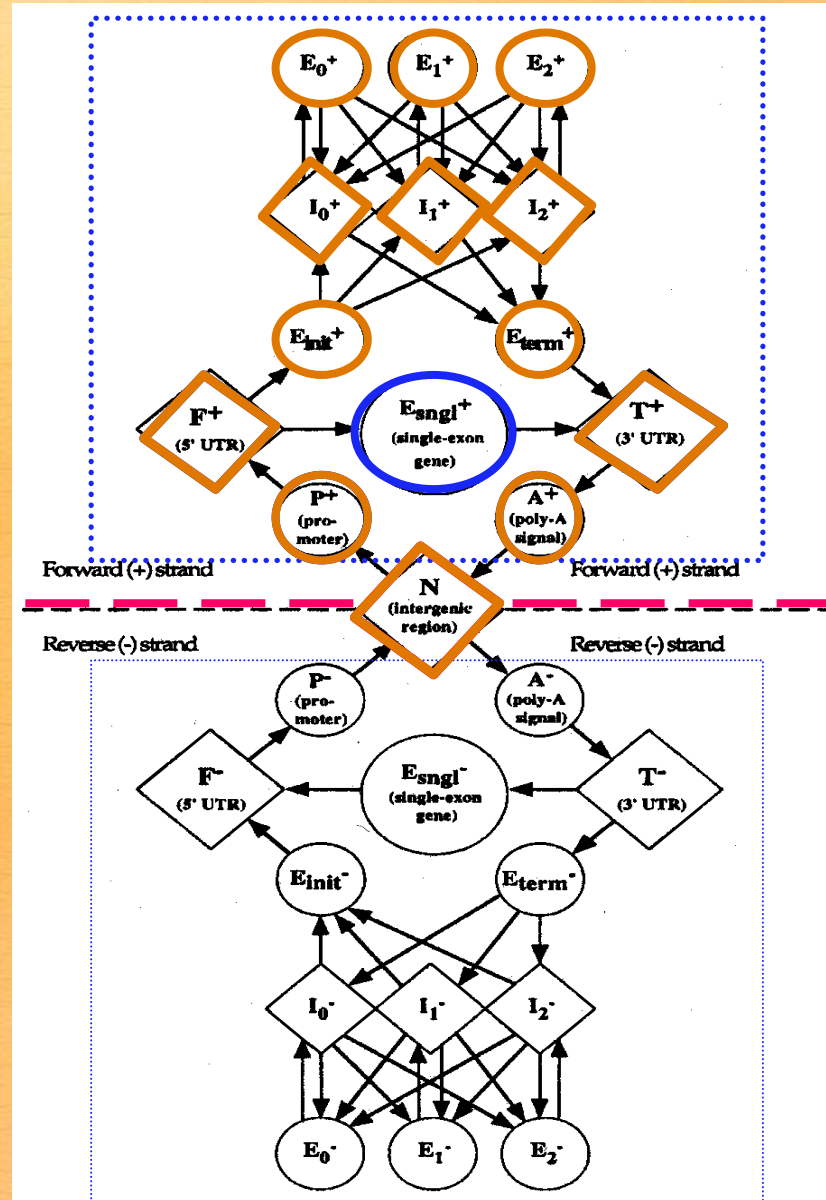
Osnova

- Tradiční použití
- Hierarchické HMM
- Párové HMM
- Kontextové HMM

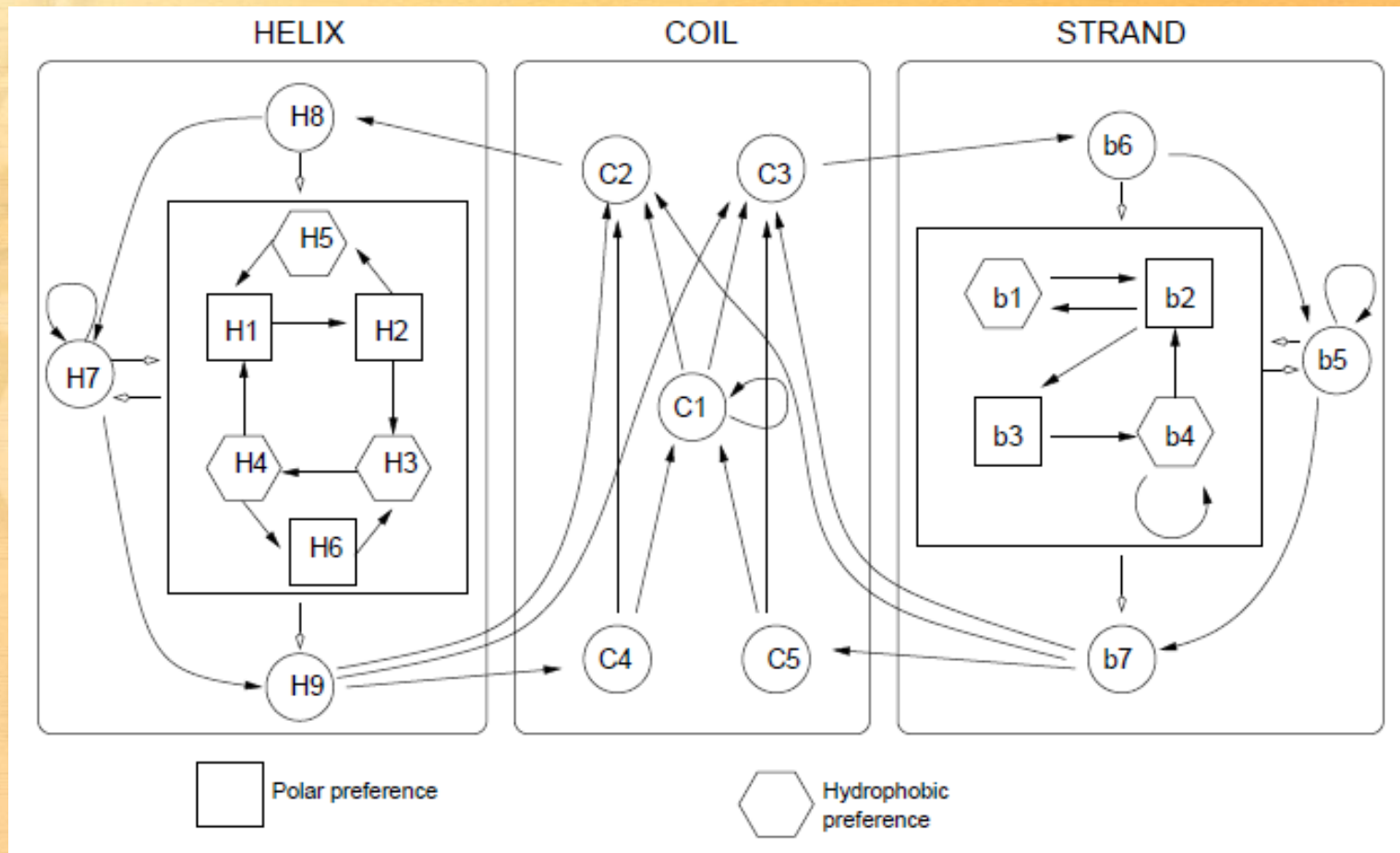
Tradiční použití

- Hledání genů
- Predikce sekundární struktury
- Topologie transmembránových proteinů

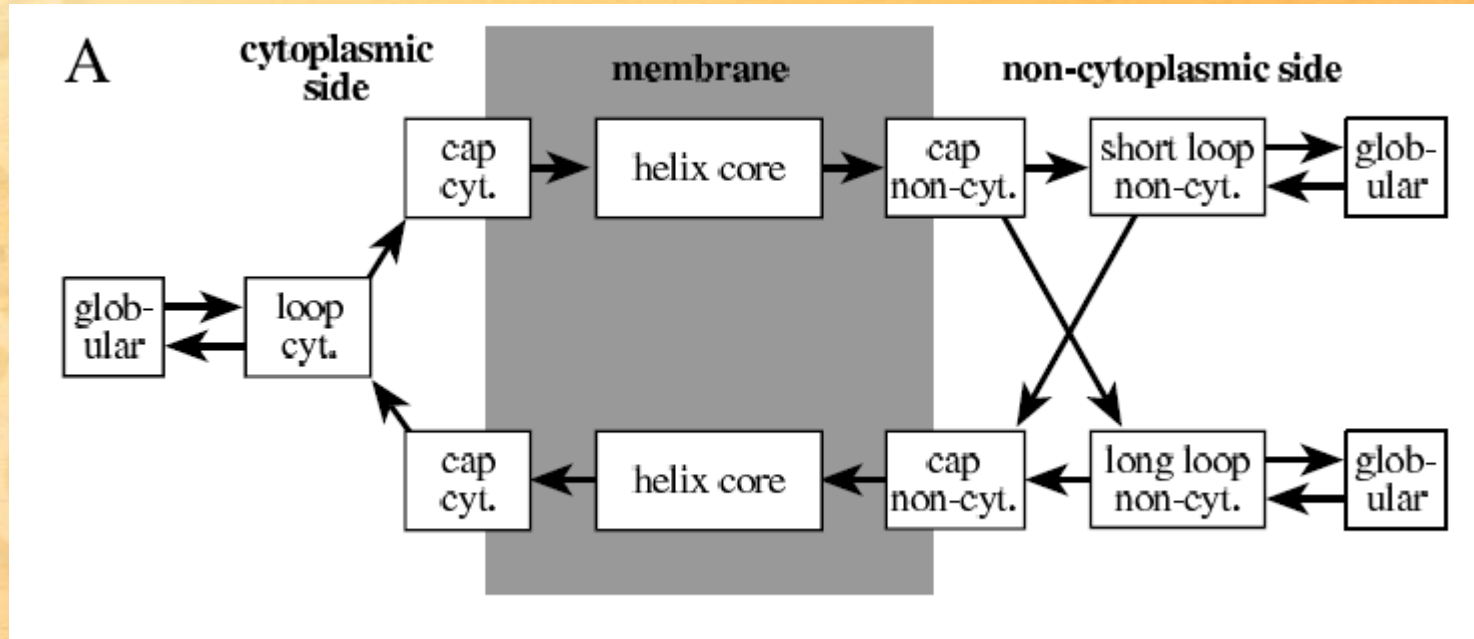
GenScan



Sekundární struktura



Transmembranové proteiny

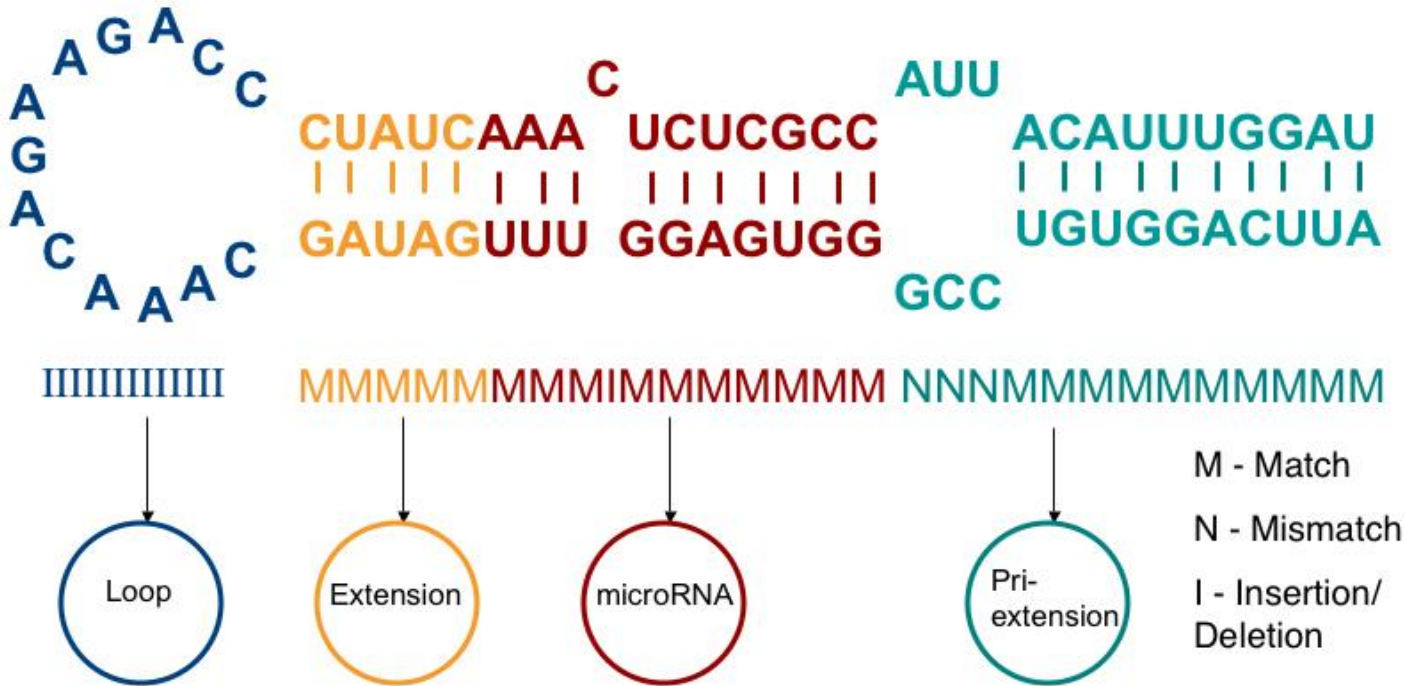


Hierarchické HMM

- **Každý stav HHMM může být další HMM**
- **Ukázka použití**
 - **miRNA topology prediction**
 - **Joint analysis of ChIP-chip and ChIP-seq data**

miRNA topology and input

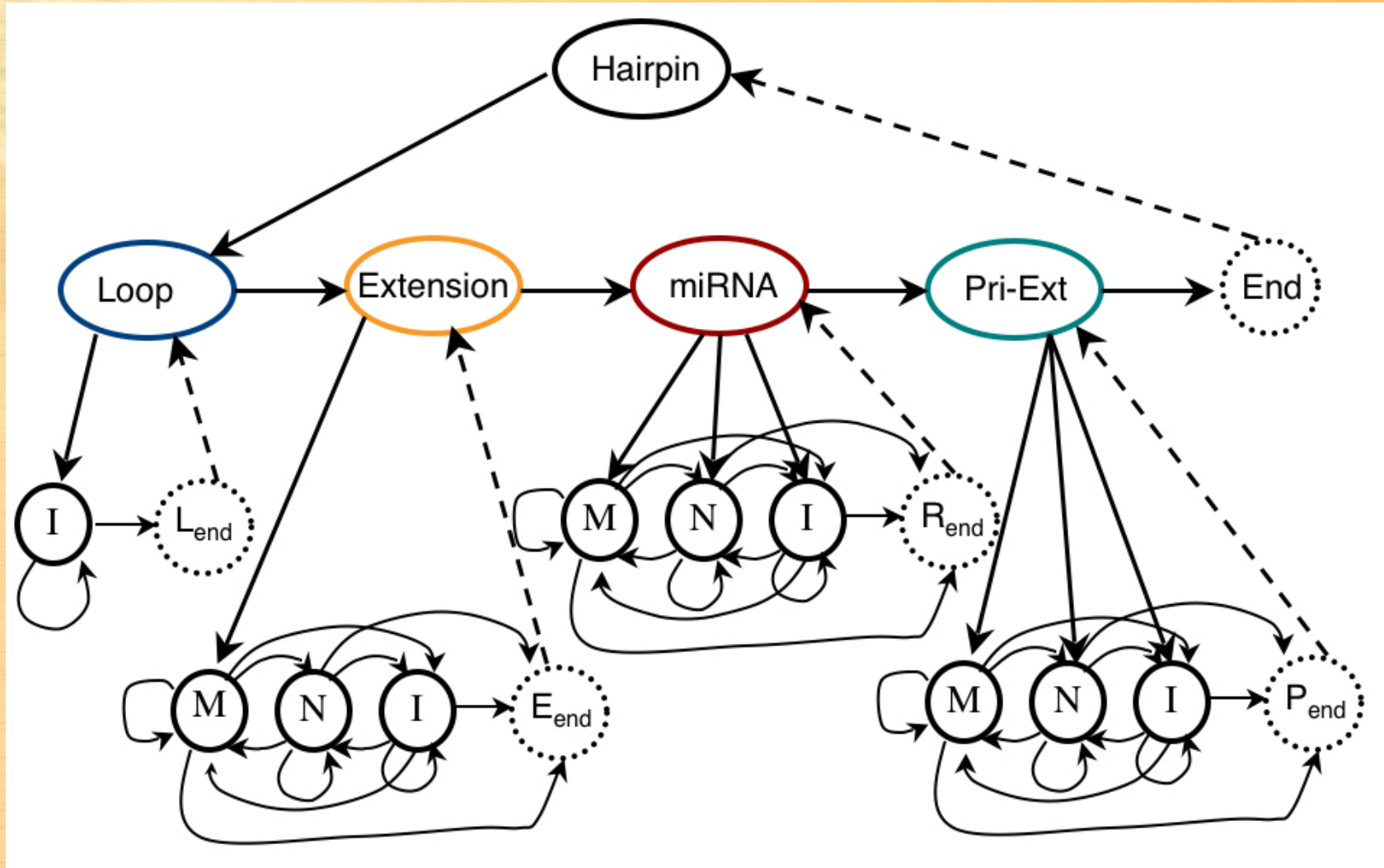
a.



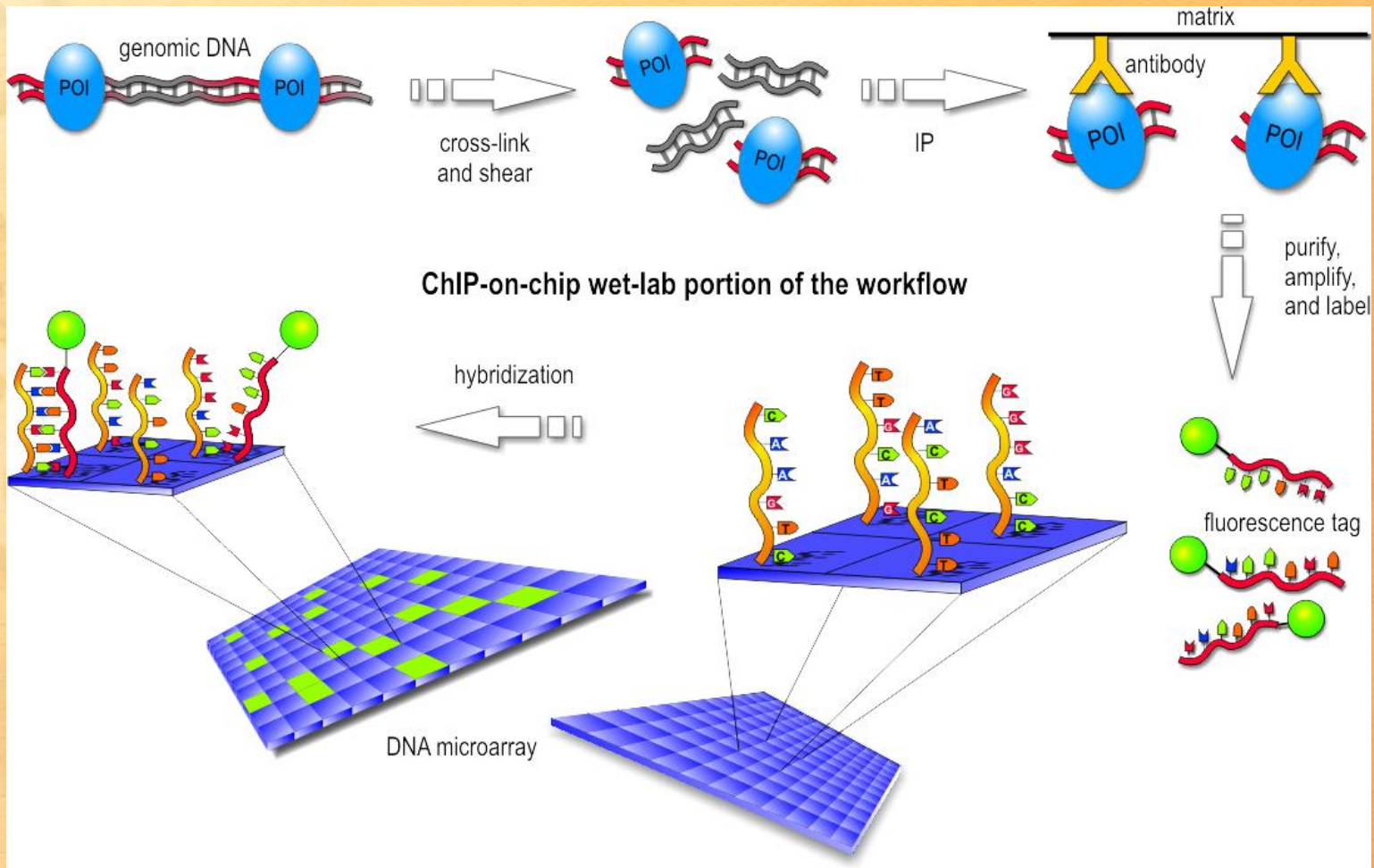
b.



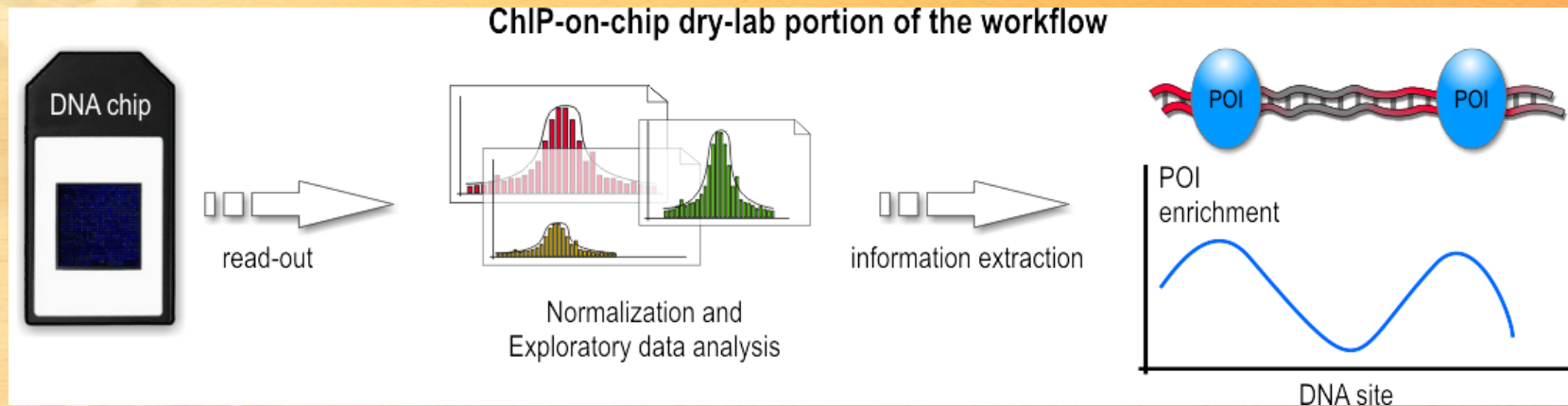
HHMM topology



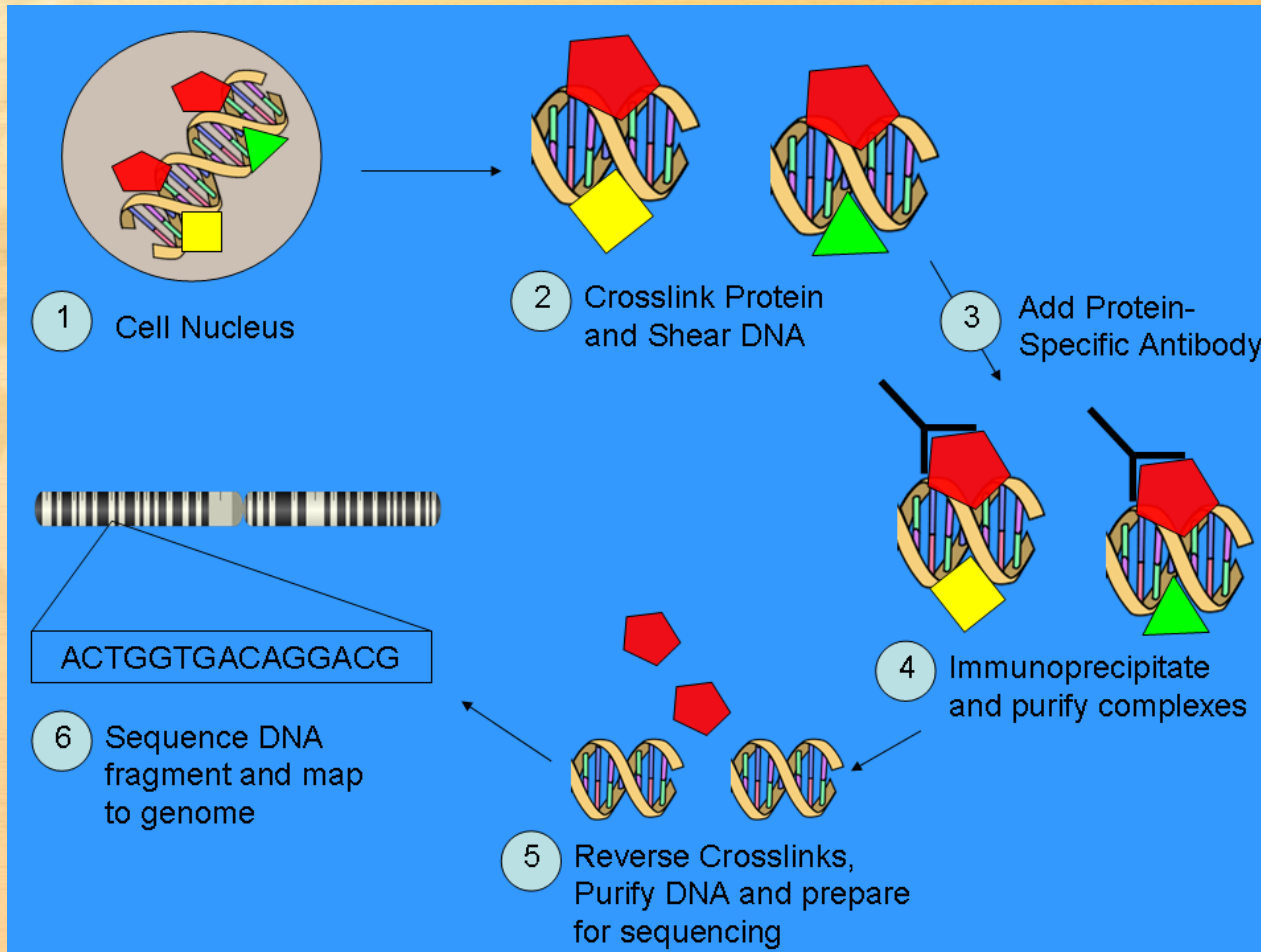
ChIP-chip



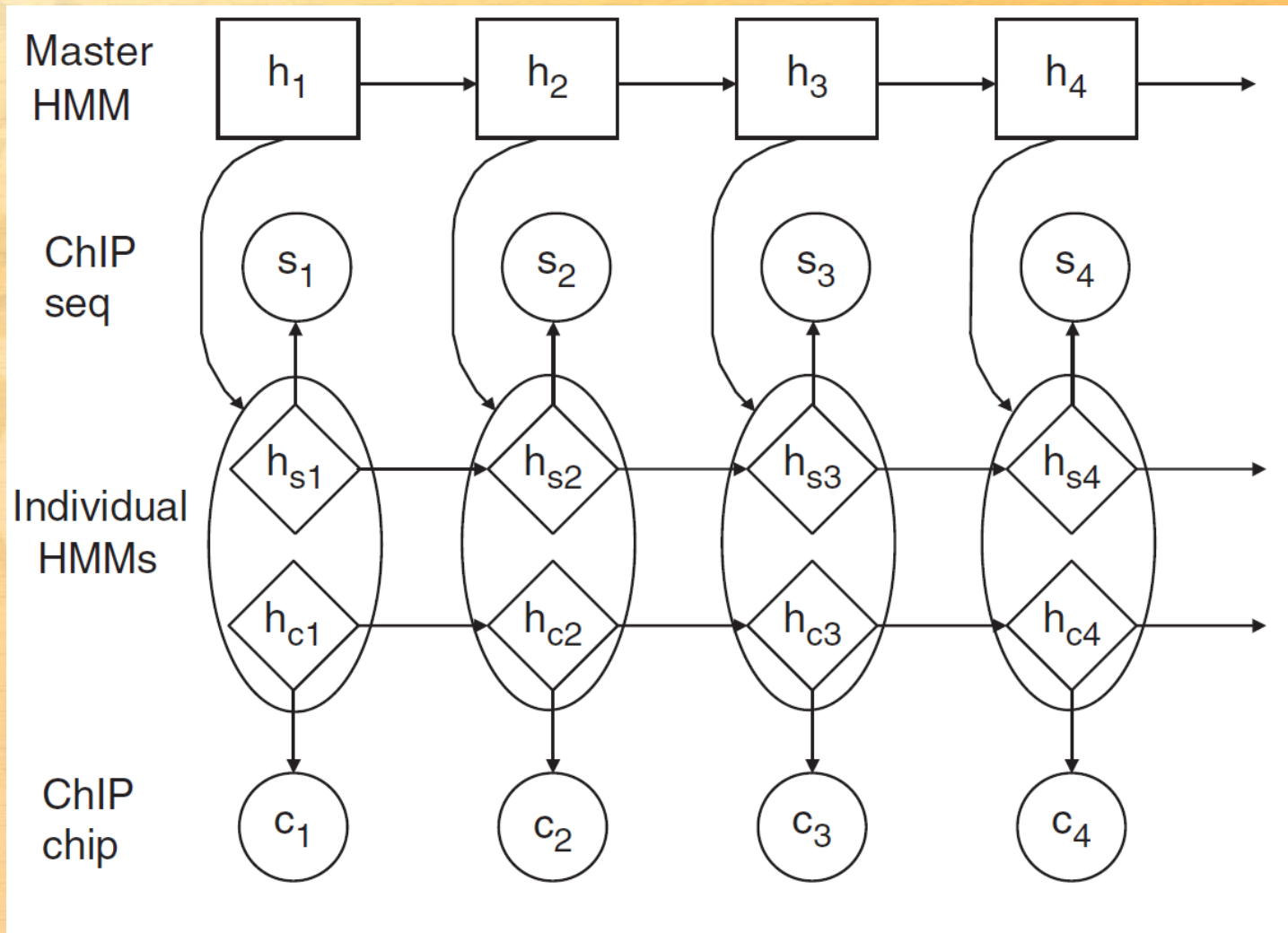
ChIP-chip



ChIP-seq



Hierarchické HMM



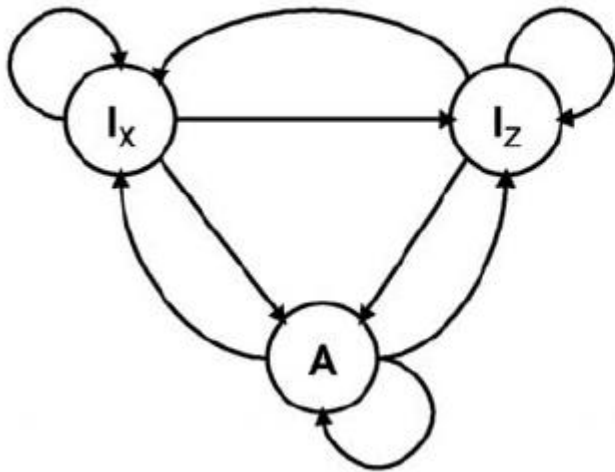
Párové HMM

- *pair-HMM* variant of HMM that is useful for finding sequence alignments and evaluating the significance of the aligned symbols.
- Unlike the original HMM, which generates only a single sequence pair-HMM generates an aligned pair of sequences.

Párové HMM

- Jednoduchý příklad

Pair HMM



I_x : insertion in x (seq 1)

I_z : insertion in z (seq 2)

A: aligned symbols in x and z

x (seq 1) : T T C C G - -

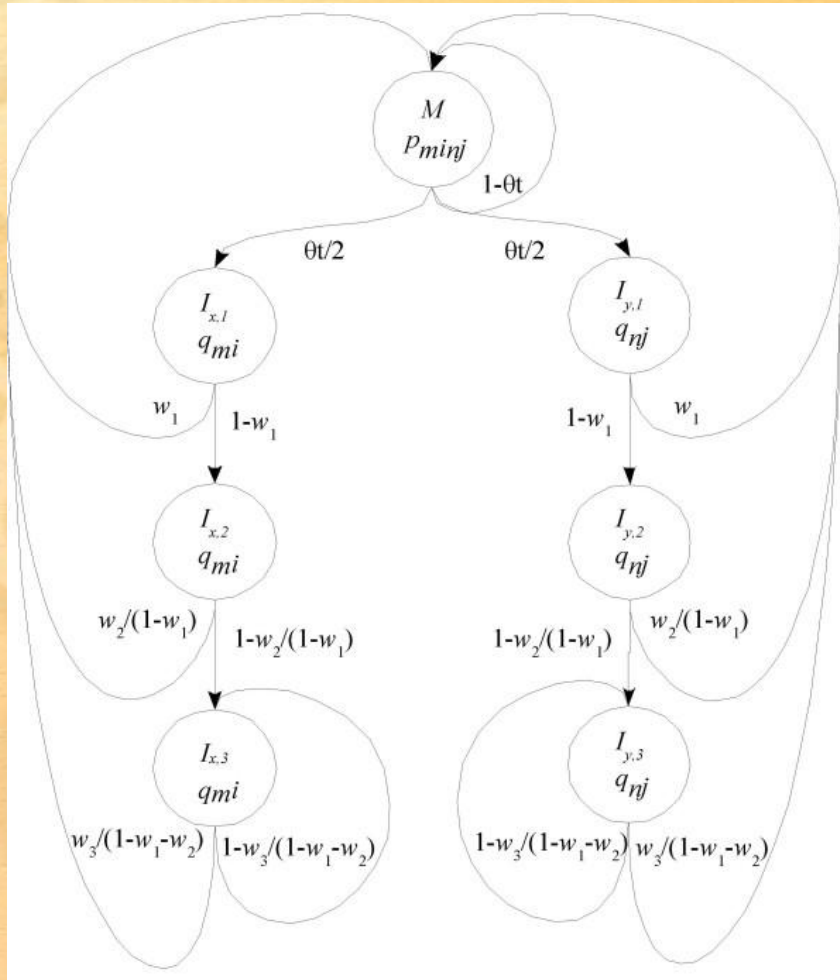
z (seq 2) : - - C C G T T

y (states) : I_x I_x A A A I_z I_z

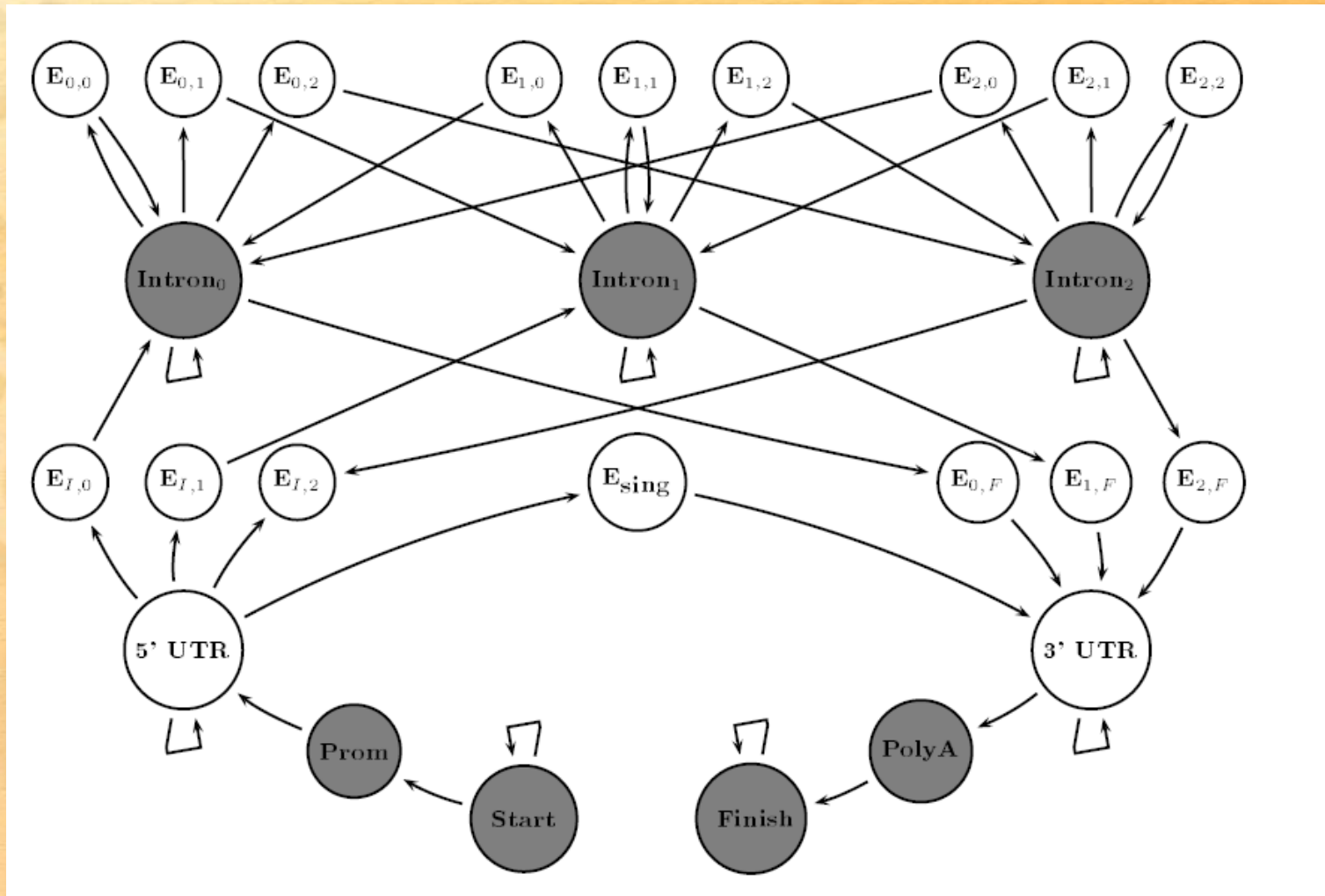
Párové HMM

- Příklady použití
 - MCALIGN2: global pairwise alignment of non-coding DNA
 - comparative gene prediction

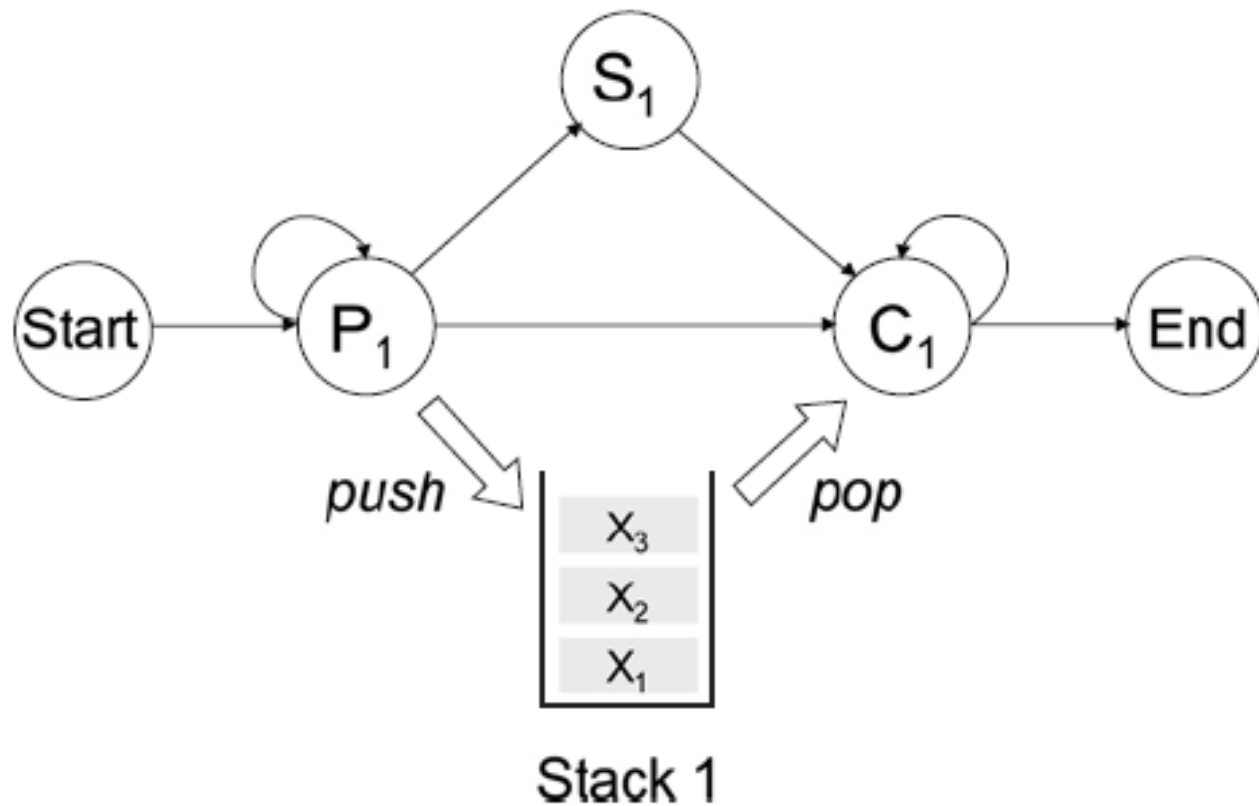
MCALIGN2



Comparative gene prediction



Kontextové HMM

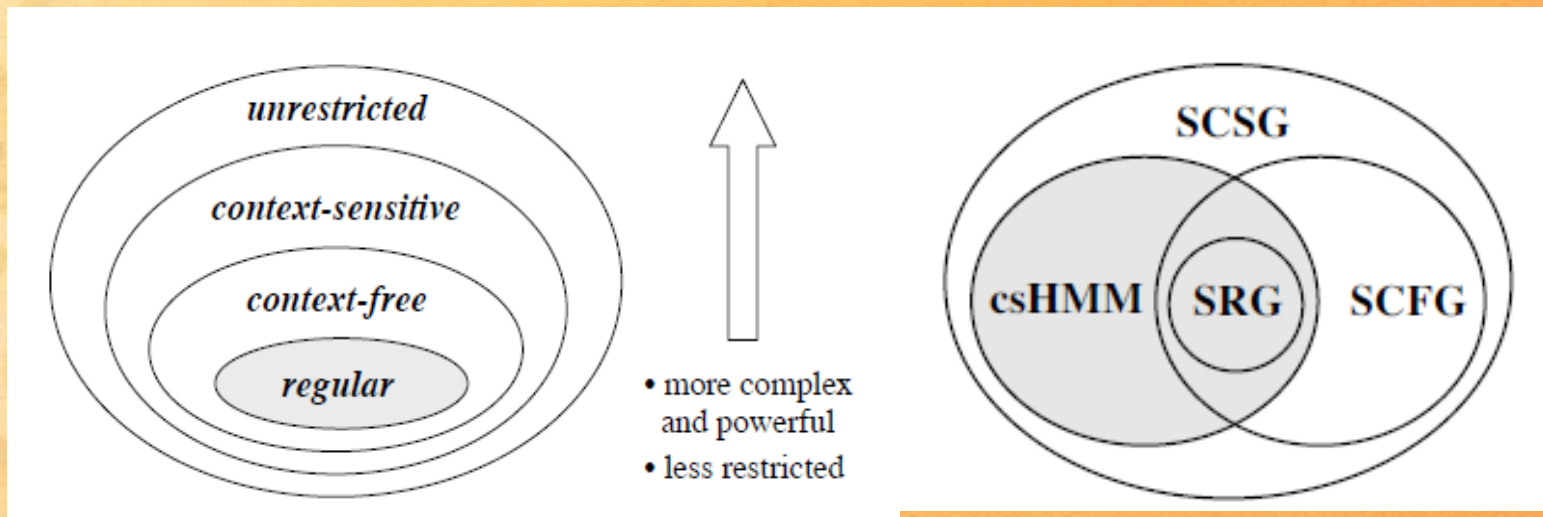


Kontextové HMM

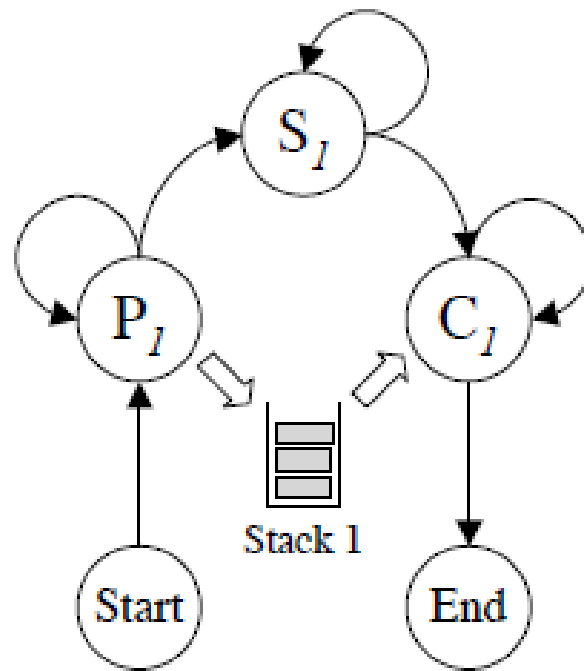
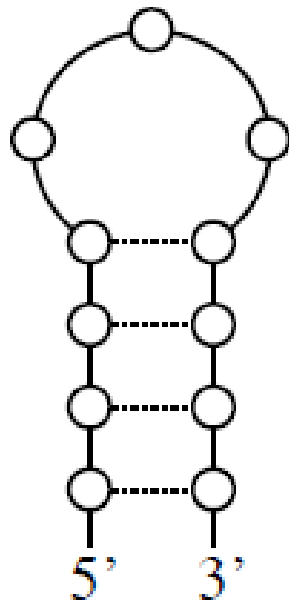
- Použití
 - RNA secondary structure modeling

Kontextové HMM

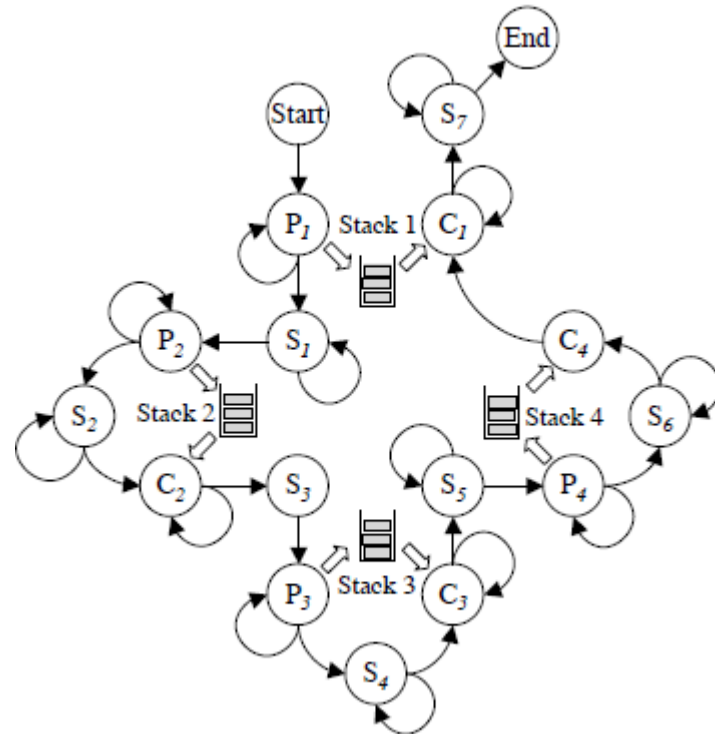
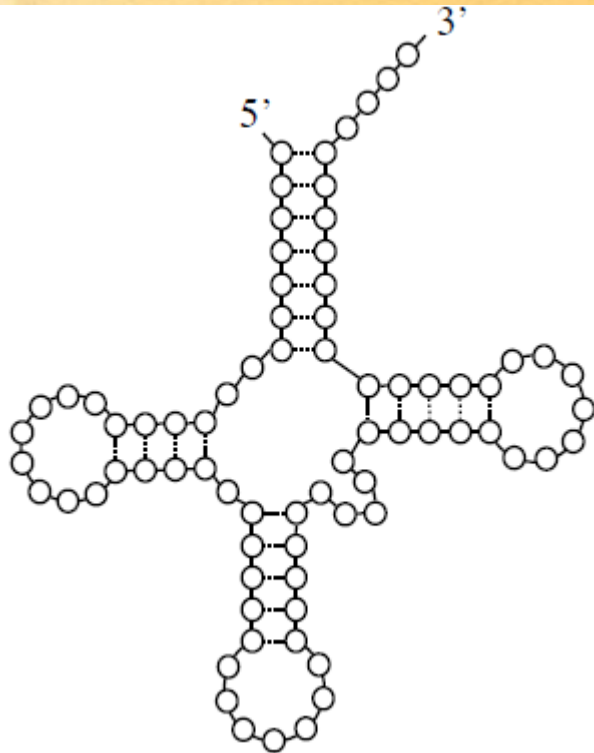
- Nevýhoda obrovská výpočetní náročnost



Kontextové HMM



Kontextové HMM



Kontextové HMM

