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# Alignment

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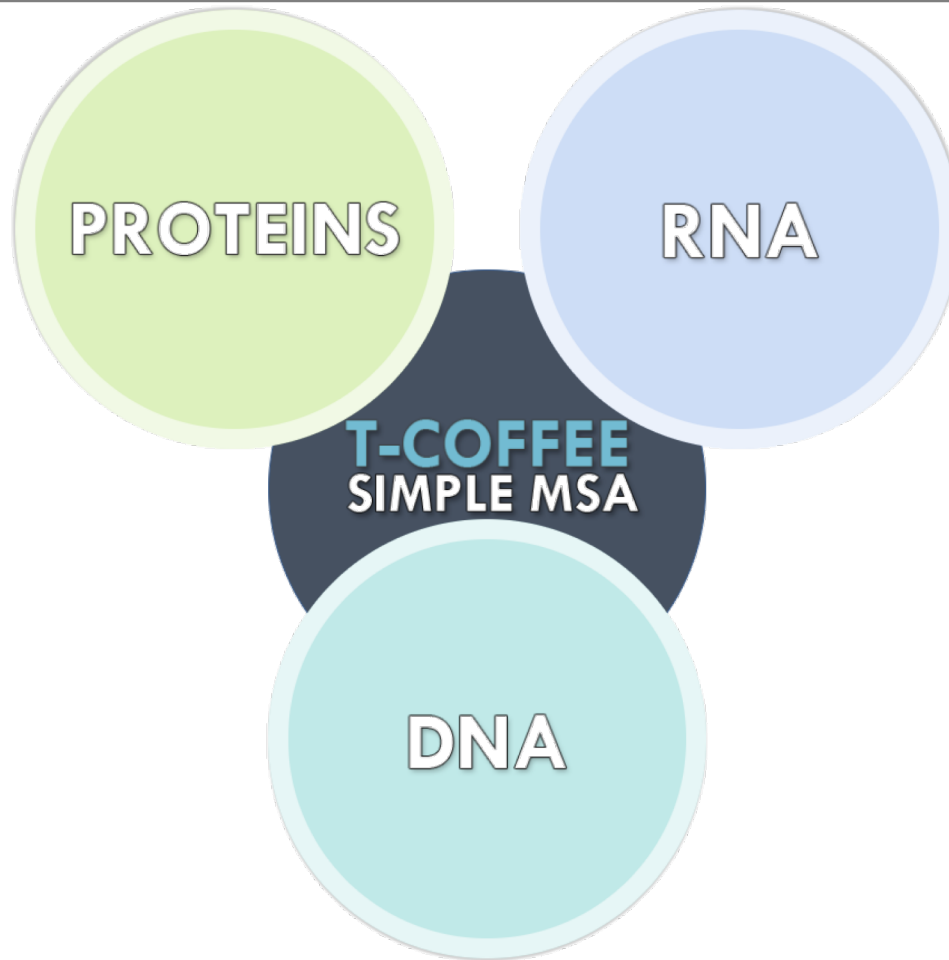
C2138 – POKROČILÁ BIOINFORMATIKA



# Využití alignmentu - opakování

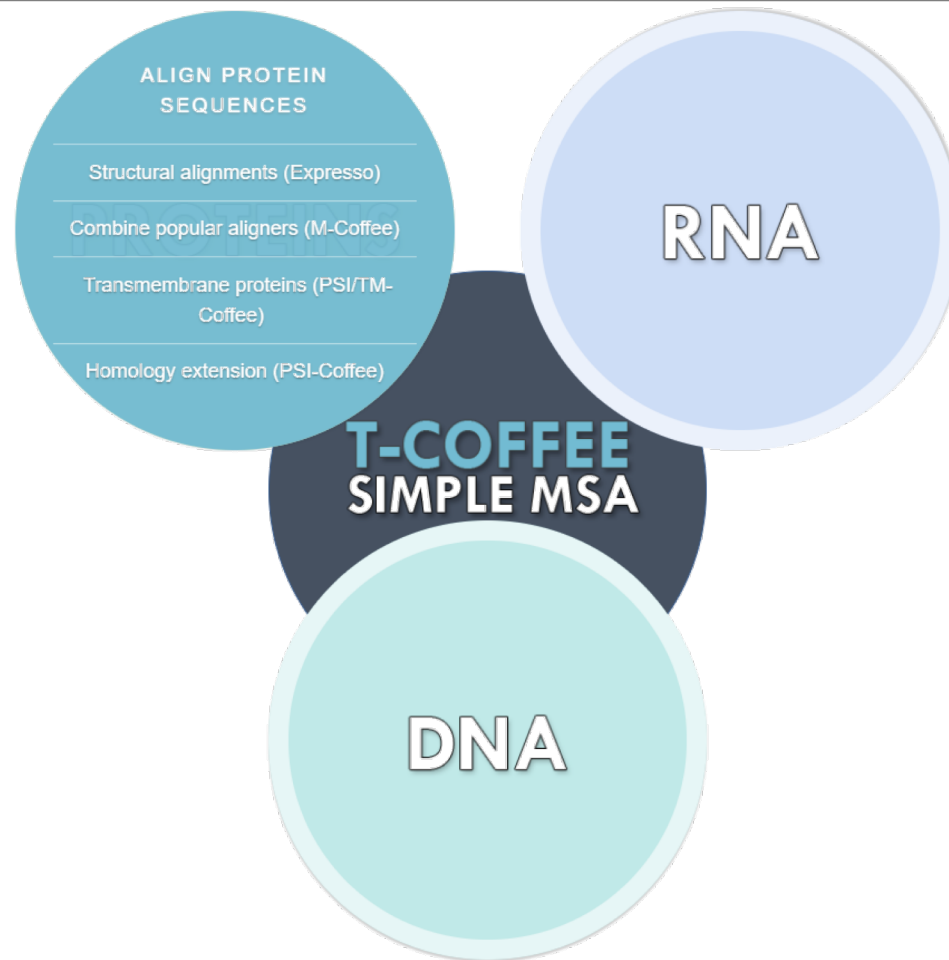
# Využití alignmentu - opakování

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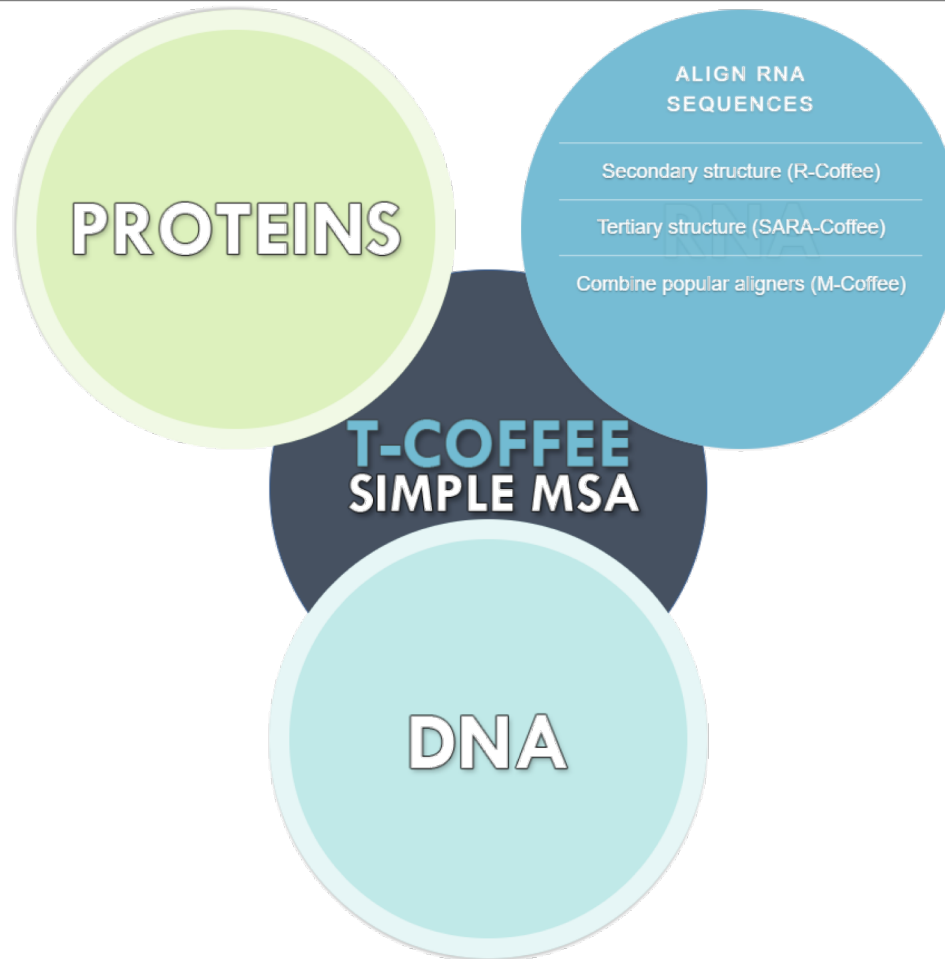
# Využití alignmentu - opakování

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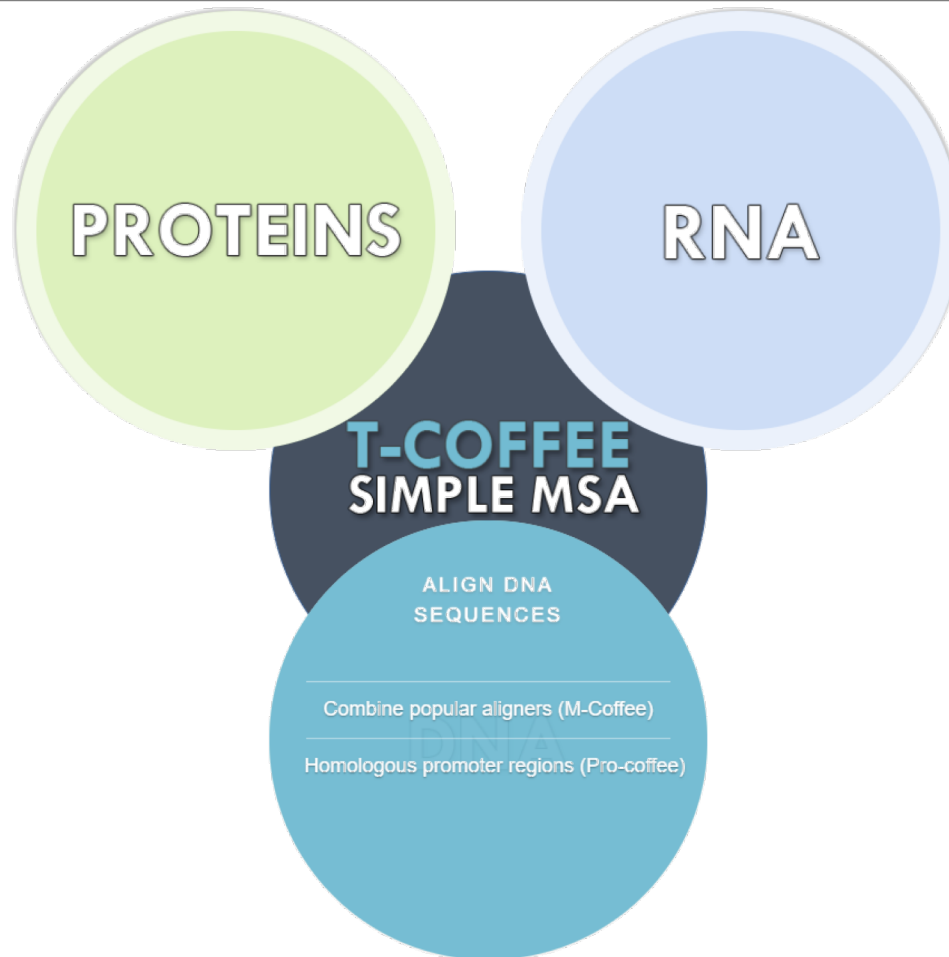
# Využití alignmentu - opakování

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# Využití alignmentu - opakování

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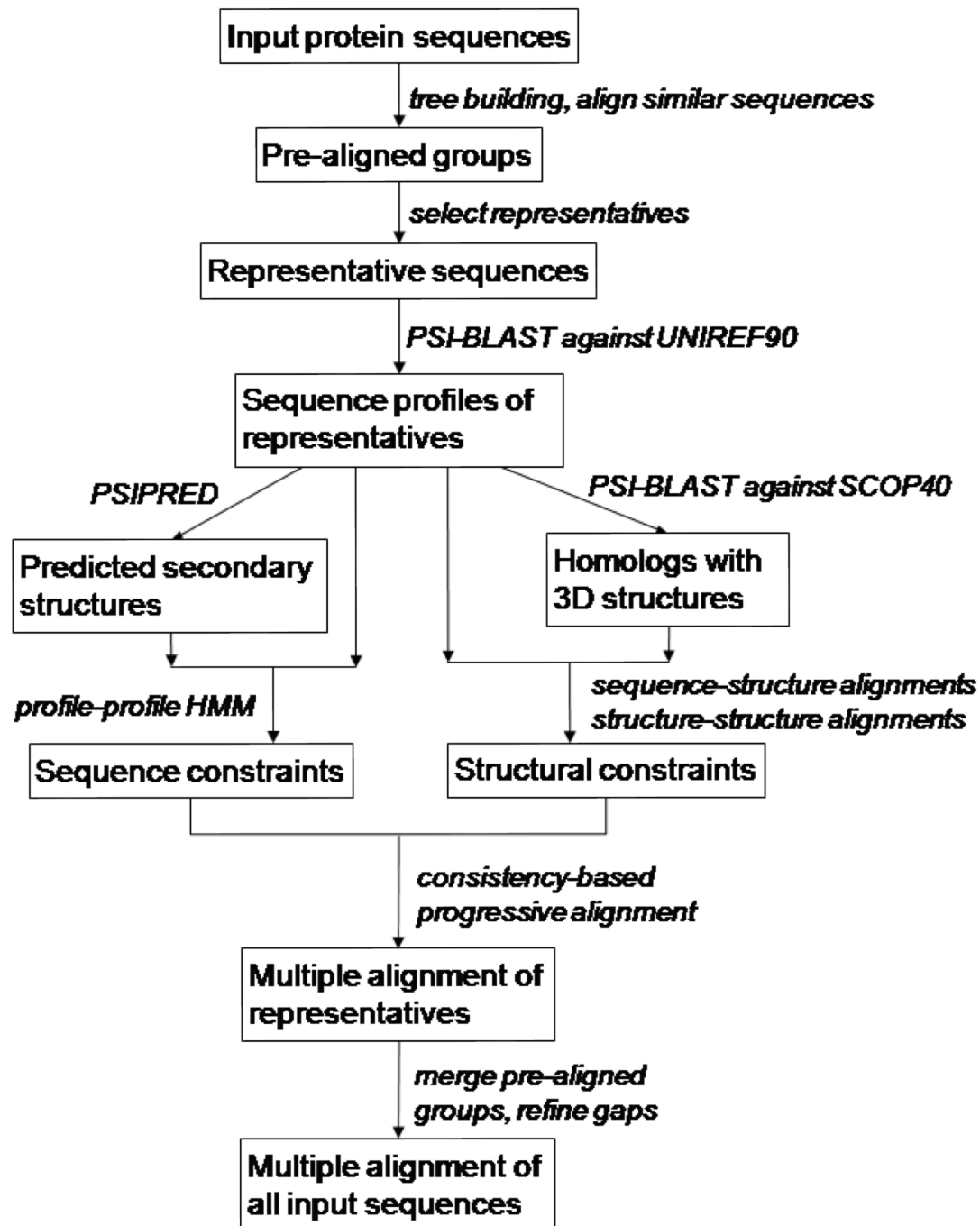


# Rozšíření alignmentu

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- ❖ Zahrnutí dodatečných informací
- ❖ Predikce sekundární struktury
- ❖ Známá 3D struktura
- ❖ Homologní sekvence se známou 3D strukturou

# PROMALS3D flowchart





# Rozšíření alignmentu

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- ❖ Porovnejte výsledky alignmentu sekvencí
  - ❖ **PDB ID: 4FIX, 2FFU**
- ❖ Clustal Omega <https://www.ebi.ac.uk/Tools/msa/clustalo/>
- ❖ Espresso <http://tcoffee.crg.cat>
- ❖ Promals3D <http://prodata.swmed.edu/promals3d/promals3d.php>
- ❖ MASS <http://bioinfo3d.cs.tau.ac.il/MASS/>

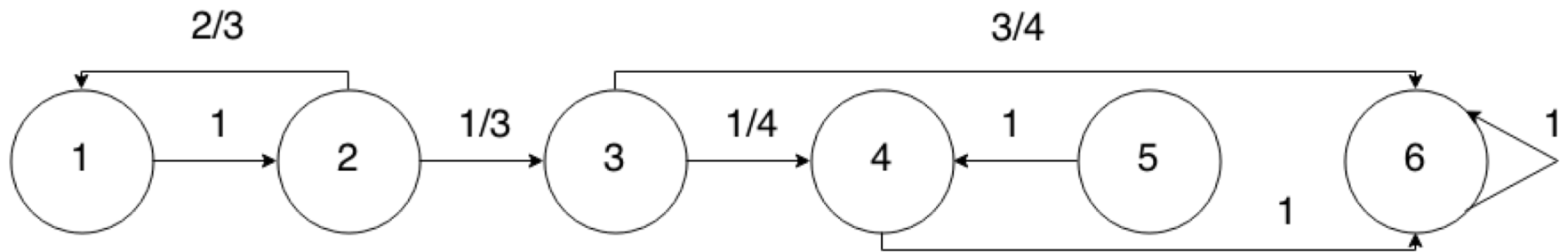
# Metody strojového učení

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- ❖ Data-mining vs. Metody strojového učení
- ❖ Statistické modely
- ❖ HMM, Neural networks, Support Vector Machines, Geneticke algoritmy, Bays network...

# Markovův řetězec

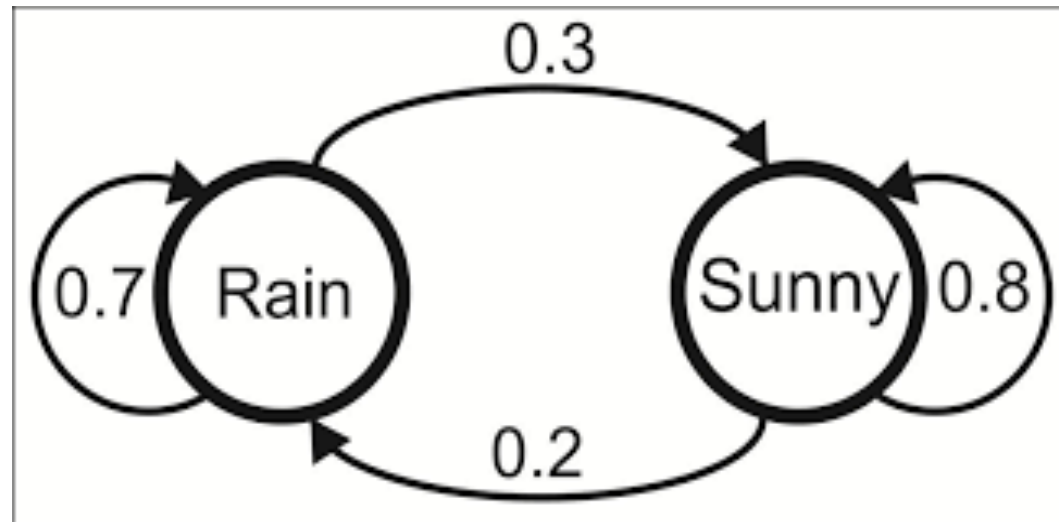
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# Markovův model

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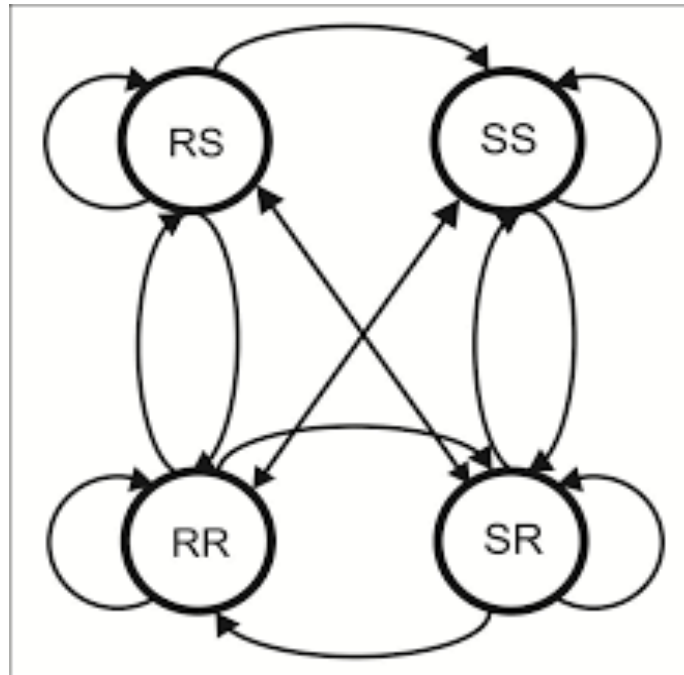
**RRRSSSRSSRRSS**



# Markovův model

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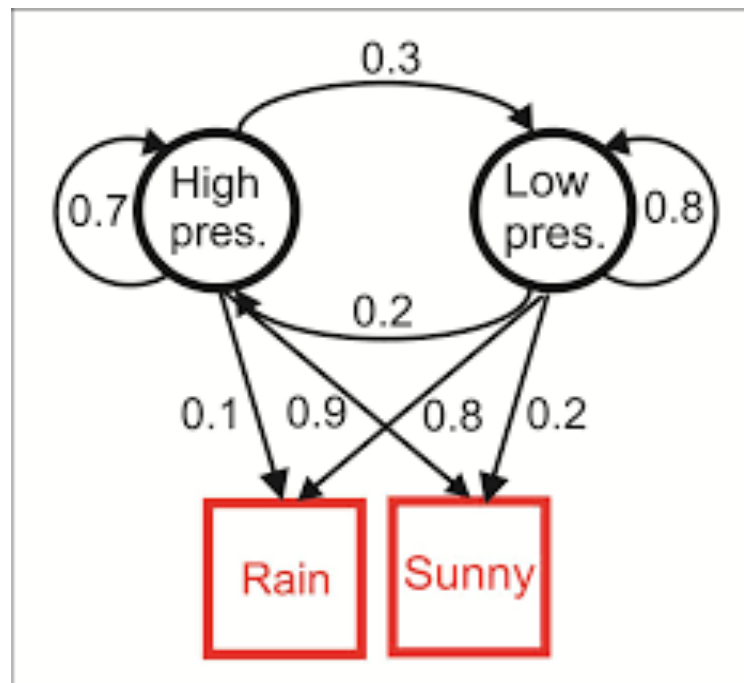
**RRRSSRRSSRRSS**



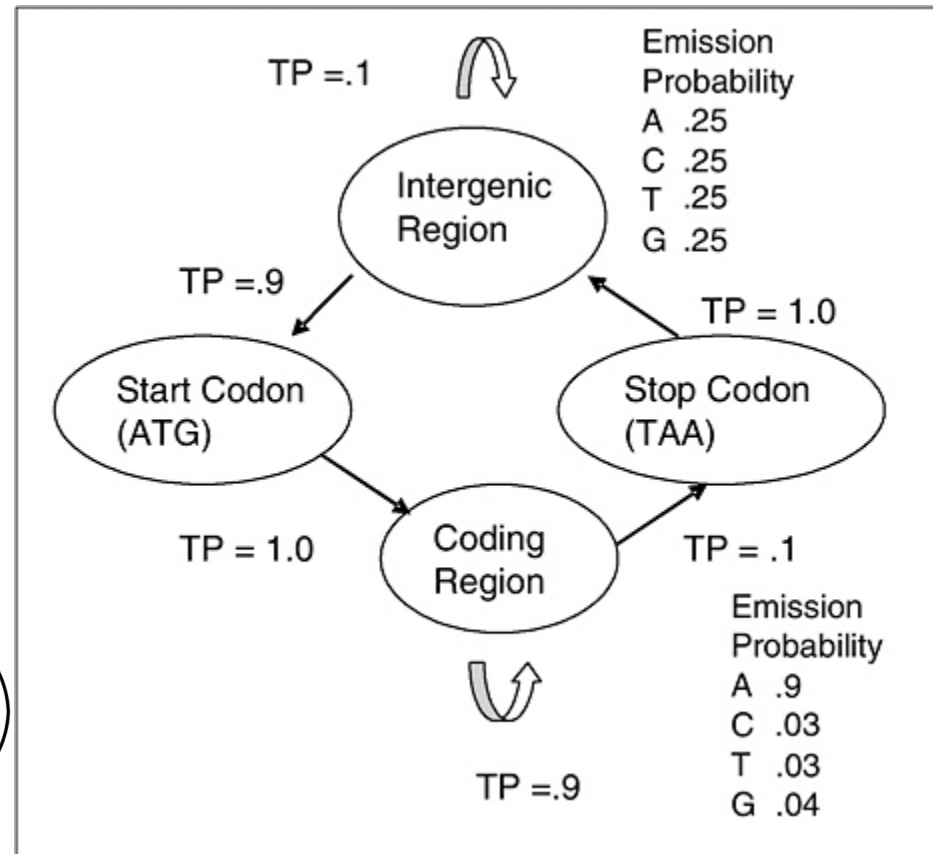
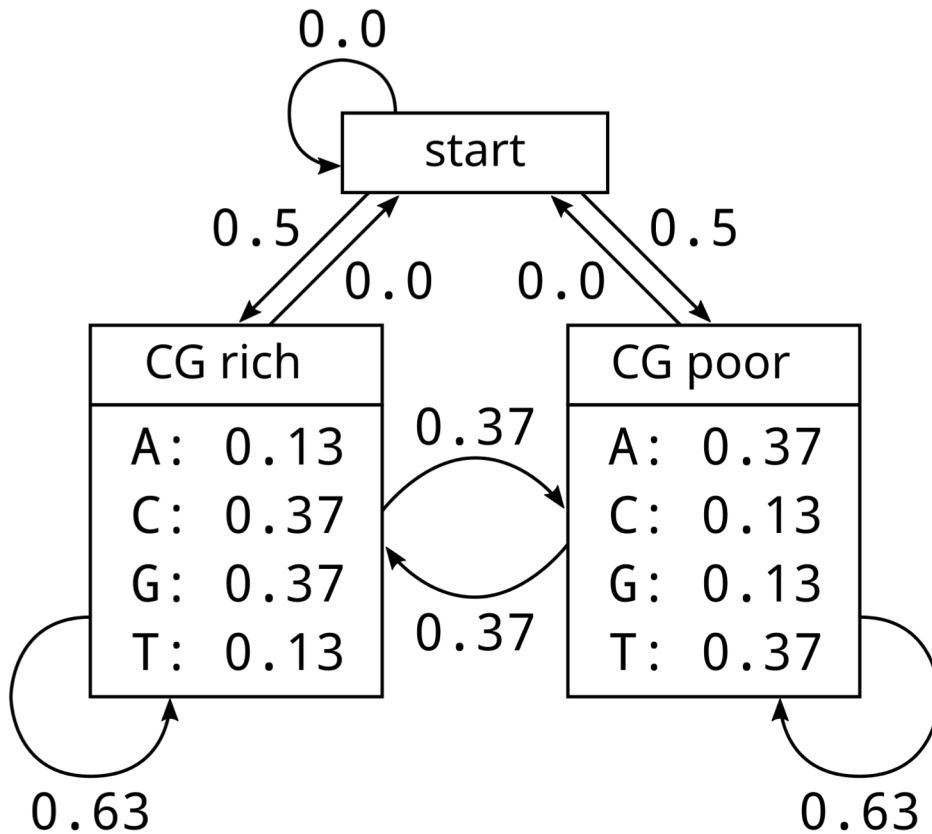
# Skrytý Markovův model (HMM)

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**RRRSSSRSSRRSS**

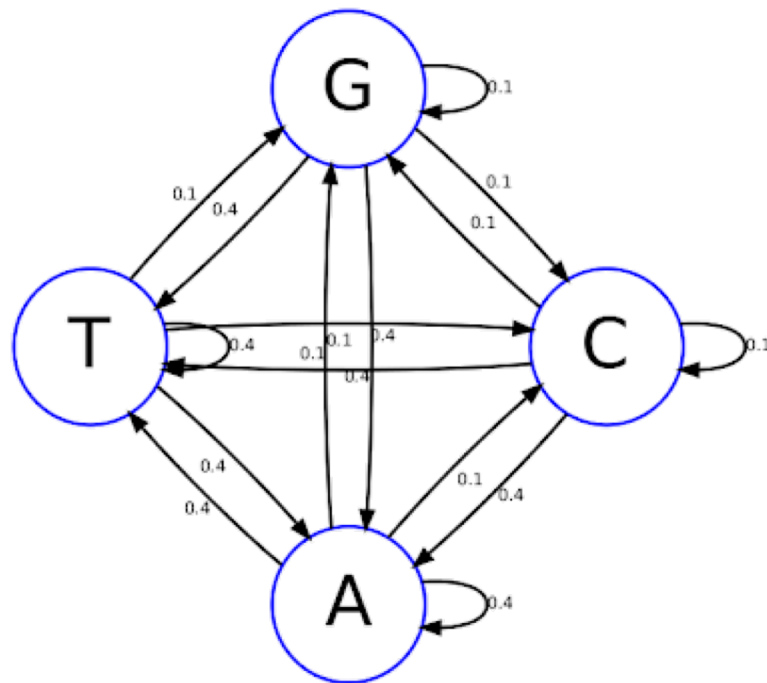


# HMM v bioinformatiche



# HMM v alignmentu

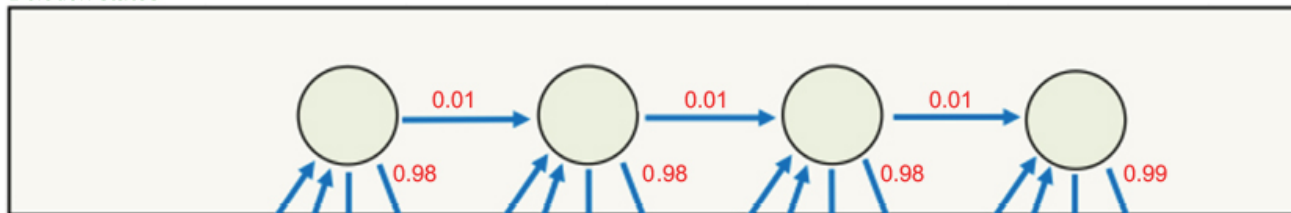
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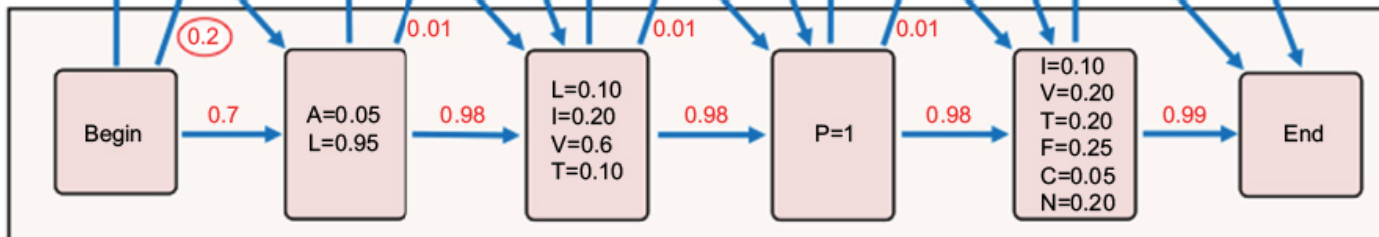
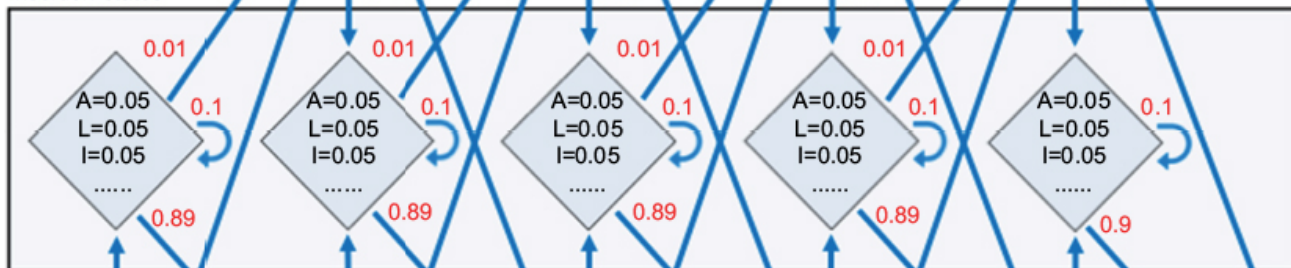


# Profilové HMM

Deletion states



Insertion states



Match states