BIOINFORMATIKA V PRAXI

CVIČENÍ 3 – DRUHÁ ČÁST

IDENTIFIKACE GENŮ, PROTEINŮ A JEJICH FUNKCE

STUDIJNÍ MATERIÁLY

Studijní materiály předmětu **C2130 Úvod do chemoinformatiky a bioinformatiky**, přednáška **Predikce genu, Sequence-evolution-function: Computational Approaches in Comparative Genomics**.

ÚKOL 1

Charakterizujte část genomu *neznámého organismu* pomocí predikčního programu **GeneMark** (http://exon.gatech.edu/GeneMark). Využijte *heuristický* predikční program.

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ÚKOL 2

Charakterizujte část genomu *neznámého organismu* pomocí predikčního programu **GeneMark** (http://exon.gatech.edu/GeneMark). Využijte „self-training“ program.

TTAAGAAATTCCGGTTATCAACTTCGAGGCCCCTTTCAGGTCACCGTTGGCGTATTTCGGGGCGATAGATTTGTATTTGTAGCCGCGAATACTGCGATCGCCCCCGGCGAAAAAACGCAGATCCGGCGGTACTTTGTCGAAATCACCGGTT
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PREDIKCE GENŮ U EUKARYOT

Genomy j**ednobuněčných** eukaryot se navzájem výrazně liší (frekvence intronů, jak velká část genomu je tvořená geny kódujícími proteiny). Pro některá jednobuněčná eukaryota (s nízkou frekvencí intronů) je možné použít stejné postupy jako pro prokaryota.

ÚKOL 3

Charakterizujte část genomu *Candida albicans* (kvasinka) pomocí programu **GeneMark** (http://exon.gatech.edu/GeneMark), verze pro nižší eukaryota. U identifikovaných genů určete možnou funkci.

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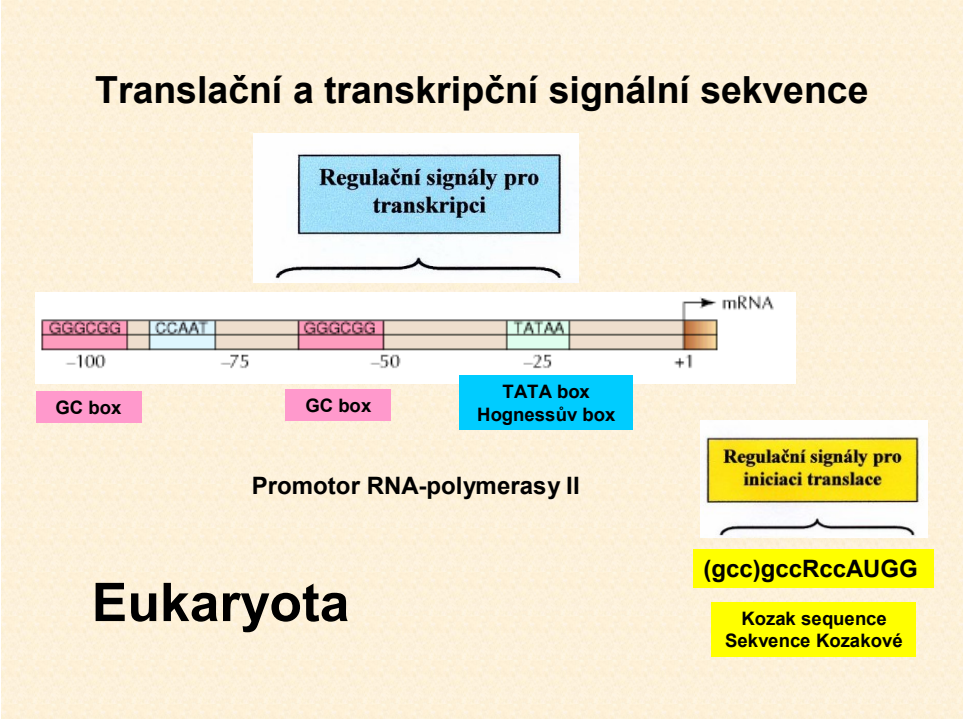
PREDIKCE GENŮ U MNOHOBUNĚČNÝCH EUKARYOT



Mnohobuněčná eukaryota se vyznačují komplexní organizací genomu, geny jsou separovány dlouhými intergenovými úseky, geny obsahují mnoho intronů, i velmi dlouhých. Exony/introny jsou identifikovány pomocí míst sestřihu (GT na 5´konci intronu, AG na 3´konci). Vzniká velké množství chyb! Dlouhé introny jsou určeny jako intergenové úseky, krátké intergenové úseky jako introny, krátké exony nemusí být identifikovány.

ÚKOL 4

Analyzujte část genomu mnohobuněčného eukaryotického organismu *(Arabidopsis thaliana)* pomocí programu **GeneMark** (http://exon.gatech.edu/GeneMark), verze pro eukaryota.

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ÚKOL 5

Analyzujte část genomu mnohobuněčného eukaryotického organismu pomocí programu **GENSCAN** (http://genes.mit.edu/GENSCAN.html).

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