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# FACULTY OF ENGINEERING AND TECHNOLOGY

## Department of Biotechnology

# Gene Prediction Tools

abc

# GRAIL

- Gene finder for human, mouse, arabidopsis, drosophila, E. coli
- Based on neural networks
- Masks human and mouse repetetive elements
- Incorporates pattern-based searches for several types of promoters and simple repeats
- Accuracy in 75-95% range

# Glimmer

- Genefinder for bacterial and archaebacterial genomes
- Uses an "interpolated Markov model" approach (a Markov model is a model for computing probabilities in the context of sequential events)
- Predicts genes with around 98% accuracy when compared with published annotations
- No web server

# GENSCAN

- Genefinder for human and vertebrate sequences
- Probabilistic method based on known genome structure and composition: number of exons
  per gene, exon size distributions, hexamer composition, etc.
- Only protein coding genes predicted
- Maize and arabidopsis-optimized versions now available
- Accuracy in 50-95% range

# GeneMark

- Gene finder for bacterial and archaebacterial sequences
- Markov model-based
- GeneMark and GeneMarkHMM available as web servers
- Accuracy in 90-99% range

# GeneParser

- Predicts the most likely combination of exons and introns using dynamic programming.
- The intron an exon positions are aligned subject to the constraint that they alternate.
- A neural network is used to adjust the weights given to the sequence indicators of know exon and intron regions such as codon usage, information content, length distribution, hexamer frequencies, and scoring matrices.

# Other software

- Generation
- GeneID
- Genie
- GenView
- EcoParse
- etc...

# XYZ

abc

# XYZ

abc

# XYZ

abc

# XYZ

abc

# XYZ

abc

# XYZ

abc

# MCQs

1. A
2. A
3. A
4. A
5. A
6. A
7. A
8. A
9. A
10. A