

# CSC 334: TOPICS IN COMPUTATIONAL BIOLOGY

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“Algorithms for Genomic Data”

Fall 2015

Smith College

Instructor: Prof. Sara Sheehan

# Sub-fields of Computational Biology

- Biological Modeling
  - Drug entering the body
  - Tissue and surgical modeling
  - Models of DNA, RNA, protein, gene networks
  - Intersects with computer vision and computer graphics
- Genomics/Genetics
  - Phylogenetics (speciation, tree of life)
  - Population genetics (evolution of a single species)
  - Disease genetics (link between genotype and phenotype)
- Neuroscience
  - Analyzing brain data, creating brain models
- Disease biology
  - Infectious disease models
  - Cancer biology

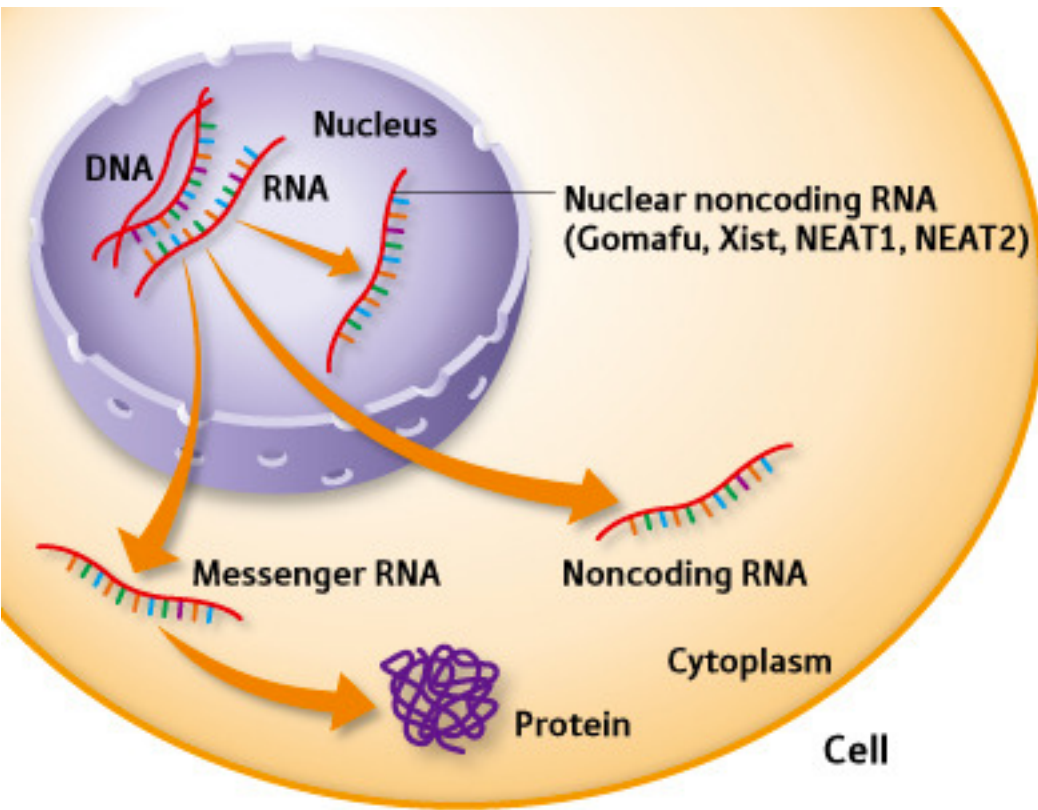
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Today



# RNA

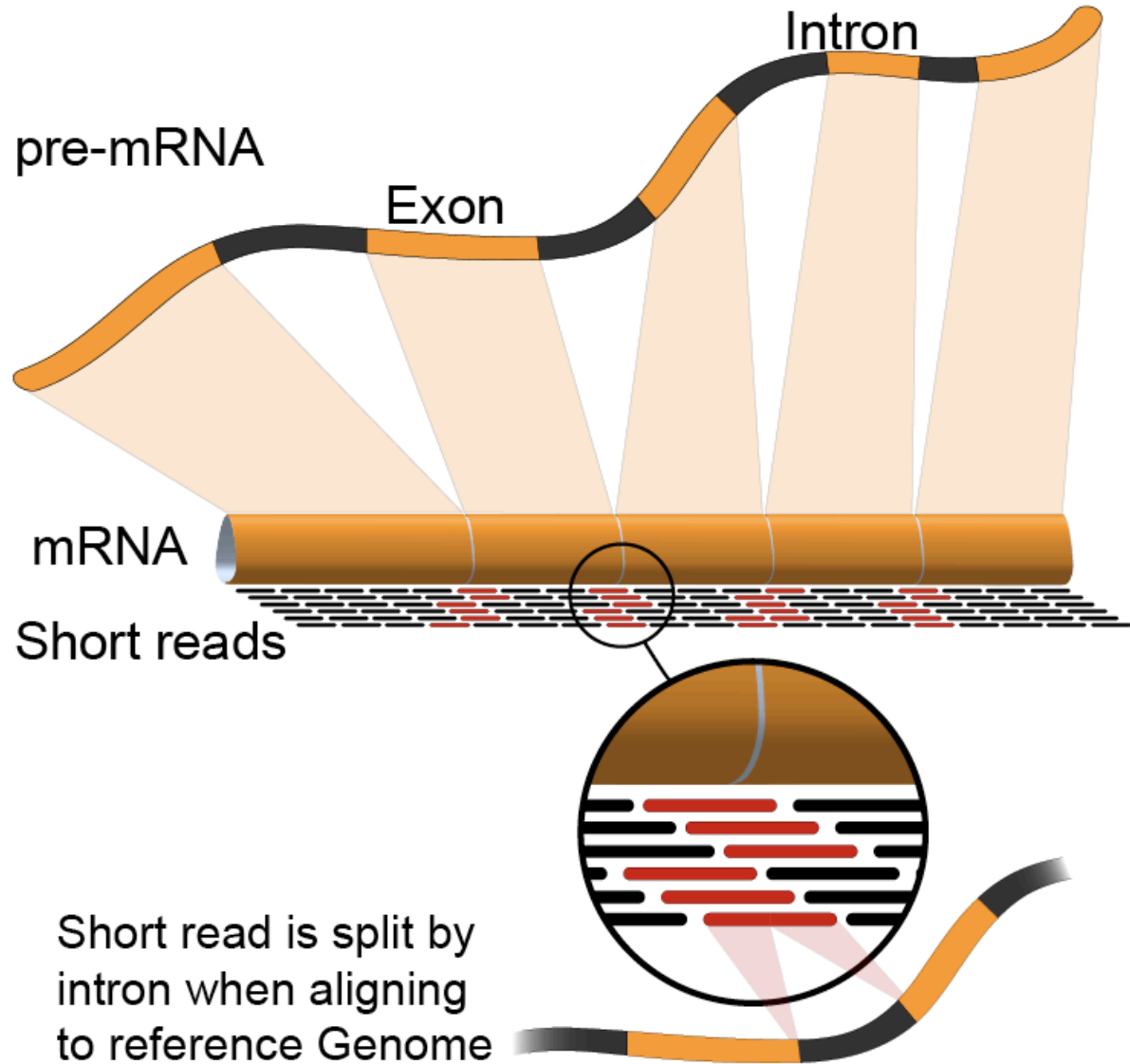


- Transcription: DNA to RNA

- <http://www.wehi.edu.au/wehi-tv/dna-central-dogma-part-1-transcription>

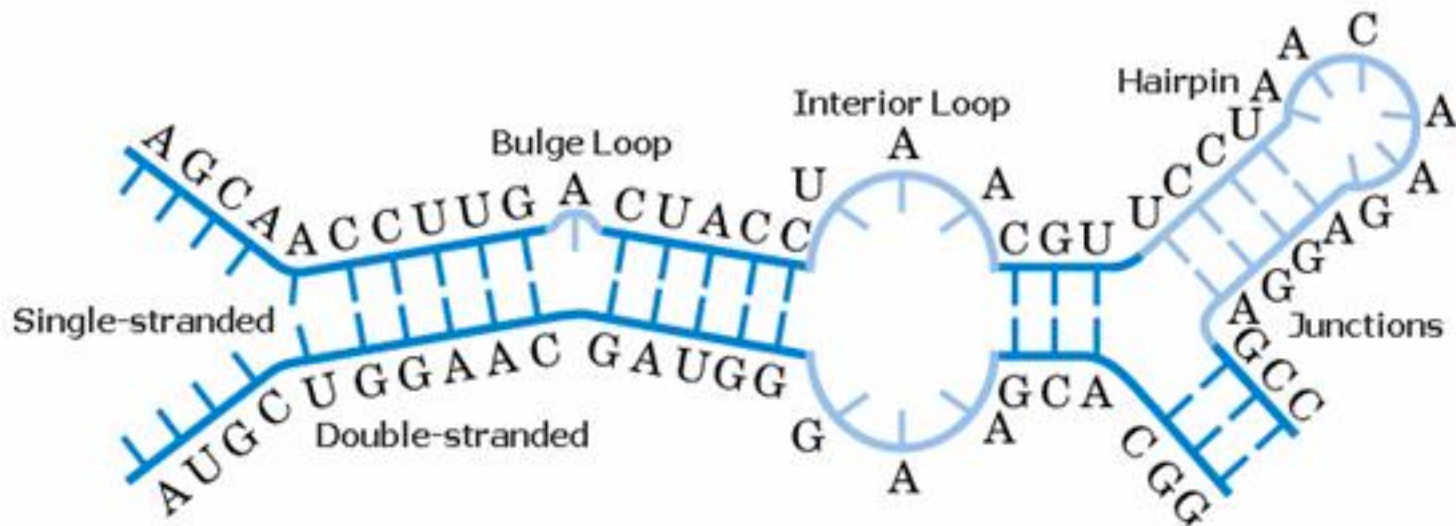
# RNA-Seq

RNA expression is often used as a proxy for protein expression



# RNA secondary structure

(Primary structure: single-stranded sequence of A,C,U,G)



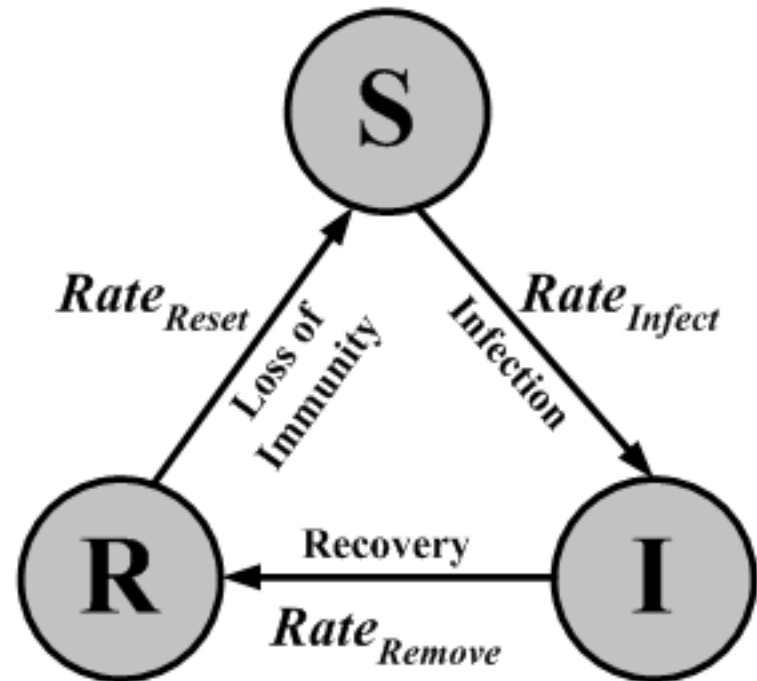
# Enter: computational biology

<https://www.youtube.com/watch?v=KBI69y2ziXw>

- Goal: how could we predict RNA secondary structure?
- Inspiration: sequence alignment
- Answer: dynamic programming (Nussinov's algorithm)

# SIR models for infectious disease

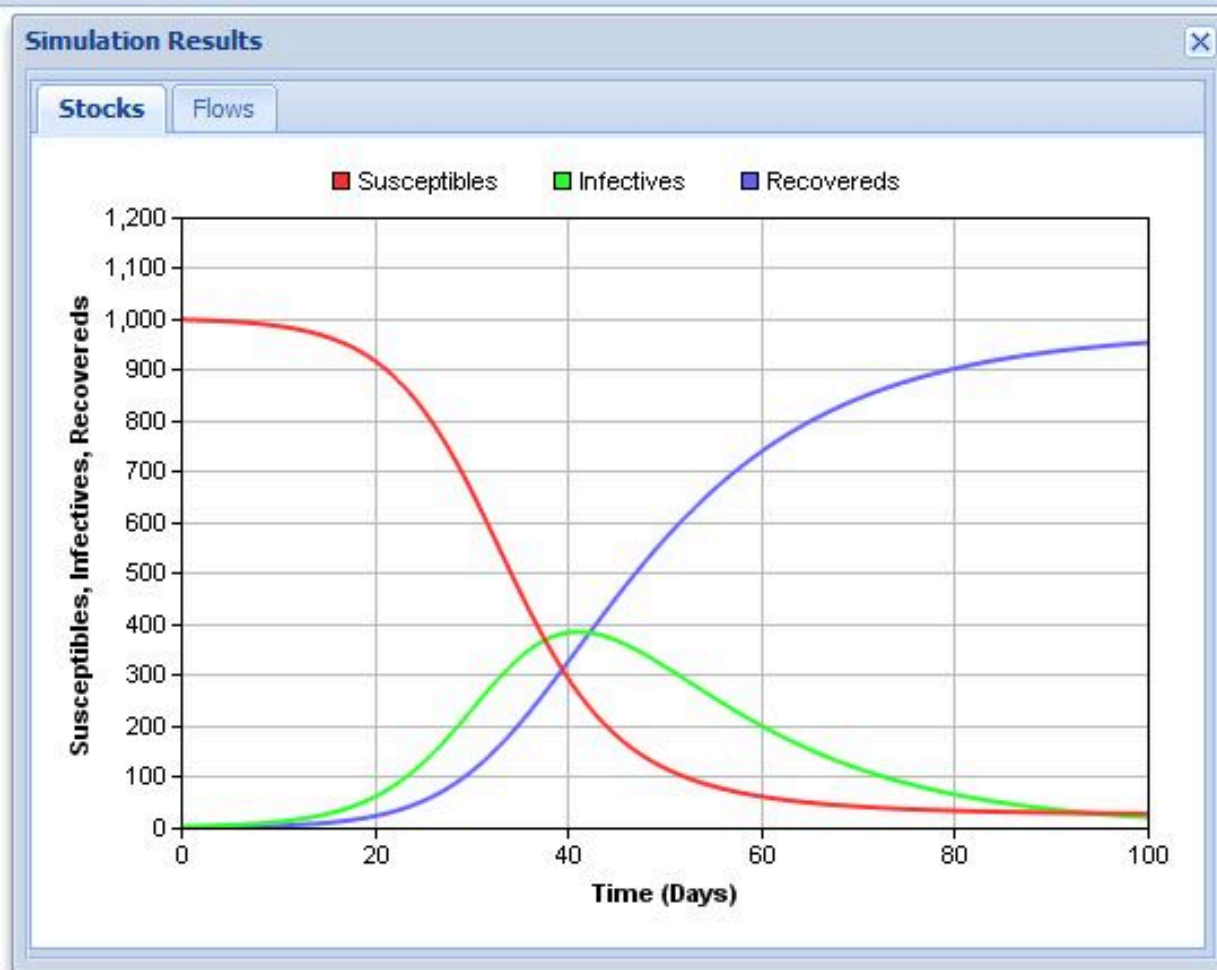
- Recent applications:
  - H1N1, “swine flu”, 2009
  - Ebola, 2015



“Influence of Local Information on Social Simulations in Small-World Network Models” (2005)



# SIR models for infectious disease



This is a simple SIR infectious diseases 3 stock model with Susceptibles, Infectives and Recovereds stocks. In the initial description the R signified Removed and could include Deaths, Recovered with immunity to infection (Resistant) or those who had fled the epidemic. Note the need to initiate the epidemic by adding a pulse of a single infected person at time 0.

