CSC 334: TOPICS IN COMPUTATIONAL BIOLOGY

“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
RNA expression is often used as a proxy for protein expression.

"RNA-Seq-alignment" by Rgocs
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.

Contacts per day: 5
Infectivity: 0.05
Days infected: 15