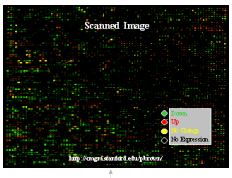
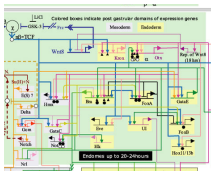
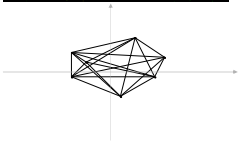
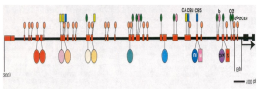
ECS 289A- Introduction to Computational Functional Genomics









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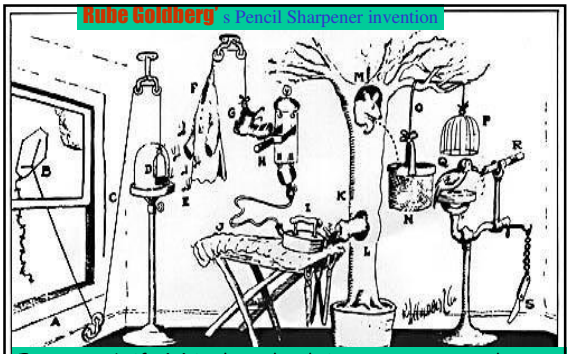
Rube Goldberg's Pencil Sharpener invention



Emergency knife (S) is always handy in case opossum or the woodpecker gets sick and can't work.

ECS 289A

- Prof. Vladimir Filkov
  3023 Engineering II
  filkov@cs.ucdavis.edu
- Office Hours: Tuesday, 2:00pm-4:00pm

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Administrativia

- ECS289A, 4 credits
- CRN 73358
- Tue/Thu 4:40-6pm, 70 SocSci
- http://www.cs.ucdavis.edu~/filkov/289a/
- No text required, papers and handouts
- Grading:
  - 60% project
  - 30% presentation(s)
  - 10% class participation

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Projects

- Projects will ideally combine biological knowledge and computational methods
- Some projects and reading lists out this week
  - Project proposals are due **April 14**
  - Progress reports are due **May 17**
  - Project presentations during last 2 weeks of classes
  - Final reports are due **Jun 14**
- If you have an idea come and talk to me asap

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Presentations

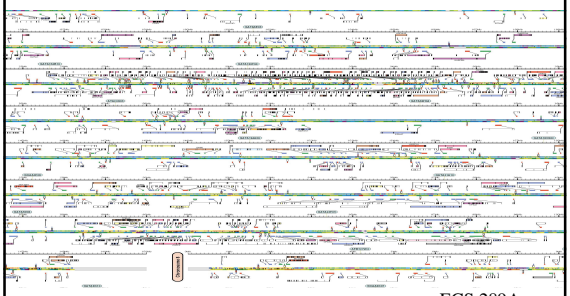
- Presentations can be of papers or software
- Each student will give 2 presentations during the class (40 min each)
- Need 2 volunteers to give first presentations on (1) Genomic Databases (GenBank, SGD, etc.) and (2) Microarray Resources (tools etc.)

Computational Biology

- Computational Scientists working on Molecular Biology Problems
- Different Scientific Cultures: CS vs Biology vs Statistics

- No unique definition: bioinformatics, computational biology, etc.
- Sub-areas in Comp Biology:
  - Genomics
  - Functional Genomics
  - Proteomics
  - Phylogenetics
  - Etc.

What good is Comp. Bio?



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What This Course is About

- Computational Functional Genomics
  - Genomics = molecular biology + robotics + informatics
    - Depends on tools and techniques of recombinant DNA technology (e.g. DNA sequencing)
    - The technologies used are high-throughput (e.g. sequencing, microarraying, etc.)
    - Data proceesed and analyzed by computers
  - Functional = exploration of gene and protein function in the cell processes (e.g. regulation, interactions, pathways, networks)
  - Computational = using computational/algorithmic methods

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Course Overview

Intro: Biology, Biotechnologies, Computational Methods

A. Central Dogma of Molecular Biology
B. High-Throughput technologies: DNA sequencing, Gene Expression Arrays, Protein-DNA, and Protein-Protein Interactions
C. CS for Biologists

Systems Modeling

A. Modeling, Simulation, Inference
B. Levels of modeling of genomic systems
C. Large-Scale Data Modeling

Bioinformatics and Data Mining of Large-Scale Data

A. Gene Expression analysis (statistics, classification, clustering)
B. Sequence analysis (promoter region analysis)
C. TF-DNA and Protein-Protein interactions analysis (topological properties and comparison)

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Course Overview, contd.

Gene Network Inference
- A. Graph Models
- B. Boolean Networks
- C. Bayesian Networks
- D. Linear Additive Models

Combining Heterogeneous Data Sources
- A. Sequence + gene expression
- B. Gene Expression + protein-protein interactions
- C. Methods for general data integration

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Lecture 1: Biological Preliminaries

- Life is survival of information
- Properties of life:
  - Information exchange (communication)
  - Procreation (passing on information)
  - Evolution (change)

- A machine that's set in motion and never stops

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Preliminaries

- Top-down Organization of life
  - Social groups etc.
  - Organisms
  - Species, etc.
  - Organs, Tissues
  - Cells: units of life

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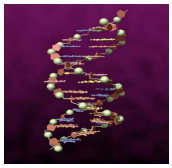
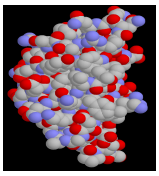
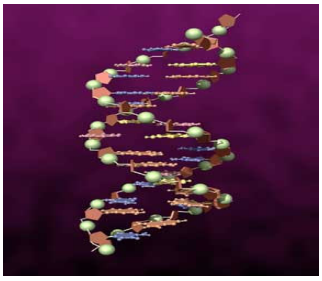
Preliminaries

- Inheritable information: Chromosomes (DNA)
- Day-to-day footwork: Proteins
- Both are complex polymer molecules





DNA



- DNA: String over the alphabet {A,C,G,T}
- A,T and C,G are complementary bases
- DNA codes for genes (proteins): genomics
- DNA codes for regulation: functional genomics

Genes and Proteins

- Nucleodtides, i.e. bases, A, C, G, and T
- Genes: units of inheritability
- Genes code for proteins!

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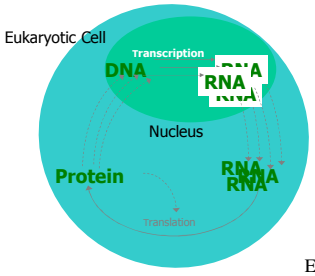
Genes to Proteins

Central Dogma: DNA ⇒ RNA ⇒ Proteins



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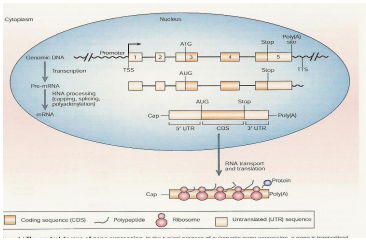
Central Dogma



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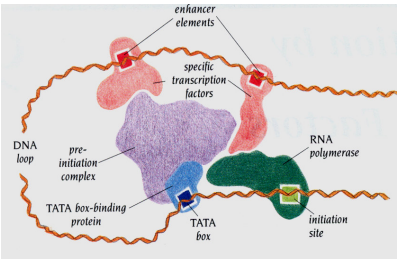
Regulating Gene Expression



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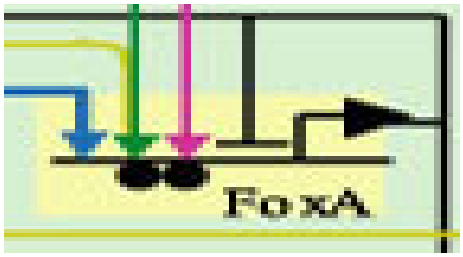
Gene Regulation Simplified



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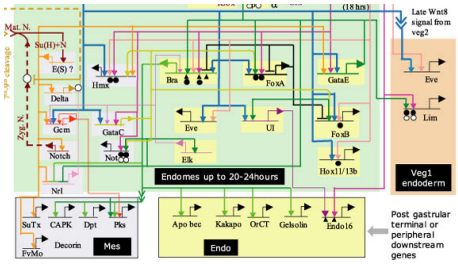

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Transcription

- Protein Binding
- Initiation
- Elongation
- Copying
- Termination

Translation

Second Base of Codon

First Base of Codon	U		C		A		G		Third Base of Codon
U	UUU	phe	UCU	ser	UAU	tyr	UGU	cys	U
	UUC	phe	UCC	ser	UAC	tyr	UGC	cys	C
	UUA	leu	UCA	ser	UAA	STOP	UGA	STOP	A
	UUG	leu	UCG	ser	UAG	STOP	UGG	trp	G
C	CUU	leu	CCU	pro	CAU	his	CGU	arg	U
	CUC	leu	CCC	pro	CAC	his	CGC	arg	C
	CUA	leu	CCA	pro	CAA	gln	CGA	arg	A
	CUG	leu	CCG	pro	CAG	gln	CGG	arg	G
A	AUU	ile	ACU	thr	AAU	asn	AGU	ser	U
	AUC	ile	ACC	thr	AAC	asn	AGC	ser	C
	AUA	ile	ACA	thr	AAA	lys	AGA	arg	A
	AUG	met*	ACG	thr	AAG	lys	AGG	arg	G
		* = START							
G	GUU	val	GCU	ala	GAU	asp	GGU	gly	U
	GUC	val	GCC	ala	GAC	asp	GGC	gly	C
	GUA	val	GCA	ala	GAA	glu	GGA	gly	A
	GUG	val	GCG	ala	GAG	glu	GGG	gly	G