

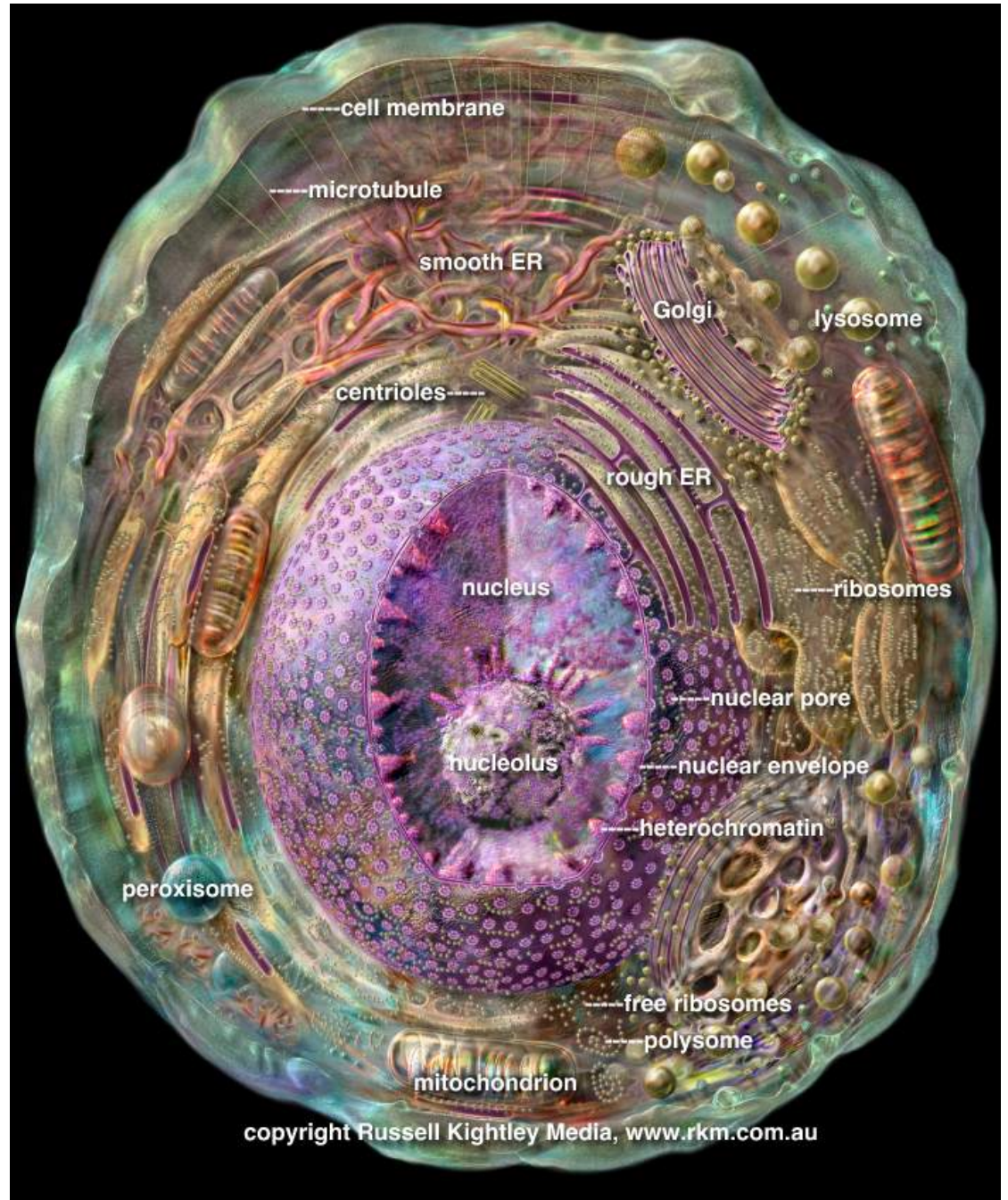
How can computers help cure cancer?  
(computational biology and  
bioinformatics)

COS116

Instructor: Olga Troyanskaya

Molecular biology 101  
or  
“why bother?”

Cells are  
fundamental  
working units  
of all  
organisms



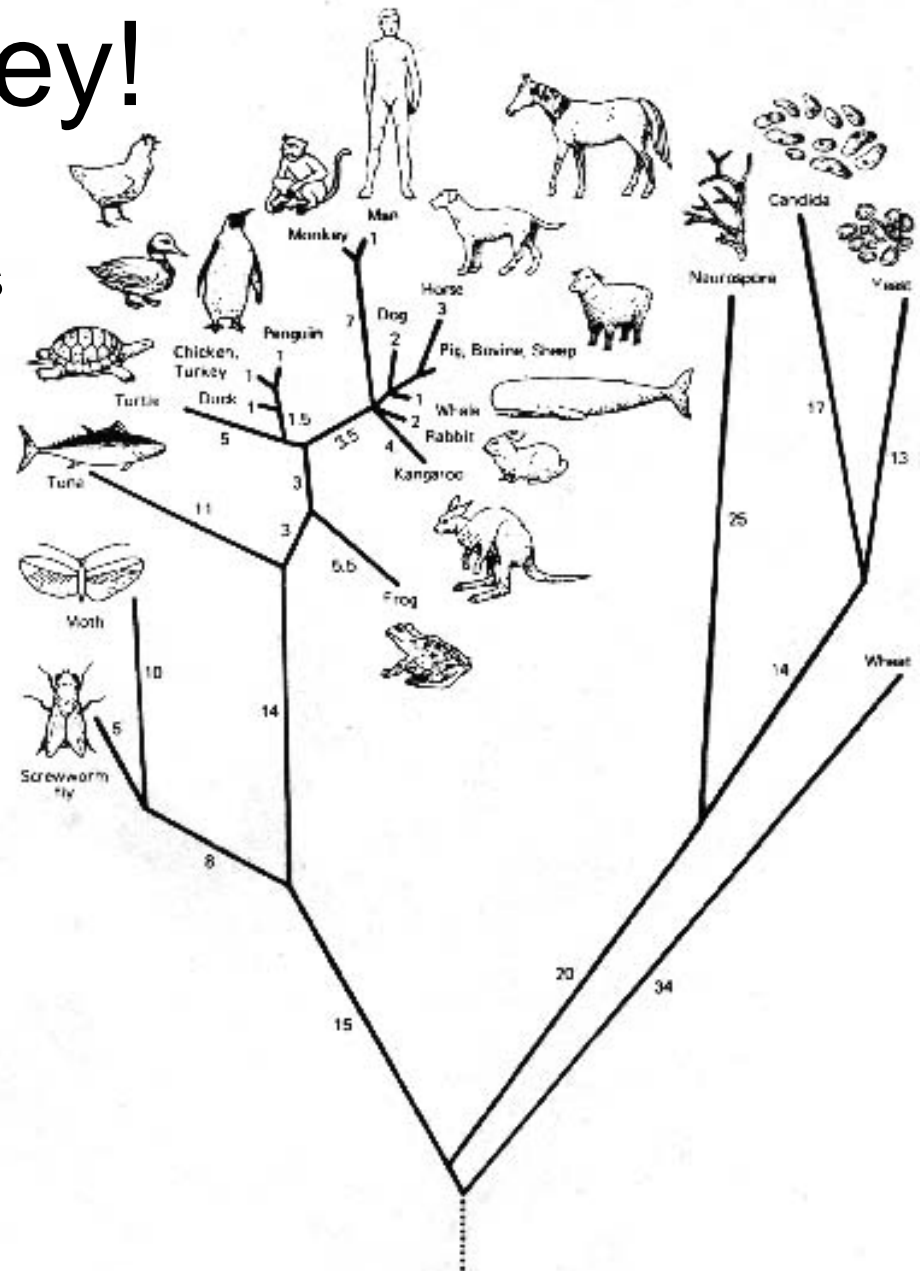
# Evolution is key!

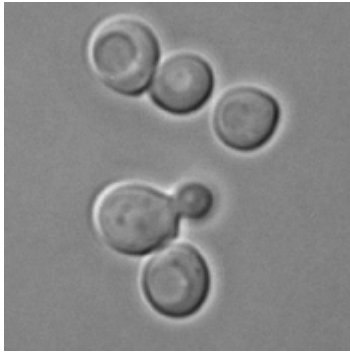
Common descent of organisms implies that they will share many “basic technologies.”

Development of new adaptations in response to environmental pressure can lead to “specialized technologies.”

More recent divergence implies more shared technologies between species.

All of biology is about two things: understanding shared or unshared features.





Yeast are unicellular organisms



Humans are multi-cellular organisms

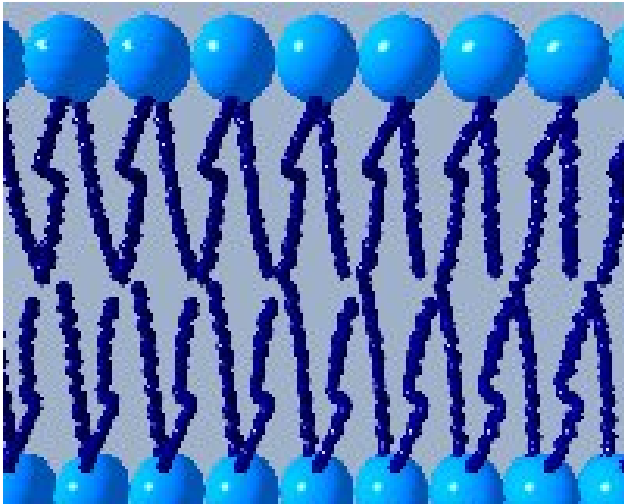
Understanding **how a cell works** is critical to understanding how the organism functions

Because of evolutionary similarities – we can use yeast and other small organisms to study human biology and disease!

# Biological macromolecules

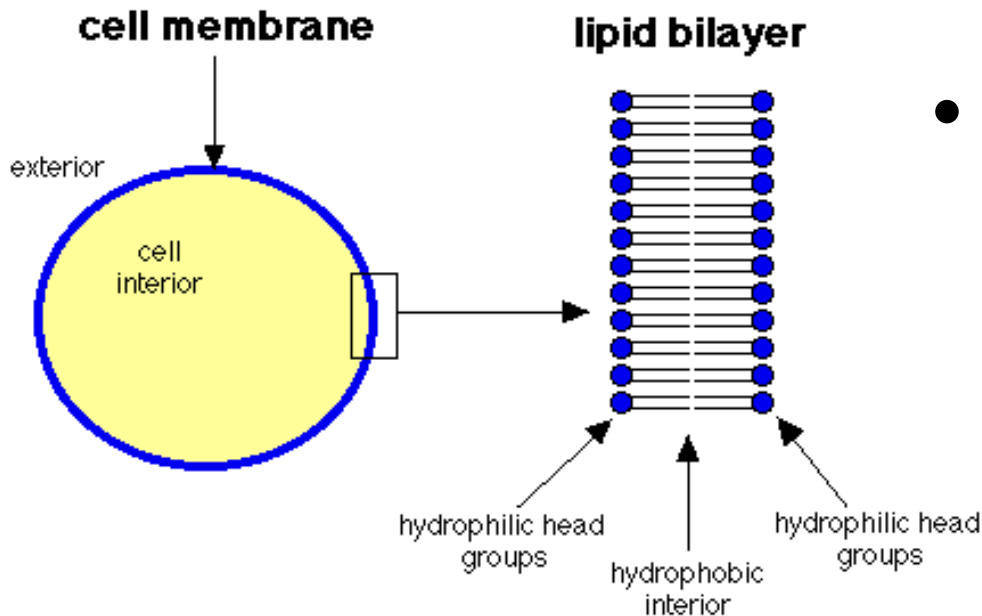
What are the main players in  
molecular biology?

What is DNA, RNA, protein, lipid?

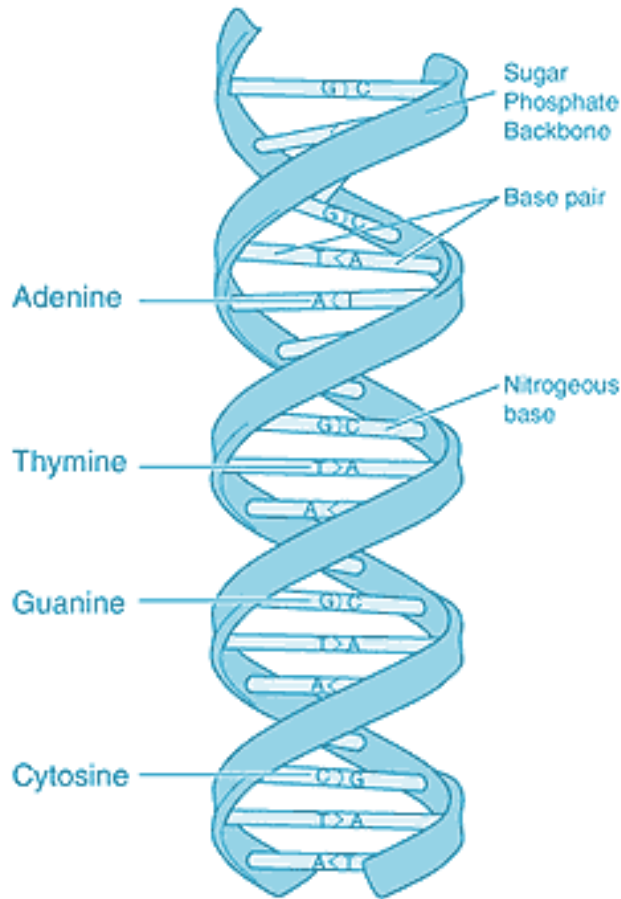


# Lipids

- Each lipid consists of a hydrophilic (water loving) and hydrophobic fragment
- Spontaneously form lipid bilayers => membranes



# DNA



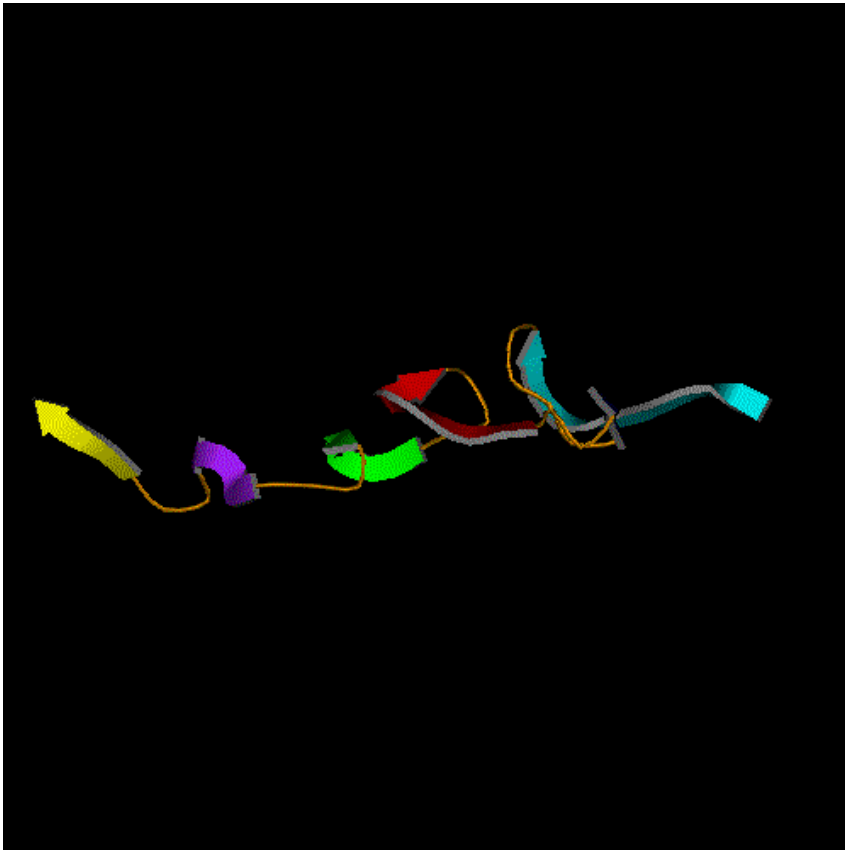
- Uses alphabet of 4 letters {ATCG}, called bases
- Encodes genetic information in triplet code
- Structure: a double helix





# Proteins

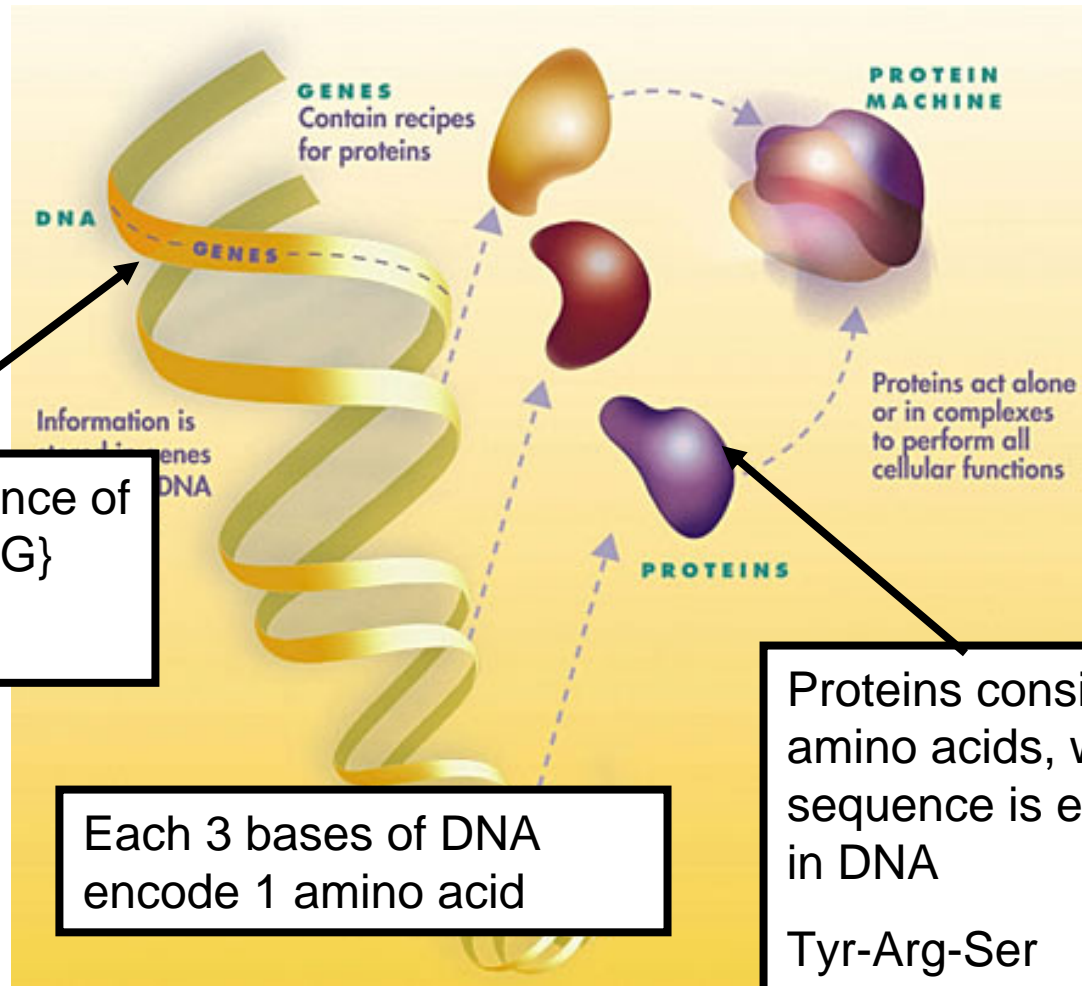
- A sequence of amino acids (alphabet of 20)
- Each amino acid encoded by 3 DNA bases
- Perform most of the actual work in the cell
- Fold into complex 3D structure



How does a cell function?  
The “Central Dogma” of biology

How are proteins made?  
What are translation & transcription?

# How does a cell function?



DNA is a sequence of bases {A, T, C, G}  
TAT-CGT-AGT

Each 3 bases of DNA encode 1 amino acid

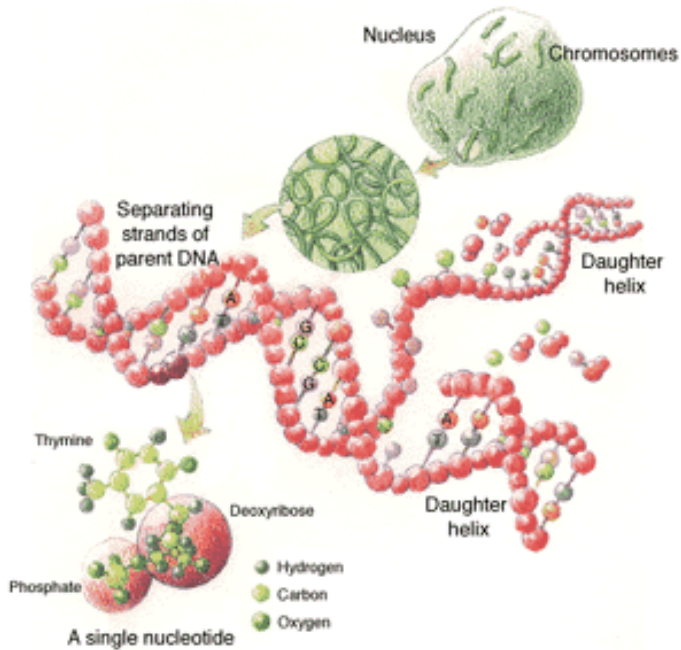
Proteins consist of amino acids, whose sequence is encoded in DNA  
Tyr-Arg-Ser

So what can computer science do  
to help study biology?

Case study 1:

sequencing the human genome

# How is the genome sequenced?



```
000001  gttgctggaggggagctggcggatgggacatgggggctggggcttgggtttcgtgctgt  
000045  ttggggggggttgggttggtagggcggcggctgggggggggggggggggggggggggggg  
000129  tccacgggggtacccctgtcccccacatctccggctcgggaccgggtgggttccgggtc  
000193  cgggggggtgggtgggttggaggggggttccgggggggggggggggggggggggggggg  
000257  gttctgggggggggggggggttccaaatgaacggcgggggtgggggggggggggggggg  
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000577  aattgggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
000641  gttctcaacgggtgcatgcatctcaacgggggggggtgggggggggggggggggggggg  
000705  aggtttgggggtatcgtggtgggggggggggggggggggggggggggggggggggggggg  
000769  aggtgggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
000833  ggtgggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
000897  gtttccgggggggggggggggggggggggggggggggggggggggggggggggggggggg  
000961  accccacatccgggggggggggggggggggggggggggggggggggggggggggggggg  
001025  ctacatccgggggggggggggggggggggggggggggggggggggggggggggggggg  
001089  gttttgcatcaatgaatgggggtgggggggggggggggggggggggggggggggggggg  
001153  cgtgggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001217  cgtgggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001281  tgggggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001345  aggggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001409  aggggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001473  aggggggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001537  cgttgggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001601  aggttgggggggggggggggggggggggggggggggggggggggggggggggggggg  
001665  gggtgggggggggggggggggggggggggggggggggggggggggggggggggggggg  
001729  aattgggggggggggggggggggggggggggggggggggggggggggggggggggggg  
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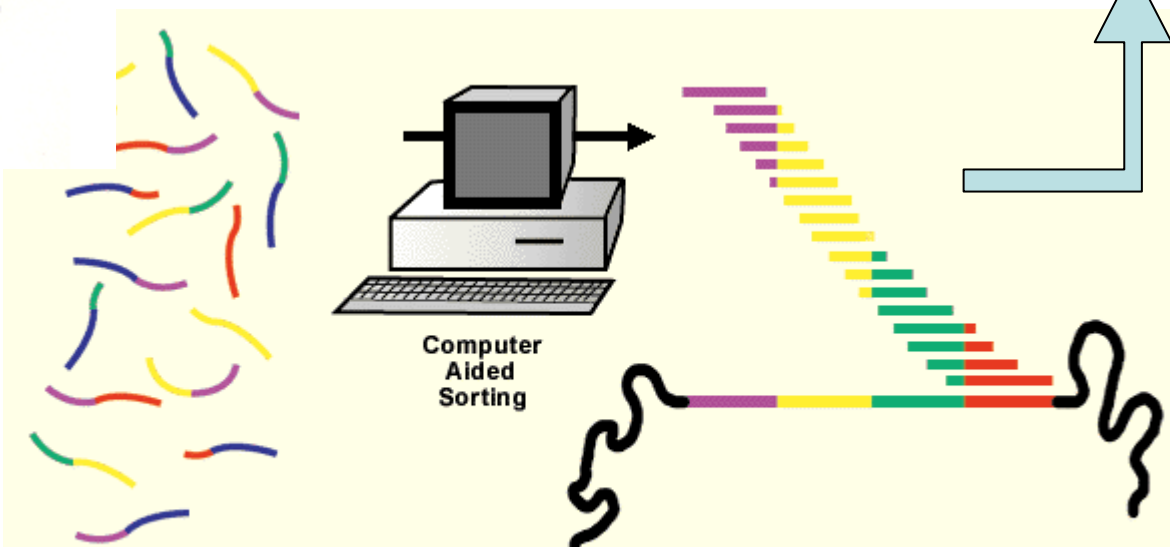


Fig 2: Short fragments of DNA sequence are ordered by overlapping data to recreate the whole genome sequence

# We have a sequence – now what?

Where are the genes?

\*start with “atg”

\*go in triplets

\*end with “act”

So how do we find them?

```
000001 gctgctggaaggggagctggccggtgggccatggccggctgcaggctctgggttccgtgctgc
000065 tggcggcggcgttggcttgcctggccacggcactgtggccgtggccccagtacatccaaaccta
000129 ccaccggcgctacacctgtaccccaacaacttccagttccggtagcatgtcagttcggccgg
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000513 taagacttccctcgattccctcaccggggcgtactgctggatacatctcgcattacctgcca
000577 ttgtctagcatcctggatacactggatgtcatggcacaataaatcaacgtgtccactggc
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000897 ggtgaaccccagctctcaacagcacctatgactcatgagcacactcttccctggagatcagctc
000961 gtcttccggacttttatctccacctgggaggggatgaagtgcacttccctgctggaagtcca
001025 accccaacatccaggccttcatgaagaaaagggttactgacttcaagcagctggagctctt
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001217 cagttagatcatgttggagatgcaagatataccagggtggctcggggccctgctgtctgc
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001729 actgcctcccggccaggggagagcacccttgcccgtgtgcccctgtgactacagagaaggagg
001793 ctggtgctggcactgggtgttcaataaagatctatgtggcattttctc
```

1 ctggegcegcg cggccctgcg ggtgacaggc aggcgggaag gggcggggcc tggggcgggg  
61 ccgcccgtggg gaggagggcg gtgggagggg aggagtggag atggcggcgg cggcggctca  
121 gggggggcggg ggcggggagc cccgtagaac cgagggggtc ggcccggggg tcccggggga  
181 ggtggagatg gtgaaggggc agccgttcga cgtgggcccg cgctacacgc agttgcagta  
241 catcggcgag ggcgcgtacg gcatggtcag ctcgccctat gaccacgtgc gcaagactcg  
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481 tgacctgtac aagttgctga aaagccagca gctgagcaat gaccatatct gctacttct  
541 ctaccagatc ctgcccggggc tcaagtacat ccactccgce aacgtgctcc accgagatct  
601 aaagccctcc aacctgctca tcaacaccac ctgcgacctt aagatttgtg atttcggcct  
661 ggcccgggatt gccgatcctg agcatgacca caccggcttc ctgacggagt atgtggctac  
721 gcgctggtac cgggccccag agatcatgct gaactccaag ggctatacca agtccatcga  
781 catctggtct gtgggctgca ttctggctga gatgctctct aaccggccca tcttccctgg  
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1141 ggggctgggg gcaggggagc aggggggac gtaggcatcc cccatgccag gcctgagcct  
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1681 gggcagaggt ggagggtggg gggcgctgag tagggactca gggccatgcc tgccccctc  
1741 atctcattca aaccccacc tagtttccct gaaggaacat tccttagtct caagggctag  
1801 catccctgag gagccagccc gggccgaatc cctcctctgt caaagctgtc acttcgcgtg  
1861 ccctcgctgc ttctgtgtgt ggtgagcaga agtggagctg gggggcgtgg agagcccggc  
1921 gcccctgcca cctcctgac ccgtctaata tataaatata gagatgtgtc tatggctgaa  
1981 aaaaaaaaaa aaaaaaaaaa aaaaa

P53

how  
would  
you  
find  
this?

# Where is this gene in the genome?

- Human genome is 3 billion bases long
- TP53 is on:
  - Chromosome 17
  - Small arm
  - Position 17.3
  - Around base 9.5 mil in chromosome 17  
(Human chromosomes range in length from 51 million to 245 million base pairs )
- Could you find this by hand?



# Need **large** databases for all the information!

http://www.ncbi.nlm.nih.gov/mapview/maps.cgi?taxid=9606&build=previous&chr=17&MAPS=genec,ughs,genes-r&cmd=focus&fill=40&query=uid(6554)&Q5TR=p53

Map Viewer Introduction to Human Genetics

Build 36.1 (Previous) Human genome overview page (Build 36.1) Human genome overview page (Build 35.1) Map Viewer Home

Master Map: Genes On Sequence

Region Displayed: 5,650K-11,870K bp

Summary of Maps

Download/View Sequence/Evidence

Genes\_cyto HsUnig Genes\_seq

Symbol	LinkOut	E	Cyto	Description
KIAA0523	sv pr dl mm hm	C	17p13.2	KIAA0523 protein
HSXIAPAF1	OMIM sv pr dl mm hm ccds	C	17p13.1	XIAP associated factor-1
CLECSF14	OMIM sv pr dl mm hm ccds	C	17p13.1	C-type (calcium dependent, carbohydrate-re
ASGR2	OMIM sv pr dl mm hm ccds	C	17p	asialoglycoprotein receptor 2
ASGR1	OMIM sv pr dl mm hm ccds	C	17p13.2	asialoglycoprotein receptor 1
DLG4	OMIM sv pr dl mm hm	C	17p13.1	discs, large homolog 4 (Drosophila)
DVL2	OMIM sv pr dl mm hm ccds	C	17p13.2	dishevelled, dsh homolog 2 (Drosophila)
GABARAP	OMIM sv pr dl mm hm ccds	C	17p13.1	GABA(A) receptor-associated protein
DERP6	sv pr dl mm hm ccds	C	17p13.1	S-phase 2 protein
CLDN7	sv pr dl mm hm ccds	C	17p13	claudin 7
SLC2A4	OMIM sv pr dl mm hm ccds	C	17p13	solute carrier family 2 (facilitated glucose tra
YBX2	sv pr dl mm hm ccds	C	17p11.2-p13.1	germ cell specific Y-box binding protein
GPS2	OMIM sv pr dl mm hm ccds	C	17p13	G protein pathway suppressor 2
MGC40107	sv pr dl mm hm ccds	C	17p13.1	hypothetical protein MGC40107
NLGN2	OMIM sv pr dl mm hm ccds	C	17p13.1	neuroligin 2
FLJ36878	sv pr dl mm hm ccds	C	17p13.1	hypothetical protein FLJ36878
TNFSF13	OMIM sv pr dl mm hm ccds	C	17p13.1	tumor necrosis factor (ligand) superfamily, m
SAT2	sv pr dl mm hm ccds	C	17p13.1	spermidine/spermine N1-acetyltransferase 2
TP53	OMIM sv pr dl mm hm ccds	C	17p13.1	tumor protein p53 (Li-Fraumeni syndrome)
ALOXE3	OMIM sv pr dl mm hm ccds	C	17p13.1	arachidonate lipoxygenase 3
AURKB	OMIM sv pr dl mm hm ccds	C	17p13.1	aurora kinase B
ODF4	sv pr dl mm hm ccds	C	17p13.1	outer dense fiber of sperm tails 4
LOC124751	sv pr dl mm ccds	C	17p13.1	hypothetical protein LOC124751

Region shown: 5,650K to 11,870K

You are here: Ideogram

Find: million ba Match case

So what can computer science do  
to help study biology?

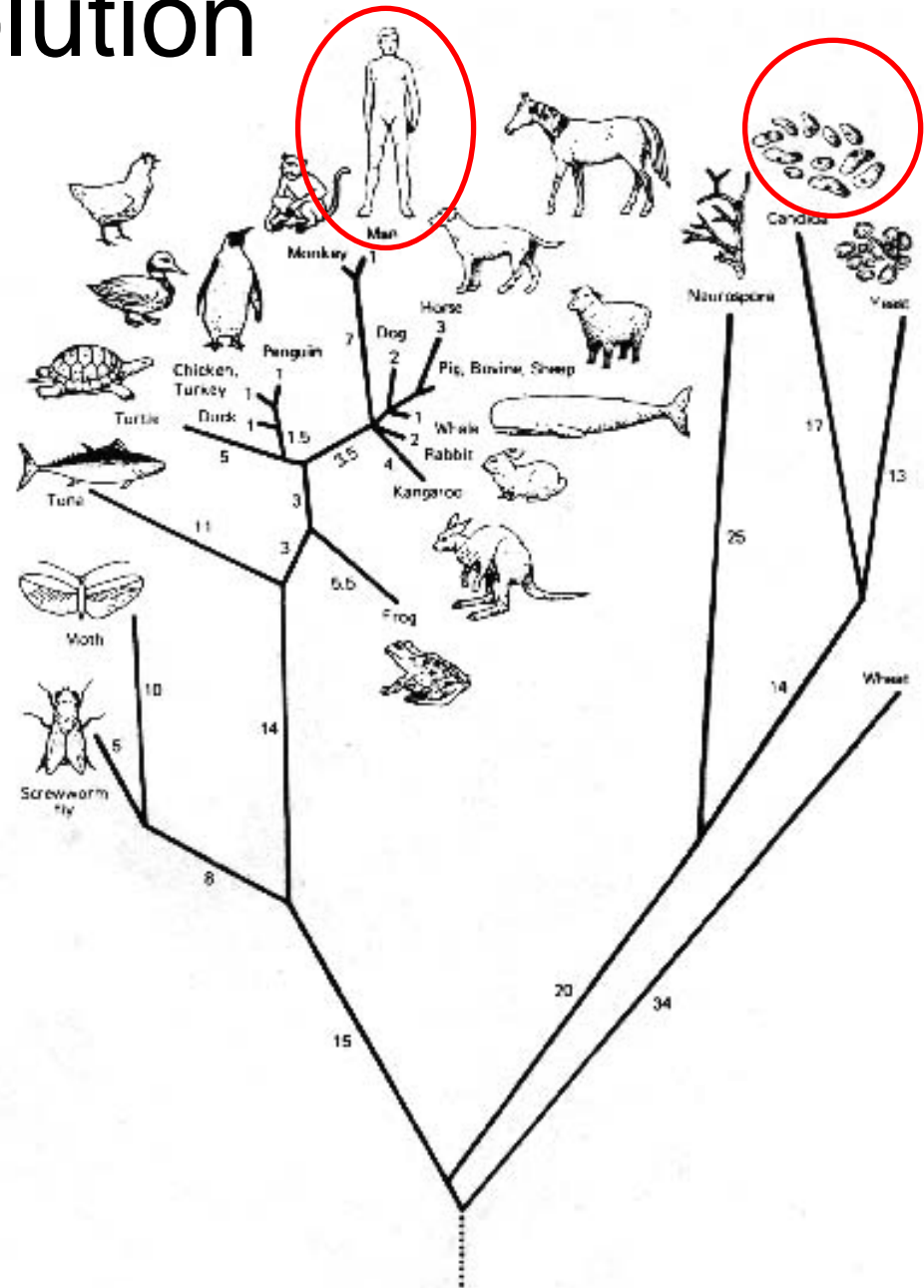
Case study 2:

so what do these genes do?

# Remember – evolution can help!

Common descent of  
organisms implies that  
they will share many  
“basic technologies.”

Thus, can use yeast to  
understand what  
proteins do in humans!



Human hereditary colon cancer gene was found by looking for a gene similar to MSH2 gene in yeast (these genes are 65% similar)!

(Yeast sequence on top).

**BLAST P-value: 3.8e-255**

Percent Similarity (|+|): 64.7      Percent Identity (|): 43.0

```

  1 MSSTRPELKFSDVSEERNFYKKYTGLPKKPLKTIKLVKGDYYTVIGSDA  50
    | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
  1 MAVQPKETLQLESAAEVGFVRRFFQGMPEKPTTIVRLFDRGDFYTAHGEDA  50

 51 IFVADSVYHTQSVLKNCQLDPVTAKNFHEPTKYVTVSLQVLATLLKLCLL  100
    || . | . || . || || || . . || || . . . | . || . . || || ||
 51 LLAAREVFKTQGVIKY. .MGPAGAKNLQS. . . .VVL SKMNFESFVKDLLL  94

101 DLGYKVEIY. . . . .DKGWKLIKASPGNIEQVNELMNMNIDSSII  140
    . || || || . . . | . || | . || || || . | . || || | || |
 95 VRQYRVEVYKNRAGNKASKENDWYLAYKASPGNLSQFEDILFGNNDMSAS  144

141 IASLKVQWNSQDGNCIIGVAFIDTTAYKVGMLDIVDNEVYSNLESFLIQL  190
    || | | . . || . . || || || . . . || || || . || || || || || ||
145 IGVVGVKMSAVDQQRQVGVGYVDSIQRKLGLCEFPDNDQFSNLEALLIQI  194

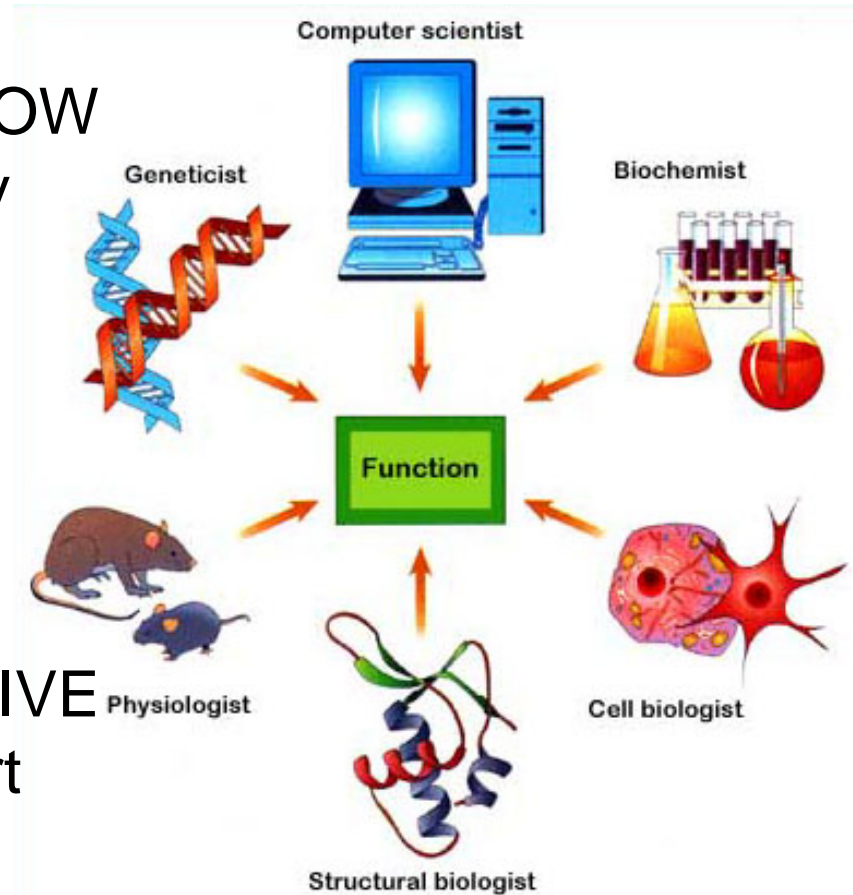
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    | . || || || . | . . || . . || || . || || || . . || || . || || |
195 GPKECVLPG. . . .GETAGDMGKLRQIIQRGGILITERKKADFSTKDIYQD  240

241 LTKLL. . . .GDDL. ALSLPQKYSKLSMGACNALIGYLQLLSEQDQVGKYE  285
    | . || || . . || || . . || || . . || || || || || || . . | . ||
241 LNRLKGGKKGEMNSAVLPENQVAVSSLSAVIKFLELLSDDSNFGQFE  290
```

# So what's next?

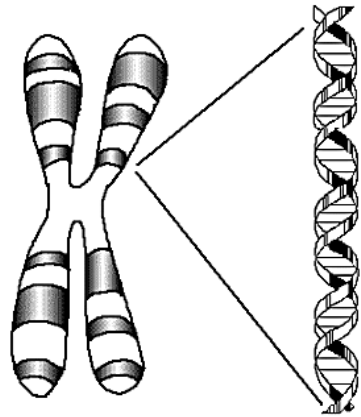
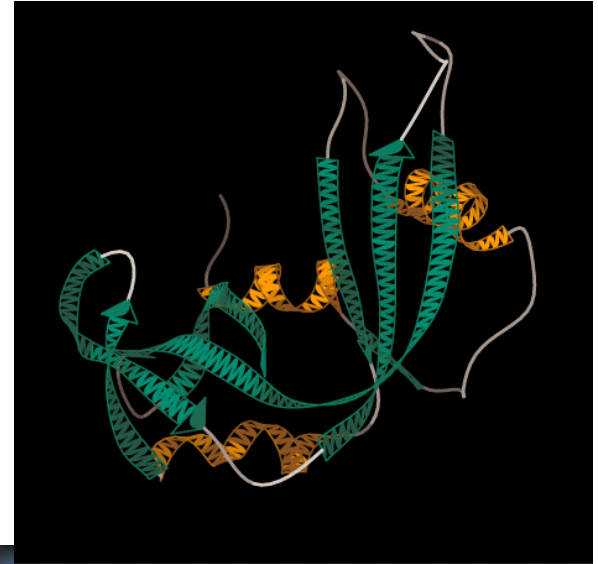
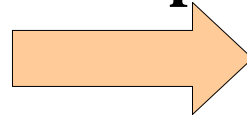
## Genomics is a collaborative discipline

- To study **WHAT** proteins **DO**, **HOW** they **INTERACT**, and **HOW** they are **REGULATED**, need data beyond genomic sequence
- Genomics/Bioinformatics is fundamentally a **COLLABORATIVE** and **MULTIDISCIPLINARY** effort



Now we are trying to understand how small differences in DNA lead to large differences in <sup>Proteins</sup> phenotypes

**Gene Expression**



Chromosome

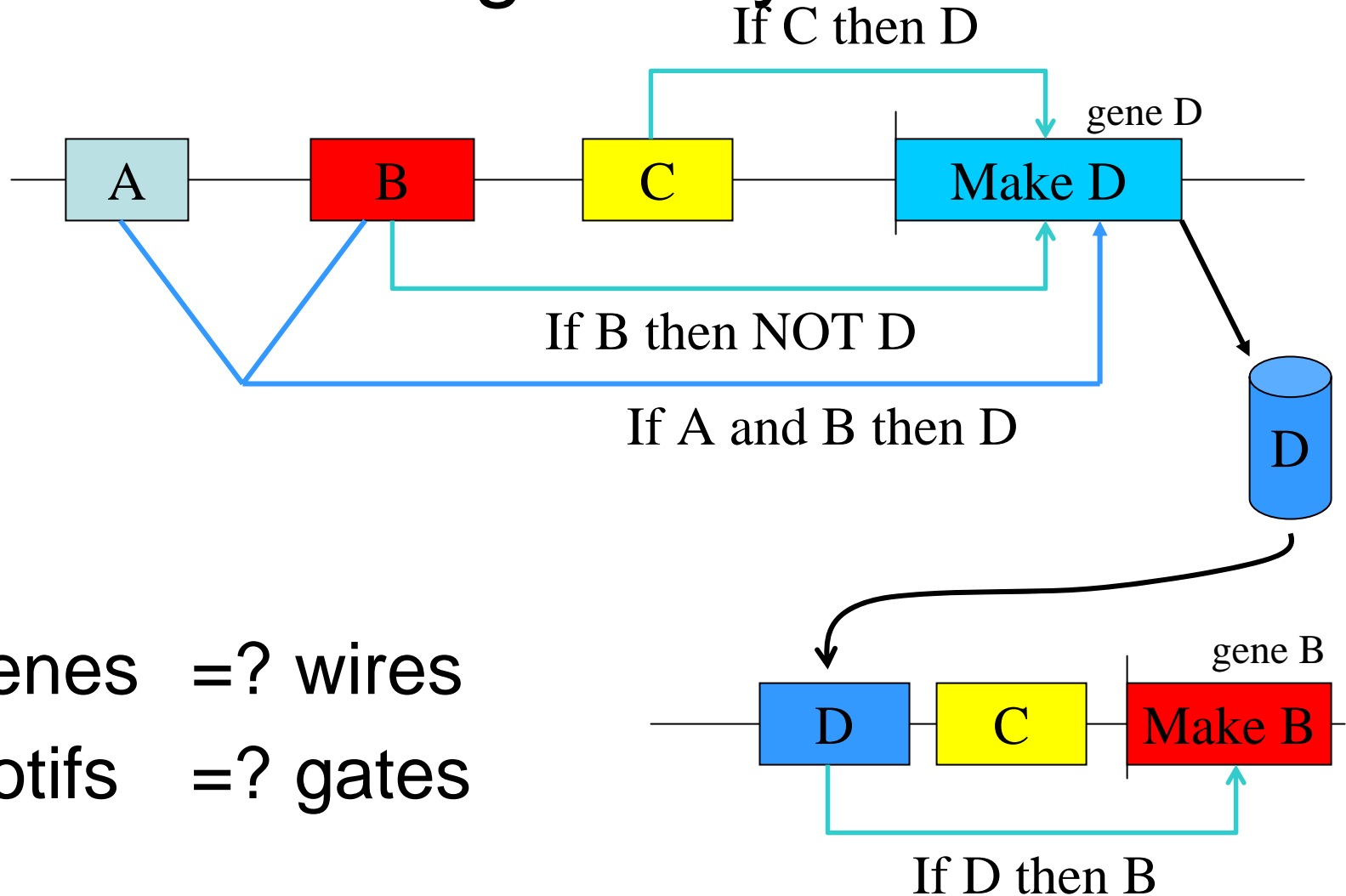
DNA

DNA



People

# The answer is probably in regulation “Gene Regulatory Circuits”

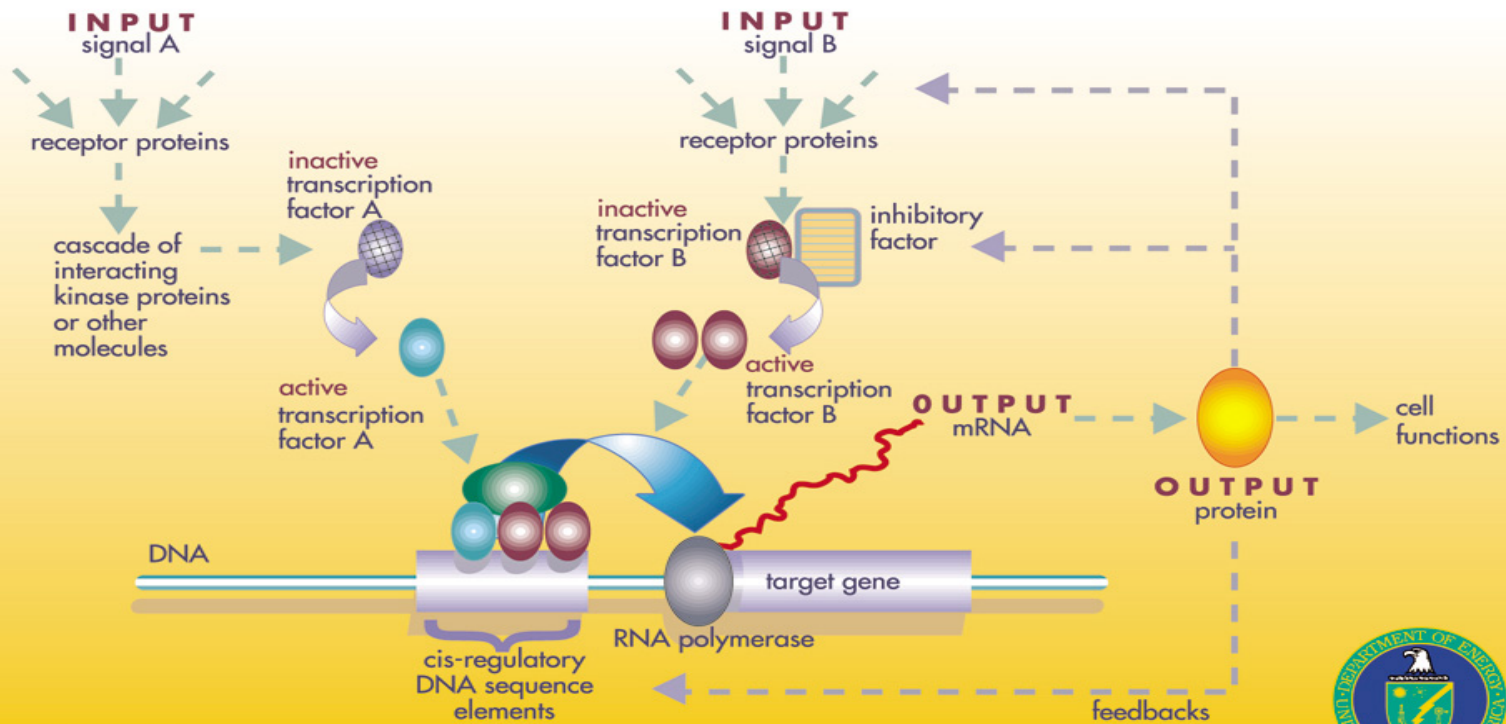


- Genes =? wires
- Motifs =? gates

# Regulatory Networks

GENOMES *to* LIFE

## A GENE REGULATORY NETWORK





Any questions?

# What is genomics all about?

The “omes” in biology.

Why bioinformatics?

What is “systems biology”?

# The “omes”

- Genome – organism’s complete set of DNA
  - Relatively stable through an organism’s lifetime
  - Size: from 600,000 to several billion bases
  - Gene is a basic unit of heredity (only 2% of the human genome)
- Proteome – organism’s complete set of proteins
  - Dynamic – changes minute to minute
  - Proteins actually perform most cellular functions, they are encoded by genes (not a 1-to-1 relationship)
  - Protein function and structure form molecular basis for disease

# Beyond the “omes” – systems biology

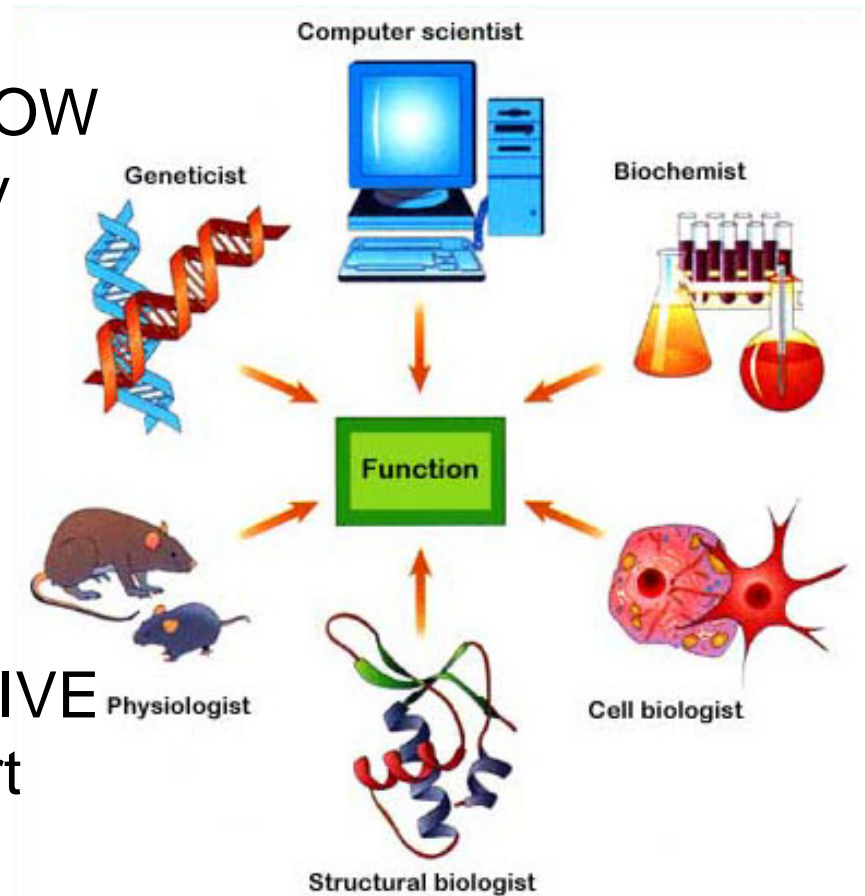
- Understanding the function and regulation of cellular machinery, as well as cell-to-cell communication on the molecular level
- Why? Because most important biological problems are fundamentally systems-level problems
  - Systems-level understanding of disease (e.g. cancer)
  - Molecular medicine
  - Gene therapy

# Systems-level challenges

- **Gene function annotation – what does a gene do**
  - ~30,000 genes in the human genome => systems-level approaches necessary
  - A modern human microarray experiment produces ~500,000 data points => computational analysis & visualization necessary
  - Many high-throughput functional technologies => computational methods necessary to integrate the data
- **Biological networks – how do proteins interact**
  - Large amounts of high-throughput data => computation necessary to store and analyze it
  - Data has variable specificity => computational approaches necessary to separate reliable conclusions from random coincidences
- **Comparative genomics – comparing data between organisms**
  - Need to map concepts across organisms on a large scale => practically impossible to do by hand
  - High amount of variable quality data => computational methods needed for integration, visualization, and analysis
  - Data often distributed in databases across the globe, with variable schemas etc => data storage and consolidation methods needed

# Function

- To study **WHAT** proteins **DO**, **HOW** they **INTERACT**, and **HOW** they are **REGULATED**, need data beyond genomic sequence
- Genomics/Bioinformatics is fundamentally a **COLLABORATIVE** and **MULTIDISCIPLINARY** effort



# Biological networks

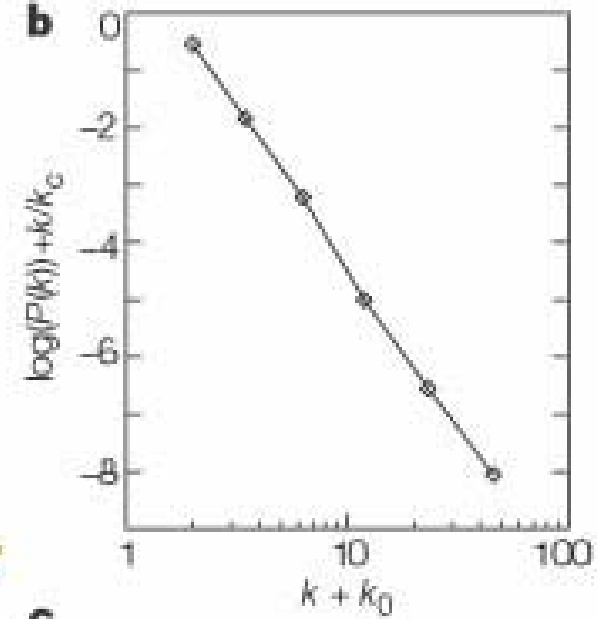
- Interaction maps (no directions)
- Pathway models (dynamic or static)
- Metabolic networks
- Genetic regulatory networks

# Yeast interaction network

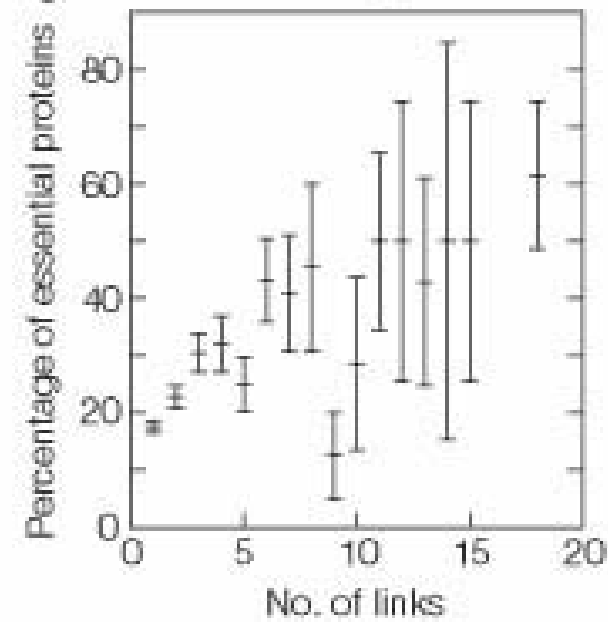
**a**



**b**

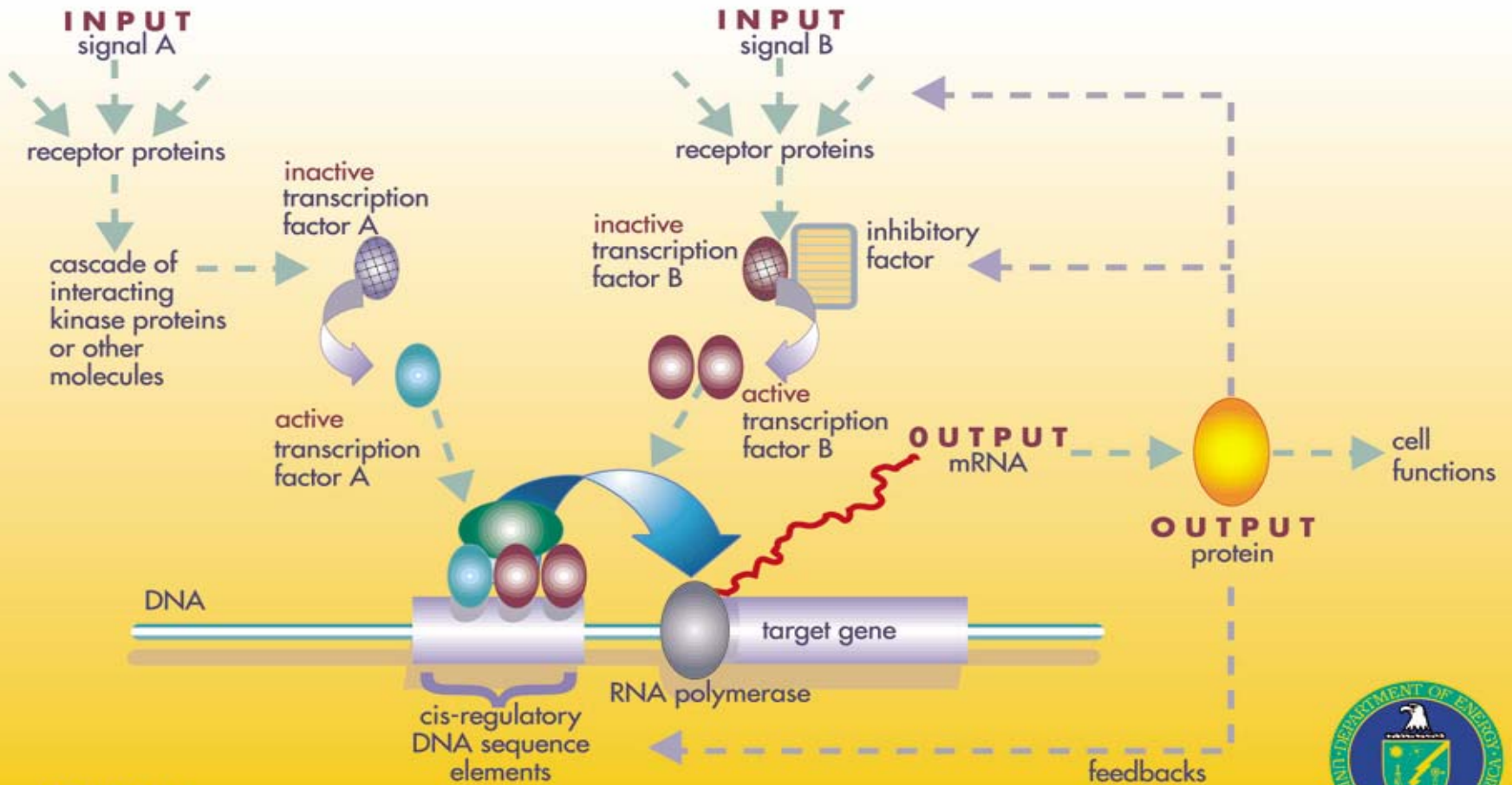


**c**





## A GENE REGULATORY NETWORK



Gene expression microarrays  
– one type of high-throughput  
functional data

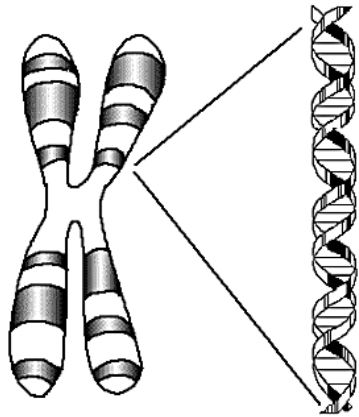
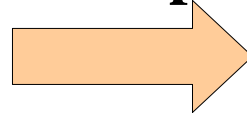
# Why microarray analysis: the questions

- Large-scale study of biological processes
- What is going on in the cell at a certain point in time?
- On the large-scale genetic level, what accounts for differences between phenotypes?
- Sequence important, but genes have effect through expression

# Why study gene expression

Proteins

Gene Expression



Chromosome

DNA

DNA



People

# Computational biology/bioinformatics

What does it study?

Where do we get the data?

# Computational Molecular Biology

- In order to gather insight into the ways in which genes and gene products (proteins) function, we:
  1. Analyze DNA and protein sequences, searching for clues about structure, function, and control.

## SEQUENCE ANALYSIS

- 2. Analyze biological structures, searching for clues about sequence, function and control.

## STRUCTURE ANALYSIS

- 3. Understand how cellular components function in living systems.

## FUNCTION ANALYSIS

# What are functions of genes?

- Signal transduction: sensing a physical signal and turning into a chemical signal
- Structural support: creating the shape and pliability of a cell or set of cells
- Enzymatic catalysis: accelerating chemical transformations otherwise too slow.
- Transport: getting things into and out of separated compartments

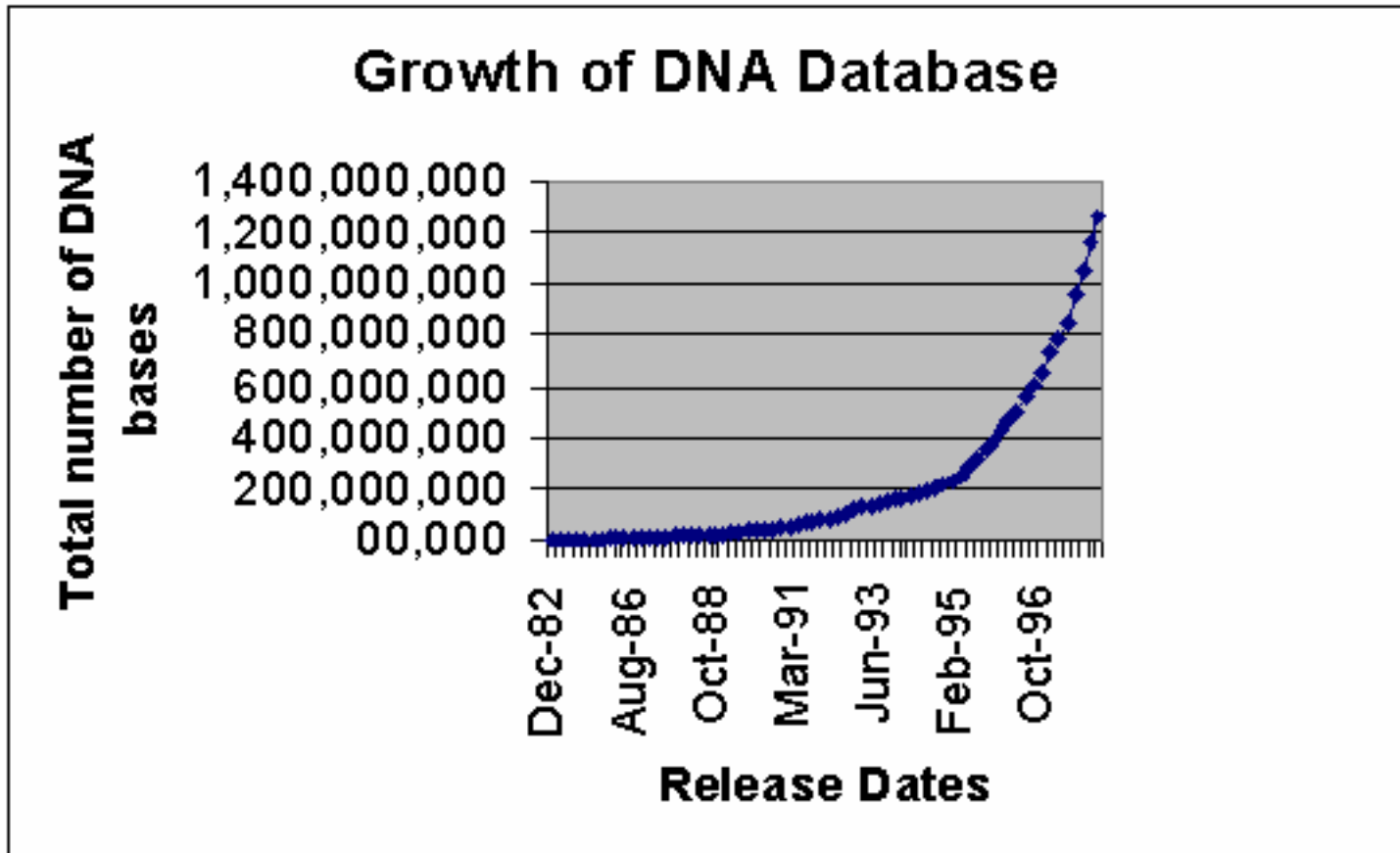
# What are the functions of genes?

- Movement: contracting in order to pull things together or push things apart.
- Transcription control: deciding when other genes should be turned ON/OFF
- Trafficking: affecting where different elements end up inside the cell



# Biology and Medicine are fundamentally information sciences.

<http://www.ncbi.nlm.nih.gov/Genbank/genbankstats.html>



# Complete Genomes Known (900 currently available publically)

- Aquifex aeolicus
- Archaeoglobus fulgidus
- Bacillus subtilis
- Borrelia burgdorferi
- Chlamydia trachomatis
- Escherichia coli
- Haemophilus influenzae
- 
- Methanobacterium thermoautotrophicum
- Caulobacter crescentus
- Helicobacter pylori
- Methanococcus jannaschii
- Mycobacterium tuberculosis
- Mycoplasma genitalium
- Mycoplasma pneumoniae
- Pyrococcus horikoshii
- Treponema pallidum
- Saccharomyces cerevisiae
- Drosophila melanogaster
- Arabidopsis thaliana
- Caenorhabditis elegans
- Homo sapiens

<http://www.ncbi.nlm.nih.gov:80/PMGifs/Genomes/org.html>

# Computer Science & Genomics

- Computer science a discipline of itself
- BUT: it's also a tool applied to study of other disciplines
  - Bioinformatics: cs applied to biology & biochemistry
  - Neuroscience
  - Security and policy
  - Economics
  - Physics

# Computational Molecular Biology (bioinformatics)

In order to gather insight into the ways in which genes and gene products (proteins) function, we:

1. Analyze DNA and protein sequences, searching for clues about structure, function, and control.

## SEQUENCE ANALYSIS

2. Analyze biological structures, searching for clues about sequence, function and control.

## STRUCTURE ANALYSIS

3. Understand how cellular components function in living systems.

## FUNCTION ANALYSIS

Chromosome Bands Localized by FISH Mapping Clones

17q21.31

Chromosome Band

STS Markers on Genetic (blue) and Radiation Hybrid (black) Maps

Gap Locations

Gap

Known Genes Based on SWISS-PROT, TrEMBL, mRNA, and RefSeq



BRCA1

RefSeq Genes

RefSeq Genes

Ensembl Gene Predictions

Ensembl Genes

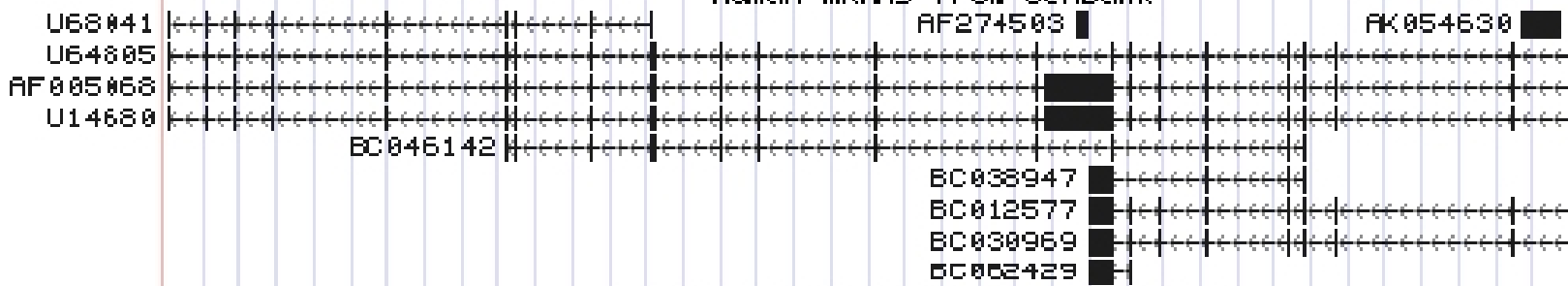
AcView Gene Models With Alt-Splicing

AcView Genes

Genscan Gene Predictions

Genscan Genes

Human mRNAs from GenBank



Human ESTs That Have Been Spliced

Spliced ESTs

Human/Chimp/Mouse/Rat/Chicken Multiz Alignments & PhyloHMM Cons

Conservation

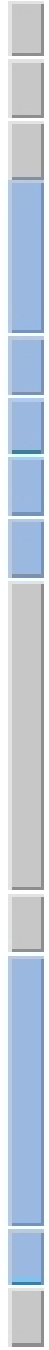
chimp  
mouse  
rat  
chicken

Takifugu rubripes Translated Blat Alignments

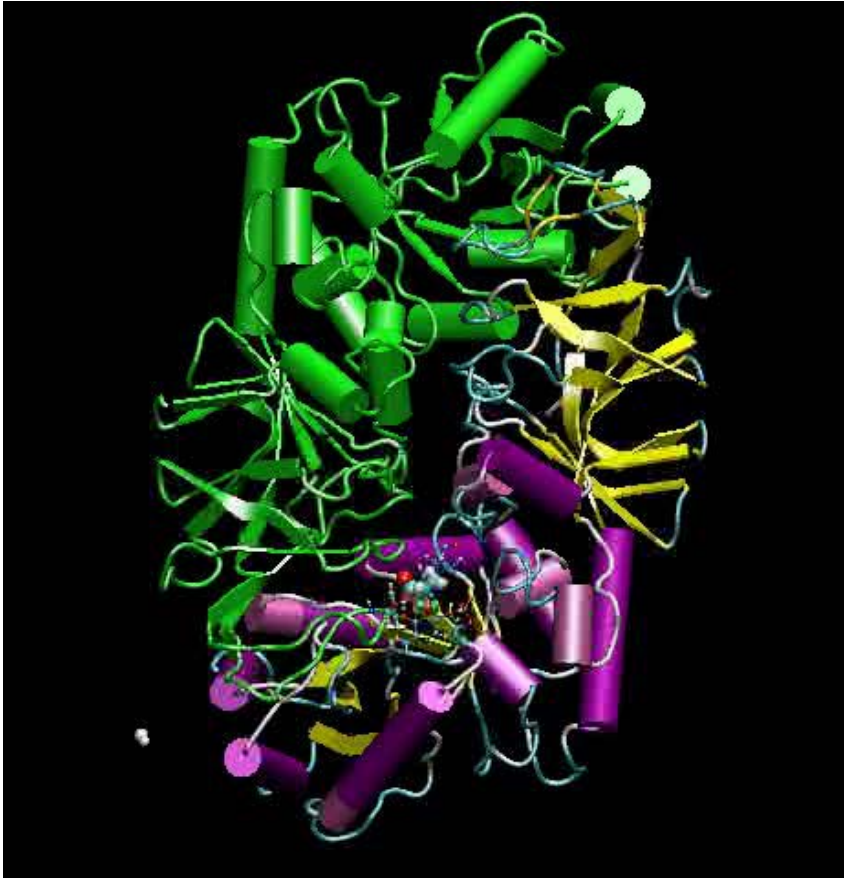
Fugu Blat

Repeating Elements by RepeatMasker

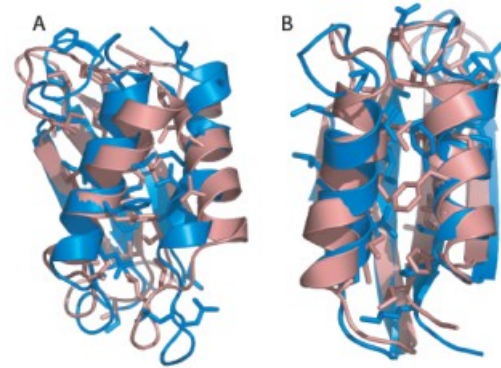
RepeatMasker



# Structure analysis



Protein dynamics of secondary structure

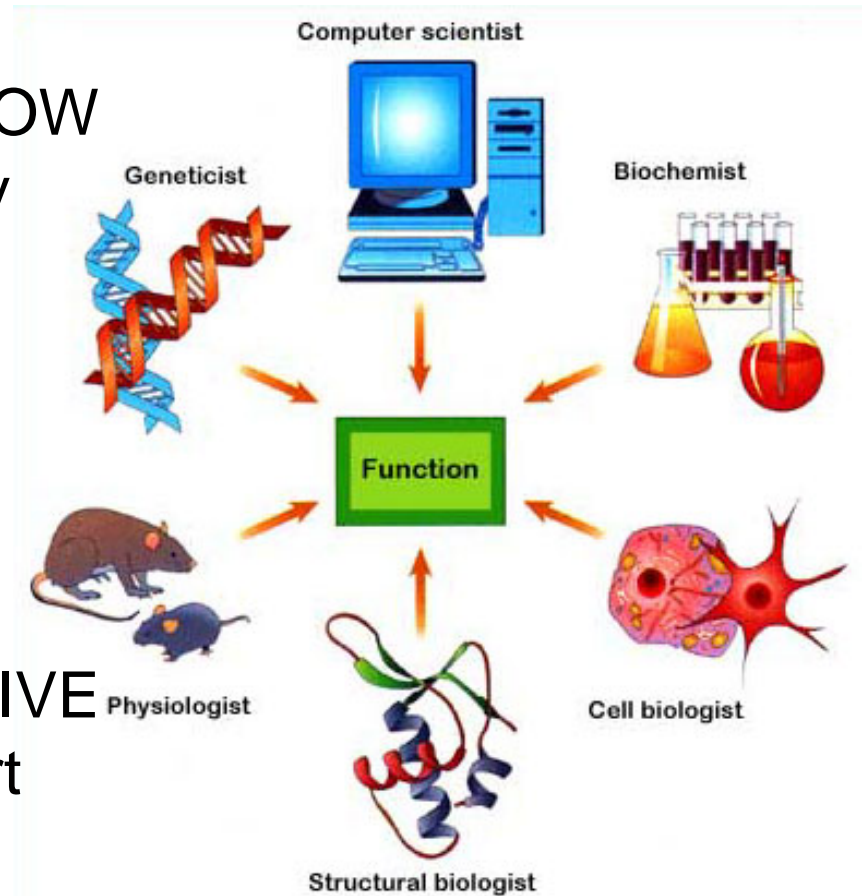


Protein structure prediction

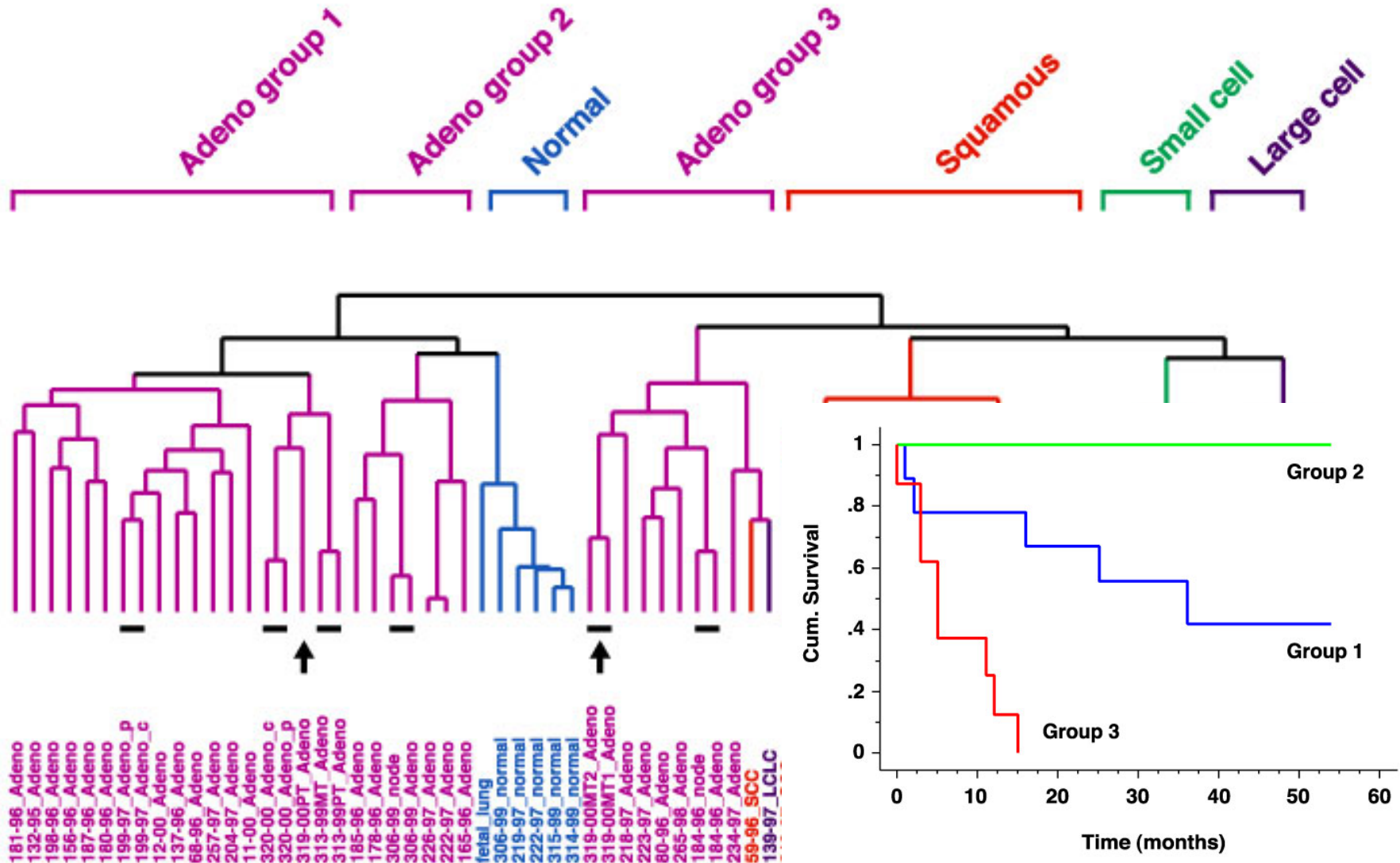
- Protein structure prediction
- Docking
- Small molecule binding
- Molecular dynamics

# Function analysis

- To study **WHAT** proteins **DO**, **HOW** they **INTERACT**, and **HOW** they are **REGULATED**, need data beyond genomic sequence
- Genomics/Bioinformatics is fundamentally a **COLLABORATIVE** and **MULTIDISCIPLINARY** effort



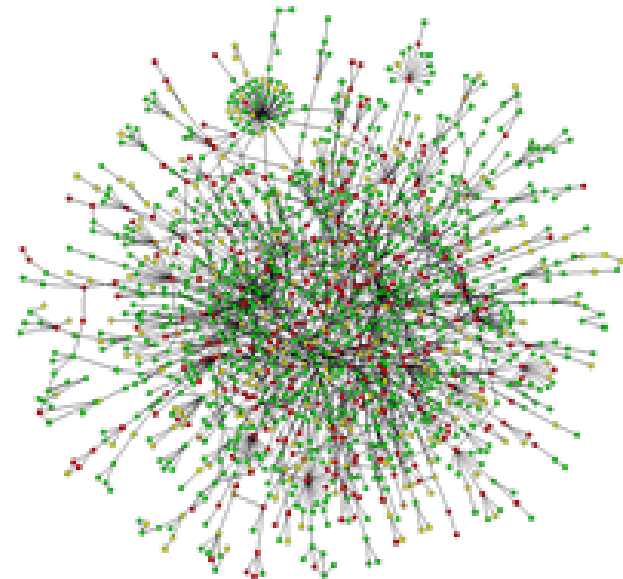
# Microarray analysis





# Biological networks

- Interaction maps (no directions)
- Pathway models (dynamic or static)
- Metabolic networks
- Genetic regulatory networks



## A GENE REGULATORY NETWORK

