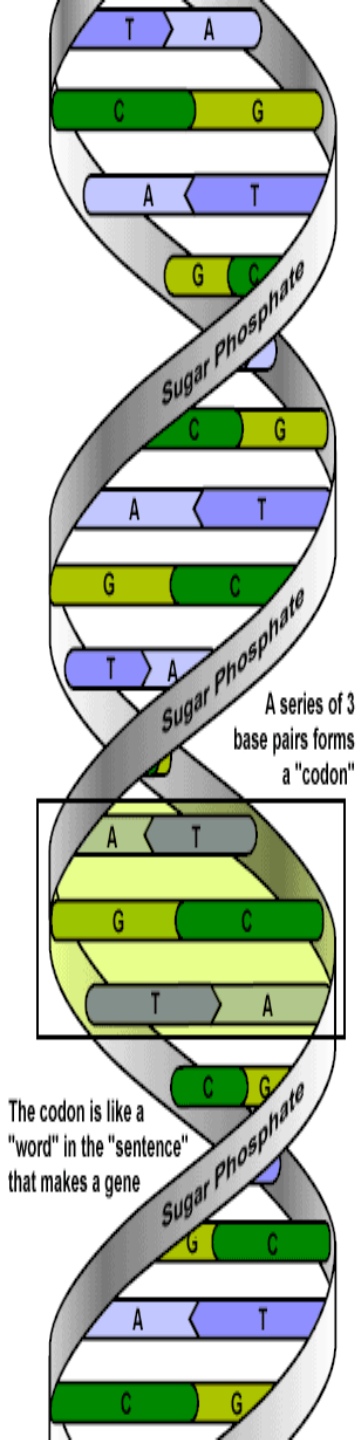

Bioinformatics

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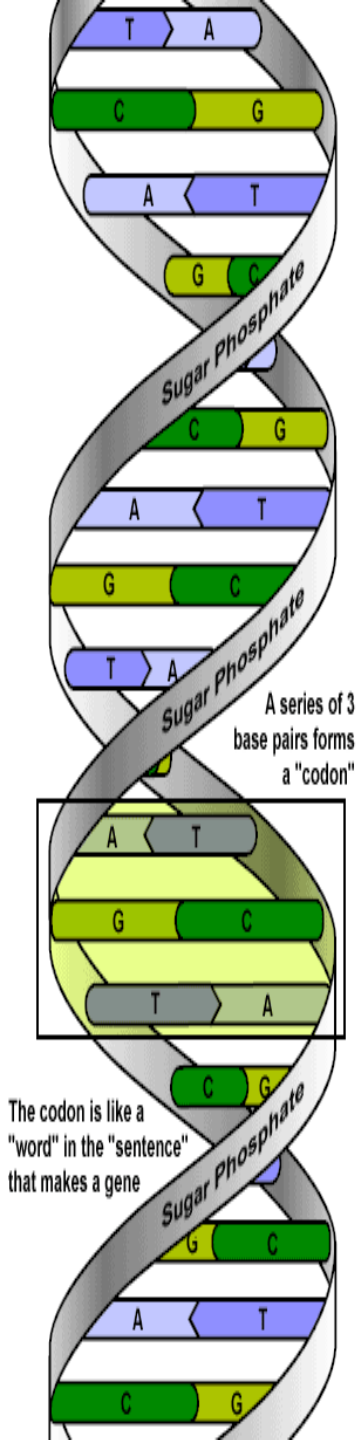
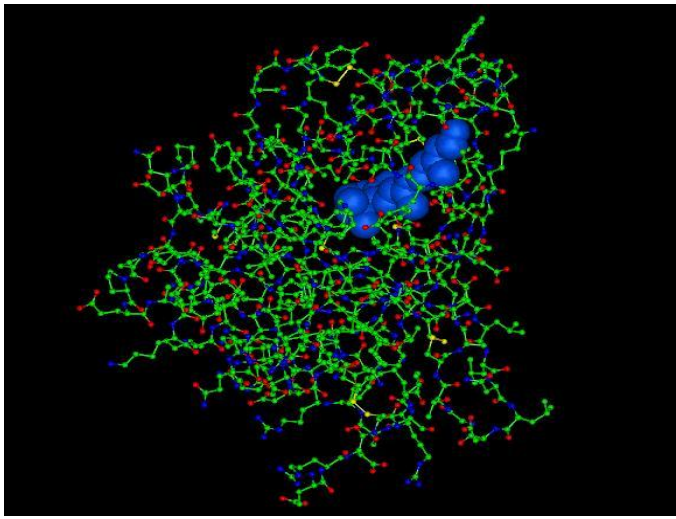
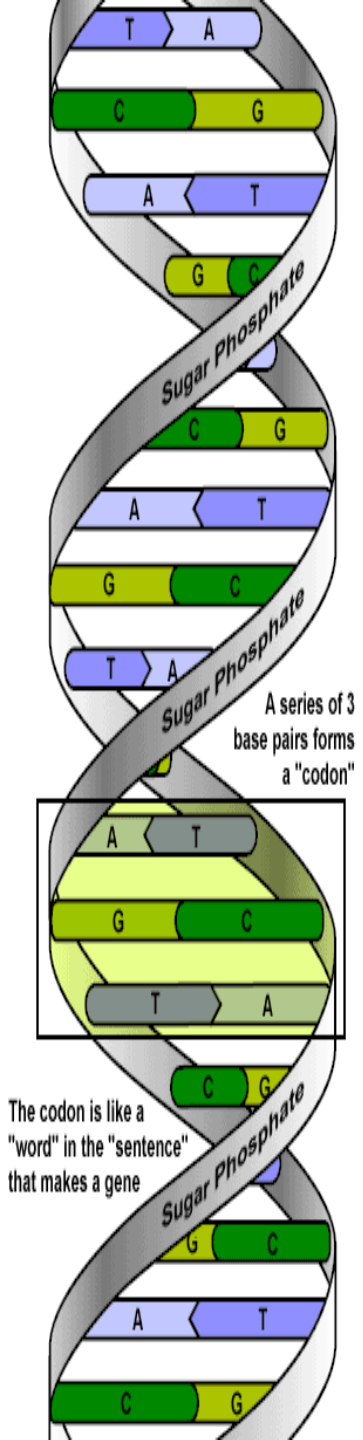


Objectives

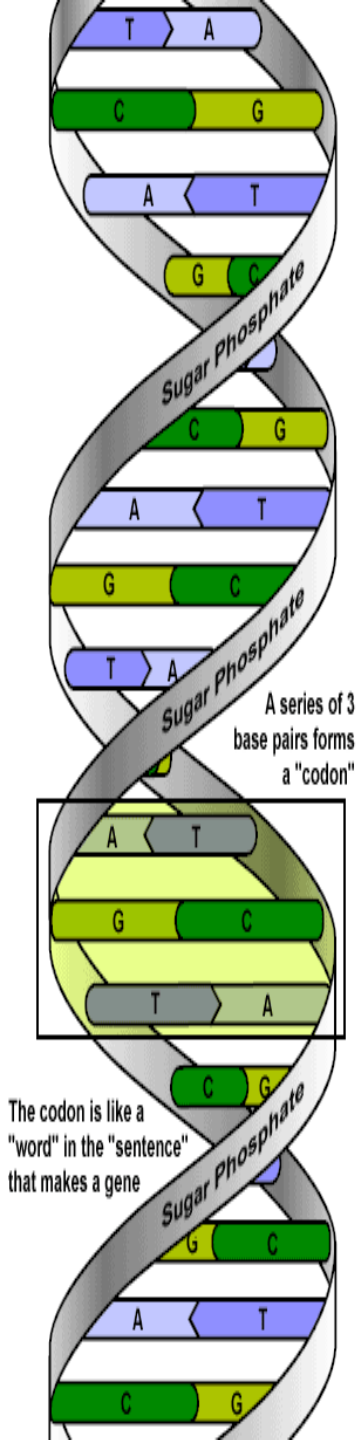
1. Introduction and historical background
2. How it is changing the society
3. Hot areas in Bioinformatics
4. Future perspective
5. Conclusion





Introduction

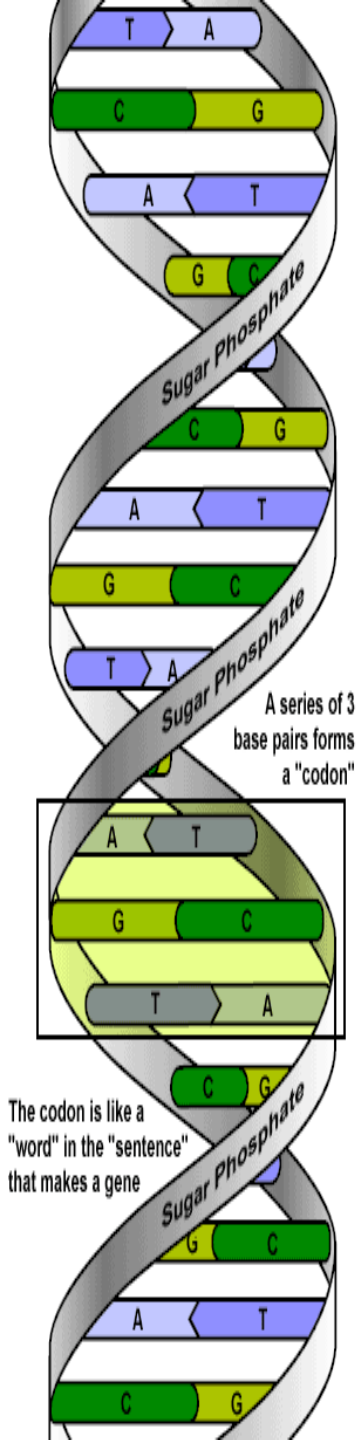
- ✓ We are drowning in data but starving for knowledge!
- ✓ We are rich in data but poor in information!
- ✓ Data is growing faster than human imagination!
- ✓ *Every day the world creates 92000 TB of data.*

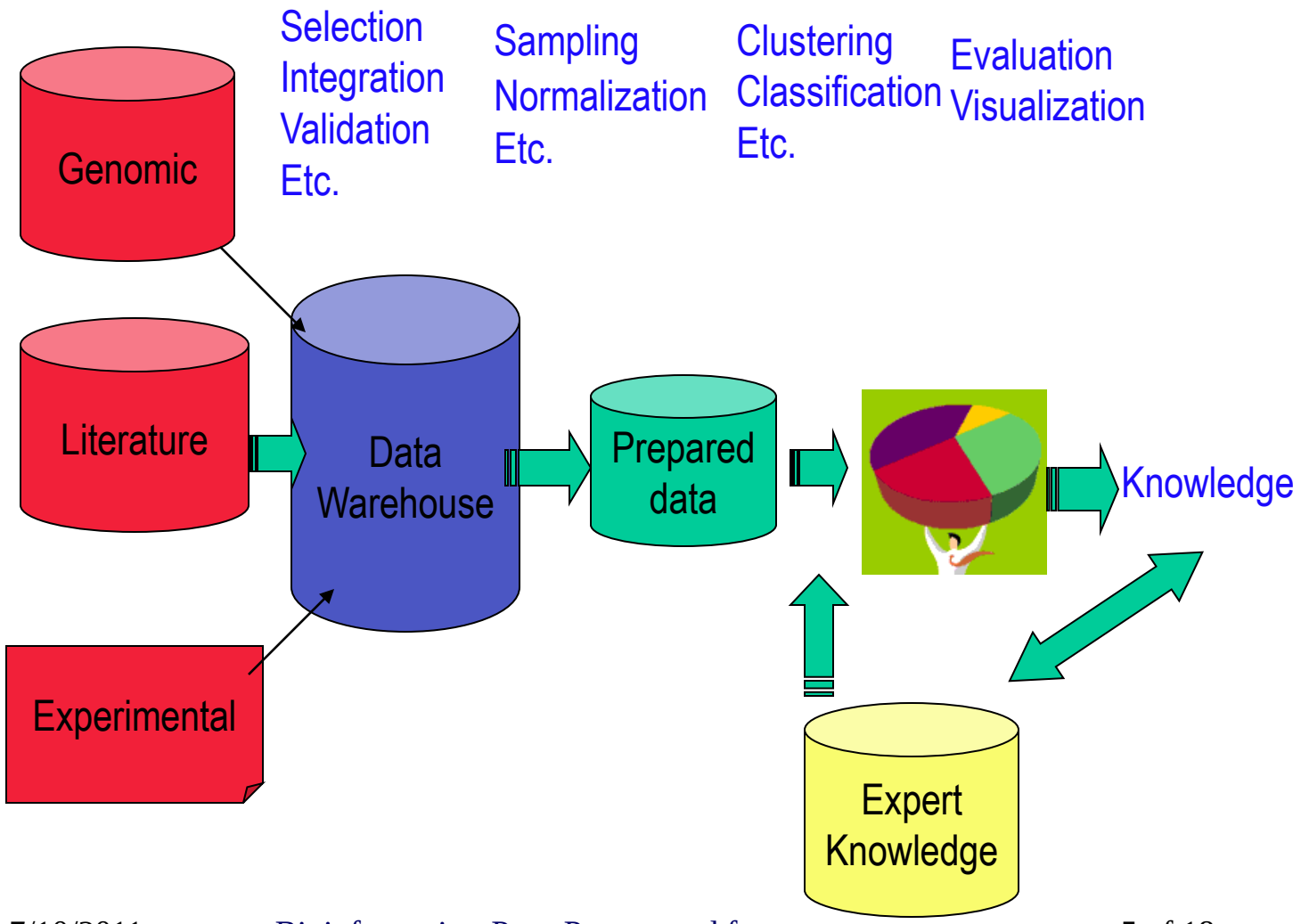


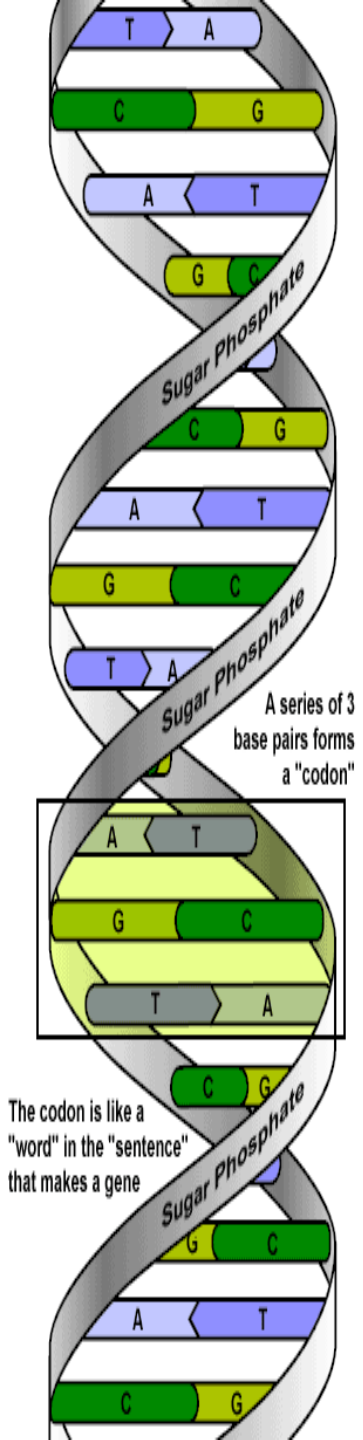
Need of Bioinformatics

- Biology is as old as the age of the planet
- Tons of material lying in
  - * Libraries across the world
  - * in hospitals as patient records
  - * Research centers
  - * Pharmaceutical companies
  - * Agriculture related organizations
  - * 400 Genome and Protein Databases
  - * 4300 tools for different aspects of bioinformatics

KDD for Bioinformatics







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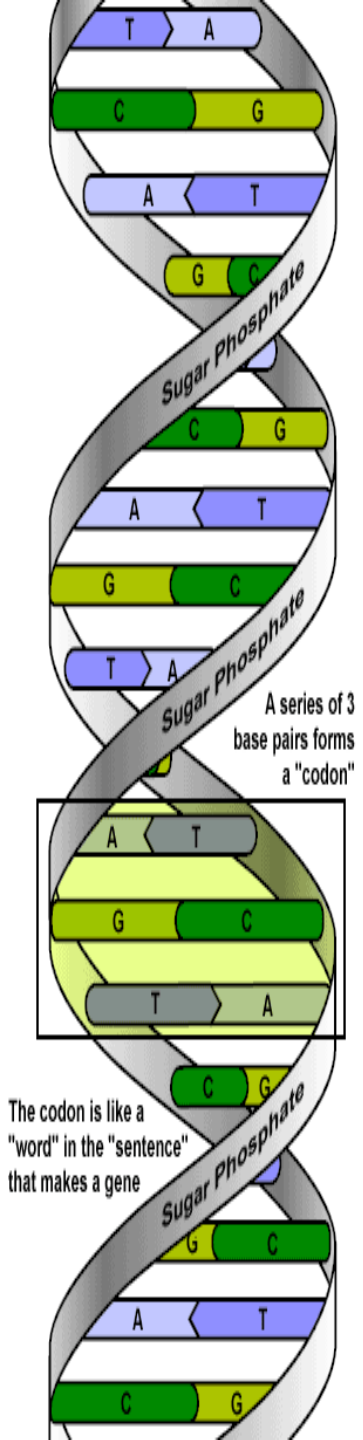
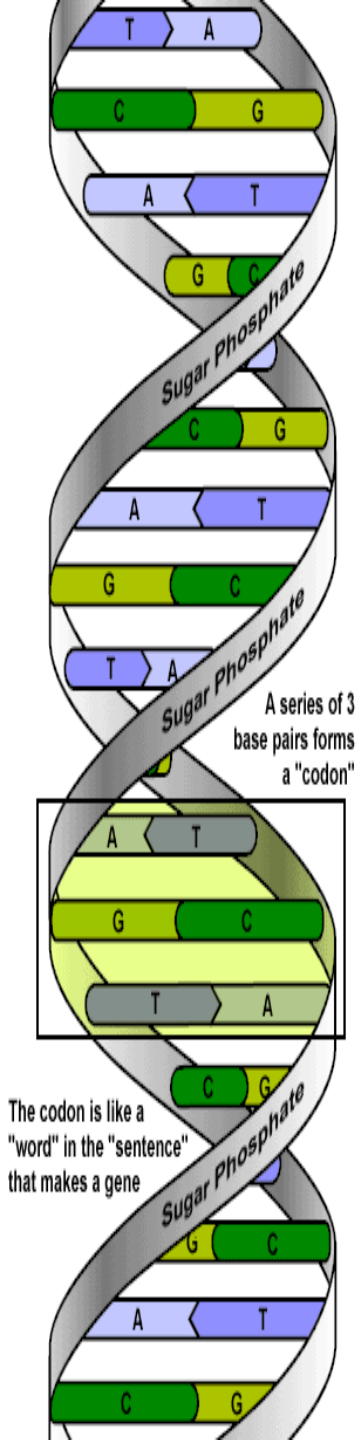


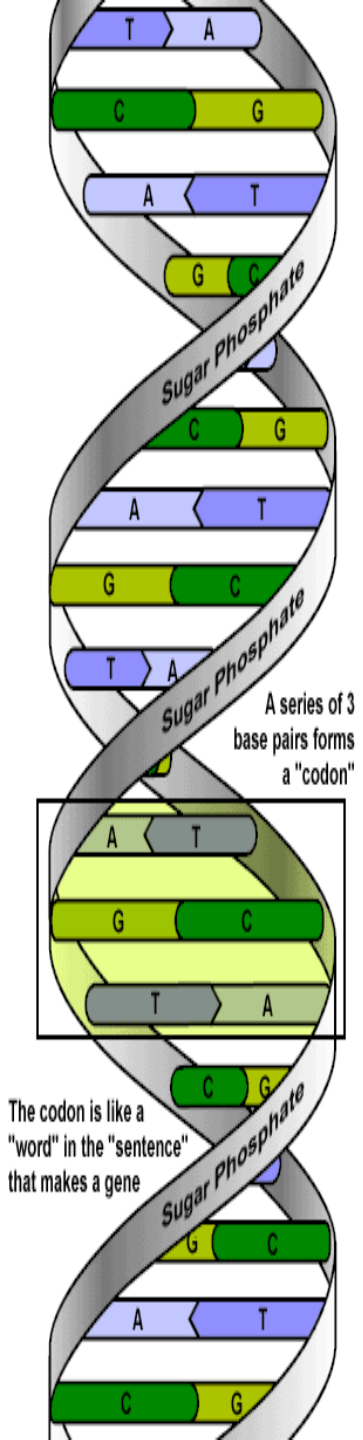
Applications bringing changes in society

- *Detection of genetic diseases*
- *Medical transcriptions*
- *Bio-product showrooms*
- *Bio-marts like data-marts*
- *Classification of DNA sequences*



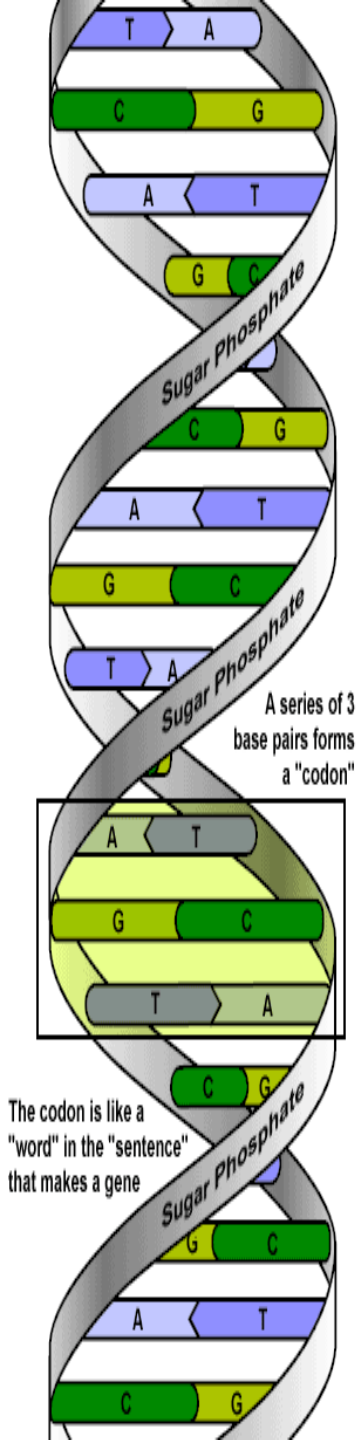
Applications bringing changes in society

- *Prediction of protein secondary & tertiary structures*
- *Investigation of structure function relationship*
- *Rational drug design*
- *Discovering global patterns of life*



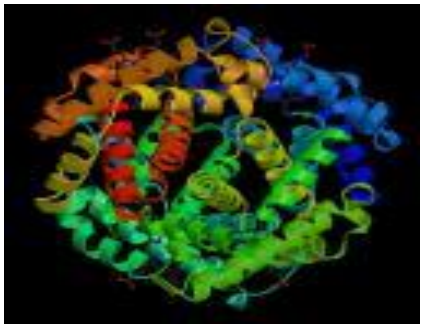
Definition

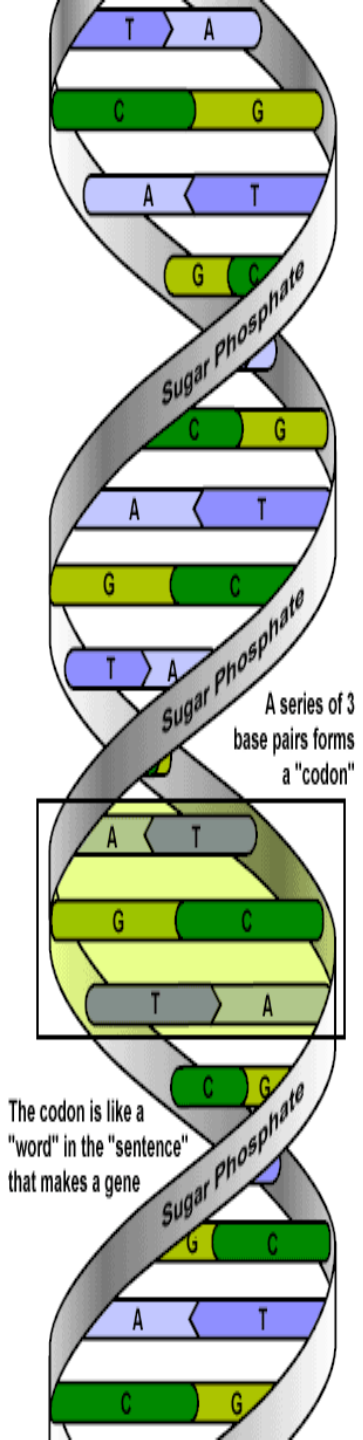
Bioinformatics is most important in enhancing the capability of biologists to competently design experiments and effectively interpret obtained data with high end personal computers and without using major equipments, expensive chemicals and fancy labs.



Hot areas in Bioinformatics

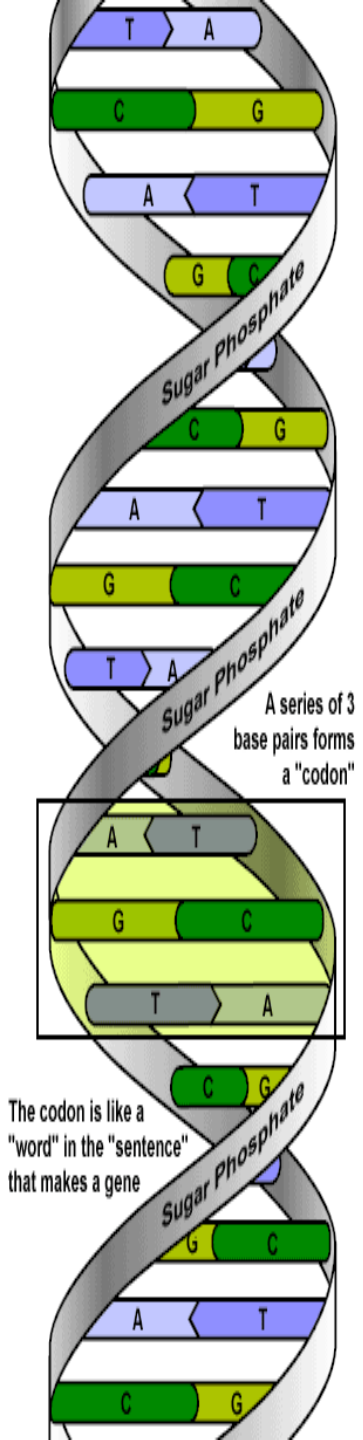
1. Intelligent Algorithms – the usage of Genetic and neural algorithms for bioinformatics has already started.
2. Sequence Analysis
3. Genome analysis
4. Structural bioinformatics
5. Protein structure prediction and protein modeling





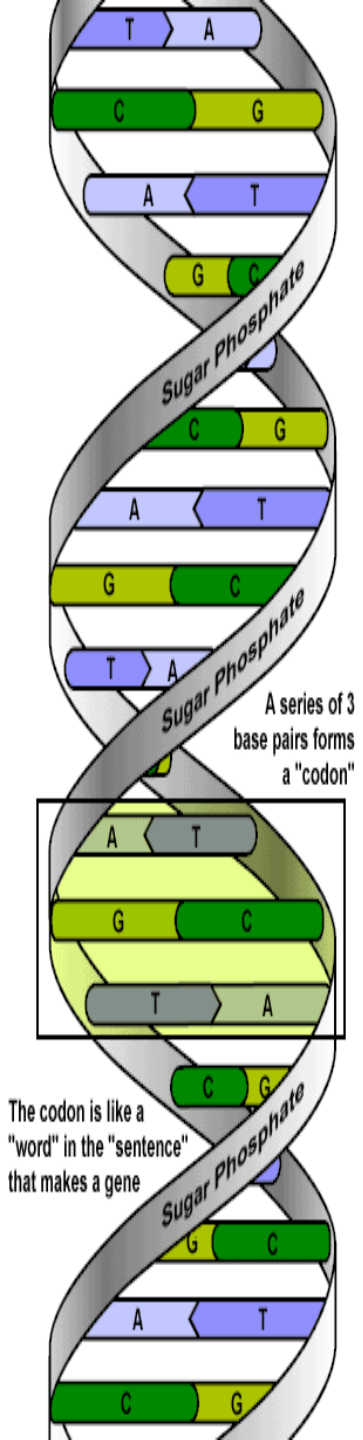
Sequence Analysis

1. Protein sequences can be predicted with the translation of DNA sequences
2. Only consists of A C T G
3. APIs and library files for bioinformatics are available in Java and C.
4. BioPerl has automated the sequence analysis
5. Use of Dynamic Programming



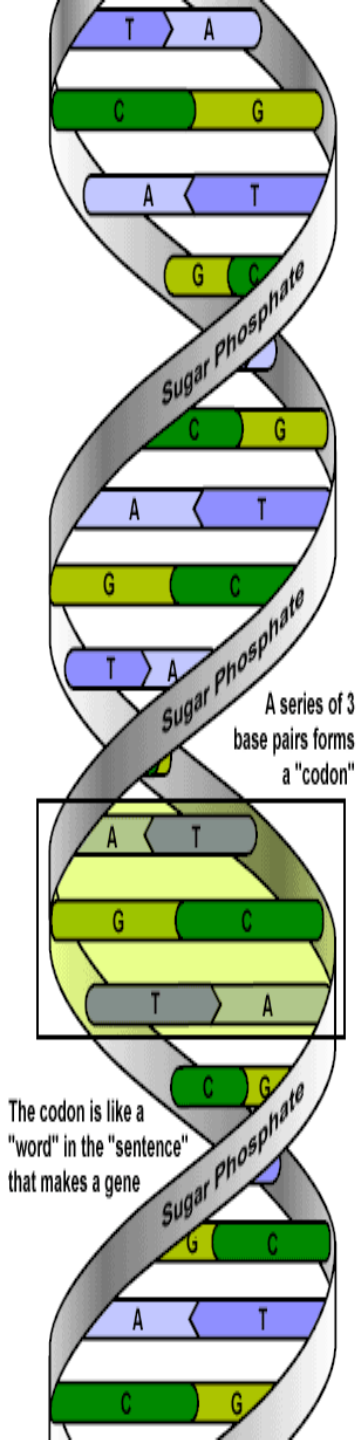
Genome analysis

1. Genome sequences of individuals vary
2. Genome anatomy has been studied in Prokaryotes (Single cell species) and Eukaryotes
3. Human Genome Project completion accelerated the pace of Genome sequencing



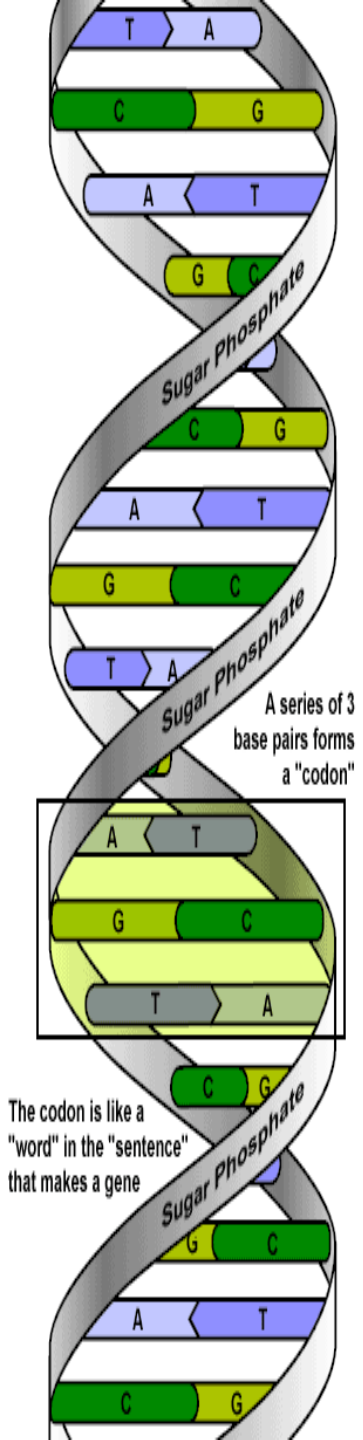
Structural bioinformatics

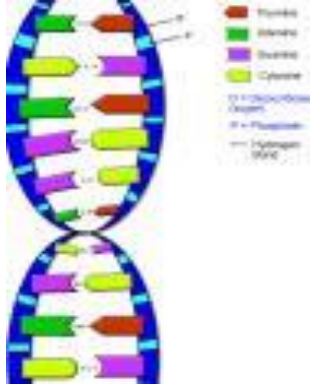
1. Structural alignment is difficult then sequence alignment
2. Proteins are classified based on structural similarity
3. Molecular viewers display protein structures
4. Very advance tools on structure modeling are available



Future perspective

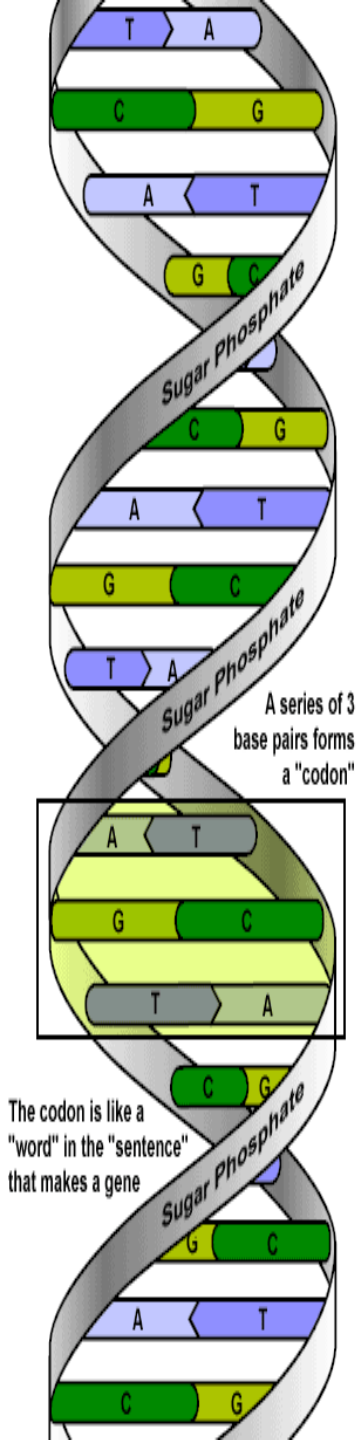
1. Data Warehouses for storing, manipulating and analyzing Bioinformatics data
2. Inter-disciplinary approach
3. Better tools and software for 3D modeling and Multiple Sequence Alignment
4. Distributed and parallel algorithms for the grid environment
5. Global Classification of evolution of life

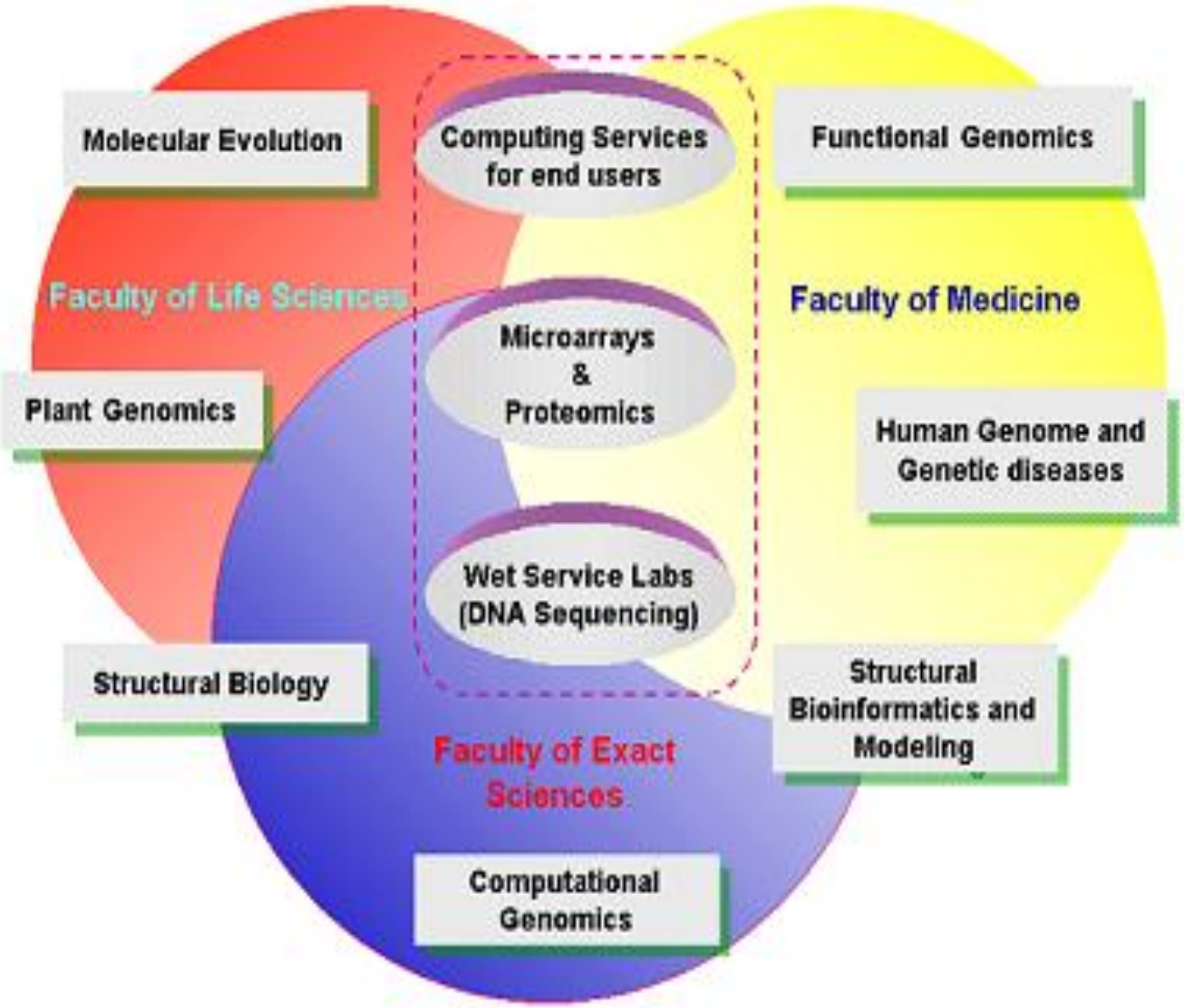




Conclusion

- Given the energy & the resources you have to do the development and research work; there is enough that can be done in bioinformatics that will be commercially and socially beneficial.
- The work done in this field will be satisfying also because that is for the welfare of every living being on the universe.
- There are many open-ended questions & problems.


T A
C G
A T
G C
Sugar Phosphate
C G
A T
G C
T A
Sugar Phosphate
A series of 3 base pairs forms a "codon"
A T
G C
T A
C G
The codon is like a "word" in the "sentence" that makes a gene
Sugar Phosphate
G C
A T
C G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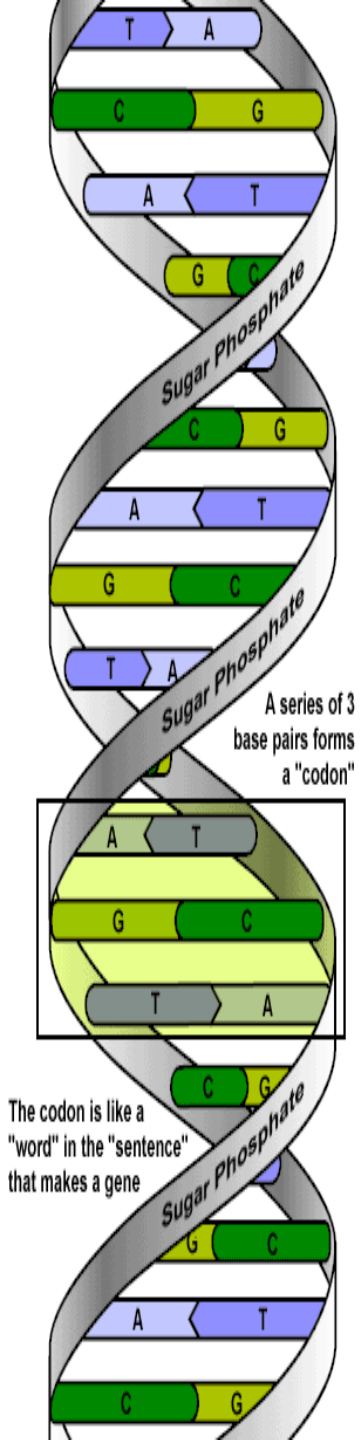
Functional Genomics
Faculty of Life Sciences
Faculty of Medicine
Microarrays & Proteomics
Plant Genomics
Human Genome and Genetic diseases
Wet Service Labs (DNA Sequencing)
Structural Biology
Structural Bioinformatics and Modeling
Faculty of Exact Sciences
Computational Genomics



Thanks!

Questions are welcome…