

# Proteomics Course

## LECTURE-8 Proteomics and Systems Biology

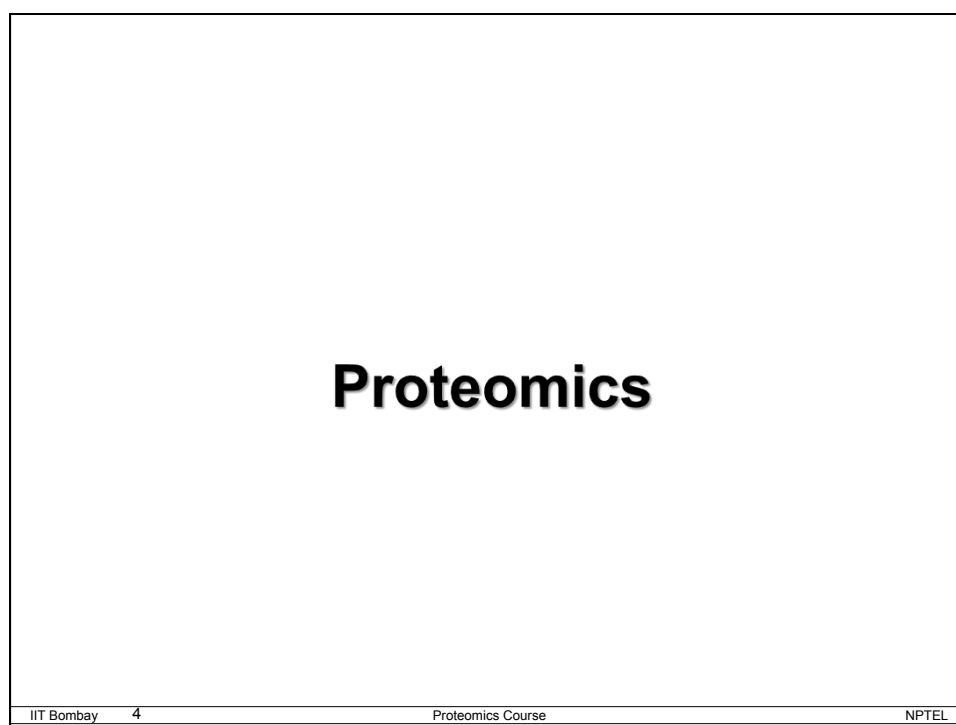
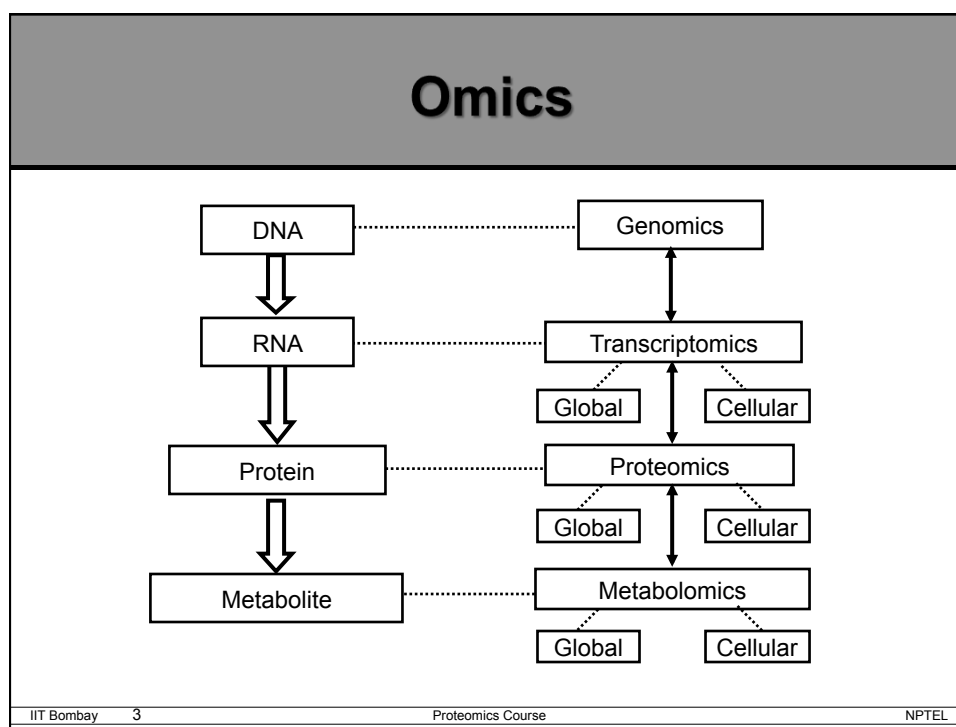


Dr. Sanjeeva Srivastava  
IIT Bombay



### Lecture outline

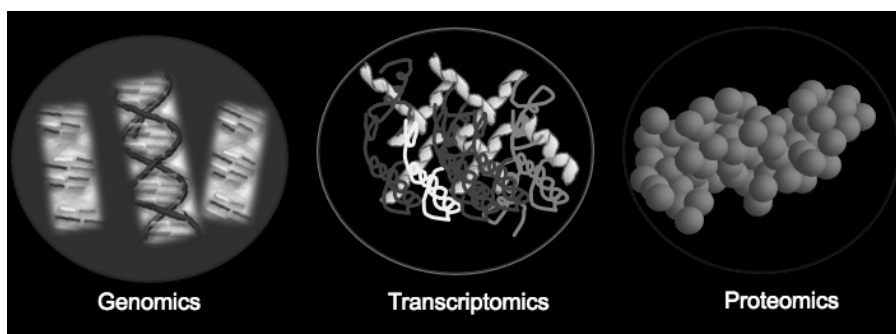
- Proteomics
- Systems Biology



## Proteomics

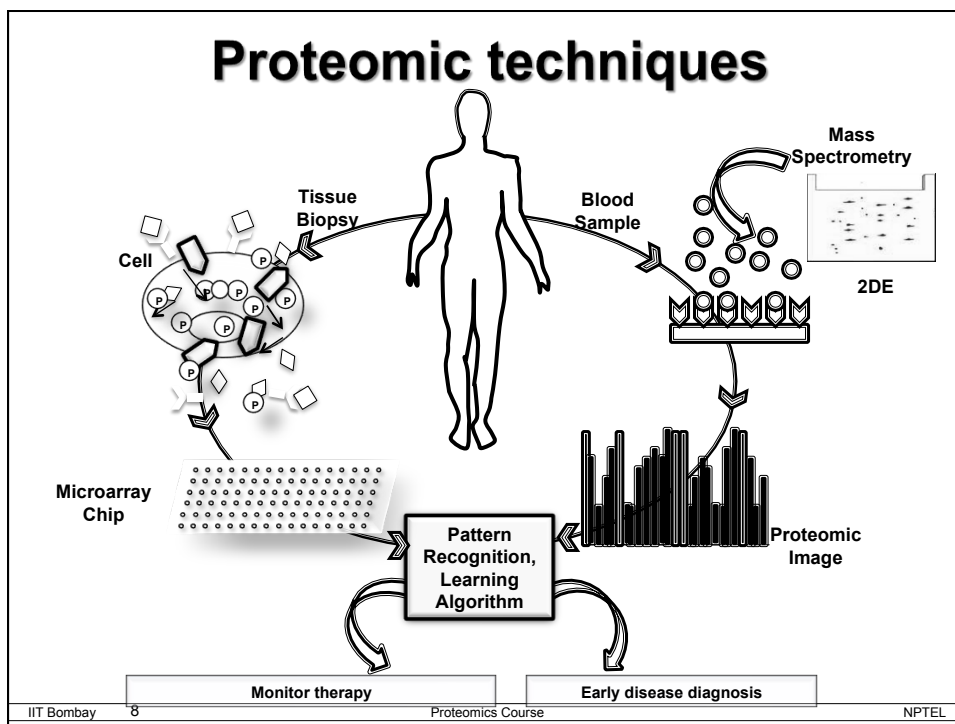
- Proteome: set of all the PROTEins expressed by a genOME
- Proteomics: study of full set of proteins encoded by a genome for their expression, localization, interaction and post-translational modifications

## Significance of Proteomics



Proteomic techniques				
Gel-based methods	Gel-free MS	Mass Spectrometry	Interactomics	Structural Proteomics
<ul style="list-style-type: none"> <li>• SDS-PAGE</li> <li>• 2-DE</li> <li>• DIGE</li> <li>• BN-PAGE</li> </ul> <p><u>Staining</u></p> <ul style="list-style-type: none"> <li>• Coomassie Blue</li> <li>• Silver</li> <li>• Fluorescent (Sypro ruby)</li> <li>• PTM stains (Pro-Q Diamond) (Pro-Q Emerald)</li> <li>• Multiplex staining</li> </ul>	<ul style="list-style-type: none"> <li>• SILAC</li> <li>• CDIT</li> <li>• ICAT</li> <li>• VICAT</li> <li>• MCAT</li> <li>• QUEST</li> <li>• iTRAQ</li> <li>• GIST</li> <li>• [<sup>18</sup>O] water</li> <li>• ICPL</li> <li>• AQUA</li> <li>• QCAT</li> <li>• SISCAPA</li> <li>• COFRADIC</li> <li>• MudPIT</li> </ul>	<p><u>Ionization</u></p> <ul style="list-style-type: none"> <li>• MALDI</li> <li>• ESI</li> </ul> <p><u>Mass analyzer</u></p> <ul style="list-style-type: none"> <li>• Quadrupole</li> <li>• Ion trap</li> <li>• TOF</li> <li>• FT-ICR</li> </ul> <p>Mass spectrometers</p> <ul style="list-style-type: none"> <li>• MALDI-TOF</li> <li>• Tandem MS (MS/MS)</li> <li>• DIOS</li> <li>• SELDI-TOF</li> </ul>	<ul style="list-style-type: none"> <li>• IP</li> <li>• Yeast two hybrid</li> </ul> <p><u>Protein microarrays</u></p> <ul style="list-style-type: none"> <li>• Antibody based</li> <li>• NAPPA</li> <li>• MIST</li> </ul> <p><u>Detection</u></p> <ul style="list-style-type: none"> <li>- Labelled</li> <li>- Label-free</li> <li>• SPR</li> <li>• Carbon nanowires</li> </ul>	<ul style="list-style-type: none"> <li>• X-ray crystallography</li> <li>• NMR</li> <li>• TROSY</li> <li>• Electron crystallography</li> <li>• Electron tomography</li> <li>Label-free</li> <li>• Atomic Force Microscopy</li> <li>• CD</li> </ul>

IIT Bombay 7 Proteomics Course NPTEL



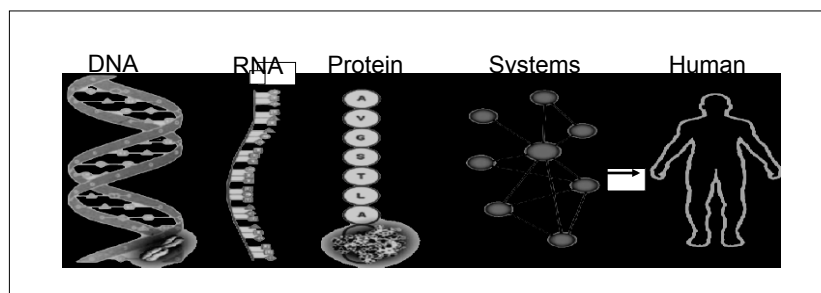
# Systems Biology

# Systems Biology

- Examination of a biological entity as an integrated system, rather than study of its individual characteristic reactions and components

## Systems Biology

- System level understanding of biological networks
- Common elements of systems biology
  - Networks
  - Modeling
  - Computation
  - Dynamic properties

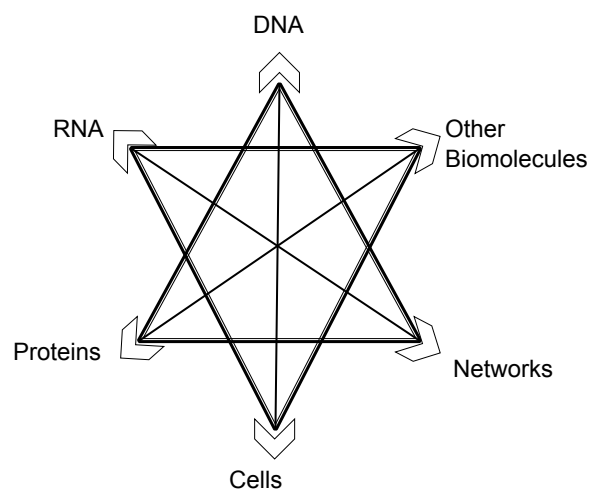


IIT Bombay 11

Proteomics Course

NPTEL

## Biological Systems



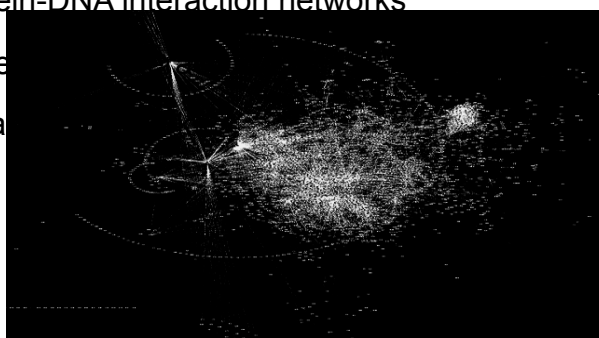
IIT Bombay 12

Proteomics Course

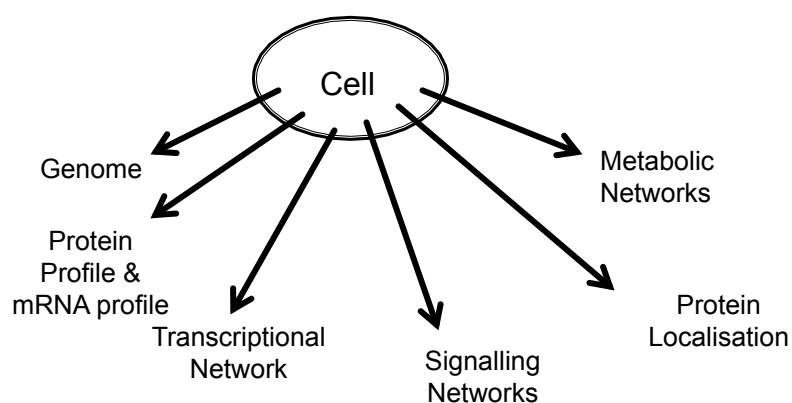
NPTEL

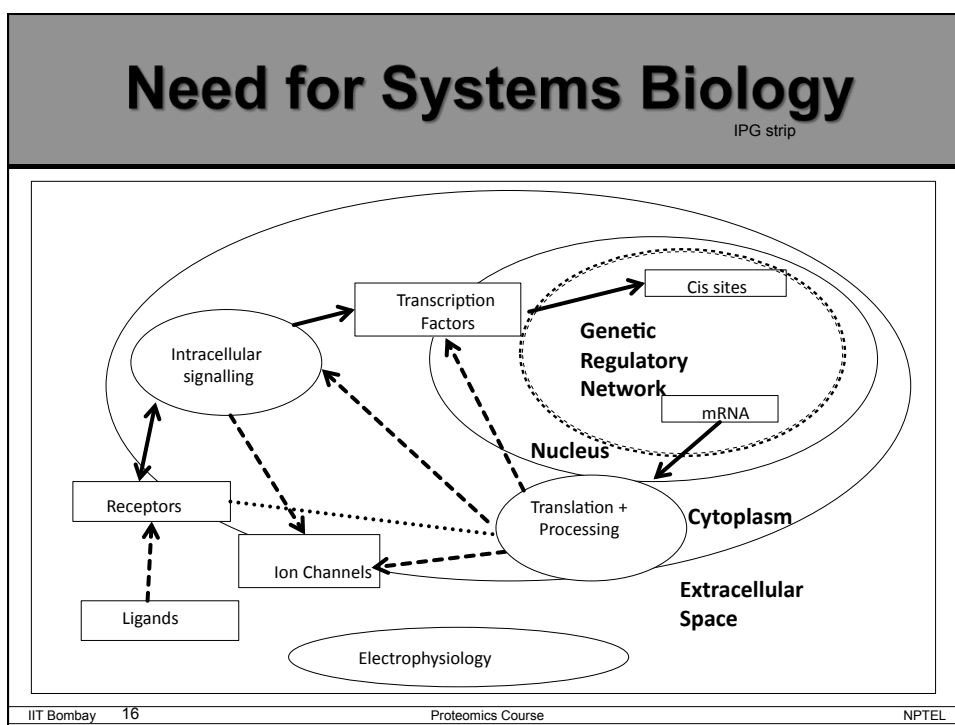
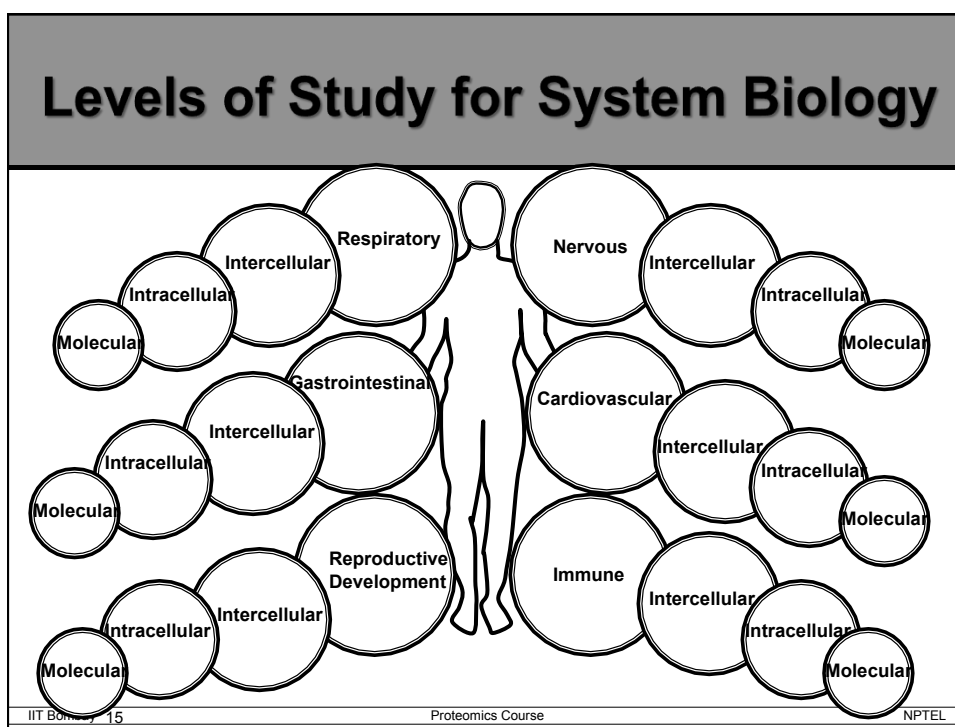
## Biological networks

- Protein-protein interaction networks
- Gene regulatory networks
- Protein-DNA interaction networks
- Prote
- Meta



## Ingredients of Systems Biology





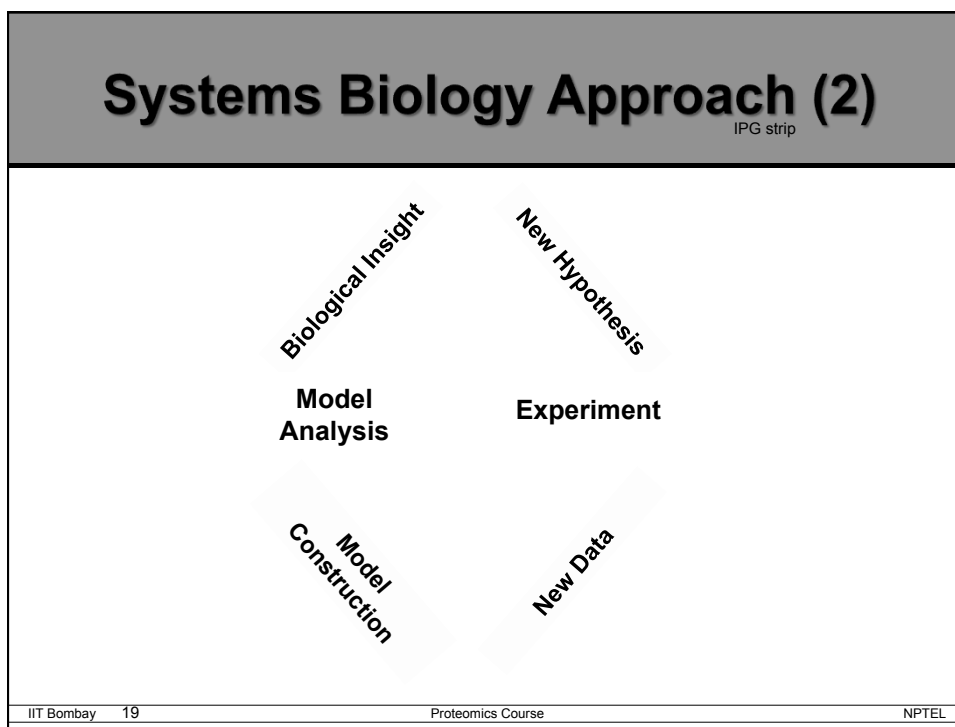


## Aim of Systems Biology

- Understanding biology in “holistic” rather than the “reductionist” approach
- Quantitate the qualitative biological data
- To make biology a predictive science

## Systems Biology Approach

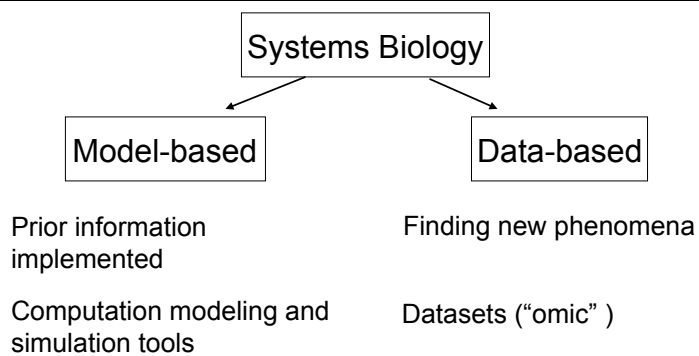
- Systems biology involves:
  - Experimental data set collection
  - Mathematical models



## Systems Biology: Different Approaches

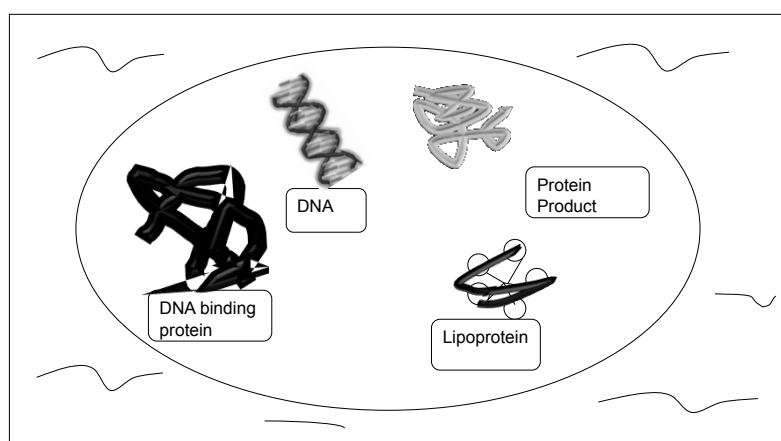
IIT Bombay 20      Proteomics Course      NPTEL

## Systems Biology: Distinct Approaches



## Studying Systems Components

IPG strip



## Systems Biology: Distinct Approaches

Reductionist Approach: Disintegrating the system into its component parts and studying them

**SYSTEMS**

**PARTS**

Reductionist Approach

---

IIT Bombay 23 Proteomics Course NPTEL

## Systems Biology: Distinct Approaches

Integrative Approach: Integrating the study of individual components to form conclusions about system

**SYSTEMS**

**PARTS**

Integrative Approach

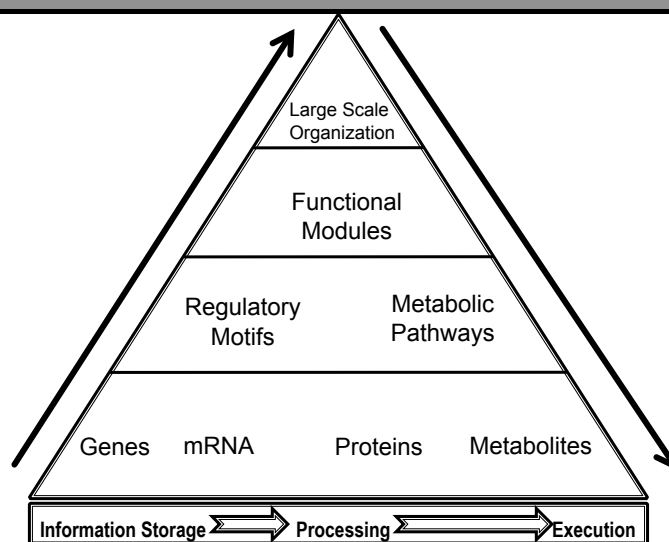
---

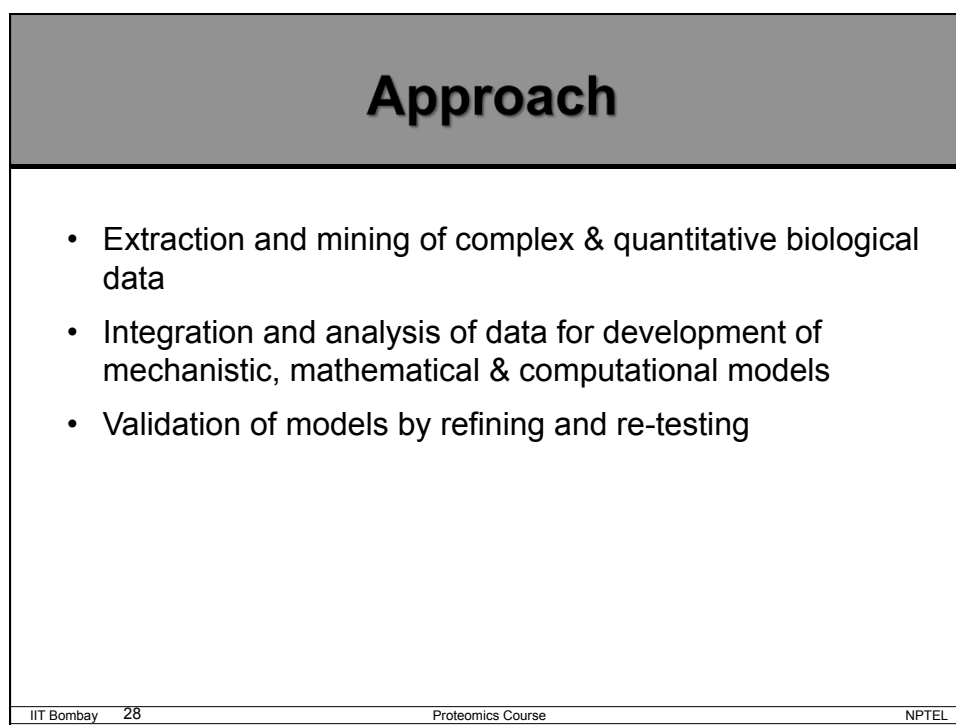
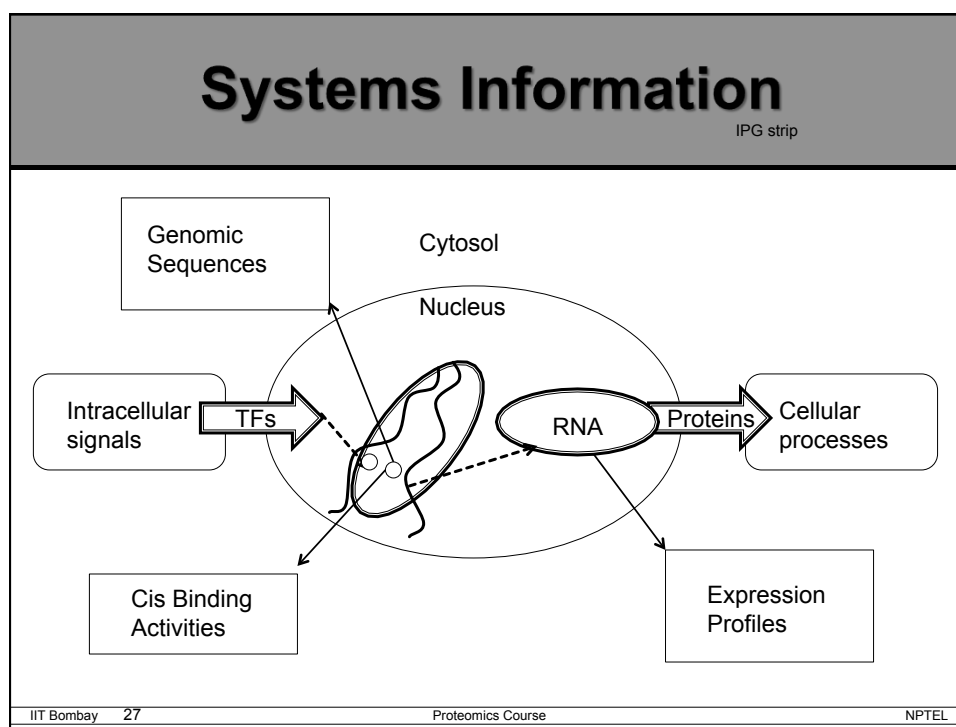
IIT Bombay 24 Proteomics Course NPTEL

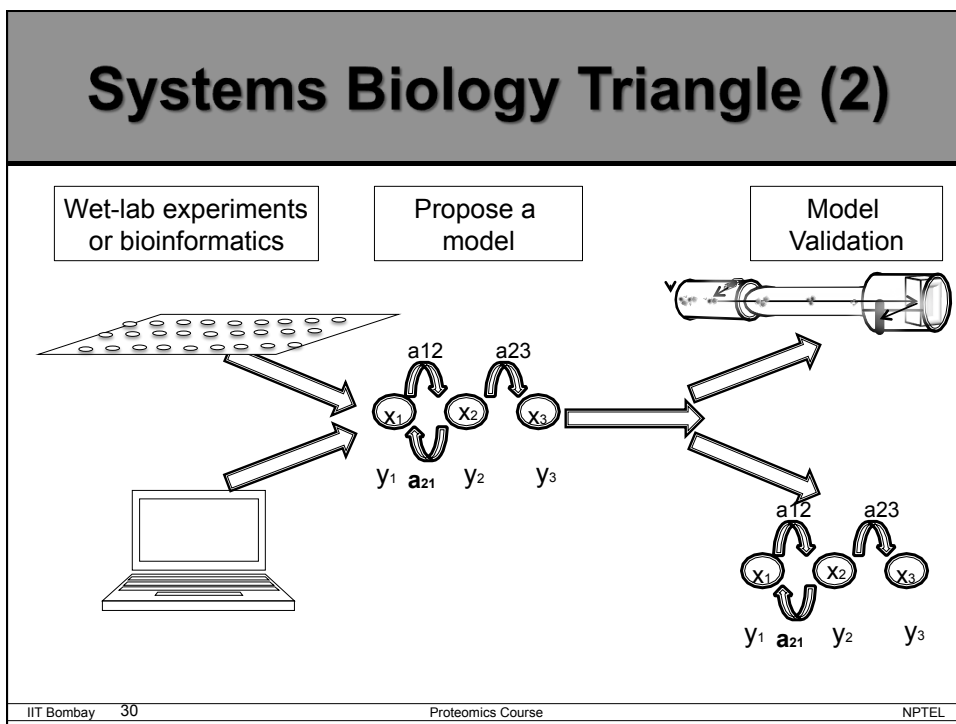
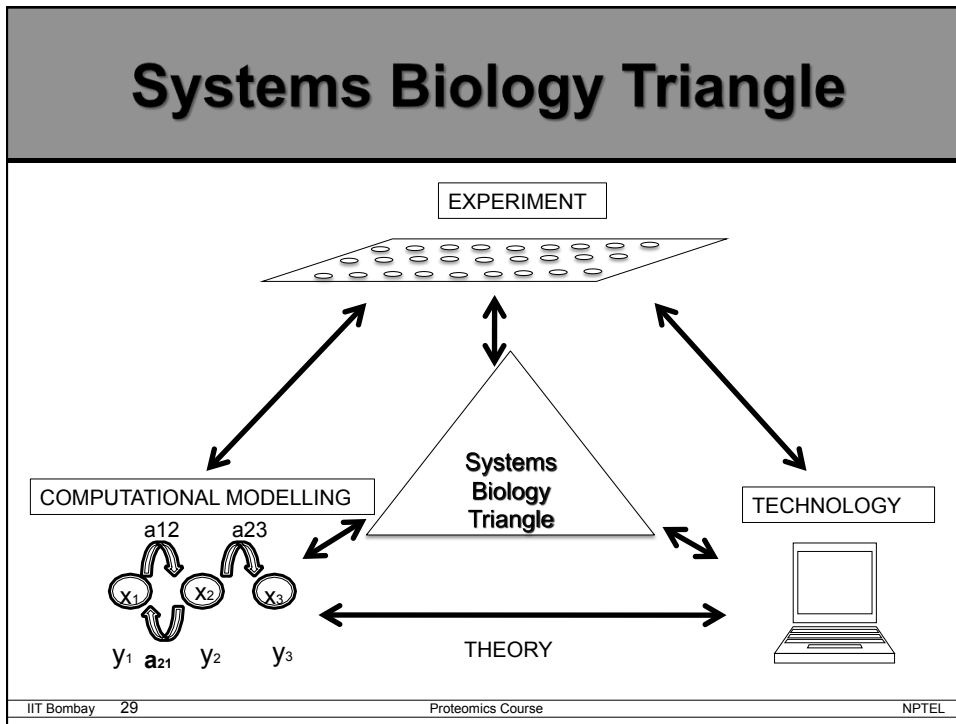
# Systems Biology Triangle

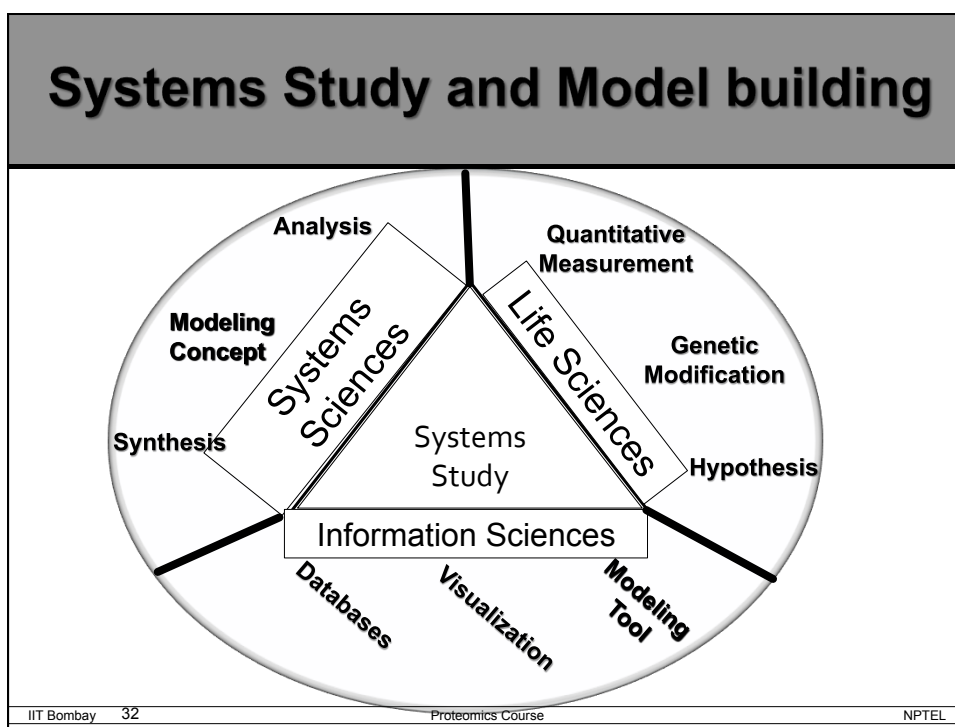
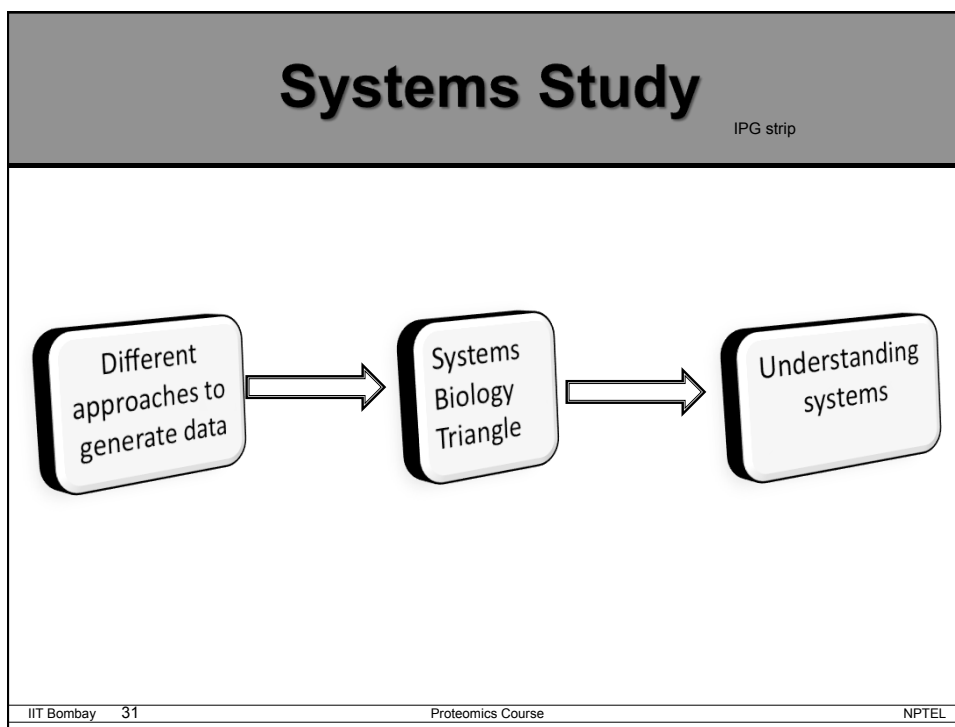
# Systems Information

IPG strip







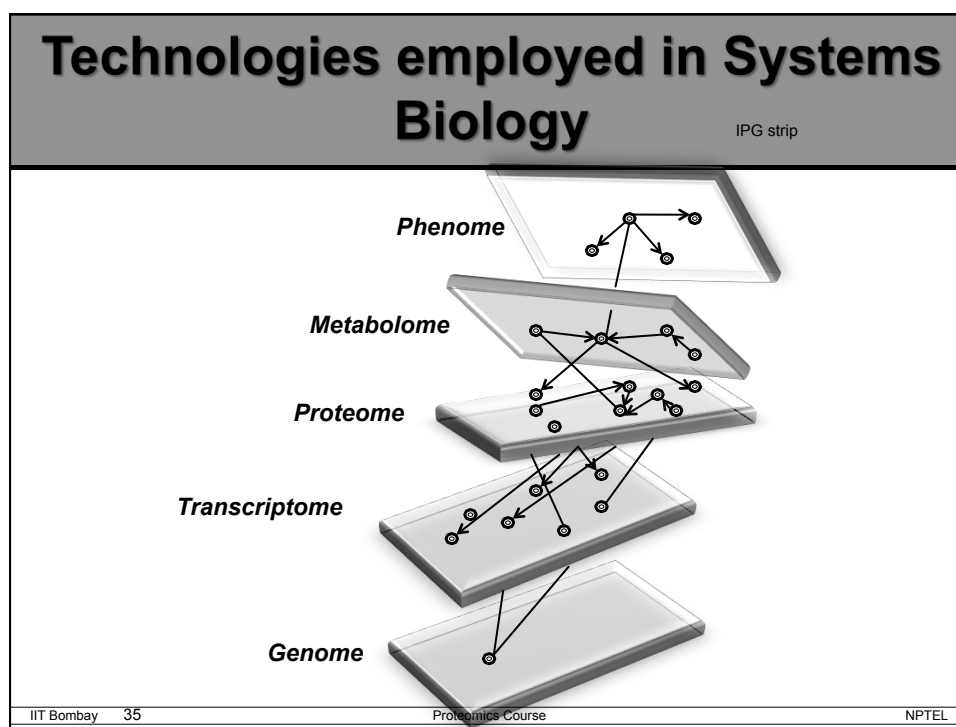




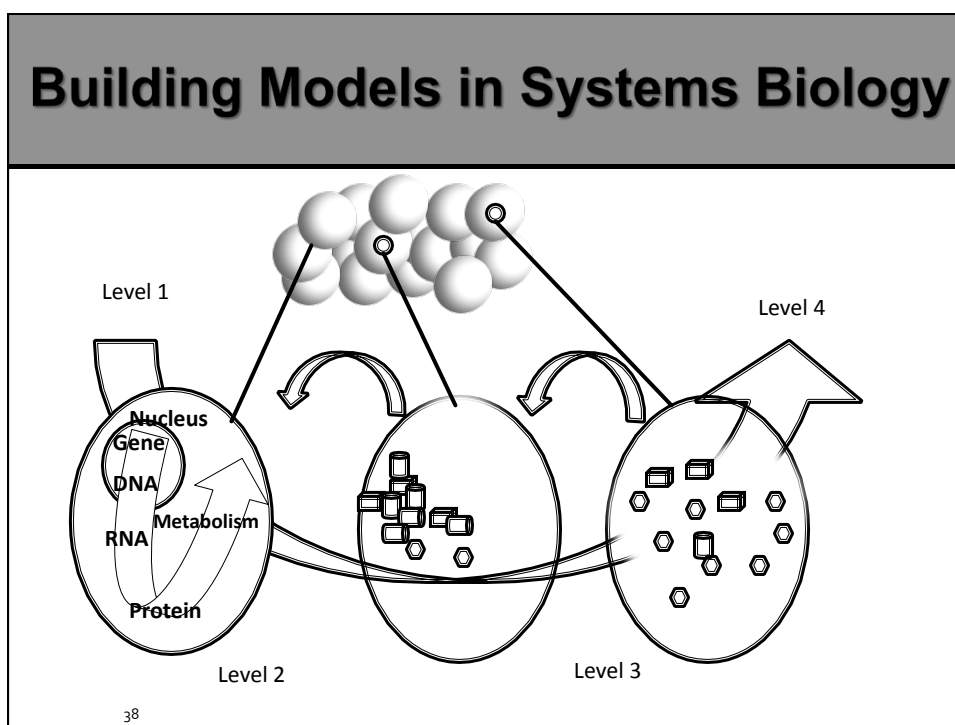
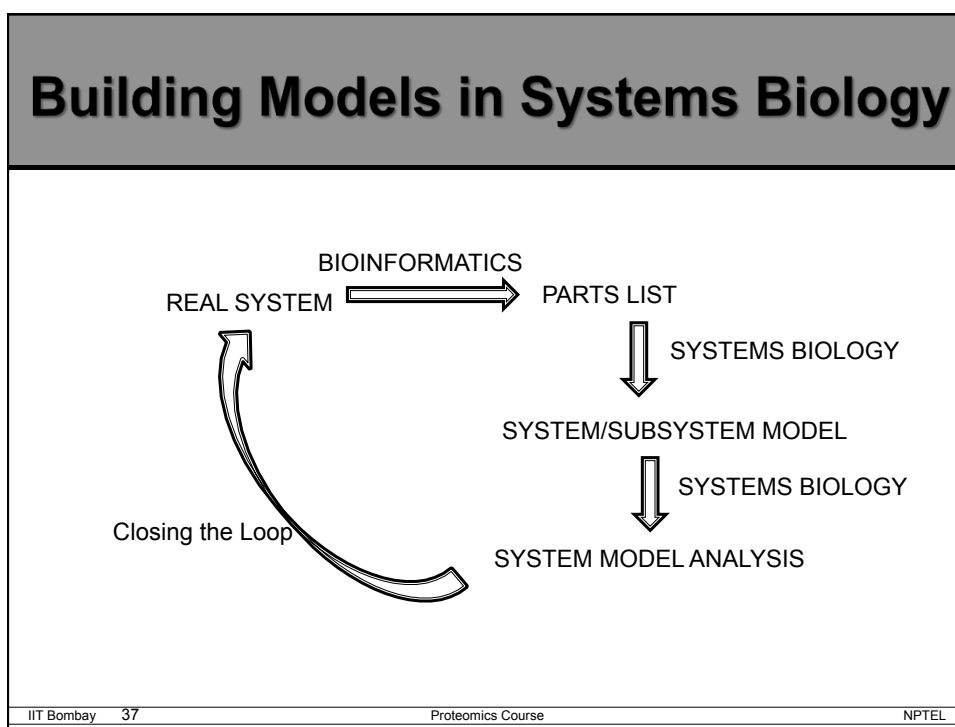
## **Technologies to Study Systems Biology**

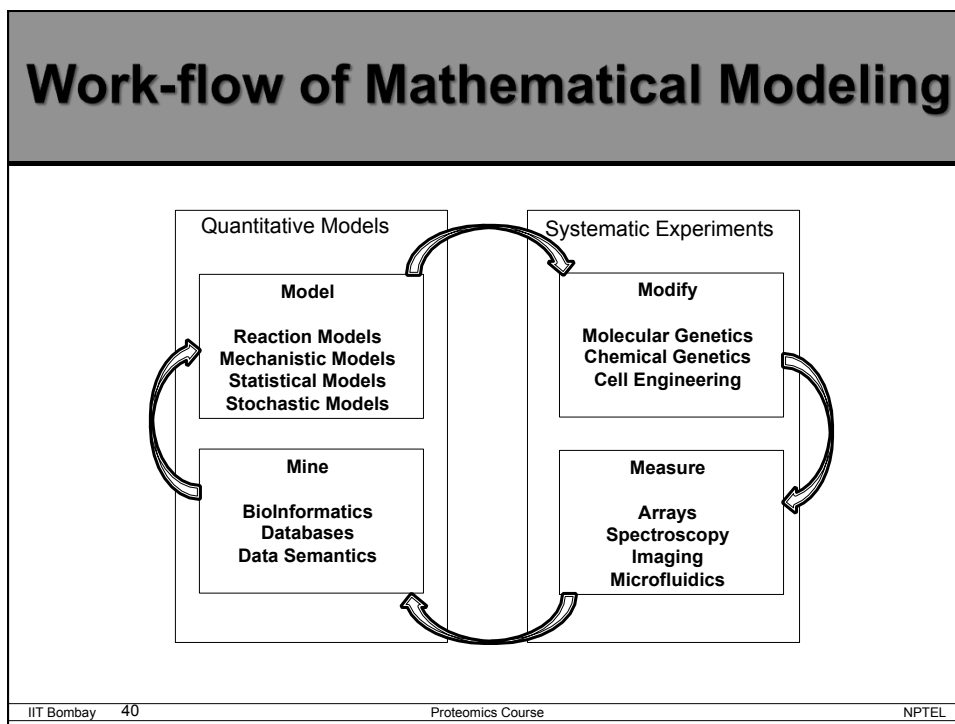
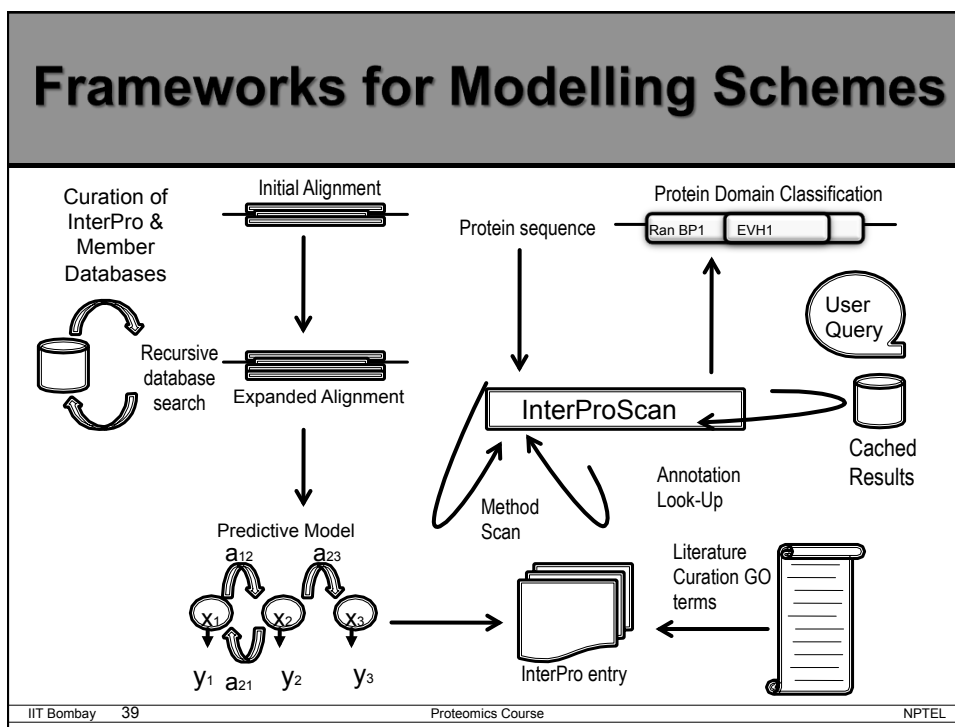
## **Systems Biology: Technologies employed**

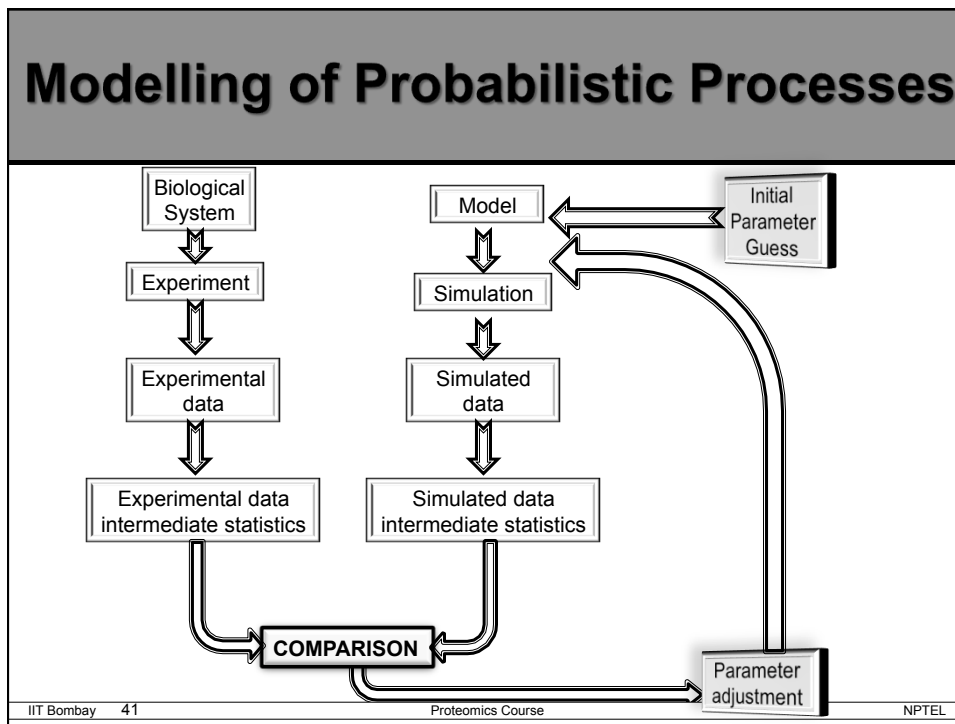
- HT-DNA sequencing, SNPs
- Microarrays, SAGE, RNA-Seq
- MS, 2D-PAGE, Protein chips, Yeast-2-hybrid
- NMR, X-ray



## Modeling Biological Networks







## ODE and Stoichiometric models

- Ordinary Differential Equations (ODE): mathematical relation that can be used for modeling biological systems
- Stoichiometric model: modeling a biological network based on its stoichiometric coefficients, reaction rates and metabolite concentrations

IIT Bombay 42      Proteomics Course      NPTEL

# Systems approaches for studying biological networks: from post-transcriptional control to drug discovery

Dr. Sarath Chandra Janga

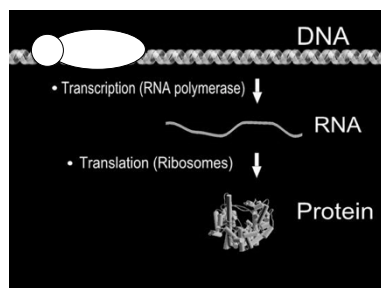
- Indiana University & Purdue University Indianapolis (IUPUI)

IIT Bombay 43

Proteomics Course

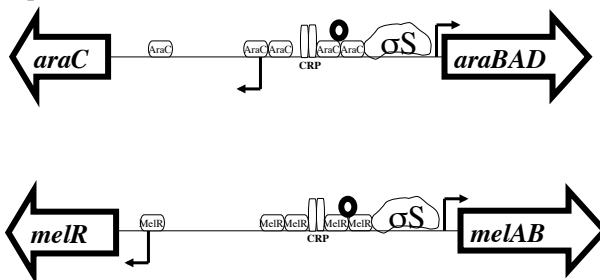
NPTEL

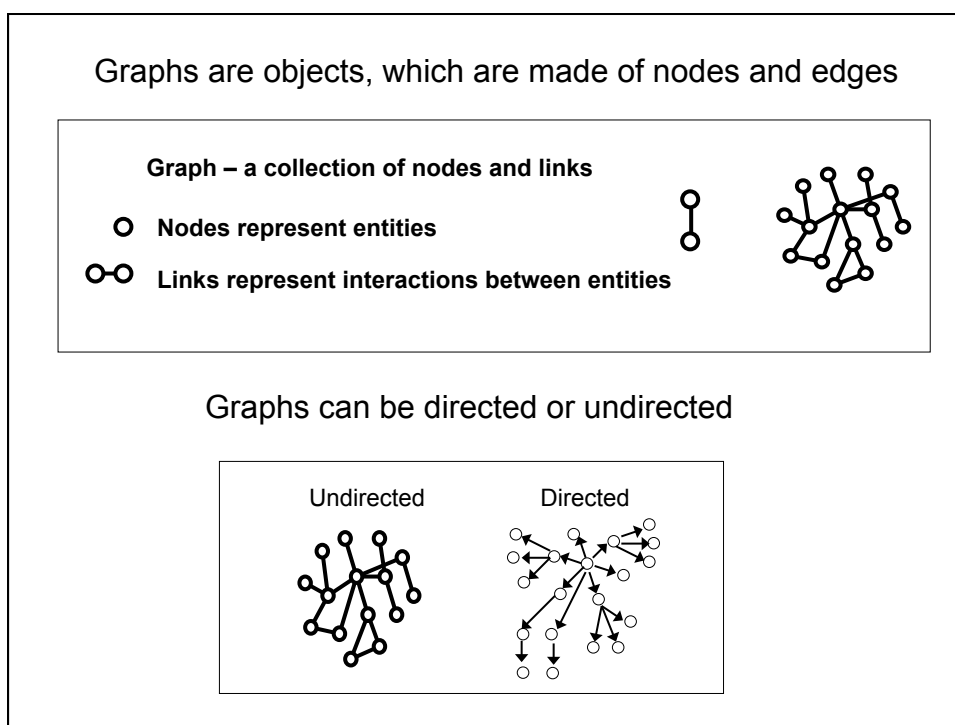
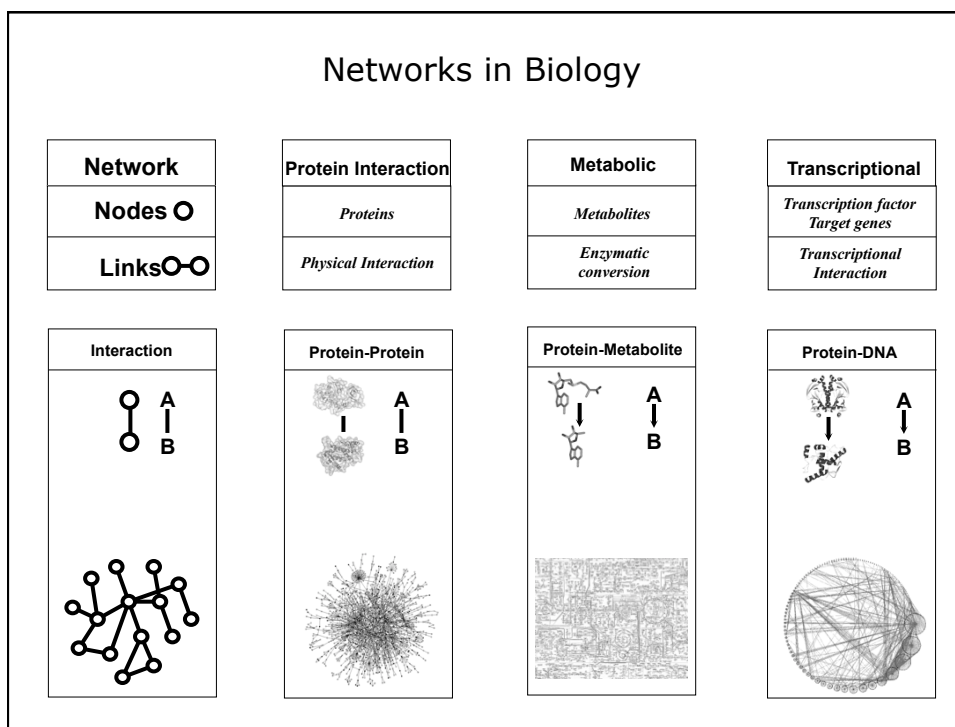
## Central Dogma of Molecular Biology

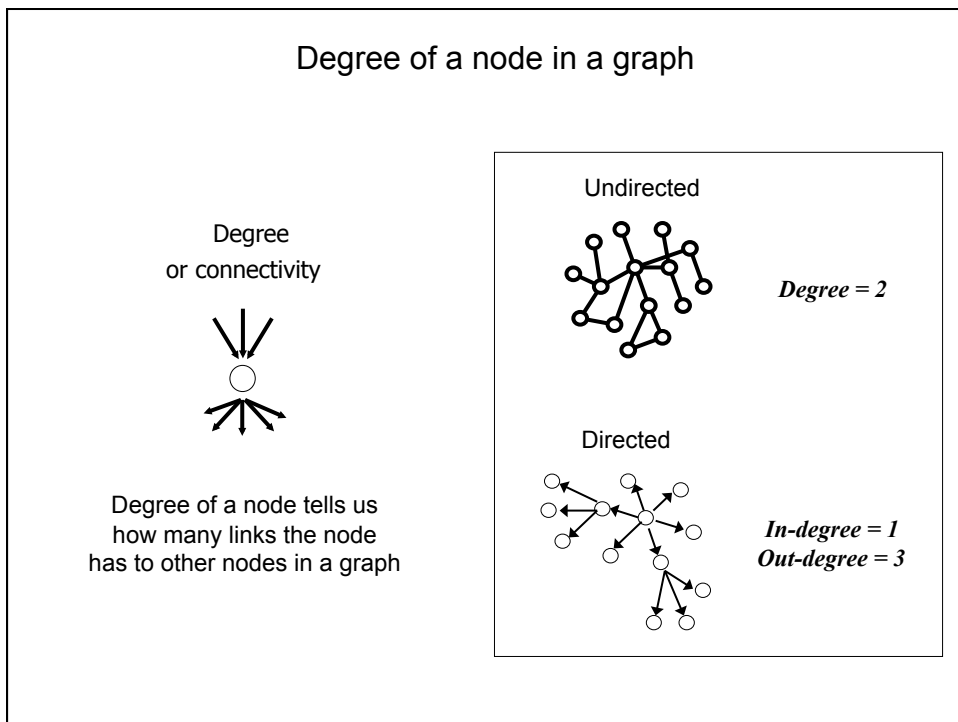
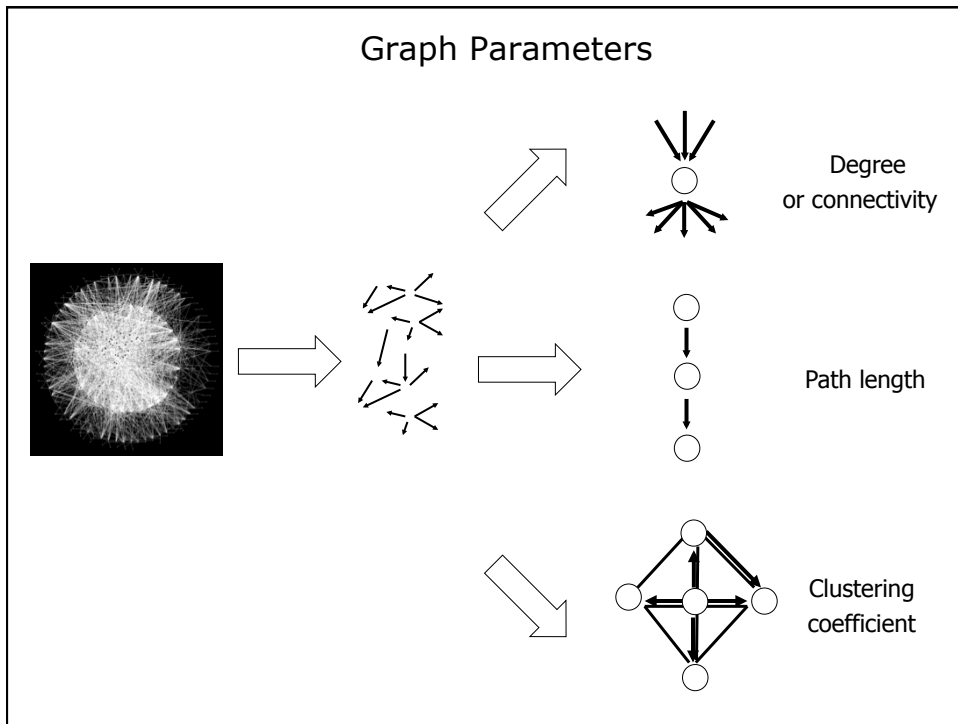


*Transcription is regulated by a class of proteins called transcription factors that bind DNA and affect expression of the nearby genes*

*An example*










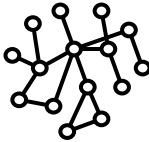
### Path length between two nodes in a graph

Path length



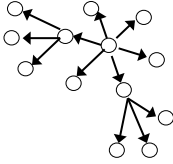
Path length is the shortest number of links needed to connect two nodes in a graph

Undirected



*Path length = 1*

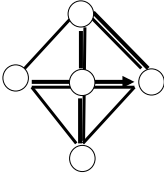
Directed



*Path length = 2*

### Clustering coefficient of a node in a graph

Clustering coefficient




Clustering coefficient tells us how interconnected are the neighbors of a give node


$$CC = \frac{\# \text{ links among neighbors}}{\# \text{ all possible links among neighbors}}$$

$$CC = \frac{2 \times M}{N \times (N - 1)}$$


N, neighbors of a node  
M, links between neighbors of a node



N=3, M=0  
CC=0

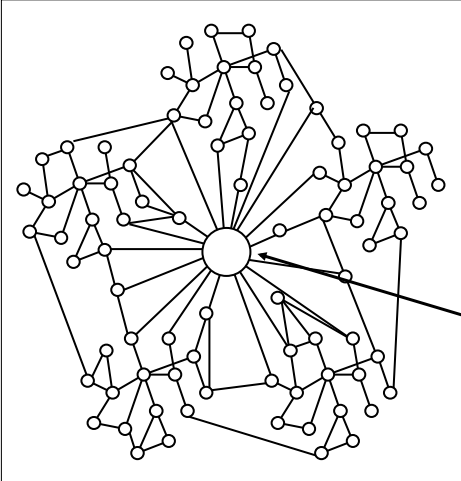


N=3, M=2  
CC=0.66



N=3, M=3  
CC=1

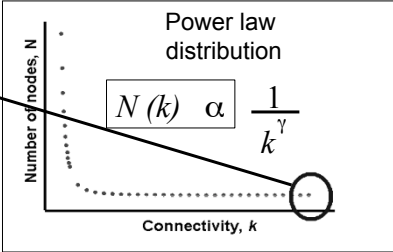
### Transcriptional networks are scale-free



**Scale-free structure**

*Presence of few nodes with many links and many nodes with few links*

Power law distribution

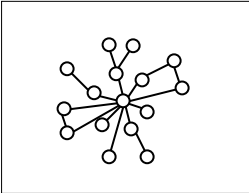
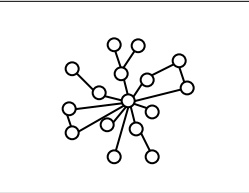
$$N(k) \propto \frac{1}{k^\gamma}$$


Scale free structure provides robustness to the system

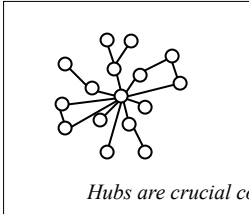
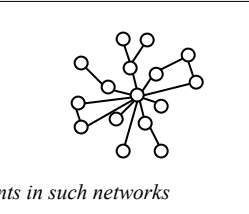
### Scale-free networks exhibit robustness

*Robustness – The ability of complex systems to maintain their function even when the structure of the system changes significantly*

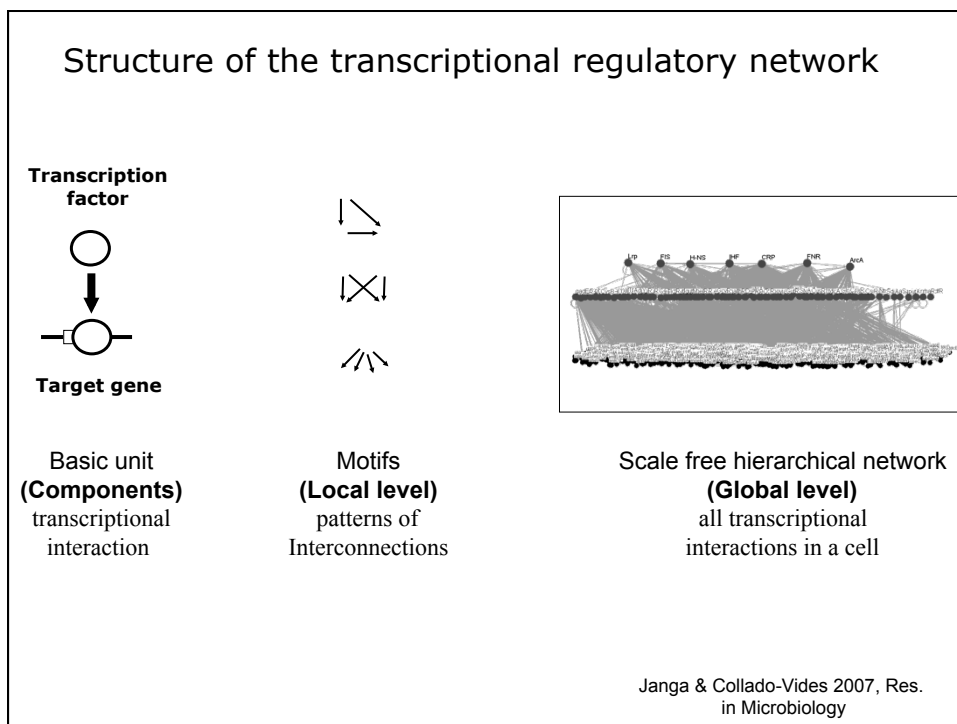
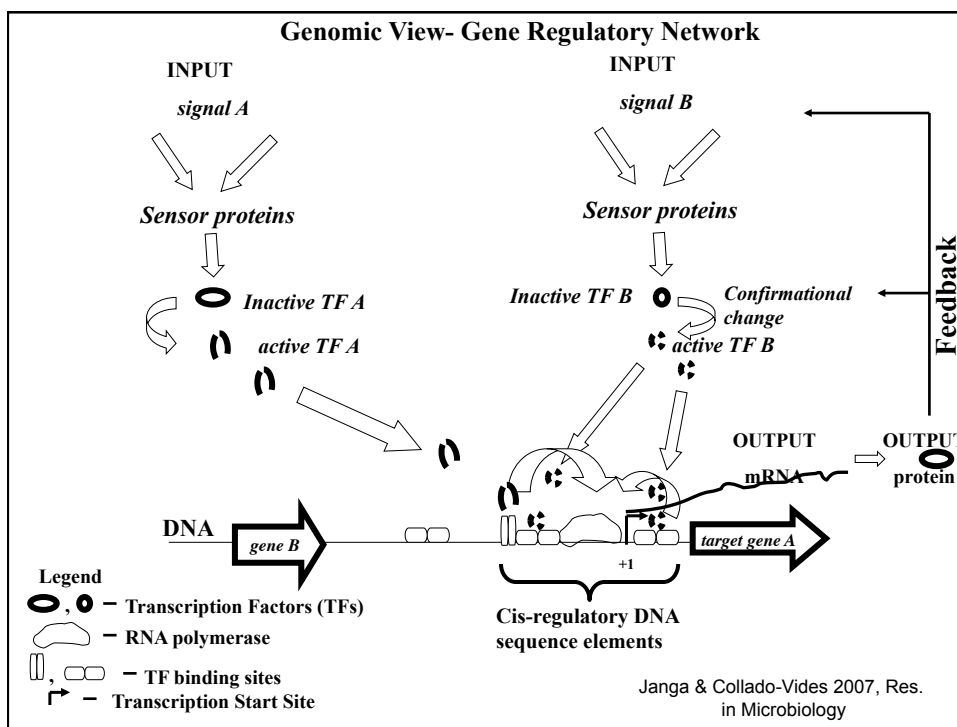
**Tolerant to random removal of nodes (mutations)**

**Vulnerable to targeted attack of hubs (mutations) – Drug targets**

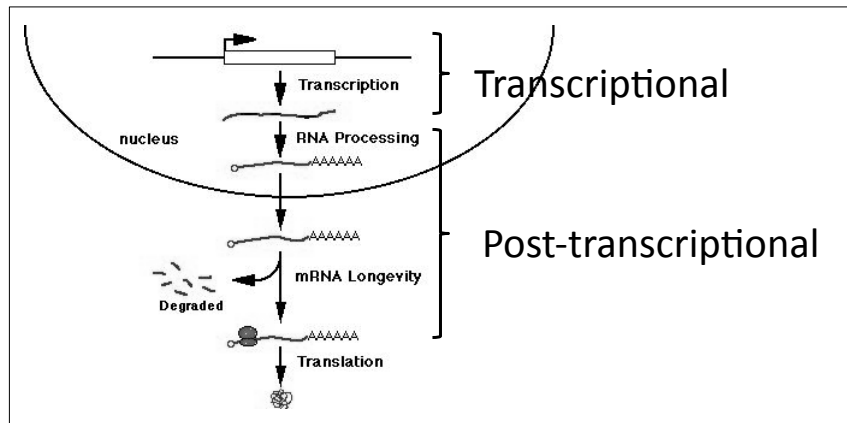



*Hubs are crucial components in such networks*

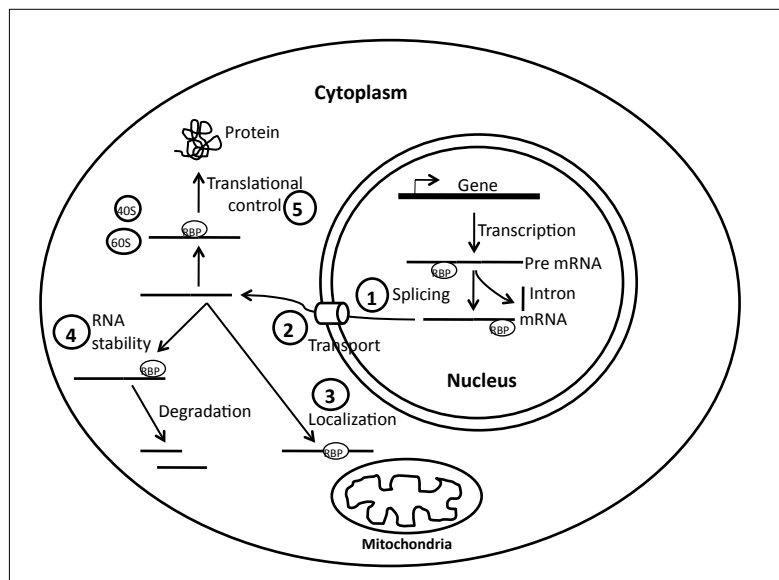


## Gene regulation beyond transcription

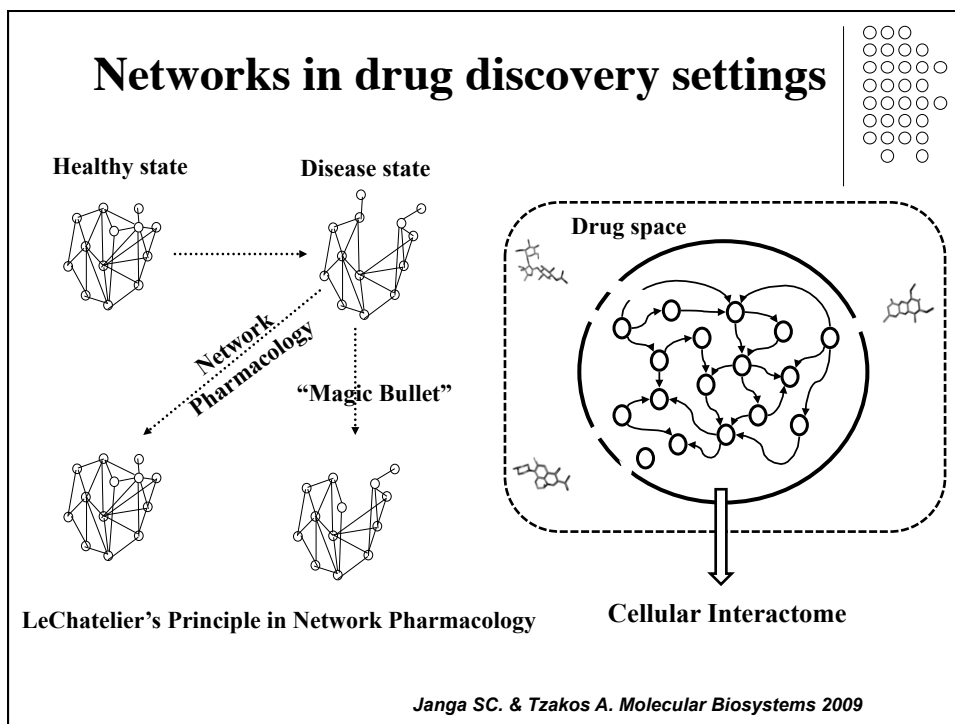
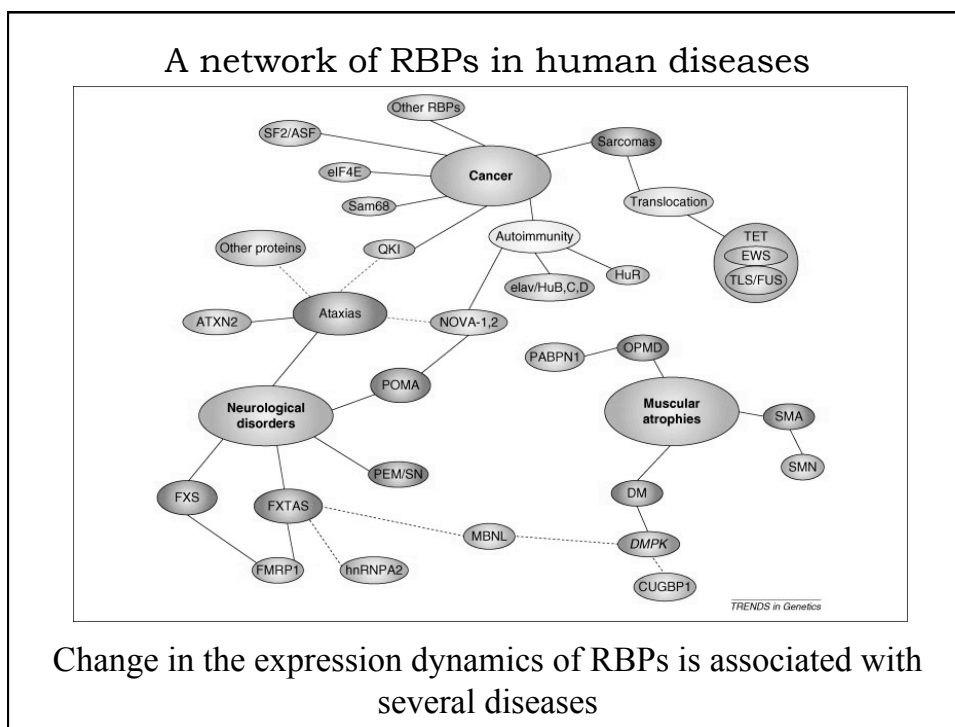
- Gene regulation is a highly regulated and complex process
- Gene regulation takes place at several steps

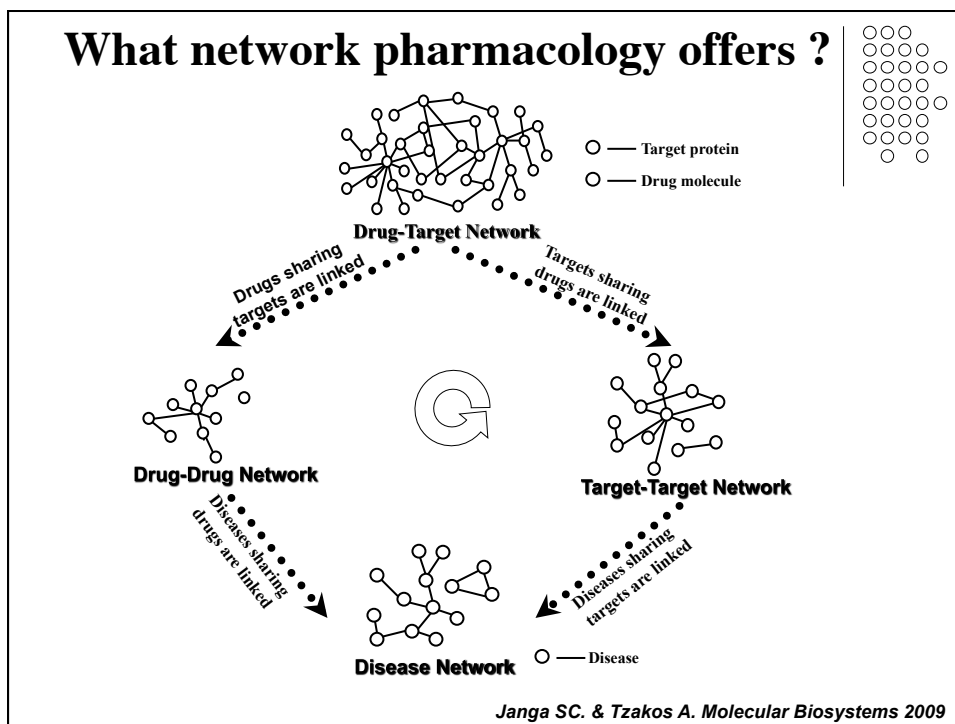
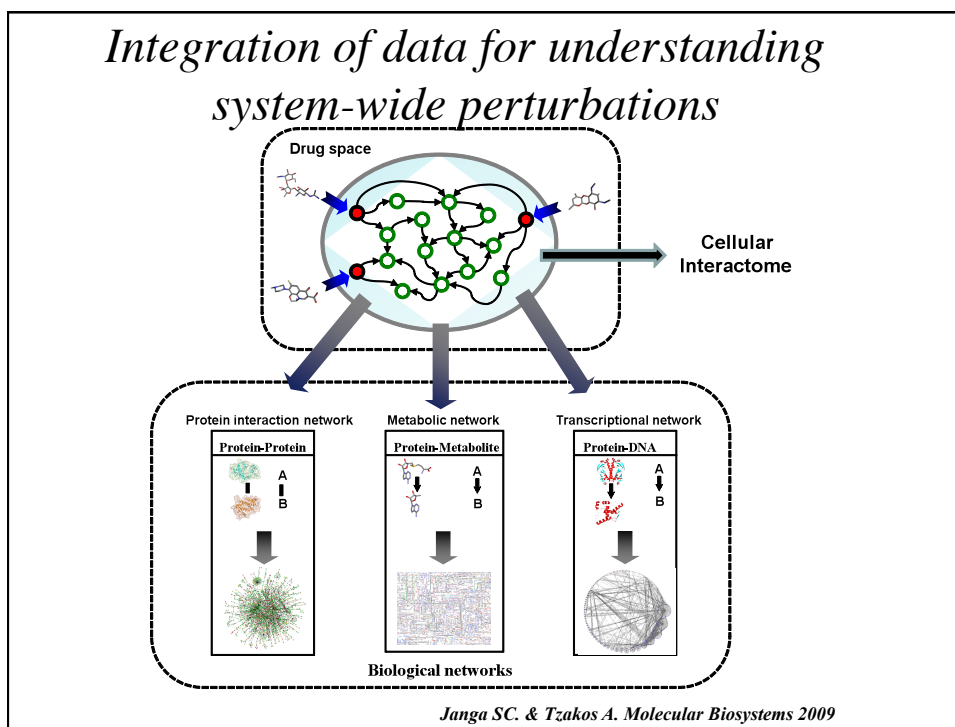


## Diverse functions of RNA-Binding Proteins (RBPs)



Mittal et al., 2009 PNAS



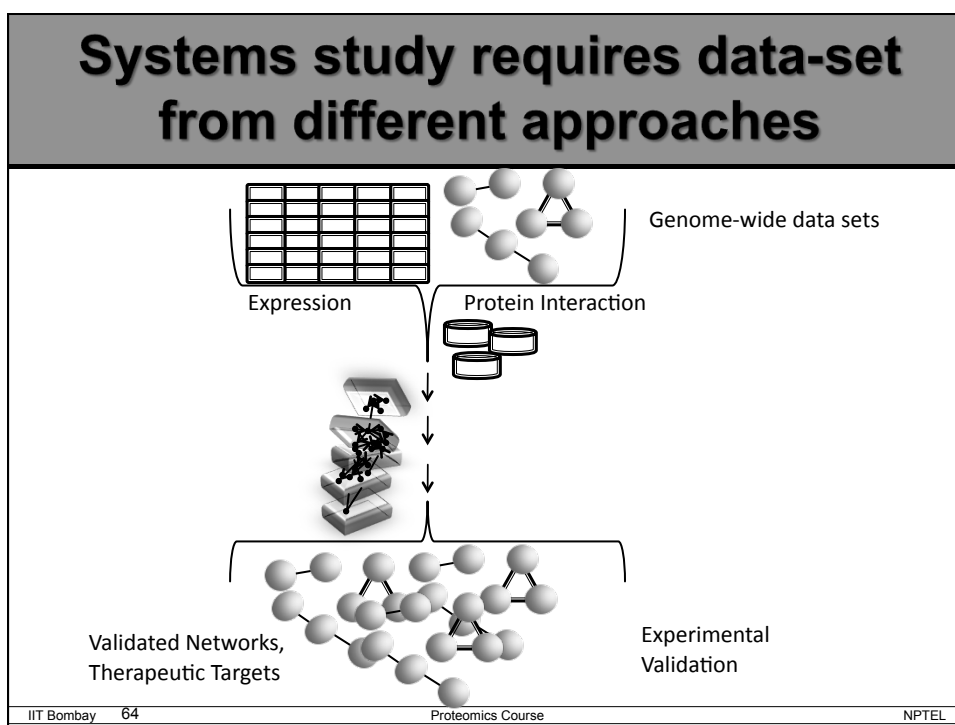
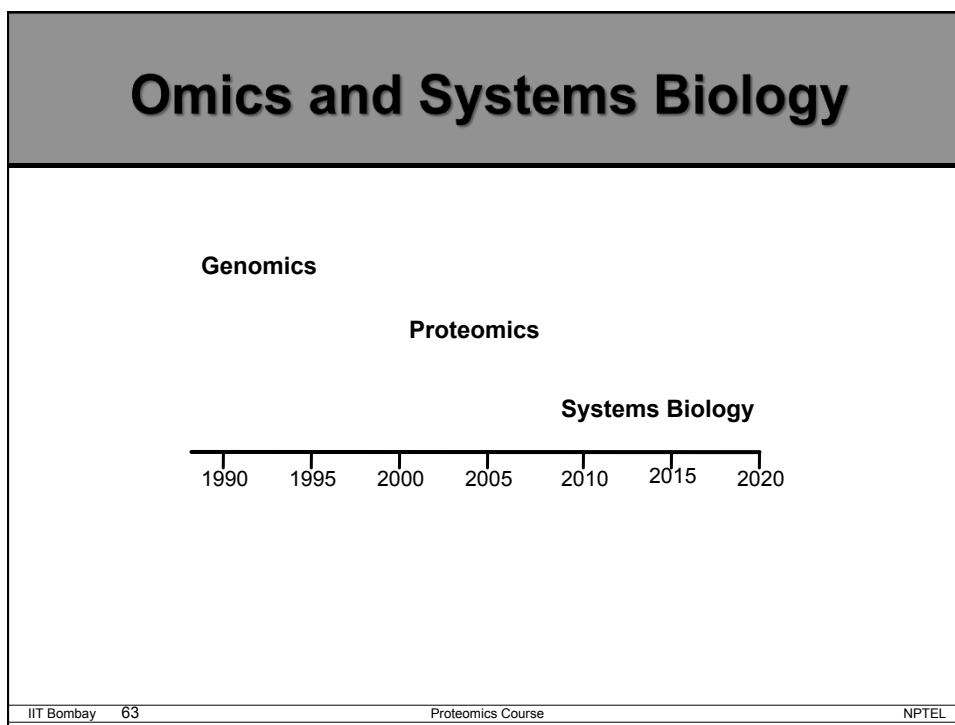


## Conclusion



- Network-based approaches are essential for dissecting the design principles of biological systems
- They play an important role in biomarker identification and elucidation of key players responsible for the disease phenotype.
- Systems medicine can lead to the development of personalized medical treatment options in years to come with developments in high-throughput sequencing and other technologies.

## “Omics” and Systems Biology





## Systems study requires collaboration!

IPG strip

Biology  
Physics  
Engineering  
Chemistry  
Computer Science  
Mathematics  
Medicine  
Statistics

**SYSTEMS  
BIOLOGY**

IIT Bombay 65 Proteomics Course NPTEL

## “Omics” to Physiology

IPG strip

Genomics      Transcriptomics      Proteomics

Systems Biology

Physiology and medicine

IIT Bombay 66 Proteomics Course NPTEL

## Challenges: Systems Biology

- Systems biology is extremely challenging
- Understanding dynamics of biological networks requires modeling, simulation and understanding of biology
- Requires mathematical & statistical approaches

## Proteomics and Systems Biology

- Proteomics is useful to understand complex signaling networks in biological systems
- Proteomics is indispensable for systems biology

## Summary

- Proteomics
- Systems biology

## REFERENCES

- Systems Biology: A Brief Overview, Hiroaki Kitano,, 1662 (2002); 295 Science
- Simpson R. J. Proteins and Proteomics: a laboratory manual ed., Cold Spring Harbor laboratory press, 2002. ISBN: 0879695544.
- Trey Ideker, L. Raimond Winslow, A. Douglas Lauffenburger. Bioengineering and Systems Biology. Annals of Biomedical Engineering. February 2006, Volume 34, Issue 2, pp 257-264
- Trey Ideker, et al., Integrated Genomic and Proteomic Analyses of a systematically Perturbed Metabolic Network, Science, 2001.
- Sarath Chandra Janga and Julio Collado-Vides. Structure and evolution of gene regulatory networks in microbial genomes. Research in Microbiology , 2007 158(10):787-94.

## REFERENCES

- Mittal N, Roy N, Babu MM, Janga SC. Dissecting the expression dynamics of RNA-binding proteins in posttranscriptional regulatory networks. Proc Natl Acad Sci U S A. 2009 Dec 1;106(48):20300-5.
- Sarath Chandra Janga and Andreas Tzakos. Structure and organization of drug-target networks : Insights from genomic approaches for drug discovery. Molecular Biosystems , 2009, 5 (12):1536-48
- Ernesto Perez-Rueda, Sarath Chandra Janga \* and Agustino-Martinez-Antonio. Scaling relationship in the gene content of transcriptional machinery in bacteria. Molecular Biosystems, 2009, 5(12):1494-501

## Acknowledgements

- Dr. Sarath Chandra Janga for stimulating discussion and presentation on Systems approaches for studying biological networks: from post-transcriptional control to drug discovery.