BHARATHIDASAN UNIVERSITY

Tiruchirappalli- 620024,
Tamil Nadu, India.

Programme : M.Sc., Biomedical Science

Course Title : Bioinformatics

Course Code : BM35S1BI

Unit – I

TOPIC: RESEARCH IN BIOINFORMATICS

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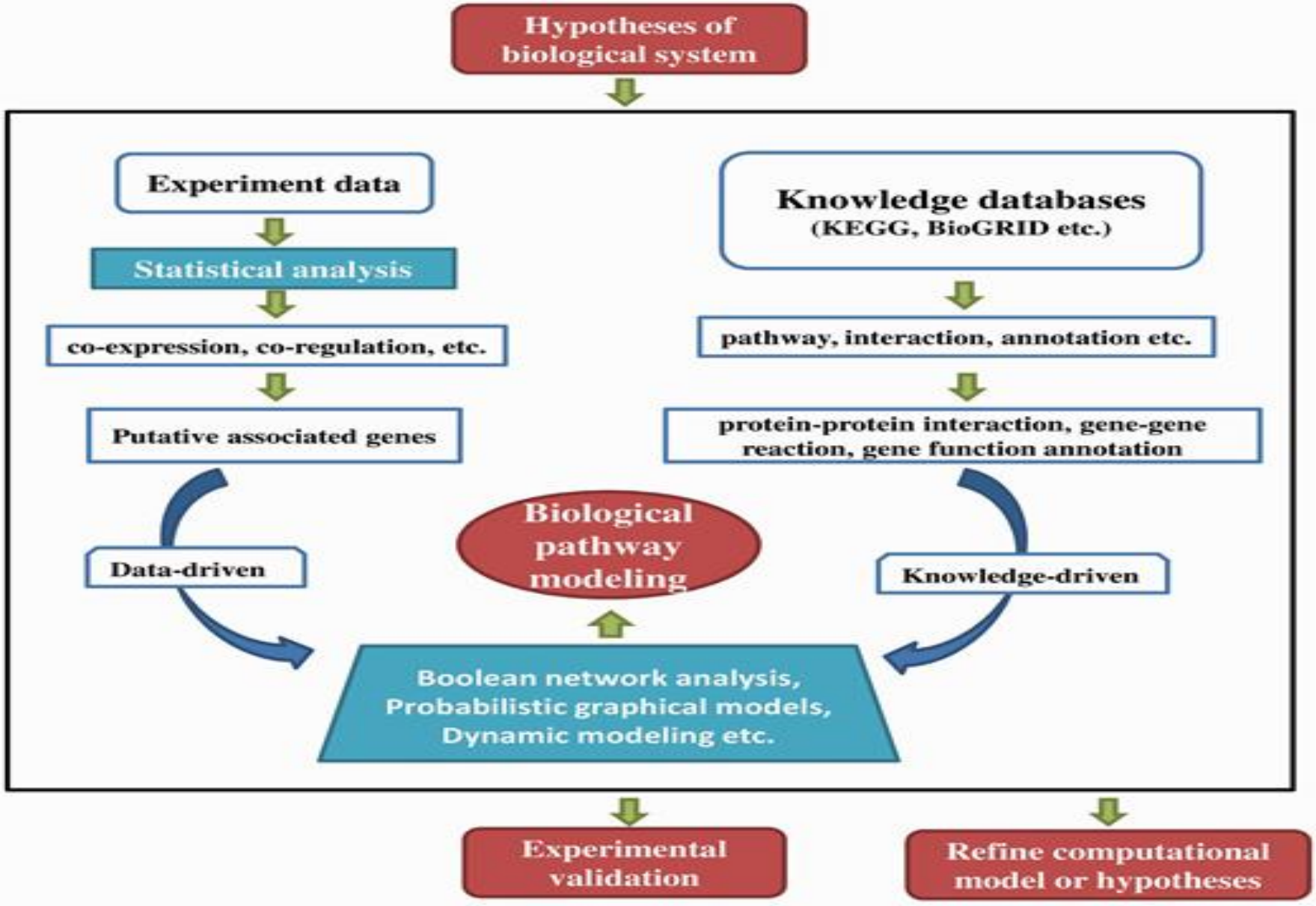
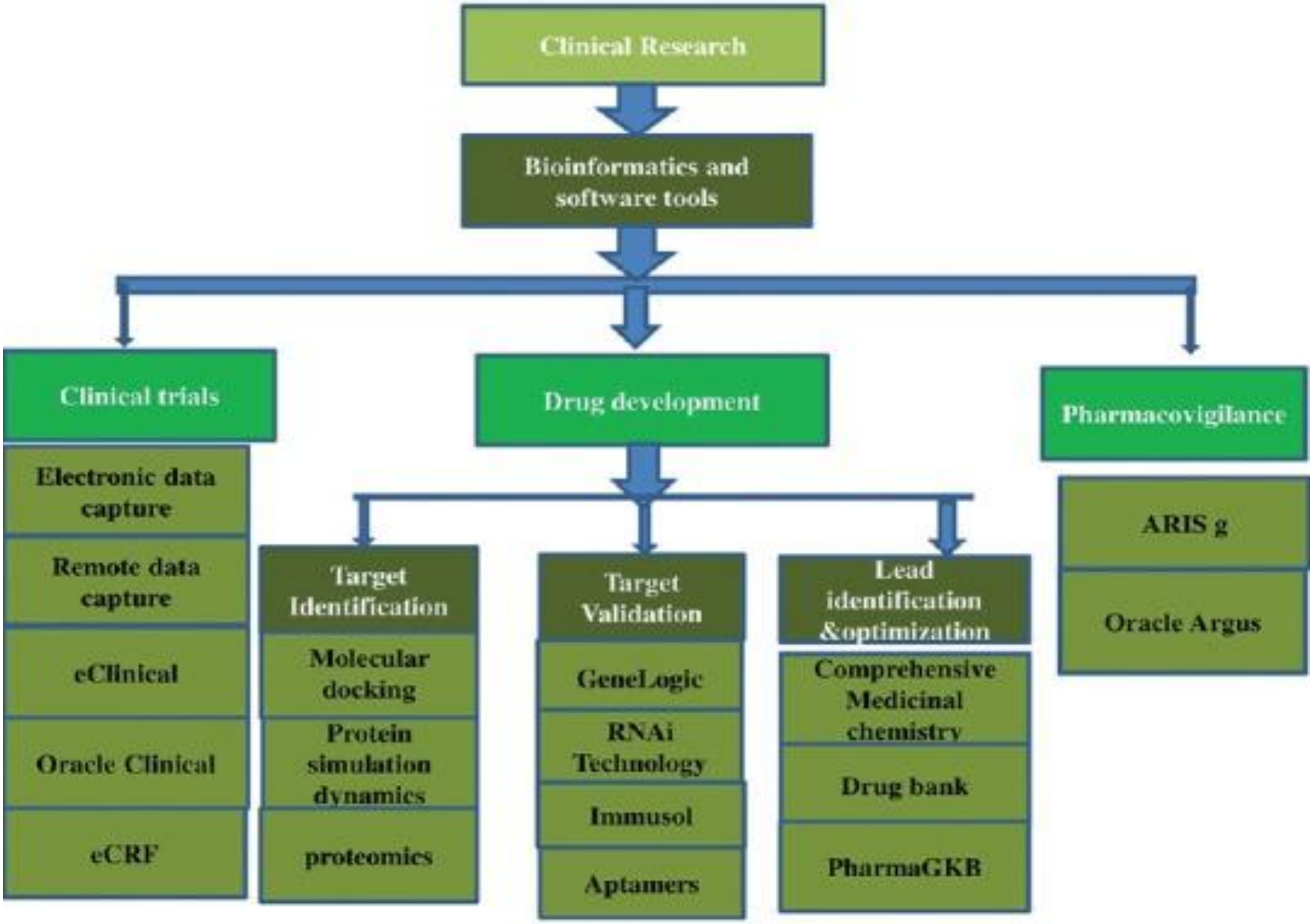
RESEARCH IN BIOINFORMATICS

- Bioinformatics is a field of study that uses computation to extract knowledge from biological data. It includes the collection, storage, retrieval, manipulation and modeling of data for analysis, visualization or prediction through the development of algorithms and software.
- **Bioinformatics is** not only combination of Bio and Informatics but it also includes various fields like Drug Designing, Genomics, Proteomics, System Biology, Machine Learning , Advanced Algorithm, Structural Biology, Computational Biology and many more.


Hypotheses of biological system
Experiment data
Statistical analysis
co-expression, co-regulation, etc.
Putative associated genes
Knowledge databases (KEGG, BioGRID etc.)
pathway, interaction, annotation etc.
protein-protein interaction, gene-gene reaction, gene function annotation
Biological pathway modeling
Data-driven
Knowledge-driven
Boolean network analysis, Probabilistic graphical models, Dynamic modeling etc.
Experimental validation
Refine computational model or hypotheses


Clinical Research
Bioinformatics and software tools
Clinical trials
Drug development
Pharmacovigilance
Electronic data capture
Remote data capture
eClinical
Oracle Clinical
eCRF
Target Identification
Molecular docking
Protein simulation dynamics
proteomics
Target Validation
GeneLogic
RNAi Technology
Immusol
Aptamers
Lead identification &optimization
Comprehensive Medicinal chemistry
Drug bank
PharmaGKB
ARIS g
Oracle Argus

Drug Discovery & Development

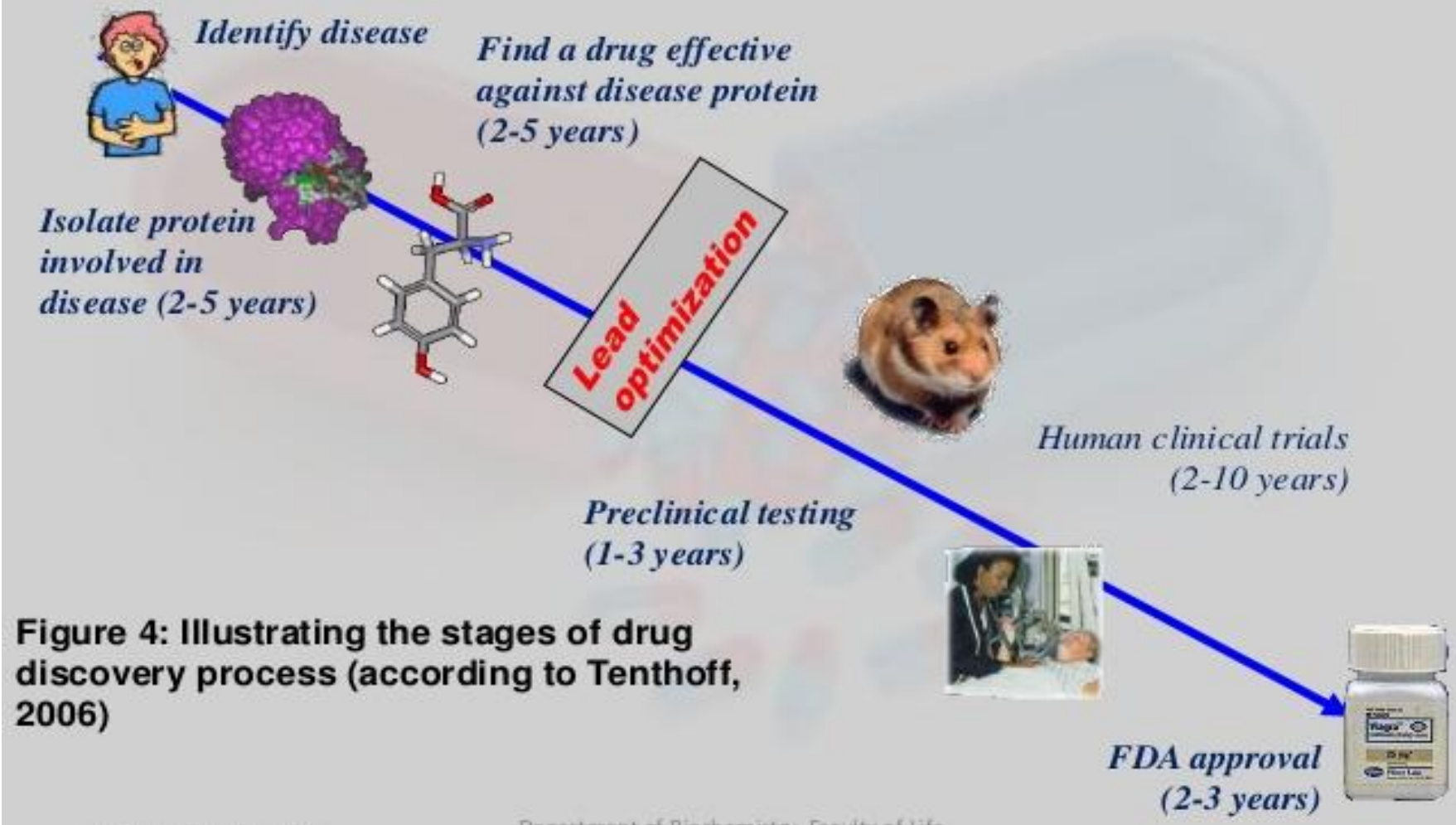
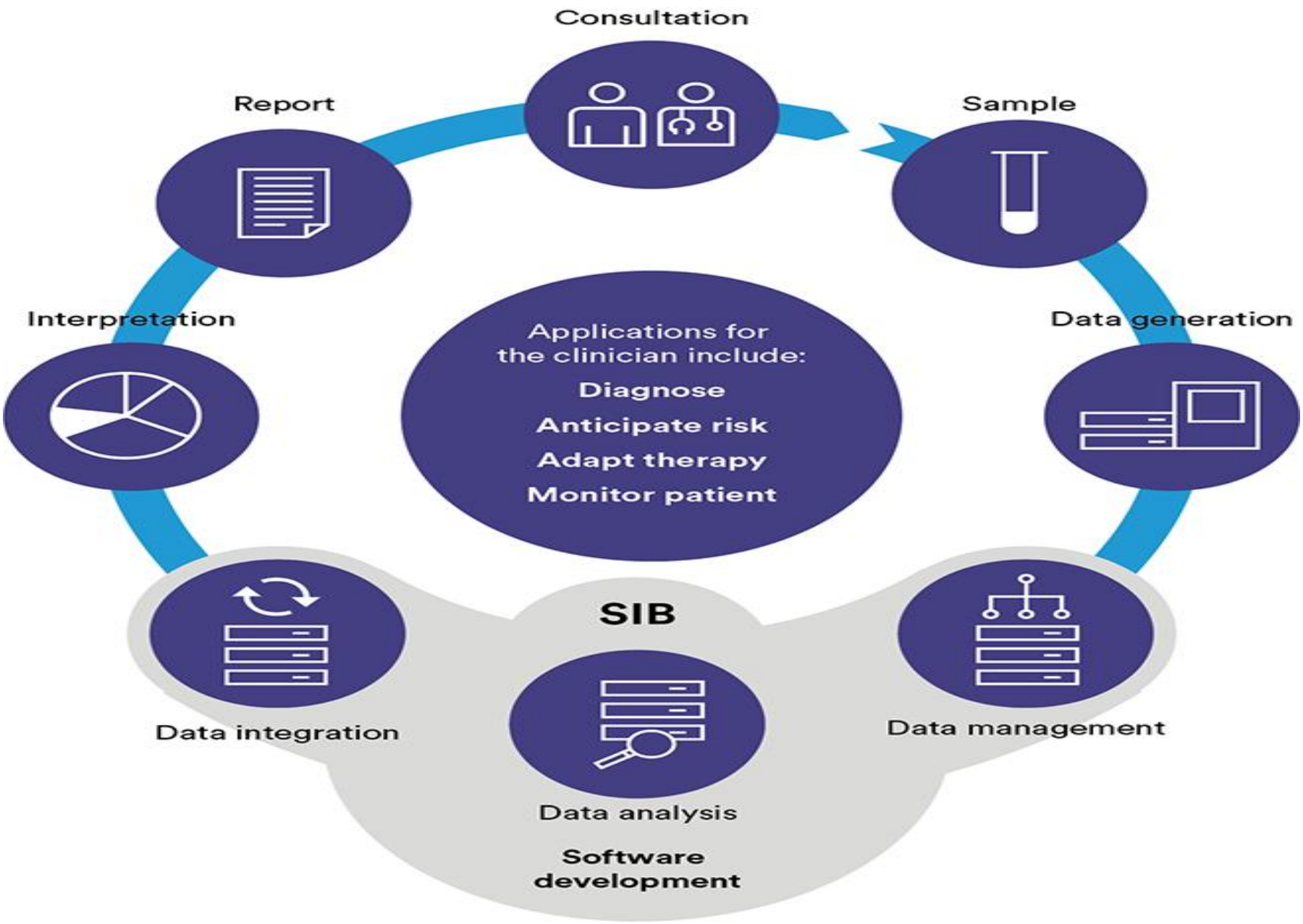


Figure 4: Illustrating the stages of drug discovery process (according to Tenthoff, 2006)


Consultation
Sample
Data generation
Data management
Data integration
Interpretation
Report
Applications for the clinician include:
Diagnose
Anticipate risk
Adapt therapy
Monitor patient
SIB
Data analysis
Software development

The role of bioinformatics in cancer research

- Diagnosis - identify classifiers to better sub-divide cancer etiologies into groups. Better individual data to put treatment and individual together.
- Treatment - identify better methods to track treatment progress and indicate problems earlier.
- Prevention - understand mechanisms for cancer initiation, progression and development and identify targets in this process.
- Connect cancer patient data from geographically distributed cancer patients for more complete analysis.

JOB OPPORTUNITIES OF BIOINFORMATICIANS

- Bioinformatics Software Developer
- Research Scientist / Associate
- Network Administrator / Analyst
- Computational Biologist
- Database Programmer
- Science Technician
- Content Editor
- Pharmacogenomics
- Proteomix
- Professor

DEFINITIONS

A **homolog** is a gene inherited in two species by a common ancestor. While **homologous** genes can be similar in sequence, similar sequences are not necessarily **homologous**.

Both **orthologs and paralogs** are types of **homologs**, that is, they denote genes that derive from the same ancestral sequence. **Orthologs** are corresponding genes in different lineages and are a result of speciation,whereas **paralogs** result from a gene duplication.

Paralog is a pair of genes that derive from the same ancestral gene.

DEFINITIONS

xenolog is a type of ortholog where the homologous sequences are found in different species because of horizontal gene transfer.

Types of homology

- **Homologues** (**homologous genes**) are genes that derive from a common ancestor-gene
- **Orthologues** (orthologs) are homologous genes in different species
- **Paralogues** (paralogs) are homologous genes in one species that derive from gene duplication

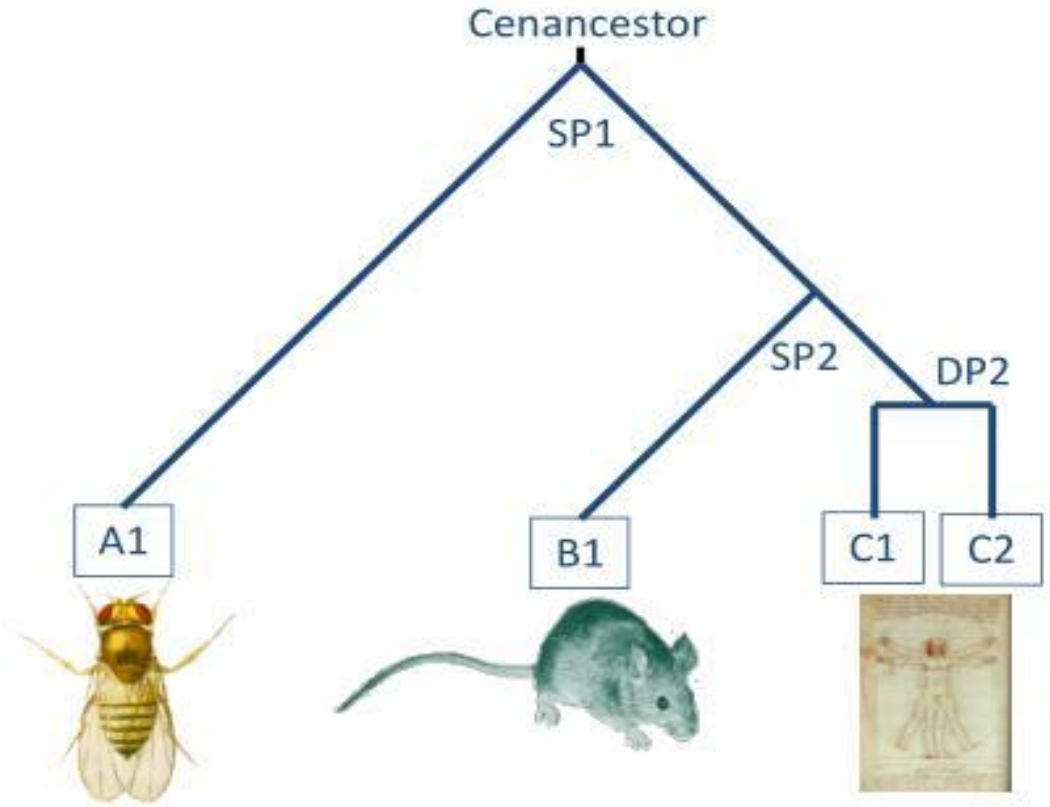
When one gene is duplicated, the duplication event results in two paralogous genes (paralogues)

Studies of paralogs have found that one paralogue of a pair often retains the ancestral gene's function, while the other paralogue is free to evolve and adopt new functions

Homologs, Orthologs and Paralogs

Identifying changes in the genome requires resolving evolutionary relationships for all bases.

Homologues: Common descent from an ancestral sequence
Paralogues: Homologues in the same genome which are the result of gene duplication; Often short hand for:
In-paralogues: Genes which have arisen from duplications in one lineage (E.g. mouse- or human- specific gene duplications)
Orthologues: Corresponding genes in two species which were derived from a single gene in the last common ancestor



C1 and C2 are paralogues
A1 and B1 and (C1 and C2) are orthologues

Orthologs vs. Paralogs

- When comparing gene sequences, it is important to distinguish between identical vs. merely similar genes in different organisms.
- **Orthologs** are homologous genes in different species with analogous functions.
- **Paralogs** are similar genes that are the result of a gene duplication.
  - A phylogeny that includes both orthologs and paralogs is likely to be *incorrect*.
  - Sometimes phylogenetic analysis is the best way to determine if a new gene is *an ortholog* or *paralog* to other known genes.

REFERENCE

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6875757

Thank You