University of Engineering and Management, Kolkata

Department of Biotechnology

In Collaboration with

Indian Institute of Technology, Guwahati

Presents

Bio-Hackathon on "Computational Drug Development"

Note:

- Select a single problem statement among the four problems
- Provide the entire solution in accordance to the manuscript template provided
- You need to submit the entire manuscript by 5PM on 21st September 2025
- In the manuscript provide a suitable title as per the problem statement

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Problem statement 1: Developing Computational Tools for Rapid Design and Validation of Diagnostic Biomarkers for High-Priority Diseases (like Tuberculosis, Hepatitis, or Malaria: any one disease).

Background

Computational tools for rapid biomarker design are revolutionizing tuberculosis, hepatitis, and malaria diagnostics by utilizing large-scale omics dataset. Traditional diagnostic methods struggles with sensitivity, early detection, and intervention. Using integrative bioinformatics, machine learning, and AI, the robust identification of disease-specific molecular signatures (proteins, genes, miRNAs) from patient sample is possible. These computational approaches facilitate development of diagnostic panels that can support point-of-care applications to meet the urgent global health priorities.

Challenge

The challenges is to frame a 'Multi-Omics data integration for biomarker discovery'

- Develop and benchmark computational pipeline that integrate and analyse transcriptomic, proteomic, and genomic dataset from publicly available repositories (Gene Expression Omnibus or European nucleotide archive or any other).

- Pipeline must employ machine learning, feature selection, and statistical method to identify potential biomarkers.

- The biomarker signatures must distinguish themselves from healthy individual or different disease stage (early onset, symptomatic, highly infectious stage etc).

Expected outcomes:

- Generation of ranked list of candidate biomarkers (proteins, genes, or metabolite molecules) associated with diseases presence or progression.

- Demonstration of pipeline sensitivity, specificity, and reproducibility using cross-validation approaches.

- Documentation of pipeline, including summary of data sources, identified biomarkers, suitability with Indian population, that can be shared with public health authorities.

- Recommendation for optimal biomarker panel that could be translated to point-of-care screening tools for further experimental validation.

Problem statement 2: Machine Learning-Driven Molecule Identification for Fluorescence-Based Detection of Cardiovascular Protein Biomarkers.

Background

Cardiovascular diseases (CVDs) remain a leading cause of death worldwide, with protein biomarkers playing crucial role in early diagnosis and risk assessment. Key biomarkers like Creatine phosphokinase-MB (CPK-MB), Troponin-I and Troponin-T, lactate dehydrogenase (LDH), atrial natriuretic peptide (ANP), and B-type natriuretic peptide (BNP), C-reactive protein (CRP) reflect heart muscle injury, inflammation, and oxidative stress. These proteins enable timely intervention and better disease management. However, sensitive and specific detection methods including fluorescence-based assays are essential to harness their full clinical potential, especially in rapid point-of-care diagnostics.

Challenge

Develop a machine learning model to predict and prioritize small molecules or dyes for molecule identification in fluorescence-based detection of cardiovascular protein biomarkers.

- Access the publicly available proteomic and transcriptomic dataset relevant to CVD from sources like UK biobank proteomics dataset (for >50,000 participants with clinical annotations). GEO and ArrayExpress repositories for transcriptomic profiles of CVD patients and healthy control can also be accessed.

- Chemical and molecular structure from database like PubChem and ChEMBL for candidate fluorescence molecules.

- Feature extraction from molecular structure using molecular fingerprints and graph embeddings.

- Use supervised learning algorithms to model molecular binding and fluorescence.

- Prediction of binding affinity (protein-ligand docking and photophysical properties) and developing an integrative modeling.

Expected outcomes

- Ranked candidate molecules with predictive fluorescence and binding efficiency to cardiovascular biomarkers.

- Model performance metric (accuracy, ROC, AUC, precision-recall) for validating predictive accuracy.

- Documentation and codebase (python-notebook preferably) for machine learning pipeline, enabling reproducibility.

Problem Statement 3: Computational Drug Development Targeting Cystic Fibrosis

Background

Cystic Fibrosis (CF) is a life-threatening autosomal recessive genetic disorder caused by mutations in the CFTR (Cystic Fibrosis Transmembrane Conductance Regulator) gene, leading to dysfunctional chloride ion transport across epithelial cells. This results in abnormally thick mucus secretions, chronic respiratory infections, impaired pancreatic function, and progressive lung damage. Despite advances in supportive care and the introduction of CFTR modulators, CF remains a major global health burden.

The current therapeutic landscape includes conventional CFTR modulators, antibiotics, mucolytics, and anti-inflammatory drugs. However, limitations such as drug resistance, partial efficacy across mutation subtypes, high costs, and side effects necessitate innovative computational approaches for drug discovery.

Natural bioactive molecules and synthetic drug design hold promise for developing next-generation therapies that can modulate CFTR function, reduce mucus viscosity, target secondary infections, and improve patient quality of life.

Challenge

Participants are invited to design computational drug discovery pipelines that integrate AI, molecular docking, virtual screening, and omics-based approaches to identify novel drug candidates for Cystic Fibrosis.

The challenge is structured into three key domains:

1. Conventional and Approved Drugs for CF

- CFTR Modulators: Ivacaftor, Lumacaftor, Tezacaftor, Elexacaftor (e.g., Trikafta® combinations)
- Mucolytics: Dornase alfa (Pulmozyme), Hypertonic saline
- Antibiotics (for chronic Pseudomonas aeruginosa and other infections): Tobramycin, Aztreonam lysine, Colistimethate, Ciprofloxacin
- Anti-inflammatory agents: Ibuprofen (high-dose), Azithromycin (anti-inflammatory role)

Task: Use computational models to analyze drug-target interactions, resistance patterns, and possible drug repurposing opportunities.

2. Natural Products and Bioactive Compounds

Natural compounds with antimicrobial, mucolytic, or anti-inflammatory properties have been investigated in CF research:

- Curcumin – potential CFTR potentiator
- Resveratrol – antioxidant and anti-inflammatory
- Quercetin – mucoregulator, CFTR modulator in preclinical studies
- Epigallocatechin gallate (EGCG) – antioxidant and CFTR stabilizer

- N-acetylcysteine (NAC) – mucolytic and antioxidant

Task: Apply molecular docking and ADMET modeling to evaluate natural compounds for their potential to modulate CFTR or secondary CF-related pathways.

3. Designing Novel Synthetic Drugs

The future of CF treatment requires synthetic small molecules or computationally designed peptides targeting specific CFTR mutations or pathways.

Task:

- Use de novo drug design algorithms to propose synthetic molecules with high binding affinity to mutated CFTR channels.
- Explore multi-target drug design strategies addressing mucus hypersecretion, infection control, and ion transport simultaneously.
- Incorporate molecular dynamics simulations to validate drug-receptor stability.

Expected Outcomes

- A prioritized list of candidate molecules (natural, conventional, and synthetic).
- Computational drug-receptor interaction maps for CFTR and secondary pathways.
- A conceptual pipeline for computational drug development in CF, integrating AI-based drug screening, pharmacogenomics, and in-silico clinical trial simulations.

Problem Statement 4: Computational Drug Development for Surface Wound Infections

Background

Surface wound infections remain a major public health challenge, particularly in trauma care, diabetic ulcers, burns, and surgical site infections. Delayed or impaired wound healing occurs due to microbial colonization, biofilm formation, antimicrobial resistance (AMR), and dysregulated inflammatory responses. Current treatments involve antibiotics, antiseptics, and advanced wound dressings, but these approaches often face limitations including:

- Emergence of antibiotic-resistant pathogens (e.g., *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*)
- Incomplete biofilm eradication
- Impaired tissue regeneration and scarring

The integration of computational drug development with natural therapeutics provides a promising pathway to identify safer, multi-functional wound healing agents with antimicrobial, anti-inflammatory, and tissue-regenerative potential.

Challenge

Participants are tasked with developing computational pipelines for drug discovery targeting infected surface wounds. The challenge will explore:

1. Conventional & Approved Therapies

- Antibiotics: Topical mupirocin, fusidic acid, silver sulfadiazine, neomycin
- Antiseptics & wound dressings: Povidone-iodine, chlorhexidine, silver nanoparticles, honey dressings
- Growth factors: Recombinant platelet-derived growth factor (becaplermin)

Task: Analyze mechanisms, resistance patterns, and drug–biofilm interactions using computational docking, pharmacophore mapping, and resistance modeling.

2. Natural Therapeutics for Wound Healing

Natural products exhibit multi-target activity across different stages of wound healing. Key candidates include:

- Curcumin – anti-inflammatory, angiogenesis promoter
- Aloe vera – re-epithelialization, collagen synthesis
- Honey – antimicrobial, biofilm disruption, osmotic wound cleaning
- Centella asiatica – fibroblast proliferation, collagen maturation
- Green tea polyphenols (EGCG) – antioxidant, ECM remodeling
- Essential oils (tea tree, neem, lavender) – antimicrobial, anti-inflammatory

Task: Use computational simulations to screen phytochemicals against wound infection pathogens and host targets (inflammatory mediators, growth factors, ECM enzymes).

3. Designing Novel Synthetic Drugs

- Apply AI-based drug design to generate synthetic small molecules targeting bacterial biofilm proteins (e.g., quorum sensing regulators, biofilm matrix enzymes).
- Develop hybrid drugs combining antimicrobial and tissue-regenerative properties.
- Incorporate molecular dynamics and ADMET modeling to predict therapeutic viability.

Model: Correlating Natural Therapeutics to Stages of Wound Healing

Stage of Wound Healing	Biological Processes	Challenges in Infected Wounds	Natural Therapeutics (Examples)	Computational Target
Hemostasis (minutes–hours)	Platelet aggregation, clot formation	Delayed clotting in infected/diabetic wounds	Honey (osmotic effect), Aloe vera (glycoproteins)	Thrombin–fibrinogen binding simulation
Inflammation (hours–days)	Immune cell recruitment, cytokine release	Excess inflammation due to infection	Curcumin (NF-κB inhibition), EGCG (antioxidant), Neem oil	Docking with NF-κB, COX-2, TNF-α
Proliferation (days–weeks)	Fibroblast proliferation, collagen deposition, angiogenesis	Impaired granulation tissue due to bacterial toxins	Centella asiatica (collagen synthesis), Aloe vera (fibroblast stim.)	VEGF–receptor docking, collagen cross-linking modeling
Remodeling/Maturation (weeks–months)	Collagen remodeling, scar formation	Scar hypertrophy, biofilm persistence	Green tea polyphenols (ECM regulation), Essential oils (scar prevention)	MMP (matrix metalloproteinase) inhibition modeling

Expected Outcomes

- A computationally ranked list of natural, conventional, and synthetic drug candidates for infected wound healing.
- Drug-pathway interaction maps linking natural therapeutics to wound healing stages.
- A computational pipeline for integrating natural and synthetic approaches to accelerate wound healing and reduce infection burden.