ATAVISM

A STUDENT-RUN SYNAPSE NEWSLETTER

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ABOUT US

The Synapse Club was created with an aim to allow students to develop and exhibit their technical, outreach, arts and other skills. And the newsletter is a tiny idea of the members of Synapse Club. Atavism is a phenotypic trait that appears suddenly in an organism. Yes, it is that feature we have always had the genes for, but have never expressed. Have you heard of the dolphin with legs or the baby born with a tail? Because if you have, you know what we're talking about! Just like its name, this newsletter is a little something that we always had the genes for, but we never expressed. We agree that the newsletter isn't as weird as the chicken with teeth but it sure is something out of the blue to bring all of us together. We aim to make this newsletter the place you can go for the latest news in the biotechnology world, bizarre but true science headlines, and conversations that you should hear more of.

When Synthetic Biology meets System Biology!!

“SysBio” comes from the concept of Systems Biology—an approach that integrates complex biological data to understand how interactions within biological systems lead to the functions and behavior of the organism.Synthetic biology combines engineering principles with biology to create new biological systems or redesign existing ones. Computational systems biology plays a critical role in the design and simulation of synthetic biological systems before they are built in the lab.

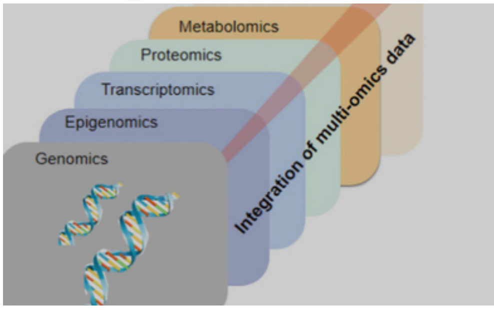
One of the most exciting applications of synthetic biology is the creation of genetically engineered organisms that can perform useful tasks, such as producing biofuels, detecting environmental toxins, or even acting as living therapeutics. Before these organisms are synthesized, computational models are used to predict how engineered genes and pathways will behave in the cell. This approach minimizes trial and error in the lab and speeds up the development of synthetic systems.

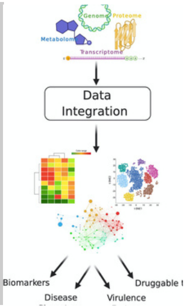
ARE YOU EVEN READING?

If you are, you're sure to have feedback for the team. Send it to 211909@juitsolan.in so that we can know. We would also love to feature your opinion on biology topics or your coverage of the latest research in the next issue. Your email could make our day!

References and Photo credits:
1. Images from Pexels, Pixabay
2. Cameron, D. E., Bashor, C. J., & Collins, J. J. (2014). A brief history of synthetic biology. Nature Reviews Microbiology, 12(5), 381-390.

Exploring the Power of Multi-Omics Integration





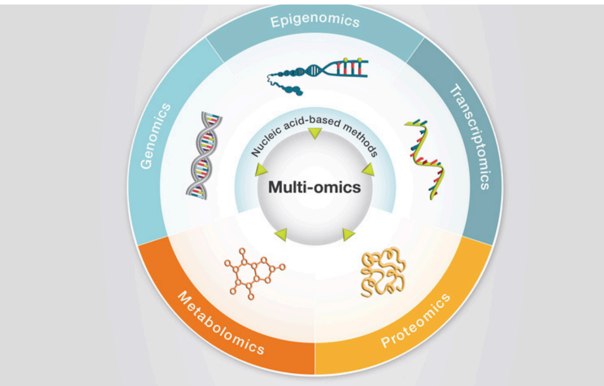
Multi-omics integration is one of the most promising advances in computational systems biology. It brings together various "omics" data—such as genomics, proteomics, metabolomics, and transcriptomics—to provide a holistic view of biological processes. By combining these datasets, researchers can identify how different molecular layers interact to drive phenotypes, disease progression, and treatment responses.

For example, in cancer research, integrating genomic mutations with proteomics data helps to understand how specific mutations alter protein expression, leading to uncontrolled cell growth. Beyond cancer, multi-omics integration is being applied to other complex diseases, such as cardiovascular disease, diabetes, and neurodegenerative disorders. In cardiovascular disease, for instance, multi-omics analyses can reveal how genetic risk factors interact with changes in lipid metabolism and inflammation, providing new insights into disease mechanisms and potential therapeutic targets.

Computational tools like iClusterPlus and MOFA (Multi-Omics Factor Analysis) are used to integrate and analyse these complex datasets. These methods help to identify biomarkers for early disease detection and targets for personalized therapies. Moreover, integrating these datasets allows researchers to move from hypothesis-driven research to data-driven discoveries, as they can uncover previously hidden patterns that drive biological function.

Challenges and Future Directions!!

While the potential of multi-omics integration is immense, several challenges remain. One of the main challenges is the standardization of data across different omics platforms. Each omics type has its own data format, noise levels, and biases, making it difficult to integrate them seamlessly. Moreover, multi-omics studies often require large datasets to account for biological variability, and generating such datasets can be expensive and time-consuming. Another challenge is the interpretation of integrated multi-omics data. With the sheer volume and complexity of data being generated, extracting biologically meaningful insights can be daunting. Advanced computational algorithms and machine learning approaches are helping to address this challenge, but there is still much work to be done in developing more accurate and interpretable models.Despite these challenges, the future of multi-omics integration is bright. Advances in computational systems biology, machine learning, and high-throughput technologies will continue to drive progress in this field, enabling deeper insights into disease mechanisms and the development of more personalized and effective treatments.



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1. Hasin, Y., Seldin, M., & Lusis, A. (2017). Multi-omics approaches to disease. Genome Biology, 18(1), 1-15.

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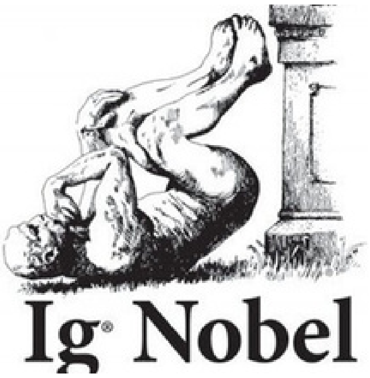
Modeling Infectious Diseases: Insights from COVID-19

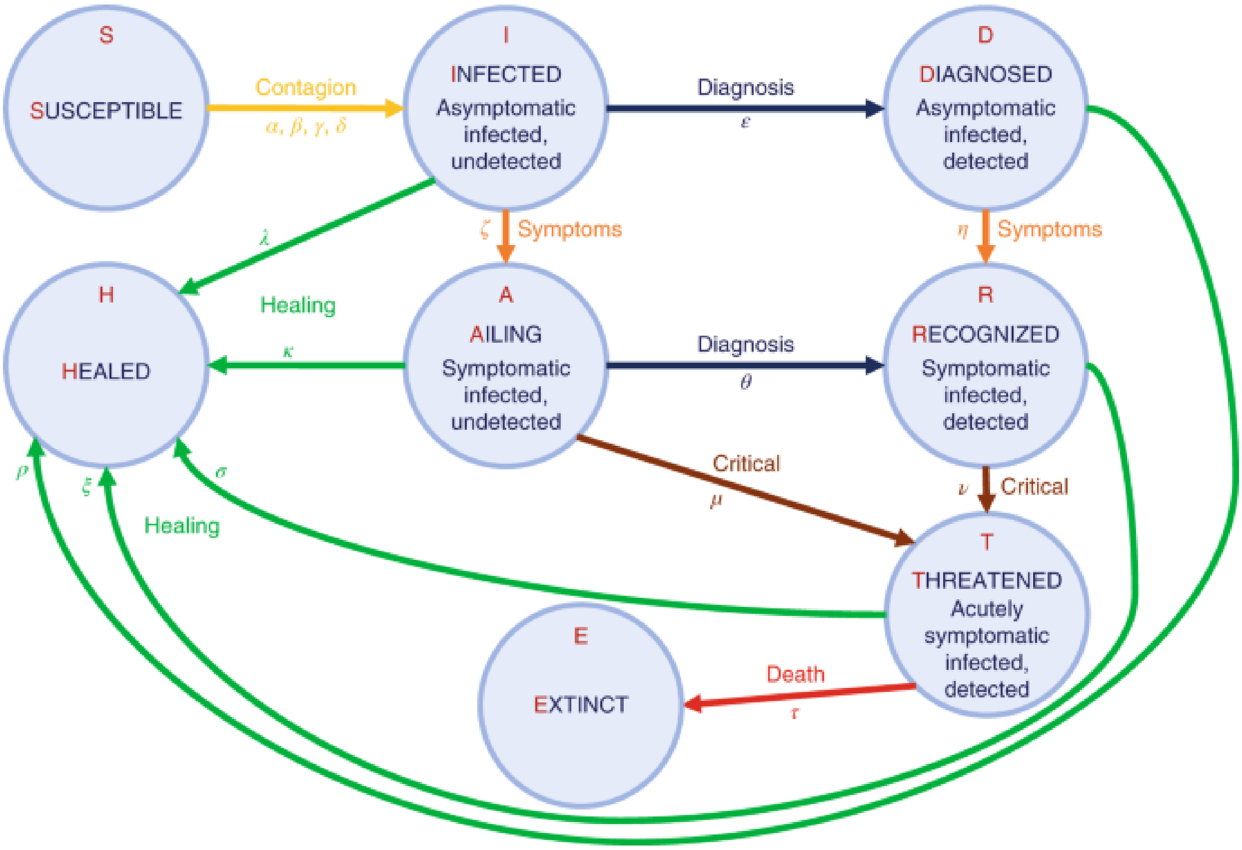
The COVID-19 pandemic underscored the pivotal role of computational modelling in managing infectious diseases. From predicting infection rates and assessing the impact of public health measures to simulating the effects of vaccination strategies, computational models helped shape the global response to the pandemic. These models, particularly epidemiological and molecular-level models, enabled scientists, public health officials, and policymakers to make informed, data-driven decisions in real time.

Epidemiological Models for Disease Spread!!!

Epidemiological models, such as the SIR(Susceptible-Infectious Recovered) and SEIR (Susceptible-Exposed-Infectious-Recovered) models, have been fundamental tools for understanding how a diseases like COVID-19 spread in populations. These compartmental models divide a population into different states or groups and use mathematical equations to predict how the disease propagates over time.



In parallel, systems biology provided insights into the molecular mechanisms of SARS-CoV-2, mapping how the virus interacts with host cells and identifying potential drug targets. Network models highlighted key protein interactions, facilitating the discovery of antiviral therapies and guiding drug repurposing efforts. Computational models also accelerated vaccine development, predicting how viral proteins fold and how vaccines could best stimulate immune responses.



References & Photo credits:
1 https://www.improbable.com/ig-about/winners/#ig2020 , https://www.improbable.com/ig-about/winners/

Artificial Intelligence in Systems Biology?

AI techniques, particularly machine learning (ML), are used to identify relationships within large-scale biological data and build models that can predict how systems behave under different conditions. These models are crucial for tasks such as, predicting gene regulatory networks, which describe how genes interact with each other to regulate gene expression, identifying protein-protein interactions, which are critical for understanding cellular functions, predicting disease progression and identifying biomarkers for early detection and targeted therapies. The application of AI in systems biology encompasses a variety of methods, including deep learning, random forests, support vector machines, and Bayesian networks, all of which contribute to understanding complex biological systems in unprecedented ways.

1. Alpha Fold: Revolutionizing Protein Structure Prediction

One of the most ground-breaking applications of AI in systems biology is Alpha Fold, an AI system developed by DeepMind.

2. AI in Drug Discovery

AI is revolutionizing drug discovery by enhancing the prediction of how chemical compounds will interact with biological targets.

3. Predicting Gene Regulatory Networks

Machine learning has proven invaluable in reconstructing GRNs from experimental data, such as gene expression profiles. Algorithms like random forests and support vector machines can analyze the relationships between genes, identifying which genes are likely to regulate others.

4. AI for Modeling Biological Systems and Disease Progression

AI-based network models can simulate how metabolic networks in cells respond to changes in nutrient availability or drug treatments.

AI and machine learning are transforming systems biology by enabling researchers to analyze vast amounts of complex biological data. From predicting protein structures and modeling gene regulatory networks to accelerating drug discovery and understanding disease progression, AI is driving innovation across multiple domains. As AI continues to evolve, its applications in systems biology will become even more powerful, offering new opportunities to understand life at its most fundamental levels and translate that understanding into therapeutic advances.

Written by: **Manshita Jindal**
Edited by: **Manshita Jindal, Synapse Club, Department of BT & BI,**
Jaypee University of Information Technology, Solan

References & Photo credits:
1. Photos credits: https://images.app.goo.gl/9BcMDKszH9pabEk96
2 Jumper, J., et al. (2021). Highly accurate protein structure prediction with AlphaFold. Nature, 596(7873), 583-589.3 Ekins, S., et al. (2019).
3 Exploiting machine learning for end-to-end drug discovery and development. Nature Materials, 18(5), 435-441.