Department of Bioengineering
Indian Institute of Science

#420, TCS Smart X Hub, Department of Bioengineering, Indian Institute of Science, Bengaluru, 560012, India
Phone: +91 80 2293 2452 siddharth@iisc.ac.in https://be.iisc.ac.in

---

Course Title: AI for Biomedical Research
Course Code: BE 301
Couse Schedule: January Semester
Credits: 3:0

Course Instructors: Siddharth Jhunjhunwala and Arvind Rao

Pre-Requisites (all 3 required):

1. BE-207 (Mathematical Methods for Bioengineers) OR equivalent
2. BE-229 (Statistics for Bioengineers) OR equivalent
3. BE-230 (Data Science for Bioengineers) OR equivalent

Description

This course intends to build on the fundamentals of machine learning to explore concepts from these areas in the context biomedical research. Students will learn about applications of advanced approaches (like transformers, Graph Neural Networks, Large Language Models, or their combinations) for problems in biomedical data sciences. Motivating examples from cancer genomics, biomedical imaging, spatial transcriptomics and drug discovery will be used to examine these principles. The course will comprise instructor-led lectures, student presentations, and course projects. Schedule permitting, guest lectures from the Institute and companies (pharma, research labs etc) might also be incorporated.

References

There is no prescribed textbook for this course. Comprehensive reading lists are provided for each topic. Key references include:

- McElreath R. Statistical Rethinking: A Bayesian Course with Examples in R and Stan
- Van Der Maaten L, Postma E, Van den Herik J. Dimensionality Reduction: A Comparative Review
- Hoffmann et al. Machine learning in medicine (arXiv:1807.00123)
- Deep learning reviews from Annual Reviews in Bioengineering

Course Outcomes

Upon completion of the course, students will be able to:

- Apply advanced signal processing and machine learning techniques to solve cancer bioinformatics problems
- Critically evaluate research papers in computational biology and bioinformatics

- Build intuition around state-of-the-art computational methods used for analysis of spatial transcriptomics and single-cell multi-omics data
- Understanding deep learning architectures (CNNs, GANs, transformers, GNNs) for biological imaging and genomics data
- Integration methods for multimodal and multi-omics datasets to derive comprehensive biological insights
- Communicate complex computational methods effectively through oral presentations and written reports