APBJC 2024
1st Asia & Pacific Bioinformatics Joint Conference
~JSBi, GIW, InCoB, APBC, and ISCB-Asia~
CREATING BIOINFORMATICS SYNERGY ACROSS THE ASIA & PACIFIC REGIONS
Dates: 22Tue - 25Fri October 2024
Venue: Okinawa, JAPAN
NAHA CULTURAL ARTS THEATER NAHArt
APBJC Asia & Pacific Bioinformatics Joint Conference

Workshops

Workshop 1

23 Oct. 13:00-14:30 Small Studio

An Introduction to Graph Neural Network (GNN) and Its Applications in Drug Response Prediction

Coordinated by

Dennis Wang

Imperial College London

Learning outcomes:

1. Gain basic knowledge of GNNs and their application in biomedical data analysis.
2. Understand the process of developing a GNN model for drug response prediction through a live demonstration.
3. Engage in hands-on learning and experimentation with the provided Google Colab notebook post-workshop.
4. Access additional materials and resources to further explore the subject.

Teaching delivery:

1. Interactive PowerPoint Presentation:
    1. Intro to graph data in biomedical research
        1. Protein-protein interaction, disease association network, and small molecule representation.
    2. Overview of popular GNN algorithms
        1. Graph convolutional network, message passing graph neural networks, and their variants.
    3. Case Studies
        1. Successful applications of GNN in predicting drug responses.
2. Demo Demonstration:
    1. Conduct a high-level walkthrough of a pre-prepared GNN model on drug response prediction.
    2. Demonstrate the steps involved in building and understanding a GNN model using Pytorch and torch_geometric, without delving into complex coding details.
    3. Show the evaluation of the model.
3. Discussion + Q&A.
4. Supplementary Materials:
    1. Access to the presentation slides and take-home Jupyter notebook on Colab for future reference.
        1. Step-by-Step Tutorial: Building a basic GNN model for drug response prediction.
        2. Dataset Overview: Understanding and preparing biomedical data for GNN.
        3. Model Training and Evaluation: Practical insights into tuning and interpreting GNN models.

    2. List of key resources for further learning: Articles, tutorials, and datasets.

Workshop 2

23 Oct. 14:50-16:20 Small Studio

Exploring the ISCB Competency Framework Version 3.0

Coordinated by
ISCB
International Society for Computational Biology

Workshop Objective:

The workshop aims to familiarize participants with the ISCB Competency Framework, with focus on the latest Version 3.0 release, covering some history of its development, understanding the competencies themselves, and exploring how one can apply the competency framework in various contexts in bioinformatics education and training.

Workshop Outline:

Introduction (10 minutes)

- Welcome and introduction to the workshop.
- Brief overview of the importance of competency frameworks in bioinformatics education and training.
- Overview of the ISCB Competency Framework development process.

Understanding the ISCB Competency Framework 3.0 (25 minutes)

- Introduction to the ISCB Competency Framework Version 3.0.
- Overview of the competency components: knowledge, skills, attitudes.
- Explanation of how competencies apply to distinct training needs and personas.
- Guided exploration of the competency framework website: https://competency.ebi.ac.uk/framework/iscb/3.0/competencies

Application of the Framework (45 minutes)

- Discussion and case studies on how the ISCB Competency Framework can be utilized in various contexts:
    - Evaluating an existing training program
    - Evaluating a short course
    - Developing a new training program or short course
    - Developing a program or course endorsement process

Wrap-Up and Q&A (10 minutes)

- Summary of key takeaways from the workshop.
- Open floor for questions and discussion.
- Closing remarks and gratitude.

Workshop 3

24 Oct. 10:45-12:15 Small Studio

Spatial Transcriptomics Data Analysis

Coordinated by

Shinn-Ying Ho, Tzong-Yi Lee,

National Yang Ming Chiao Tung University, Taiwan

Workshop Description:

In the rapidly evolving field of high-throughput sequencing, spatial transcriptomics has emerged as a transformative technology, offering unprecedented insights into the spatial organization of gene expression within tissues and organisms. This workshop aims to equip participants with the knowledge and tools necessary to harness the power of spatial transcriptomics data and extract meaningful biological insights. The workshop will be held in interactive manner, after the introduction of principles, methodologies, and challenges associated with spatial transcriptomics data analysis. Through a combination of lectures, hands-on exercises, and interactive discussions, participants will learn how to preprocess spatial transcriptomics datasets, perform quality control assessments, detect spatially co-expressed genes, and visualize spatial gene expression patterns.

Benefits of the Workshop to attendees:

From understanding the fundamentals of spatial gene expression profiling to exploring advanced computational techniques, participants will gain a comprehensive understanding of the analytical pipeline required to interpret spatially resolved transcriptomic data effectively. Additionally, we will explore cutting-edge computational approaches for spatial data integration, trajectory inference, and spatial cell type mapping, providing participants with a toolkit to address diverse biological questions across a range of spatial scales and experimental designs. Whether you are a biologist seeking to leverage spatial transcriptomics to uncover the spatial dynamics of gene regulation or a computational scientist interested in developing novel analytical methods for spatial data analysis, this workshop offers a valuable opportunity to enhance your skills and expand your research horizons. Join us as we embark on a journey through the transcriptomic landscape, where spatially resolved insights await discovery.

In this workshop on spatial transcriptomics, we will focus on the effective processing, analysis, and visualization of spatial transcriptomics data using Seurat and stLearn. Seurat, a comprehensive R package, has been extended to support spatial data with functionalities beyond basic single-cell analysis, including preprocessing, quality control, normalization, and identification of spatially relevant clusters and markers. Meanwhile, stLearn, designed to further enhance spatial data analysis, provides tools to integrate spatial information directly into the analysis pipeline, enabling deeper insights into the spatial organization of cells. Both tools employ robust statistical and machine learning methods such as PCA, t-SNE, and UMAP, which are critical for uncovering complex data structures and understanding the spatial context of gene expression. The workshop will also incorporate essential resources such as the Allen Brain Atlas, which provides comprehensive gene expression datasets invaluable for researchers wishing to compare their spatial transcriptomics data with established brain gene expression patterns. By integrating Seurat and stLearn with these databases, the workshop aims to provide participants with a comprehensive framework for conducting spatial transcriptomics research.

Speakers:

Tzong-Yi Lee, National Yang Ming Chiao Tung University, Taiwan
Chia-Ru Chung, National Central University, Taiwan
Yuxuan Pang, The University of Tokyo

Workshop 4

24 Oct. 15:05-16:35 Small Studio

Glycoinformatics

Coordinated by:
Kiyoko F. Aoki-Kinoshita, Soka University, Japan
Rene Ranzinger, CCRC, University of Georgia, USA
Issaku Yamada, The Noguchi Institute, Japan

Workshop Description:

The Glycoinformatics workshop will be held in an interactive manner, after some shortpresentations by software and database developers. The content will cover basic glycandrawing tools/software, glycan format converters, followed by more in-depth analyticaltools including GlycoMaple.

Benefits of the Workshop to attendees:

This Workshop will benefit researchers who would like to either (a) find information or references to glycan-related genes, proteins, lipids, lectins, pathways, diseases, etc. or (b) perform their own analysis on their data using the latest tools developed by the speakers, including machine-learning tools and Web tools for analyzing glycans and pathways, etc. After a set of invited talks by the developers of these databases and tools, the speakers can be directly asked questions regarding their data or tool during panel discussion. This will also be an opportunity for attendees to make requests for more data or tools that would be useful for their research; opportunities for new collaborations are possible.

Structure: Invited talks (demos), Panel Discussion, or hands-on workshop

Speakers:

Kiyoko F. Aoki-Kinoshita, Soka University, Japan
Rene Ranzinger, CCRC, University of Georgia, USA
Issaku Yamada, Noguchi Institute, Japan
Philip Toukach (online)
Thomas Luetteke (online)