WORKSHOP 1

"Exploring the new Ensembl data platform"

Date: September 14, 2026

Start Time: 09:30

End Time: 13:00

Room 1 (TBC)

Coordinated by:

Dr. Aleena Mushtaq, EMBL-EBI, United Kingdom

Description:

The Ensembl Genome Browser has been an indispensable tool in the field of genomics, aiding scientists around the world in their research for over 25 years. The Ensembl database provides visualisation and comprehensive analyses of integrated genomic data, including genes, variants, comparative genomics and gene regulation for almost 5000 eukaryotic and over 31000 prokaryotic genomes.

With the rapid growth of genomic data in the past decades, a new Ensembl data platform (https://beta.ensembl.org/) has been designed to provide a more robust and efficient platform. The new platform offers enhanced features, improved data visualisation, and a more intuitive user interface.

This three-hour workshop is an introduction to the new Ensembl platform which currently presents genomic features for almost 5000 species with a new user interface, including visualisation of genes and variants on the Human Pangenome Reference Consortium (HPRC) and the Darwin Tree of Life assemblies. Participants will have the opportunity to learn about the range of data and tools available, gain hands-on experience in navigating the new Ensembl website to retrieve and interpret data and think about how this data might be informative for their research. Importantly, participants will have the opportunity to engage with the Ensembl community and find sources of help and documentation.

Intended Audience

It is suitable for:

- beginners to practise retrieving genomic data, analysing variants and customising views for regions of interest and
- researchers to connect with Ensembl experts from EMBL-EBI to troubleshoot research challenges.

WORKSHOP 2

"Text to knowledge graph: unlocking science with semantic toolkits"

Date: September 14, 2026

Start Time: 13:30

End Time: 17:00

Room 1 (TBC)

Coordinated by:

Ms. Renu Kumari, BRIC- National Institute of Plant Genome Research (BRIC-NIPGR), India

Description

The rapid expansion of scientific literature across disciplines has made manual knowledge synthesis increasingly inefficient. Despite the availability of large corpora, much of the knowledge remains inaccessible for computational analysis due to unstructured text formats.

This tutorial addresses this challenge by introducing semantic toolkits for automated knowledge extraction from scientific publications. The session will cover:

- Retrieval of research articles from open-access repositories using pygetpapers
- Named entity recognition with docanalysis
- Linking extracted entities to trustworthy resources for example Wikidata
- Construction of simple knowledge graphs from extracted data
- Exporting interoperable, machine-readable outputs

The tutorial emphasizes semantics by demonstrating how structured vocabularies and standardized resources improve interoperability, discoverability, and reuse of scientific knowledge across domains.

Intended Audience

It is suitable for:

- beginners with basic programming knowledge and
- intermediate users interested in semantic technologies and ontology-based data integration.

WORKSHOP 3

"TA systems biology approach to building gene networks using single-cell RNA-seq data"

Date: September 14, 2026
Start Time: 09:30
End Time: 13:00
Room 2 (TBC)

Coordinated by:

Dr. Gokce Oguz), Agency for Science, Technology and Research, Singapore

Dr. Adaikalavan Ramasamy, Agency for Science, Technology and Research, Singapore

Description

Single-cell RNA sequencing (scRNA-seq) has entered a mature phase, with studies now routinely profiling millions of cells across diverse tissues and conditions. Yet most downstream analyses remain anchored to gene-by-gene differential expression testing which captures individual signals but missing the coordinated regulatory programs that drive biological phenotypes. This workshop addresses that gap by pairing foundational scRNA-seq analysis with a gene network-based framework for systems-level interpretation.

The first half covers the end-to-end scRNA-seq workflow: importing data from public repositories, quality control, preprocessing, and cell type annotation. The second half introduces high-dimensional weighted gene co-expression network analysis (hdWGCNA), which groups genes into co-expression modules reflecting coordinated biological activity. Participants will implement hdWGCNA on a real dataset, interpret the resulting networks, and understand why this approach offers a more biologically meaningful complement to standard differential expression analysis.

By the end of this half-day workshop, participants will be equipped to run a complete scRNA-seq pipeline and apply gene network methods to extract richer insight from their data. No prior single-cell experience is required, but familiarity with transcriptomics and sequencing concepts will be helpful. Hands-on exercises will be conducted in R; participants are strongly encouraged to have basic R familiarity.

Intended Audience

It is suitable for participants who are

- new to single-cell analysis, who will learn scRNA-seq pipeline and
- already familiar with single-cell methods, who will be introduced to a gene network-based framework that moves beyond standard differential expression testing.

WORKSHOP 4

"User-centered approaches for sustainable and impactful bioinformatics services"

Date: September 14, 2026
Start Time: 13:30
End Time: 17:00
Room 2 (TBC)

Coordinated by:
Patricia Carvajal-López, EMBL-EBI, United Kingdom

Description

This knowledge exchange workshop brings together members of bioinformatics service teams and infrastructures to learn from each other and from the experience of the European Bioinformatics Institute (EMBL-EBI) and Ensembl teams running next-generation web services. It is also intended for researchers, developers, and institutional representatives interested in improving the usability, accessibility, and sustainability of bioinformatics platforms within the Asia/Pacific region.

As biological data resources continue to expand in scale and complexity, web-based scientific services must evolve to better support diverse research communities and increasingly data-intensive workflows. User-centered design and user research are becoming essential components in the development of effective bioinformatics infrastructure, helping service providers better understand researcher needs, improve usability, and support efficient data exploration.

This workshop will provide participants with an opportunity to exchange experiences, discuss challenges and solutions, and explore practical approaches for integrating user research into the development of scientific web resources. Using the new Ensembl web browser as a case study, participants will gain insights into methodologies for gathering user feedback, identifying usability barriers, and translating community needs into platform improvements. Examples discussed during the workshop will draw from a range of biological data resources and use cases, including infectious disease research.

Although many of the principles discussed are broadly applicable across bioinformatics services, the workshop will also provide space to explore challenges and opportunities specific to the Asia/Pacific region, while initiating dialogue with the regional bioinformatics infrastructure and services community.

Intended Audience

Suitable for:

- bioinformatics service teams and infrastructure staff and
- researchers, developers, and institutional representatives interested in improving the usability, accessibility, and sustainability of bioinformatics platforms within the Asia/Pacific region.

WORKSHOP 5

"Computational Network Analysis of Omics Data"

Date: September 14, 2026

Start Time: 9:30

End Time: 13:00

Room 3 (TBC)

Coordinated by:

Ms. Pooja Singh, Jawaharlal Nehru University, India

Pushpender Singh Chandel, Jawaharlal Nehru University, India

Description

Recent years have seen rapid growth in biological data, posing significant challenges for data analysis and interpretation. Advanced computational approaches, such as deep learning and neural networks, have emerged as powerful tools for analyzing and extracting meaningful patterns from complex biological datasets. The AI-based methods mentioned above enable efficient analysis of multi-omics data (genomic, proteomic, and molecular interaction data), thereby improving prediction accuracy and the discovery of biological insights. Consequently, AI-driven models are transforming modern biomedical and bioinformatics research for precision medicine.

This hands-on workshop focuses on the comprehensive analysis of publicly available genomic data to derive novel molecular-level insights using artificial intelligence (AI)-driven approaches, guiding participants from raw data retrieval through to precision therapeutic target identification. Here, we employ advanced computational pipelines to systematically investigate NGS datasets, with a particular emphasis on identifying driver genes-key regulators that influence critical cellular processes and disease progression. By integrating AI-based methodologies, we aim to detect previously unrecognized patterns, reconstruct regulatory networks, and characterize functional pathways underlying complex biological systems.

Intended Audience

This tutorial is intended for:

- beginners seeking to bridge the gap between high-throughput data generation and actionable biological interpretation, advancing both biomedical research and the development of personalized therapeutic strategies.