

Pre-conference workshops



Sunday, June 7th, 2026 | 09:00 – 10:30 | Track A

From Discovery to Manufacturing: Strategies for Scalable, Efficient Biologics Production

Organized by: The Advanced Cell Technology Industrial Platform (ACTIP)

What to expect:

ACTIP, an independent non-profit association of European companies and institutions, is committed to advancing the industrial application of cell technologies for biopharmaceuticals, vaccines, and other therapeutic solutions. This workshop brings together ACTIP experts to share practical insights from the complex journey of transforming discovery into robust, scalable manufacturing processes. Manufacturers today face increasing pressure to accelerate timelines, reduce costs, and deliver high-quality biologics in a rapidly evolving market. Key strategies—such as cell line development, process intensification, advanced data analytics, and automation—are essential to optimize efficiency and ensure flexibility. Addressing challenges like pipeline heterogeneity and achieving sufficient titres for a viable business case requires innovative approaches and collaboration.

Join us for an interactive session where leading industry experts and ACTIP members will discuss how to streamline workflows, leverage artificial intelligence (AI), and apply analytical strategies to create well-characterized biologics. Learn how to save time, maximize titres, and simplify operations to build processes that meet the demands of modern biologics production.

Workshop moderators: Jochen Sieck, Merck Life Science & Andreas Castan, Cytiva

Draft agenda:

09:00-09:05	Welcome
09:05-09:20	Finding the right clone fast: CLD Platform optimization , <i>Katarzyna Sobkowiak, Merck Healthcare, Switzerland</i>
09:20-09:35	Automated computational fluid dynamics turns scale-down mimics into predictive tools for scale-up , <i>Peter Satzer, P4B, Austria</i>
09:35-09:50	GMP Drug Substance Manufacturing from Stable CHO Pools: A Far-Fetched Concept or The Future of Early Drug Development , <i>Simon Fischer, Boehringer Ingelheim, Germany</i>
09:50-10:05	Transforming biopharma process development and manufacturing with AI: from mAbs to advanced therapies , <i>Kevin Healy, DataHow, Switzerland</i>
10:05-10:20	From Data to Design: Using Omics Techniques and MVDA to Optimize Production of Biologics , <i>Sandra Klausung, Sartorius, Germany</i>
10:20-10:30	Plenary discussion & wrap up

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When is modeling in upstream process development useful?

Organized by: Moritz von Stosch, HINA Bioventures, London, UK; Madhuresh Sumit, Sanofi

What to expect:

The seemingly "sudden" progress in AI has spiked a lot of curiosity in AI applications, especially also for cell culture. Questions like: "Can we develop a model of the process? Can we predict the evolution? What would happen if...?" are now common. While interesting from a scientific perspective, these kinds of questions/applications rarely deliver value in terms of increased understanding, reduction in experiments, costs or risk. In this workshop, we propose a framework that supports the design of modeling (including machine-learning) applications such that they deliver value. Together with the participants we want to explore how modeling can be useful in cell line screening, process optimization, scale-up or process characterization. Three workstreams will run in parallel, one for CHO, gene therapy and cell therapy. Upon the discussion real use cases will be shared.

Agenda:

- Introduction to modeling & model application design framework (30 min)
- Hands-on application of framework on typical process development activities (45 min)
- Summary and Examples of case studies (15 min)

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CHO transcriptome compendium – Its uses and practical exercises on CHO transcriptome

Organized by: Meiyappan Lakshmanan

Speakers: Meiyappan Lakshmanan, Indian Institute of Technology Madras, India; Markus Riedl, BOKU Vienna, Austria; Meera Alagu Sundari P.M., Indian Institute of Technology Madras, India

What to expect:

We have recently developed a comprehensive Chinese Hamster transcriptome data set by pooling the list of available RNA-seq data from public repositories Sequence Read Archive (SRA) and European Nucleotide Archive (ENA). We focused on studies which either used Chinese Hamster tissues or different CHO cell lines grown in a vast array of conditions and shortlisted 23 unique Bio projects. Note that we also included the RNA-seq data available from in-house Chinese Hamster tissue samples. The compendium has a total of 352 RNA-seq samples from 24 different studies, comprising of 8 Hamster tissues (brain, kidney, liver, lung, muscle, ovary, pancreas and spleen) and 4 different CHO cell lines (CHO-DG44, CHO-DXB11, CHO-K1 and CHO-S) from 2 and 22 different studies, respectively. It should be noted that the CHO cell lines either express a recombinant protein such as mAb or just the parental cell lines grown in a variety of conditions such as adherent and suspension cultures in batch or fed-batch with various serum-containing or serum-free media.

In this workshop, we will present how we uniformly processed this data and used the CHO transcriptome compendium to analyze the gene expression variations between CHO cell lines and hamster tissues and uncovered the potential impact of immortalization on gene expression. Further, we compared the gene expression profile of different CHO cell lines with selected hamster tissues having active secretion mechanisms. The findings of this study will provide important insights for future research involving a comprehensive understanding of CHO cells' transcriptome and multi-omic analysis. In the workshop, if time permits, we will also cover the basics of transcriptome profiling experimental considerations and the fundamentals of transcriptome data analysis.

Going Continuous: Digital Tools in Modern Bioprocessing

Organized by: Wolfgang Sommeregger, QUBICON AG, Vienna, Austria

Speakers: Mark Duerkop, Novasign GmbH, Vienna, Austria; Christian Witz, SimVantage GmbH, Graz, Austria; Wolfgang Sommeregger, QUBICON AG, Vienna, Austria

What to expect:

This workshop explores how digitalization is transforming the design, development, and control of continuous bioprocesses. Although continuous manufacturing has achieved significant technological progress, only a limited number of approved biopharmaceutical products are currently produced using fully automated or end-to-end continuous processes. The session addresses this gap by examining the challenges that still limit broader implementation and by presenting concrete digital and modeling-based strategies to overcome them.

Central to the workshop is the role of integrated data infrastructures, advanced modeling approaches, and system-level process understanding in enabling robust and scalable continuous manufacturing. Participants will learn how tightly coupled unit operations introduce dynamic interactions that require new monitoring, control, and experimental design strategies.

Based on real-world use cases, the workshop will highlight innovative strategies for continuous upstream and downstream integration, including recent results from continuous lab-scale processes as well as an FDA-funded grant focused on understanding Residence Time Distribution (RTD) propagation across multiple unit operations in continuous bioprocessing.

Participants will gain practical insights into:

- Digitizing laboratory and pilot-scale continuous setups
- Integrating on- and offline data streams from diverse processing equipment and analytical tools
- Designing experimental plans for Quality by Design (QbD) learning in continuous processes
- Developing predictive models to visualize process behavior under varying operating conditions and autonomously control process behavior
- Applying simulation-based approaches to increase process understanding
- Use first-principal approaches to derisk scale-up and process control

The workshop demonstrates how combining mechanistic modeling, data-driven methods, and simulation enables faster iteration cycles, improved process understanding, and predictive, in-silico optimization, moving continuous bioprocessing beyond trial-and-error approaches.

Agenda:

The workshop will combine short, focused expert presentations with interactive, audience-driven elements to encourage exchange. Interactive components will include live polling, discussions on practical implementation barriers, digital maturity, and regulatory considerations. The session will conclude with an open discussion and Q&A to address technical and strategic questions from participants.

IBioNe Lunch with workshop on community efforts to make bioprocessing data AI-ready and to facilitate digital twin development: the MIAYBE minimal Information standard & HEK genome-scale metabolic models

Organized by: *IBioNe, Mike Betenbaugh (JHU), Nicole Borth (BOKU), Nathan Lewis (UGA), Dong Yup Lee (SKKU)*

Speakers: Kimberly Robasky (UGA), Ana Nikolov (OAGI), Milos Drobnjakovic (OAGI), Meiyappan Lakshmanan (IITM), Dong Yup Lee (SKKU), Nathan Lewis (UGA)

Innovations in bioprocessing and data analytics are accelerating cell line development, cultivation and purification workflows. Computational models/tools and AI are key to these advancements in animal cell biomanufacturing. However, the data needed for such applications is in disarray, so we need community efforts to collect and clarify data for modeling and analysis. Here, we present community efforts to build data & modeling resources to help develop predictive digital twin models and AI-assistants for data analysis. Speakers will describe and seek community feedback on three major aims: (1) Minimum information standards to get data AI-ready, (2) NIIMBL-supported ontology efforts for annotating bioprocessing and cell line development data, and (3) community reconstruction of mammalian metabolic networks governing the synthesis of products such as AAV vectors.

First, to make bioprocess data AI-ready for bioprocess foundation models and ChatGPT-like, no-code tools for data analysis, we need FAIR data that are structured, contextualized, and reusable. Today, the essential mammalian cell culture data remain trapped in ELNs, PDFs, spreadsheets, legacy files, and disconnected instruments. Thus, the data are difficult to compare, integrate, or learn from, especially across labs. Thus, community data standards could turn these isolated experiments into a collective resource. We will speak about MIAYBE, a minimum information framework designed to capture the experimental context needed to interpret bioprocess outcomes. To facilitate this, AI agents are being developed to gather data for easy MIAYBE reporting, allowing one to record enough context to answer real science and engineering questions, accelerating cell line selection and process optimization.

Second, to enable automated data curation and structuring, ontologies are needed. These harmonize data and guide AI agents as they crawl through our data to gather and structure the data for easier use. Thus, we will describe BMIC, a bioprocessing data ontology being developed by OAGI.

Third, rAAV production is still hindered by major challenges, including inconsistent plasmid entry and degradation, as well as the accumulation of low-quality impurities (e.g., empty or truncated capsids). Genome-scale models (GEMs), combined with multi-omics data, provide a powerful means to uncover the cellular and metabolic bottlenecks underlying these limitations. To this end, we are coordinating and leading a community effort to establish GEM-driven strategies that can decipher the cross talk between the rAAV replication and HEK293 metabolism, identify metabolic engineering targets, and address media bottlenecks, ultimately improving both rAAV productivity and quality. To reconstruct the community HEK293 GEM, we are adopting the highly successful open-source framework previously used for CHO GEM development. This effort is (re-)uniting experts in systems biology, metabolic engineering, and bioprocessing to build a comprehensive HEK293 GEM. We will present this initiative, showing how the model can be rapidly reconstructed, curated, and validated using large datasets from multiple contributors, resulting in a consensus model with strong academic and industrial value.

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Faster, Smarter Cell Line Development through Multi-Omics Integration

Organized by: Luigi Grassi, AstraZeneca

Speakers: Luigi Grassi (AstraZeneca); Kasia Kozakowska-McDonnel (AstraZeneca); Kevin Ly (Wellcome Sanger Institute); Marie Moullet (Wellcome Sanger Institute)

What to expect:

This workshop explores how multi-omics and machine-learning approaches can accelerate and enhance cell line development. The first half presents the CLD process, sequencing and analytical assays, and examples of ML-powered biological modelling. The second half is an interactive discussion on integrating advanced modelling into decision-making — covering needs, benefits, challenges, and opportunities.

Agenda:

- Overview of the CLD process and high-throughput sequencing and analytical assays used to identify optimal cell lines for large-scale manufacturing (20 minutes — Kasia & Luigi).
- A crash course on in-silico cell models: how machine learning and computational biology can predict and explain cellular behavior (25 minutes — Kevin & Marie).
- Q&A and guided discussion on combining high-throughput assays with computational modelling to accelerate and improve clone selection (45 minutes — All speakers).

Sponsored by AstraZeneca

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Technology Presentations and Industrial Workshops

Details to follow.