SBML, SBGN & COMBINE Archives — Hands-on

Get hands-on with the core standards that power modern systems biology. This module focuses on SBML for model encodings, SBGN for pathway diagrams, and COMBINE Archives for packaging simulations, so that your models can be shared, reproduced and reused across tools and collaborators.

SBML, SBGN & COMBINE Archives

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Session Index

Session 1

Fee: Rs 8800 Apply Now

SBML Essentials: Species, Reactions & Parameters

SBML structure and core constructs (Level 2/3 view)

model, listOfSpecies, listOfReactions **compartments** **parameters and constants**

Encoding biochemical reactions in SBML

reactants, products and modifiers **mass action rate laws** **enzyme kinetics (Michaelis-Menten)**

First simulations with SBML friendly tools

COPASI basics **tellurium and libRoadRunner** **time**

course and steady state runs

Session 2

Fee: Rs 11800 Apply Now

Advanced SBML, Units, Rules & Events

Units, constraints and good modeling practice

unit definitions and consistency | constraints | dimension checks

Rules and events in SBML for complex behavior

assignment and rate rules | algebraic rules | events and conditional changes

Annotations and ontology links

MIRIAM style annotations | GO, ChEBI cross references | identifiers.org URIs

Session 3

Fee: Rs 14800 Apply Now

SBGN Diagrams & Visual Encodings

SBGN languages and when to use them

process description | entity relationship | activity flow

Creating SBGN diagrams from pathways

glyphs and arcs | layout principles | mapping to SBML structures

Tooling for SBGN and SBML integration

SBGN-ED and related editors | importing SBML to diagram tools | export for publications

Session 4

Fee: Rs 18800 Apply Now

COMBINE Archives & FAIR Packaging

What goes inside a COMBINE Archive

Theory + Practical

Assembling SBML, SBGN and SED-ML into a single bundle

simulation descriptions (SED-ML) **linking models and diagrams** **metadata and manifest files**

FAIR oriented deliverables and submission readiness

checklists and validation **archiving for BioModels** **documentation and README files**