Advanced Computational Modeling of Biological Systems Training Course

Professional Development Training Course Outline

Category	Biotechnology and Pharmaceutical Development	**Duration**	10 Days
Base Fee	$4,000 USD	**Delivery Mode**	Online / On-site Hybrid

Course Introduction

This intensive, training course focused on **Computational Systems Biology** and **Multi-scale Biological Modeling**. The modern post-genomic era is defined by an explosion of **Big Data** in the life sciences, necessitating sophisticated **In Silico** approaches to translate raw biological information into actionable knowledge. This course transcends traditional bioinformatics, concentrating on the development and application of dynamic, predictive **Mathematical Models** to simulate complex living systems, from molecular interactions to whole-organism physiology. Participants will master **High-Performance Computing (HPC)** and **Machine Learning for Biology** to drive **Precision Medicine** and accelerate **Drug Discovery**, equipping them with the cutting-edge, interdisciplinary skills required to be leaders in **Quantitative Biology** and **AI in Healthcare**. Advanced Computational Modeling of Biological Systems Training Course is specifically designed for professionals and researchers aiming to tackle the most challenging problems in **Biotechnology** and **Bio-Pharmaceutical R&D**.

The program provides a deep dive into advanced **Algorithm Development** and **Scientific Computing** techniques, using powerful programming environments like **Python** and **Julia** for creating robust, validated models. By focusing on both **Deterministic** and **Stochastic Modeling**, the course covers diverse biological scales, including detailed **Kinetic Modeling** of metabolic pathways, **Network Biology** analysis, and **Spatio-Temporal Modeling** of cell behavior. A core emphasis is placed on **Model Validation** against real-world **Multi-Omics** data, ensuring the practical utility and reliability of the computational frameworks developed. Through hands-on **Case Studies** in areas like infectious disease prediction and **Cancer Modeling**, attendees will gain proficiency in building next-generation **Digital Twins** of biological processes, essential for in silico experimentation, **Hypothesis Generation**, and informing experimental design in high-stakes scientific and industrial settings.

Programme Curriculum

Advanced Computational Modeling of Biological Systems Training Course

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Course Duration

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Course Objectives

1. Master Computational Systems Biology frameworks for Multi-Scale Modeling.
2. Develop and implement advanced Kinetic Modeling and Parameter Estimation techniques.
3. Design and analyze complex Biological Network Models
4. Apply High-Performance Computing (HPC) for large-scale Biological Simulations.
5. Utilize Machine Learning (ML) for Genomics and Proteomics data integration.
6. Construct and validate Digital Twin models for Precision Medicine applications.
7. Perform Stochastic Modeling for low-copy number and single-cell dynamics.
8. Implement Spatio-Temporal Modeling for cell and tissue systems.
9. Gain proficiency in Python for Scientific Computing
10. Integrate Multi-Omics Data into predictive models.
11. Develop and run models on Cloud Computing platforms for scalable biological analysis.
12. Conduct Sensitivity Analysis and Uncertainty Quantification for model reliability.
13. Apply computational models to accelerate Drug Target Identification and Bio-Pharmaceutical R&D.

Target Audience

1. Computational Biologists / Bioinformaticians

2. R&D Scientists in Pharma/Biotech.
3. Systems Biologists.
4. Data Scientists.
5. Graduate Students and Postdoctoral Researchers in Quantitative Biology and related fields.
6. Biomedical Engineers.
7. Software Engineers.
8. Principal Investigators and Research Managers.

Course Modules

Module 1: Foundations of Computational Systems Biology

- Defining the scope: Computational Systems Biology vs. Bioinformatics.
- Introduction to ODE (Ordinary Differential Equation) and PDE (Partial Differential Equation) modeling.
- Data types for modeling: Kinetic parameters, Multi-Omics inputs.
- Concepts of abstraction, scale, and coarse-graining in biology.
- Model parameter identification and Good Modeling Practice (GMP).
- Case Study: Modeling the dynamics of a simplified gene regulatory feedback loop.

Module 2: Deterministic Kinetic Modeling

- Developing mass-action and Michaelis-Menten rate laws.
- Numerical integration methods and stability analysis.
- Steady-state analysis and bifurcation diagrams.
- Software tools: COPASI, SBML, and Python libraries.
- Sensitivity Analysis to identify key control points.
- Case Study: Modeling drug response in a cell signaling pathway

Module 3: Stochastic Modeling and Noise

- Sources of Biological Noise
- Gillespie Algorithm.
- Chemical Langevin Equation (CLE) for approximation.
- Modeling low-copy number molecular events and single-cell variability.
- Comparing deterministic and stochastic outcomes.
- Case Study: Simulating protein expression variability due to burst transcription.

Module 4: Network Biology and Pathway Analysis

- Graph theory basics for biological networks.
- Constraint-Based Modeling for metabolism.
- Topological analysis of biological networks.
- Pathway inference and reconstruction from Genomics Data.
- Dynamic analysis of network robustness and fragility.
- Case Study: Predicting metabolic engineering strategies using FBA in a microbial system.

Module 5: Spatio-Temporal Modeling (Cellular Scale)

- Introduction to Reaction-Diffusion systems (PDEs).
- Agent-Based Modeling (ABM) for cell-cell interactions.
- Modeling morphogenesis, cell migration, and tissue organization.
- Numerical methods for solving PDEs

- Application to modeling tumor microenvironments.
- Case Study: Simulating collective cell migration during wound healing using an ABM approach.

Module 6: Advanced Numerical Methods and HPC

- Numerical stability and convergence for stiff ODEs.
- Introduction to parallel computing for massive simulations.
- Optimization techniques for high-dimensional parameter spaces.
- Efficient implementation of algorithms in Julia or optimized Python.
- Managing and visualizing large-scale simulation output.
- Case Study: Speeding up Monte Carlo simulations for a large protein interaction network using parallelization.

Module 7: Machine Learning for Model Parameterization

- Using ML to infer parameters from noisy data.
- Bayesian Inference and Markov Chain Monte Carlo (MCMC) methods.
- Deep Learning for automated feature extraction from Image Data.
- Reinforcement Learning for optimizing biological control systems.
- Model order reduction techniques
- Case Study: Parameterizing an inflammatory response model using high-throughput experimental data and MCMC.

Module 8: Multi-Omics Data Integration

- Strategies for unifying Genomics, Proteomics, Metabolomics data.
- Data normalization, quality control, and batch effect correction.
- Top-down vs. bottom-up modeling strategies.
- Developing Data-Driven Models and hybrid approaches.
- Visualization of multi-layered biological information.
- Case Study: Integrating transcriptomic and metabolomic data to refine a whole-cell metabolic model.

Module 9: Model Validation and Uncertainty Quantification

- Cross-validation and model comparison metrics.
- Techniques for robust Model Validation against unseen experimental data.
- Quantifying model output Uncertainty
- Methods for model rejection and refinement.
- Best practices for reproducible research and model sharing.
- Case Study: Validating a cardiac cell model's prediction of drug-induced changes in action potential duration.

Module 10: Digital Twins and Personalized Medicine

- Conceptual framework of the Biological Digital Twin.
- Creating patient-specific models using individual Genomic and clinical data.
- Applications in predicting individual drug response and disease progression.
- Challenges in real-time data assimilation for Digital Twins.
- Ethical and regulatory considerations.
- Case Study: Building a personalized patient model to predict optimal chemotherapy dosage for a cancer patient.

Module 11: Computational Drug Discovery and Target ID

- Modeling drug-target binding kinetics and Pharmacodynamics (PD).
- Simulating the effects of perturbation on Biological Networks.
- High-throughput In Silico Screening strategies.
- Predicting Off-Target Effects and drug toxicity using whole-system models.
- Integrating Structural Biology with Systems Models.
- Case Study: Identifying novel drug targets in a bacterial resistance pathway using FBA and dynamic modeling.

Module 12: Cancer Modeling and Therapy Optimization

- Modeling tumor growth dynamics and heterogeneity.
- Spatio-temporal models of angiogenesis and metastasis.
- Simulating the tumor-immune microenvironment.
- Optimal control theory for personalized Combination Therapy.
- Predicting resistance mechanisms to targeted treatments.
- Case Study: Optimizing the timing and dosage of a combination immunotherapy and chemotherapy based on model predictions.

Module 13: Infectious Disease and Epidemiological Modeling

- SIR/SEIR Models for population-level dynamics.
- Agent-Based Models for disease spread in heterogeneous populations.
- Modeling pathogen-host interactions and immune response.
- Integrating Genomic Epidemiology into predictive models.
- Forecasting outbreak progression and evaluating intervention strategies.
- Case Study: Using a computational model to evaluate the impact of different vaccine rollout strategies on an emerging infectious disease.

Module 14: Protein and Macromolecular Modeling

- Modeling protein-protein interaction (PPI) networks.
- Fundamentals of Molecular Dynamics (MD) and Coarse-Grained MD.
- Integrating MD insights into larger systems models.
- Predicting allosteric regulation and conformational changes.
- Modeling protein stability and misfolding diseases.
- Case Study: Using Coarse-Grained MD simulations to study the assembly of a viral capsid or protein complex.

Module 15: Scientific Computing and Deployment

- Developing reusable, modular, and version-controlled model code (Git).
- Containerization for reproducibility
- Executing models on Cloud Computing platforms
- Creating user-friendly web interfaces for models
- Ethical computing and data security in biological modeling.
- Case Study: Deploying a metabolic model as a reproducible, containerized web service for collaborative use.

Training Methodology

The training adopts a highly **Interactive and Hands-on** methodology, ensuring deep practical skill acquisition.

1. Lecture & Theory.
2. Coding Workshops.
3. Real-World Case Studies.
4. Group Modeling Project.
5. Expert Q&A/Mentoring.
6. Flipped Classroom Elements.

Register as a group from 3 participants for a Discount

Send us an email: info@fineskilltrainingcenter.org or call +254769199797

Certification

Upon successful completion of this training, participants will be issued with a globally- recognized certificate.

Tailor-Made Course

We also offer tailor-made courses based on your needs.

Key Notes

a. The participant must be conversant with English.

b. Upon completion of training the participant will be issued with an Authorized Training Certificate

c. Course duration is flexible and the contents can be modified to fit any number of days.

d. The course fee includes facilitation training materials, 2 coffee breaks, buffet lunch and A Certificate upon successful completion of Training.

e. One-year post-training support Consultation and Coaching provided after the course.

f. Payment should be done at least a week before commence of the training, to Fineskill Training Center account, as indicated in the invoice so as to enable us prepare better for you.

Upcoming Scheduled Sessions

Start Date	End Date	Location	Price
23 Nov 2026	04 Dec 2026	Online	$2,000
23 Nov 2026	04 Dec 2026	Physical	$3,000
23 Nov 2026	04 Dec 2026	Physical	$6,000
23 Nov 2026	04 Dec 2026	Physical	$6,000

Start Date	End Date	Location	Price
23 Nov 2026	04 Dec 2026	Physical	$12,000
23 Nov 2026	04 Dec 2026	Physical	$9,000
23 Nov 2026	04 Dec 2026	Physical	$12,000
23 Nov 2026	04 Dec 2026	Physical	$12,000

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