



33rd CONFERENCE ON

Intelligent Systems  
for Molecular  
Biology

DATES: July 20

AND THE 24th

European Conference  
on Computational  
Biology



# Quantum Machine Learning for multi-omics analysis

Session	Topic	Type	Time
I	Welcome Remarks and Introduction	Q&A	9 – 9:20 AM
	Quantum computing fundamentals with Qiskit	Hands-on	9:20 – 10 AM
	Current state of Quantum Machine Learning	Lecture	10 – 10:45 AM
Coffee Break			10:45 – 11 AM
II	Data and Complexity measures	Lecture	11 – 11:30 AM
	Quantum Kernel methods	Lecture	11:30 – 12 PM
	Applying a Quantum-Classical machine learning benchmarking tool on omics data	Lecture + Hands-on	12 – 1 PM
Lunch break			1 – 2 PM
III	Implementing Quantum Kernel methods	Hands-on	2 – 3 PM
	Execute the benchmarking tool on omics data	Hands-on	3 – 4 PM
Coffee break			4 – 4:15 PM
IV	Review results from the benchmarking tool	Hands-on	4:15 – 5:15 PM
	Result Read-outs	Q&A	5:15 – 5:45 PM
	Future Directions & Concluding Remarks	Lecture	5:45 – 6 PM



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## Know your Hosts



Aritra Bose, PhD  
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## Learning Outcomes

- Understanding the fundamentals of quantum computing, including learning how to implement algorithms in a quantum computer with quantum gates and circuits using Qiskit.
- Practical experience of pre-processing multi-omics data and preparing it for a quantum hardware experiment.
- Gain experience on quantum algorithms for learning problems.
- Analyze machine learning methods on multi-omics data, understand their shortcomings and review the impact of data complexity measures on ML models.
- How to apply QML models on multi-omics data.
- Learn design of experiments for biomedical data using quantum computers by gaining an in-depth knowledge of quantum-classical hybrid workflows.
- Understand when to apply QML models and benchmark it with classical ML models.



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## Tutorial Materials

- All tutorial materials are available here:  
[https://github.com/IBM/qml4omics/tree/Tutorial\\_ISMB25](https://github.com/IBM/qml4omics/tree/Tutorial_ISMB25)
- Datasets used in this tutorial are available in the data directory. It contains a Melanoma Minimal Residual Disease dataset with single-cell transcriptomic data and a Breast Cancer multi-omics data containing DNA methylation and transcriptomic data.
- You can find each session's materials in the designated directory in the repo.