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ISMB Tutorial #4 Quantum-enabled multi-omics analysis

Organized by

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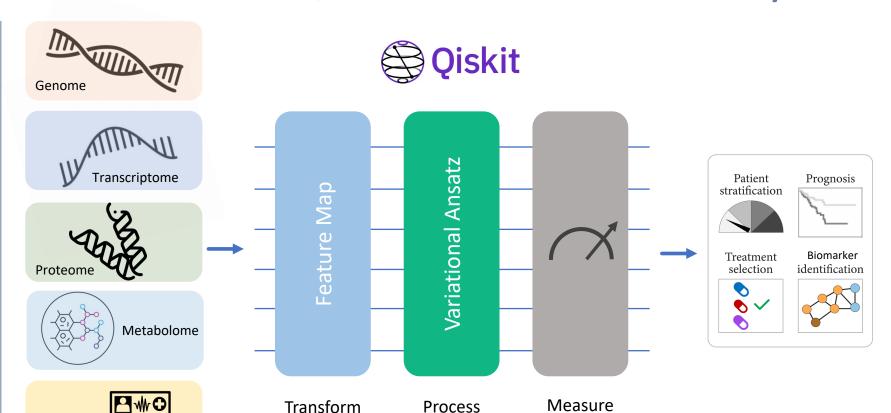
Multi-omics

Intelligent Systems For Molecular Biology Date: July 12, 2024

Palais des congrès de Montréal



Tutorial IP4: Quantum-enabled multi-omics analysis



Data

Data

Output

Organizers



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Phenome

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Quantum-enabled multi-omics analysis



FRIDAY, JULY 12, 2024 9 AM – 6 PM EDT



HTTPS://WWW.ISCB.ORG/ISMB20
24/PROGRAMMESCHEDULE/TUTORIALS#IP4



PALAIS DES CONGRÈS DE MONTRÉAL

Session Plan

Time	Session	Title
0900 - 1000	I	Quantum Information & Fundamentals
1000-1045	1	IBM Quantum setup & Introduction to Qiskit
1045-1100	-	Coffee Break
1100-1200	Ш	Introduction to Quantum circuits
1200-1300	II	Variational Quantum Algorithms & Machine Learning
1300-1400	-	Lunch
1400-1430	III	Single-cell RNAseq Data & Classical Machine Learning
1430-1600	III	Quantum Machine Learning concepts and applications in single-cell RNAseq data.
1600-1615	-	Coffee Break
1615-1700	IV	Design and Implementation of Quantum Machine Learning in single-cell RNAseq data.
1700-1800	V	Interactive Q&A

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Learning Outcomes

Participants in this tutorial will learn a new paradigm of analyzing multi-omics data with hands on experience with a quantum computer. More objectively, the major takeaways of this tutorial would be:

- Understand the basics of quantum computing including hands-on experience on quantum gates and circuits using Qiskit.
- Identify the nature of problems that are best suitable for current quantum systems.
- Process single-cell multi-omics data to a quantum computer in form of a circuit and execute it.
- How to apply quantum machine learning algorithms on single-cell multi-omics data.
- How to design experiments using quantum computers.

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Tutorial materials

- All tutorial materials are available here: https://github.com/IBM/QMLOmics
- 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.
- The first dataset is considered as an example dataset in Session III. The second one is used for the exercise in Session IV.
- You can find each session's materials in the designated directory in the repo.