



Quantum Innovation Challenge



THE UNIVERSITY
of EDINBURGH



IMPERIAL



QuSOP: a quantum learning–optimisation framework for robust dose selection in early clinical development

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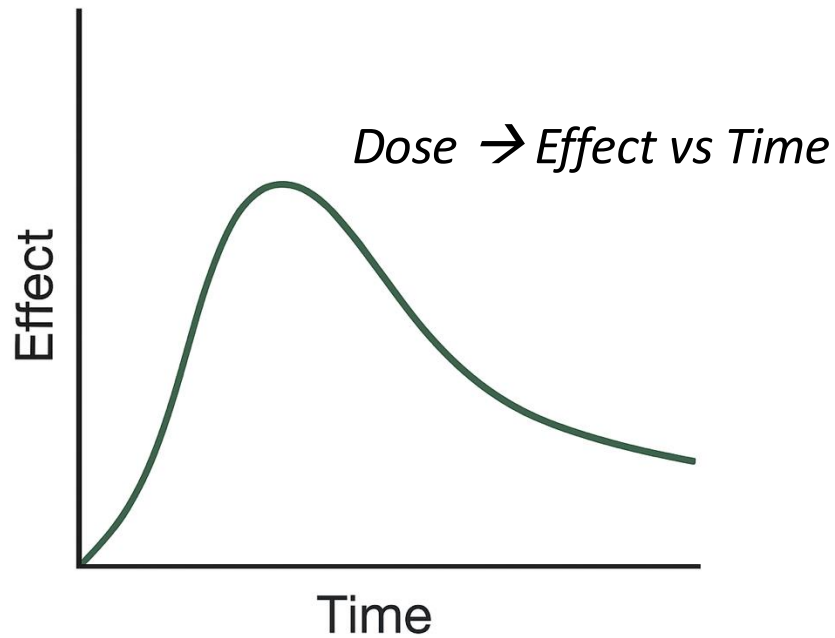


Outline

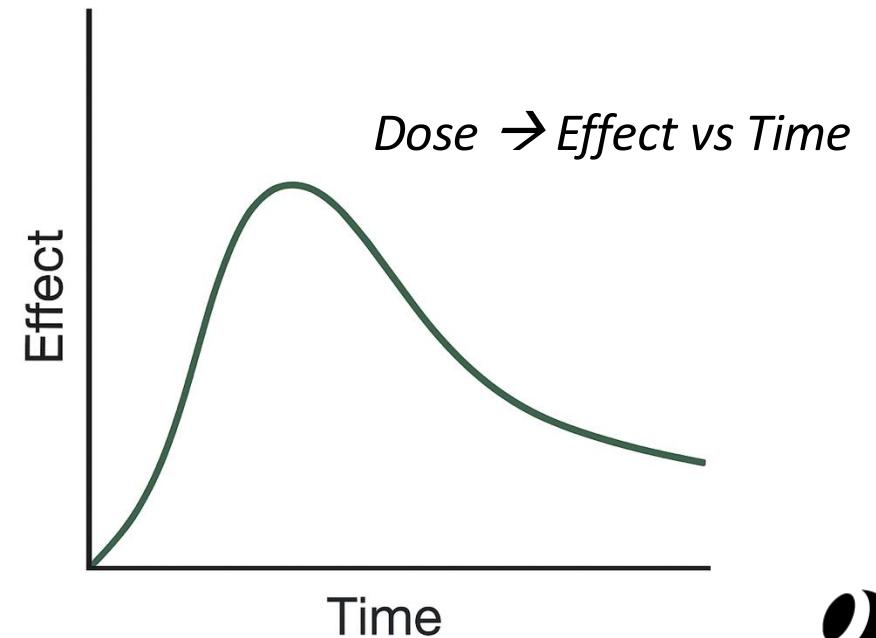
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PK/PD models: key tool in accelerating drug development

- Utilizes preclinical and clinical pharmacokinetic and pharmacodynamic data to model exposure-response of drug in target disease
- Validated PK/PD models developed in early clinical trials can reduce doses evaluated in late-stage clinical trials, reducing costs and timelines



Preclinical animal studies



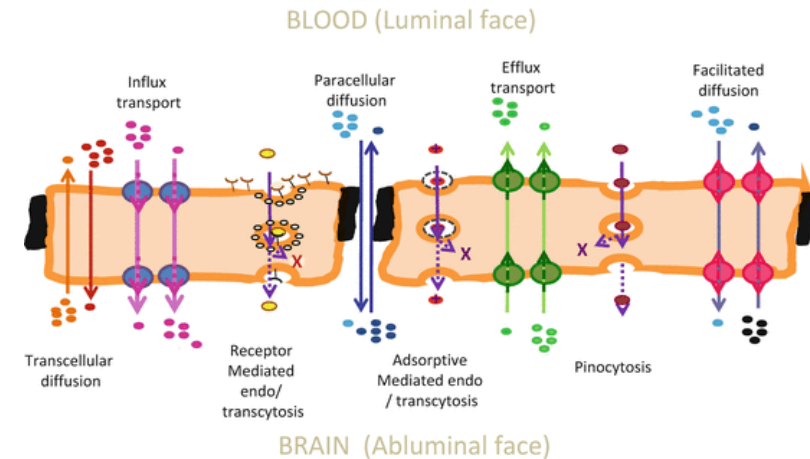
Clinical trials

Introduction and Problem Statement

1. How to accurately extrapolate to sub-populations?



2. How to describe non-linear biological processes?



From de Lange (2013)

- ML/AI approaches suffer from lack of data validation; sparse, unreliable data
- How can Quantum Computing address data limitations?
 - Propagate uncertainty as population-level attainment probabilities
 - Efficiently embed biological information from heterogenous, sparse data

Problem statement & Classical Monte Carlo

We would like to estimate the **probability of clinical success** $p(d)$ for a given **dose** d over the **discretised time window** for a **patient** $\zeta \sim P$.

$$p(d) = \mathbb{P}_{\zeta \sim P}(\mathcal{S}(d, \zeta)) \quad \text{where} \quad \mathcal{S}(d, \zeta) = \left\{ \max_{t \in \mathcal{G}_{\text{qd}}} \hat{y}(t; d, \zeta) \leq \tau_{\text{PD}} \right\},$$

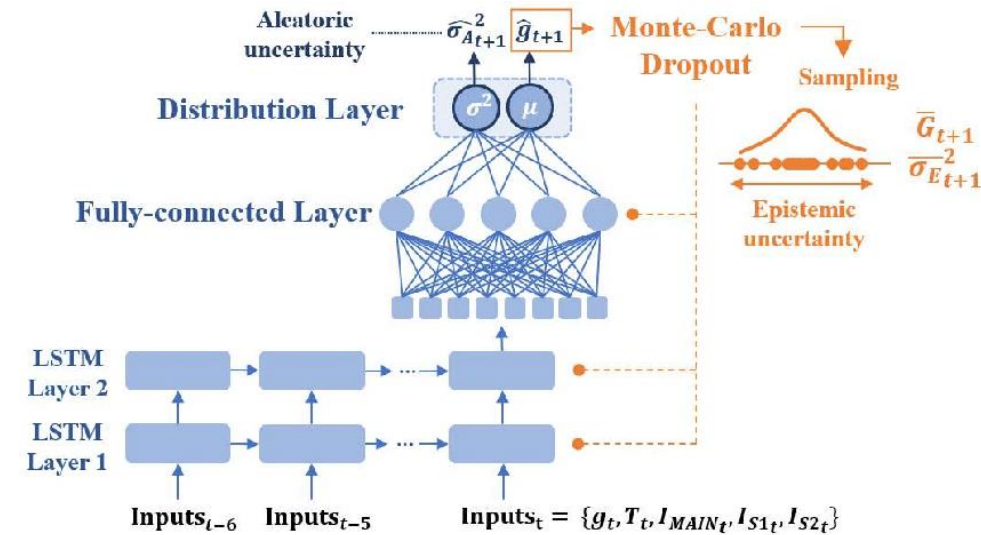
which indicates that for a dose d and a patient ζ , the **estimated biomarker path** $\hat{y}(t; d, \zeta)$ did not exceed the **safe dose** τ_{PD} .

Classical Monte Carlo is a computational method that uses **random sampling** to estimate quantities that cannot be computed analytically.

- Given i.i.d. draws $\zeta^{(1)}, \dots, \zeta^{(M)} \sim P$, the unbiased estimator of success at dose d is

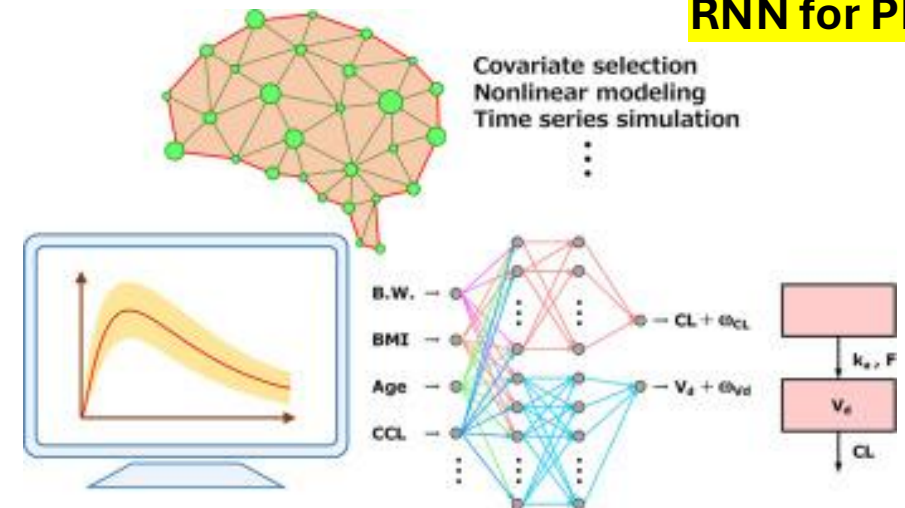
$$\hat{p}_M(d) = \frac{1}{M} \sum_{m=1}^M \mathbf{1}\{\mathcal{S}(d, \zeta^{(m)})\}.$$

Probabilistic LSTM Model



Vien, et al. IWSHM 2021

RNN for PK-PD



Uno et al. Drug Meta. and Pharm. 56 (2024): 101004.

Classical vs. Quantum Monte Carlo estimator

To estimate $p(d)$ with **accuracy** ϵ , **Classical Monte Carlo** requires $O(\sigma^2/\epsilon^2)$ **samples**, where σ^2 is the **variance** of $\mathbb{1}_{S(d,\zeta)}$. This yields to a **Computational bottleneck**.

- Evaluate ~ 80 doses per grid
 - Each dose simulated on 10^3 – 10^4 virtual subjects
 - Hundreds of replicates for ± 2 – 3% confidence
 - Each trajectory spans 24 h or 168 h
- } **Total:**
80,000
trajectory
predictions

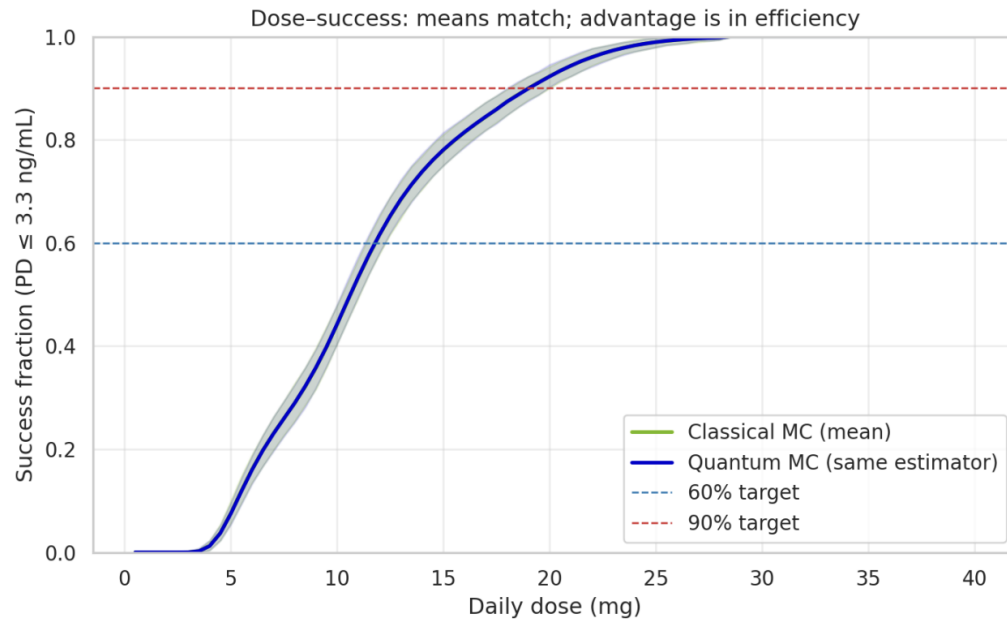
Quantum Monte Carlo: a quantum algorithm that provides a **quadratic speed-up** in the number of samples over classical MC.

- Relies on **Quantum Amplitude Estimation**.
- To estimate $p(d)$ with accuracy ϵ , one requires $O(\sigma/\epsilon)$ samples.

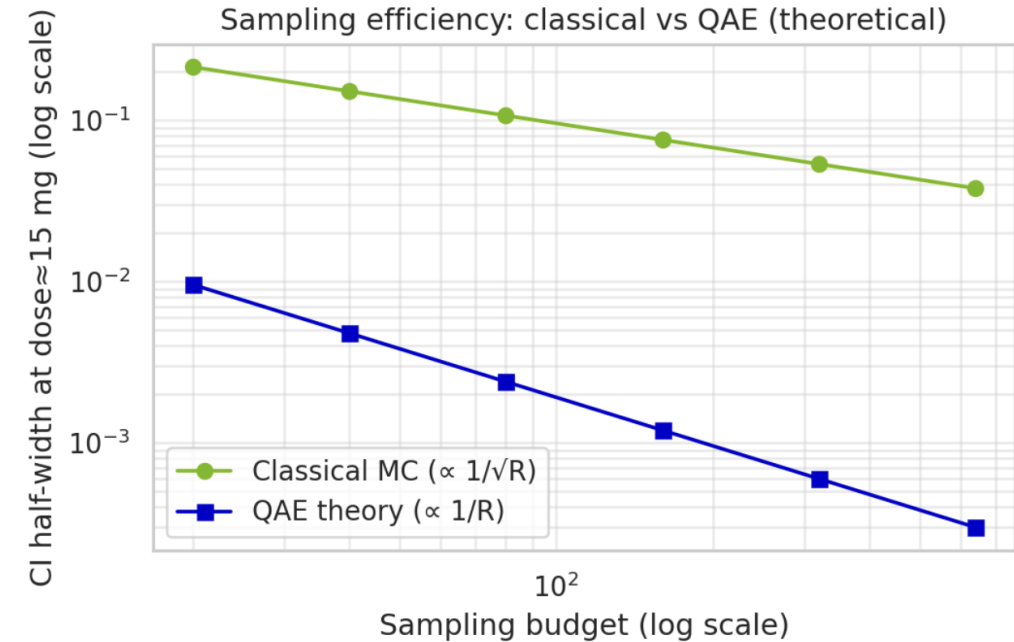
Quadratic speed-up in efficiency.



Classical vs. Quantum Monte Carlo results

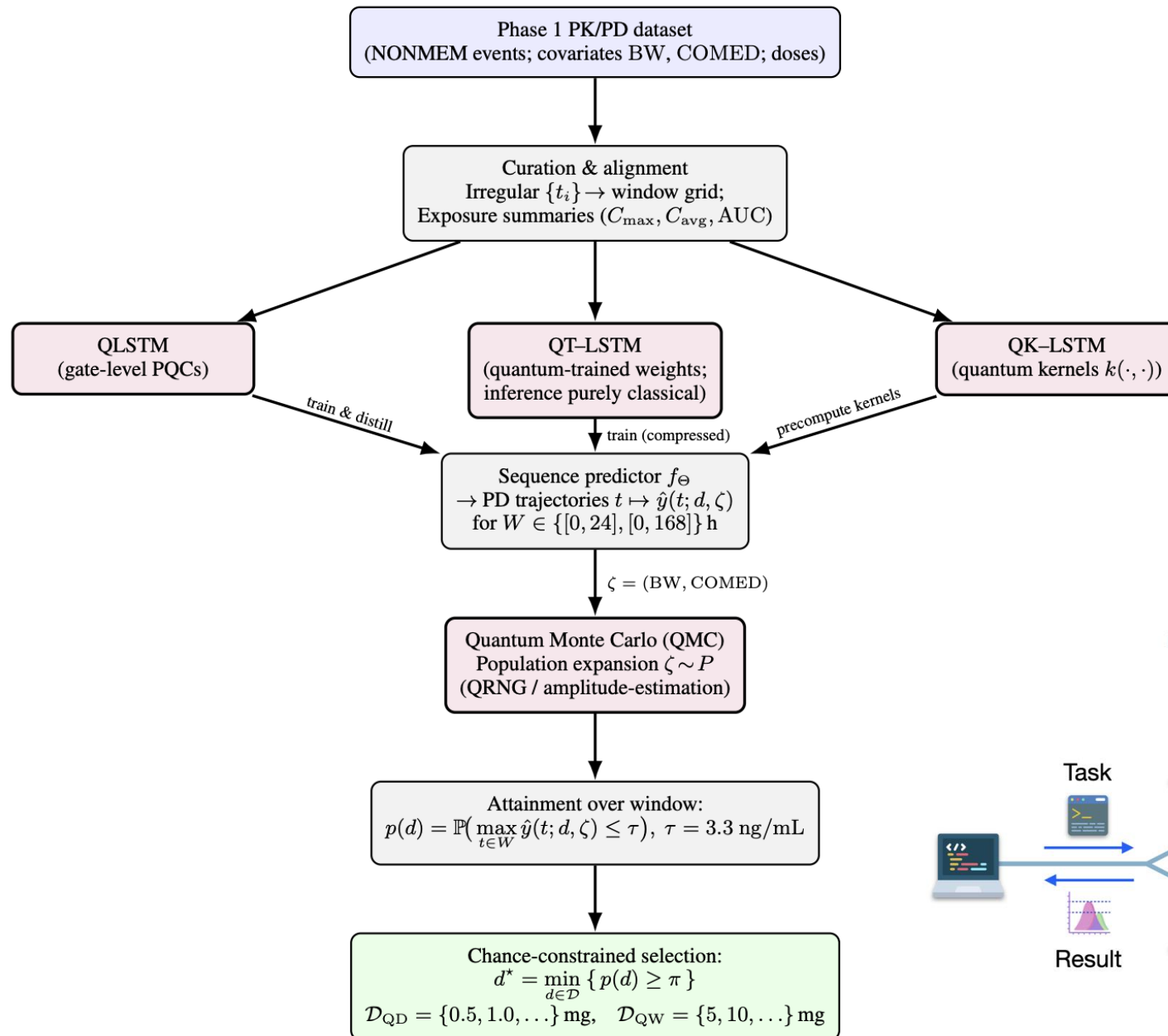


(a) Classical MC vs. quantum-augmented MC (QRNG): mean dose-success curves agree with Classical MC; efficiency gains stem from enhanced sampling (variance reduction) due to QMC.



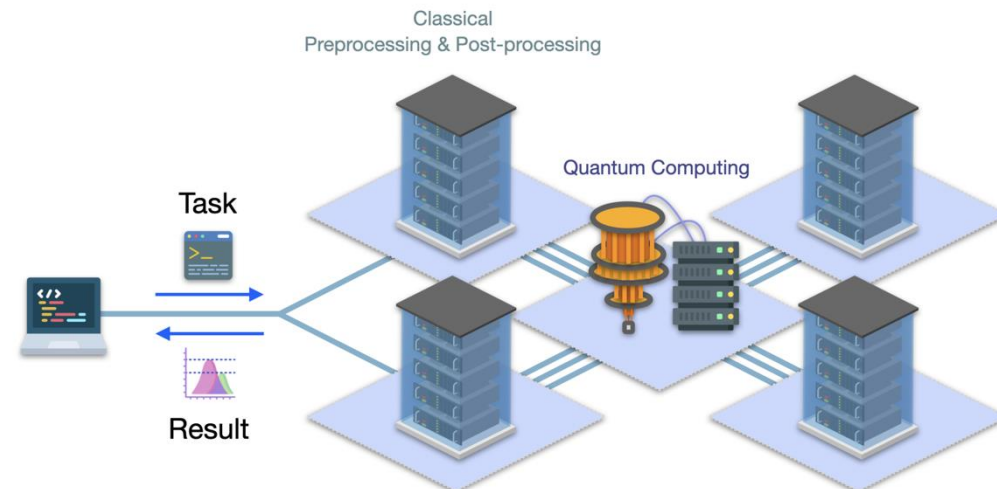
(b) Confidence-interval half-width versus sampling budget on a log-log scale. Classical MC exhibits $1/\sqrt{R}$ scaling; idealized QAE achieves $1/R$.

QuSOP framework

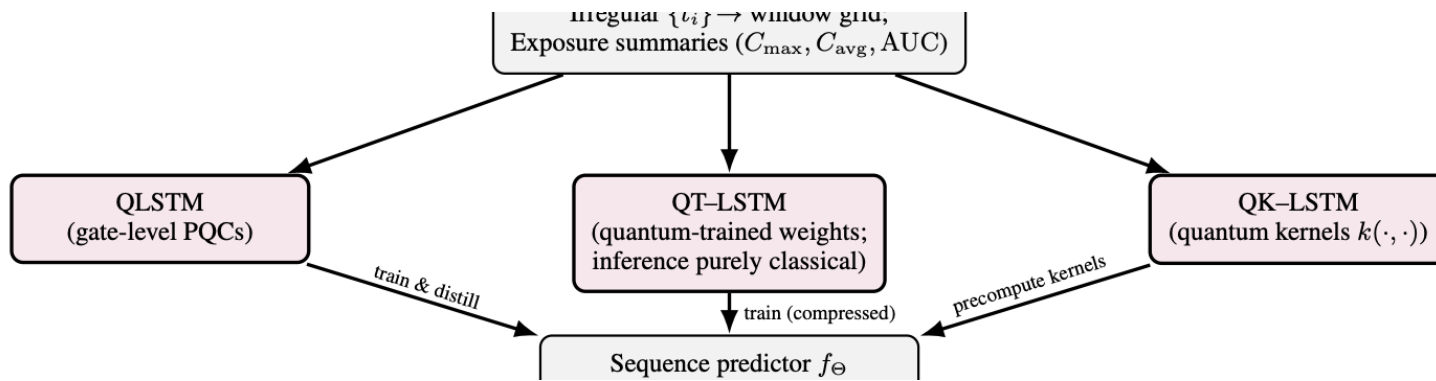


Legend

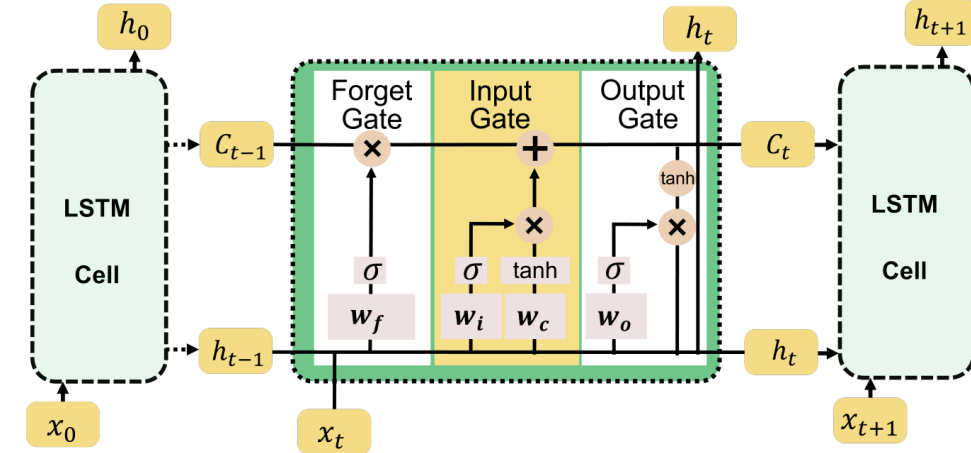
- Quantum modules (QLSTM, QT-LSTM, kernels, QMC)
- Classical preprocessing / inference
- Decision (dose policy)



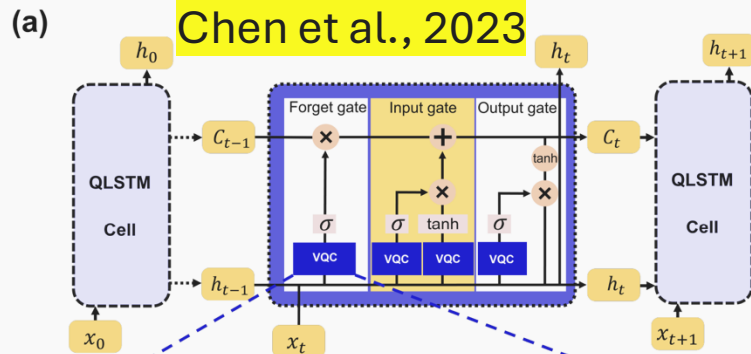
Quantum-Enhanced LSTM Model



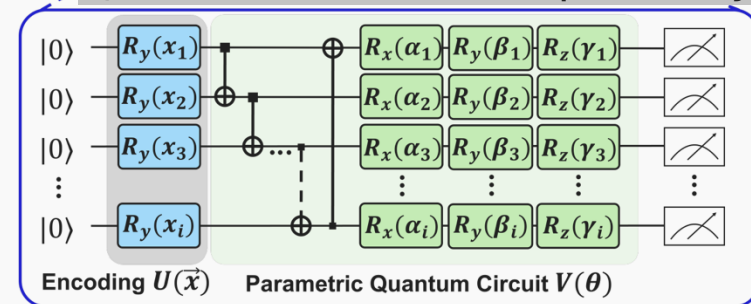
Classical LSTM Model



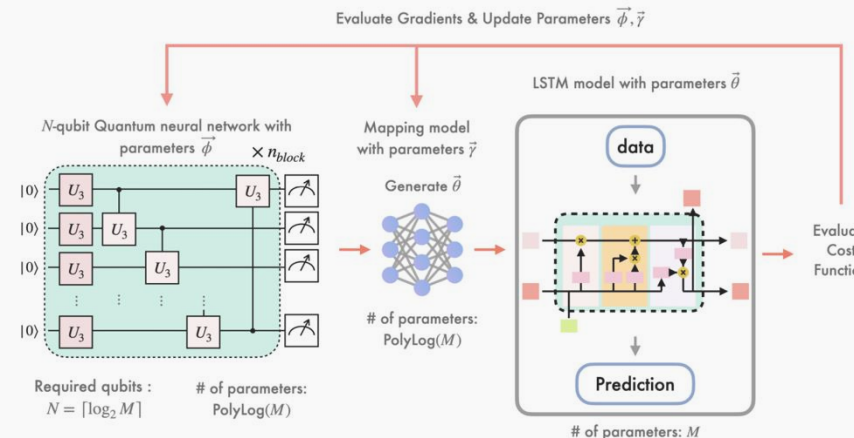
(1) QLSTM Model Chen et al., 2023



(b) Quantum-Enhanced Expressivity

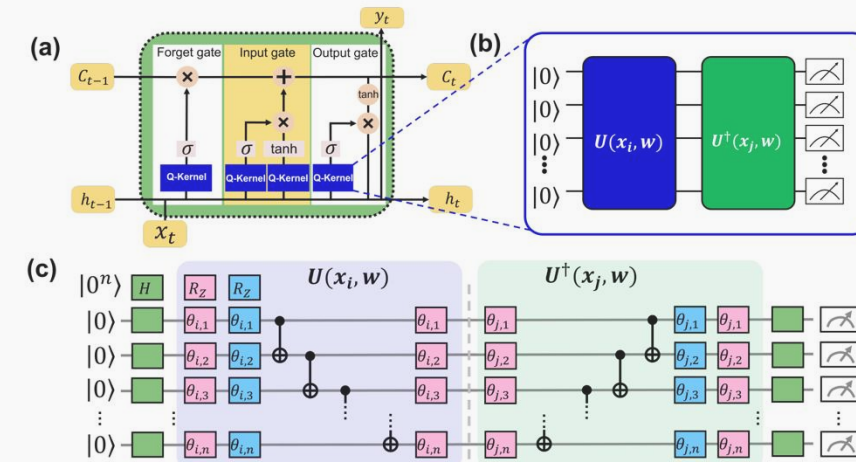


(2) QT-LSTM Model Chen et al., 2024



Quantum advantage in
space Complexity

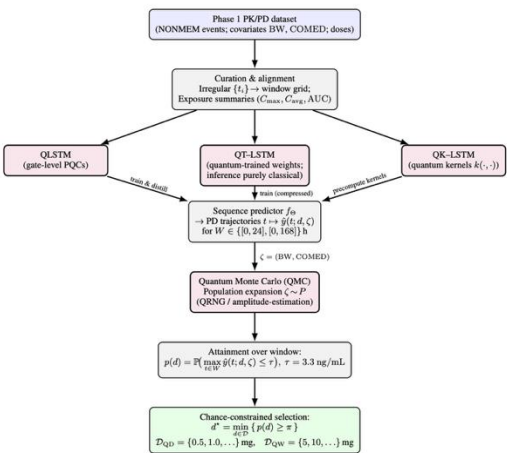
(3) QK-LSTM Model Chen et al., 2025



Hybrid deployable
architecture in Quantum-HPC

Current Result and Future Development

Decision Making Model
for pharmaceutical
companies:



Real-world and industrial level problems

What is the daily dose level (in whole multiples of 0.5 mg) that ensures that 90% of all subjects in a population similar to the one studied in the Phase 1 trial achieve suppression of the biomarker below a clinically relevant threshold (3.3 ng/mL) throughout a 24-hour dosing interval at steady state?

Which weekly dose level (in whole multiples of 5 mg) has the same effect over a 168-hour dosing interval at steady-state, if the compound was dosed once-weekly?

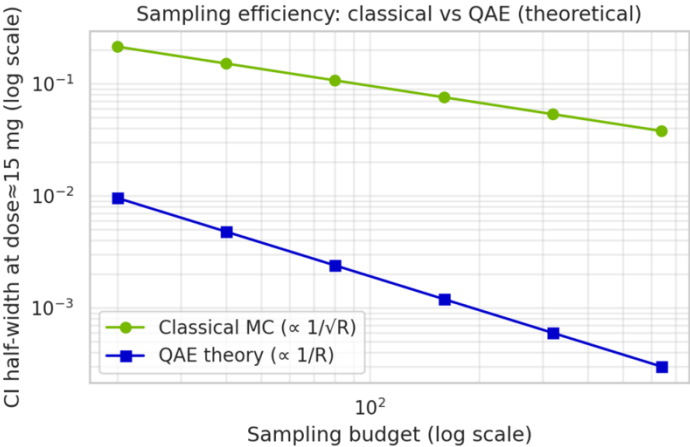
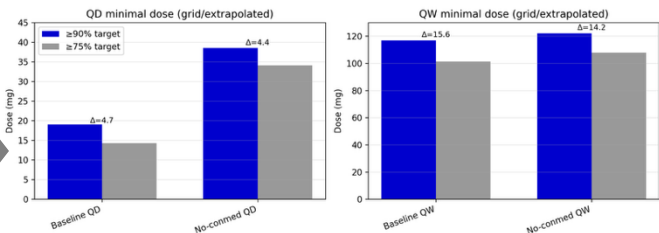
Suppose we change the body-weight distribution of the population to be treated to 70–140 kg, how does that affect the optimal once-daily and once-weekly doses?

Suppose we restrict that concomitant medication is not allowed. How does that affect the optimal once-daily and once-weekly doses?

How much lower would the optimal doses in the above scenarios be if we were to ensure that only 75% of all subjects achieve suppression of the biomarker below the clinically relevant threshold (3.3 ng/mL)

Industrial level solution

Scenario	Regimen	Dose at 90% (mg)	Dose at 75% (mg)	Reduction (mg / %)
Baseline QD	QD	19.0	14.3	4.7 / 25.0%
No-conm QD	QD	38.5	34.1	4.4 / 11.5%
Baseline QW	QW	116.9	101.3	15.6 / 13.4%
No-conm QW	QW	122.1	107.9	14.2 / 11.6%



powered by **CUDA-Q**

