Quantum approximated cloning-assisted density matrix exponentiation

Pablo Rodriguez-Grasa,[1,2,3] Ruben Ibarrondo,[1,2] Javier Gonzalez-Conde,[1,2] Yue Ban,[4] Patrick Rebentrost,[5] and Mikel Sanz[1,2,6,7]

[1]*Department of Physical Chemistry, University of the Basque Country UPV/EHU, Apartado 644, 48080 Bilbao, Spain*
[2]*EHU Quantum Center, University of the Basque Country UPV/EHU, Apartado 644, 48080 Bilbao, Spain*
[3]*TECNALIA, Basque Research and Technology Alliance (BRTA), 48160 Derio, Spain*
[4]*Departamento de Física, Universidad Carlos III de Madrid, Avda. de la Universidad 30, 28911 Leganés, Spain*
[5]*Centre for Quantum Technologies, National University of Singapore, Singapore 117543*
[6]*IKERBASQUE, Basque Foundation for Science, Plaza Euskadi 5, 48009, Bilbao, Spain*
[7]*Basque Center for Applied Mathematics (BCAM), Alameda de Mazarredo, 14, 48009 Bilbao, Spain*

ABSTRACT

Classical information loading is an essential task for many processing quantum algorithms, constituting a cornerstone in the field of quantum machine learning. In particular, the embedding techniques based on Hamiltonian simulation techniques enable the loading of matrices into quantum computers. A representative example of these methods is the Lloyd-Mohseni-Rebentrost protocol, which efficiently implements matrix exponentiation when multiple copies of a quantum state are available. However, this is a quite ideal set up, and in a realistic scenario, the copies are limited and the non-cloning theorem prevents from producing more exact copies in order to increase the accuracy of the protocol. Here, we propose a method to circumvent this limitation by introducing imperfect quantum copies that significantly enhance the performance of previous proposals. This abstract is based on Ref. [1].

The LMR protocol, introduced in Ref. [2], serves as the foundation for numerous fault-tolerant quantum machine learning algorithms [3–5] and is also significant for efficient Hamiltonian simulation [6]. Given n copies of a quantum state ρ, this protocol strives to implement the complex exponentiation of the quantum state ρ, acting on a quantum state σ for a time t, i.e. $e^{-i\rho t}\,\sigma\,e^{i\rho t}$. Each step of this methodology uses a single copy of ρ and implements an operation on the state of the system σ described by the quantum channel

$$T_{\mathrm{LMR}}(\sigma) = \mathrm{tr}_2[e^{-i\Delta t S}\,(\sigma\otimes\rho)\,e^{i\Delta t S}] = \cos^2\Delta t\,\sigma + \sin^2\Delta t\,\rho - i\,\sin\Delta t\,\cos\Delta t\,[\rho,\sigma]. \tag{1}$$

Therefore, using this operation n times and taking $\Delta t = t/n$ we can implement the target operation with error

$$\varepsilon_{\mathrm{LMR}(n)} = \left\|T^n_{\mathrm{LMR}}(\sigma) - e^{-i\rho t}\,\sigma\,e^{i\rho t}\right\|_1 = \frac{t^2}{2n}\left\|\,[\rho,\ \sigma]_2 + 2(\rho-\sigma)\,\right\|_1 + O(t^3/n^2). \tag{2}$$

Hence, to simulate $e^{-i\rho t}\,\sigma\,e^{i\rho t}$ up to an accuracy ε, $n \sim O(t^2/\varepsilon)$ original copies of ρ become needed. Additionally, in [6] this protocol was shown to be optimal with respect to the number of copies required in the asymptotic limit, reducing the opportunity for improvement of the protocol to get a better prefactor in the error term or to generate more (imperfect) copies of the state.

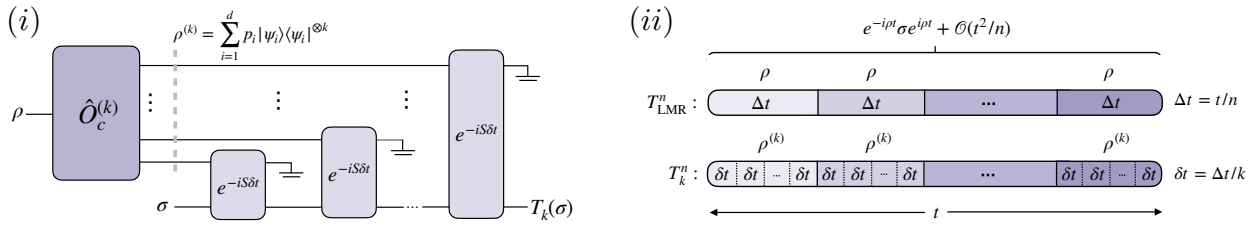

FIG. 1. (*i*) LMR protocol for a single original copy of ρ asissted by biomimetic cloning using the eigenbasis of ρ as the preferred basis for the cloning. S denotes the swap operation, p_i the eigenvalues of ρ and $T_k(\sigma)$ the output of the combined operation. (*ii*) Distribution of time intervals for the combined protocol. To implement the exponentiation of ρ for a time t with n copies, initially, time intervals of duration $\Delta t = t/n$ are considered. When introducing biomimetic copies, each interval is subdivided into k intervals of duration $\delta t = \Delta t/k$.

The no-cloning theorem in quantum information states the impossibility of perfectly copying an arbitrary unknown quantum state. However, cloning a set of orthogonal states is allowed. The biomimetic cloning of quantum observables, referred to as $\hat{O}_c$, leverages this fact by performing the operation $\hat{O}_c|\psi_j\rangle \rightarrow |\psi_j\rangle \otimes |\psi_j\rangle$, where $\{|\psi_j\rangle\}_{j=1}^{d}$ is the eigenbasis of certain observable, whose statistics will be exactly replicated by the biomimetic copies. Hence, given a quantum state $\rho = \sum_{i,j=1}^{d} \rho_{ij} |\psi_i\rangle \langle\psi_j|$, we can generate k biomimetic copies of this state that we denote as

$$\hat{O}_c^{(k)}(\rho) = \sum_{i,j=1}^{d} \rho_{ij} \left(|\psi_i\rangle \langle\psi_j|\right)^{\otimes k} \equiv \rho^{(k)}. \tag{3}$$

Now we can combine both, the LMR opearation and the biomimetic cloning machine in the following way. From each ρ we will create k biomimeitc copies taking ρ as the observable and we will apply the LMR protocol to each of those copies for time intervals of length $\delta t = \Delta t/k$ as depicted in Figure 1. Considering the limit where k is large for analytical calculation purposes, we obtain the asymptotic error of the LMR assisted with infinite biomimetic copies

$$\varepsilon_{\mathrm{BIO}(n\rightarrow nk)} = \left\| T^n_{\mathrm{BIO}}(\sigma) - e^{-i\rho t}\, \sigma\, e^{i\rho t} \right\|_1 \approx \frac{t^2}{2n} \| \, [\rho,\ \sigma]_2 + 2\, \rho \circ \sigma - \{\rho, \sigma\} \, \|_1. \tag{4}$$

The convergence behavior of the error with respect to the number of biomimetic copies, denoted as k, is shown in Figs. 2 (*ii*) and (*iii*), where we show the best and worst cases respectively. These graphics present the error in different scenarios. Firstly, the error is depicted when directly applying LMR with the original n copies, which corresponds to Eq. 2. Additionally, the graphics show the error for two cases of the combined protocol: one starting with 1 original copy and generating nk biomimetic copies, and the other starting with n original copies and generating nk biomimetic copies. Finally, the error is also displayed for the LMR with nk original copies. When provided with n copies of ρ, the improvement achieved by generating biomimetic copies versus the direct application of the LMR operation, Eq. (2), is quantified by

$$\frac{\varepsilon_{\mathrm{LMR}(n)}}{\varepsilon_{\mathrm{BIO}(n\rightarrow nk)}} \approx \frac{\| \, [\rho,\ \sigma]_2 + 2(\rho - \sigma) \, \|_1}{\| \, [\rho,\ \sigma]_2 + 2\, \rho \circ \sigma - \{\rho, \sigma\} \, \|_1} \equiv Q_1. \tag{5}$$

Here, the subscript 1 in Q denotes the norm-1 or trace norm. Therefore, although the error is suppressed in the same way with the number of copies n, thus not violating the optimality result of the original protocol from Ref. [6], the prefactors depend on the quantum states under consideration and can lead to a reduction in the error as the system size increases. In fact, we rigorously show that on average, Q_1 will scale exponentially with the size of the quantum system considered. This behaviour is experimentally depicted in Fig. 2 (*i*), where the mean, minimum and max value of Q_1 from a sample of 100,000 random cases uniformly distributed according to the Hilbert-Schmidt measure is illustrated for different number of qubits. These numerical results show a linear scaling of Q_1 with the dimension of the system for the average case. We also demonstrate the regimes in which our protocol provides an advantage, considering the cost of implementing the biomimetic cloning machine and the hypothetical cost of generating an additional copy of ρ. As a final remark, even though we have focused our study in a particular non-linear transformation, the exponentiation, our results constitute a promising starting point to enhance the implementation of many quantum protocols that require multiple copies of a quantum state, particularly when its breed resources are costly or limited.

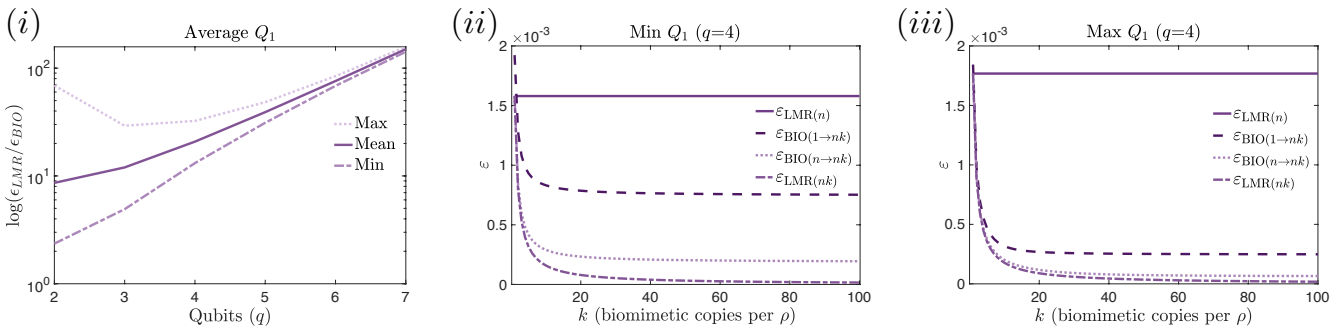

FIG. 2. We depict the results obtained from randomly generated cases distributed according to the Hilbert-Schmidt measure, with $t = 0.2$ and $n = 4$ original copies. (*i*) Mean value of Q_1 across a sample of 100,000 random cases for each number of qubits. (*ii*) Minimum (*ii*) and maximum (*iii*) value of Q_1 among the 100,000 random samples, specifically for $q = 4$.

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