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Quantum annealing versus classical machine learning applied to a simplified computational biology problem

Transcription factors regulate gene expression, but how these proteins recognize and specifically bind to their DNA targets is still debated. Here we studied the ability of a quantum machine learning approach to predict binding specificity. Using simplified datasets of a small number of DNA sequences derived from actual binding affinity experiments, we compared the performance of a commercially available quantum annealer, D-Wave (DW), with several state-of-the-art classical techniques. Despite technological limitations, we find an advantage in classification performance and nearly equal ranking performance using the quantum annealer for fairly small training datasets. (Authors: Richard Li, Rosa Di Felice, Remo Rohs, Daniel Lidar)