

Protein folding with QAOA

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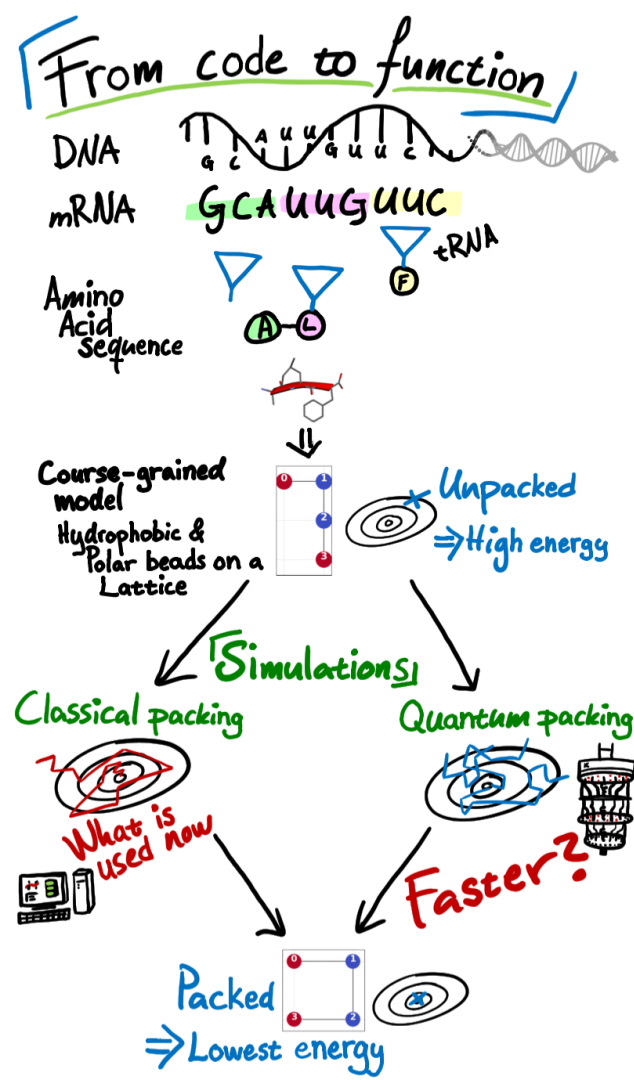
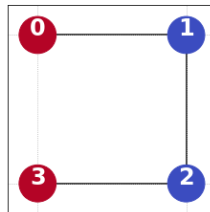


Overview

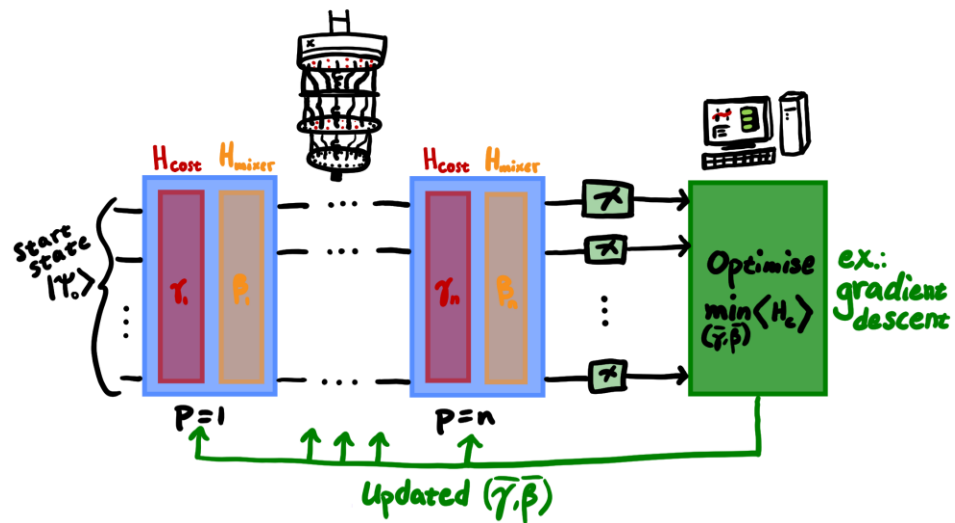
- Protein folding
- Gate based quantum computer: Quantum Approximate Optimisation Algorithm (QAOA)
- Initial parameters in QAOA inspired by quantum annealing
- What kind of quantum computers would be needed to challenge classical computers in folding proteins?

Protein folding simulations

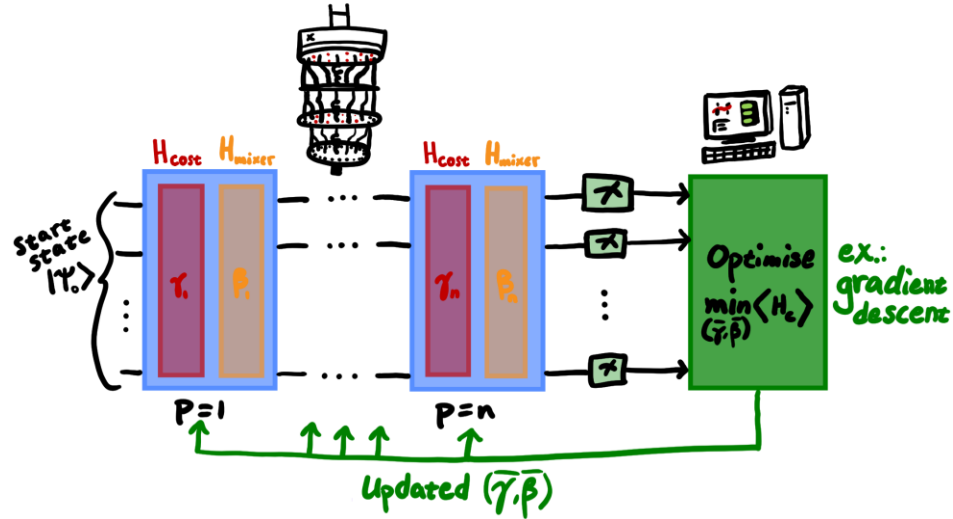
- From DNA to amino acid sequence.
- Amino acid sequence folds to functioning protein.
- Course-graining models for simplifications.
- Hydrophobic-Polar model on a lattice.



QAOA

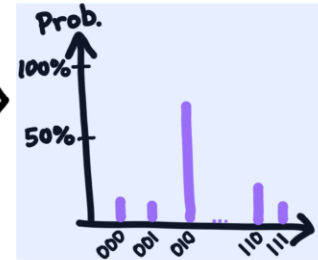


QAOA



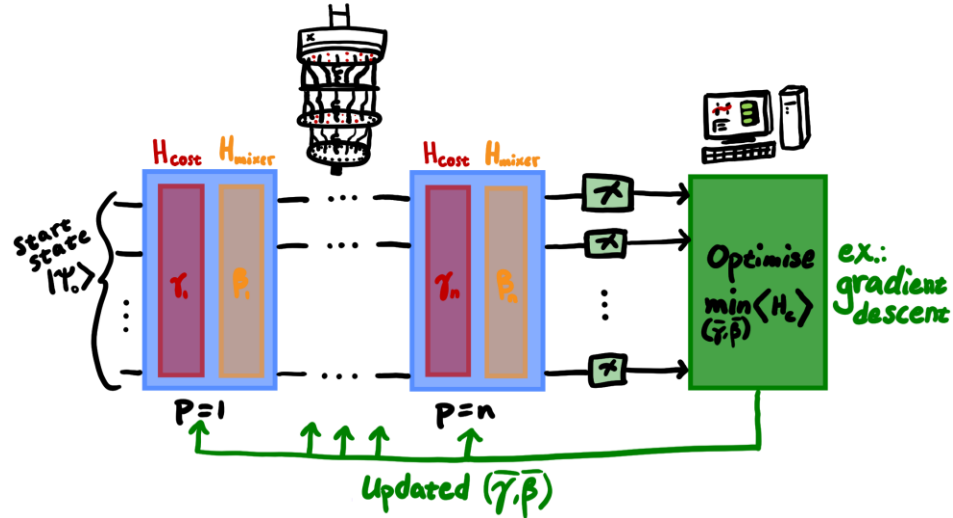
$$|\Psi(\bar{\gamma}, \bar{\beta})\rangle = e^{-i\beta_n H_m} e^{-i\gamma_n H_c} \dots e^{-i\beta_1 H_m} e^{-i\gamma_1 H_c} |\Psi_0\rangle$$

Optimise $\min\langle H_c \rangle$ ($\bar{\gamma}, \bar{\beta}$) \Rightarrow Measure $|\Psi(\bar{\gamma}_{opt}, \bar{\beta}_{opt})\rangle$ \Rightarrow



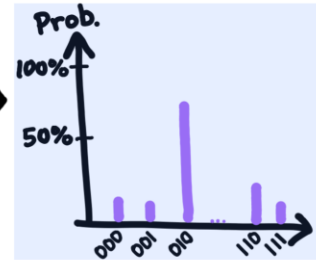
Best Solution with low cost

QAOA



$$|\Psi(\bar{\gamma}, \bar{\beta})\rangle = e^{-i\beta_1 H_m} e^{-i\tau_1 H_c} \dots e^{-i\beta_n H_m} e^{-i\tau_n H_c} |\psi_0\rangle$$

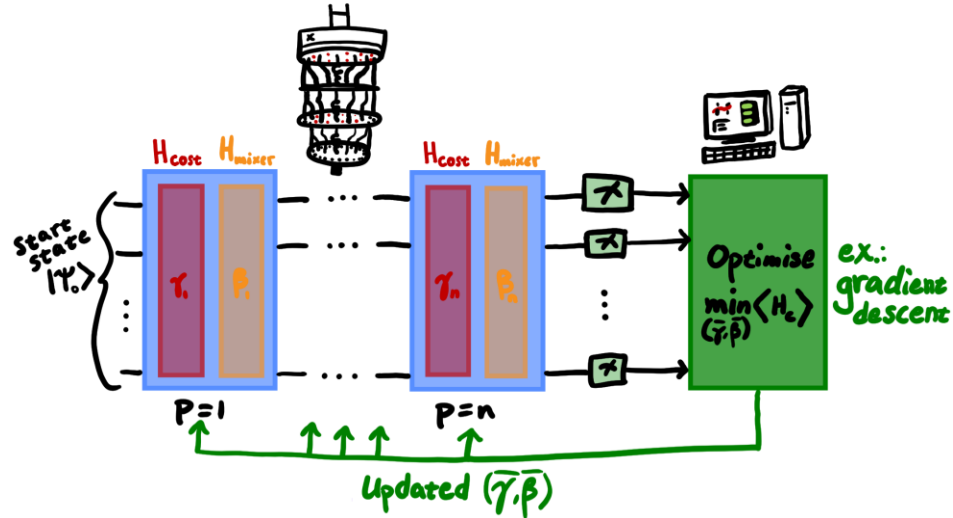
Optimise $\min \langle H_c \rangle (\bar{\gamma}, \bar{\beta}) \Rightarrow |\Psi(\bar{\gamma}_{opt}, \bar{\beta}_{opt})\rangle \Rightarrow$



Best Solution with low cost

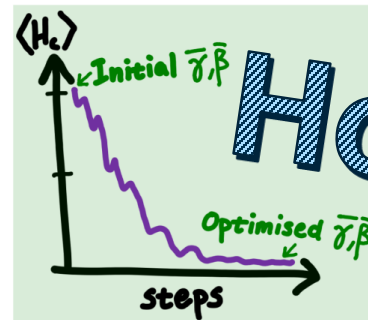
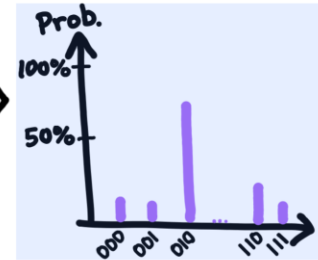


QAOA



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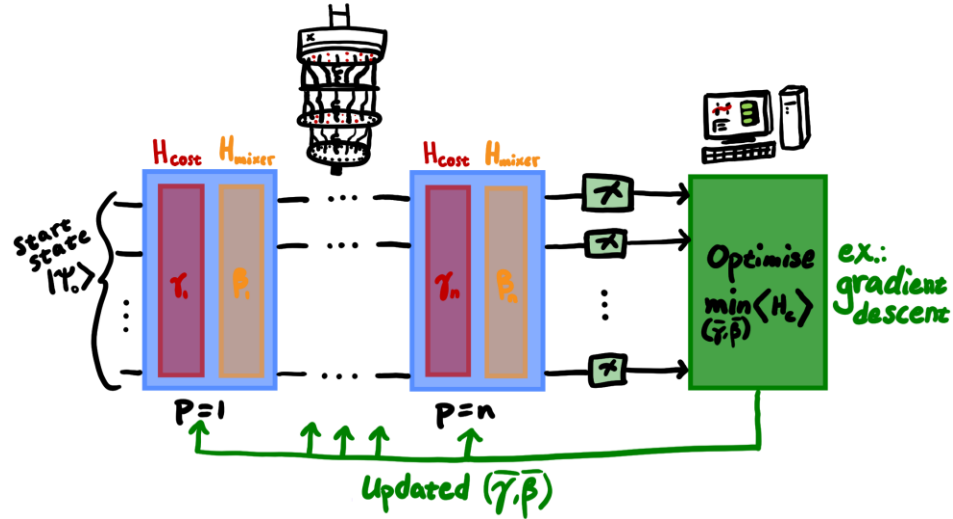
Optimise $\min_{(\vec{\gamma}, \vec{\beta})} \langle H_c \rangle \Rightarrow |\Psi(\vec{\gamma}_{opt}, \vec{\beta}_{opt})\rangle$



Hopefully

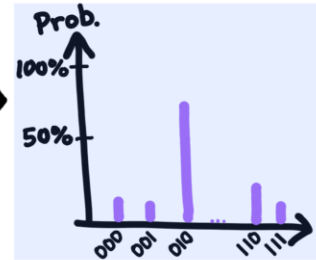
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Optimise $\min_{(\bar{\gamma}, \bar{\beta})} \langle H_c \rangle \Rightarrow |\Psi(\bar{\gamma}_{opt.}, \bar{\beta}_{opt.})\rangle$



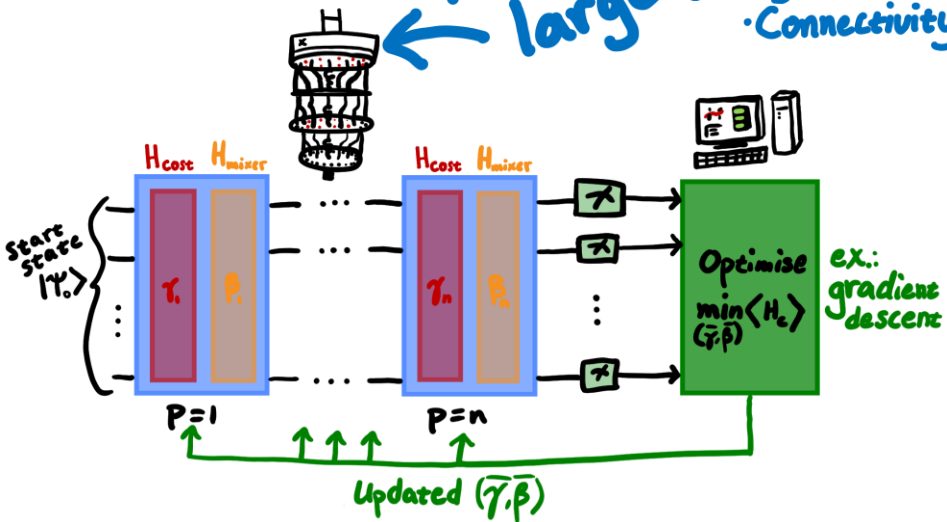
Best Solution with low cost

Where to start?

QAOA

How large?

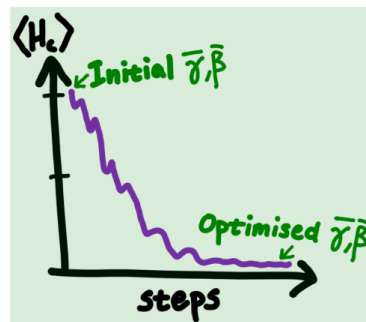
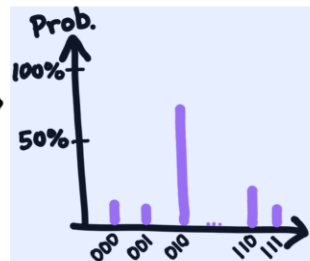
- Qubits
- Gates
- Connectivity



$$|\Psi(\bar{\gamma}, \bar{\beta})\rangle = e^{-i\beta_1 H_m} e^{-i\gamma_1 H_c} \dots e^{-i\beta_n H_m} e^{-i\gamma_n H_c} |\Psi_0\rangle$$

Optimise $\min_{(\bar{\gamma}, \bar{\beta})} \langle H_c \rangle$

Measure $|\Psi(\bar{\gamma}_{opt}, \bar{\beta}_{opt})\rangle$

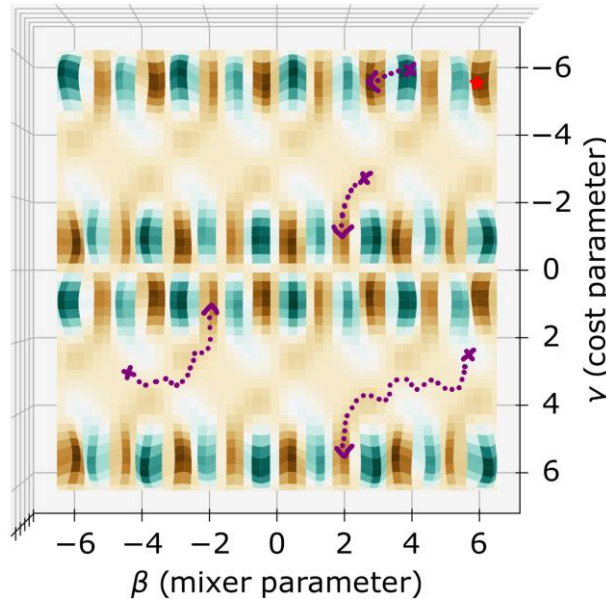
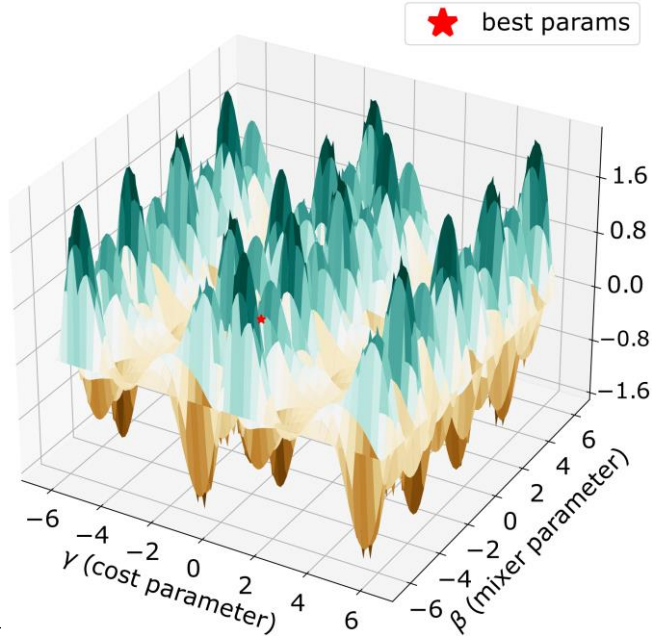
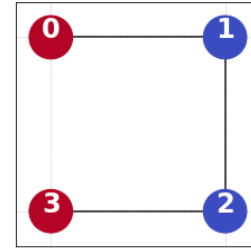


Best Solution with low cost

Where to start?

Energy landscape $p=1$

Success of measuring best solution $\approx 38\%$

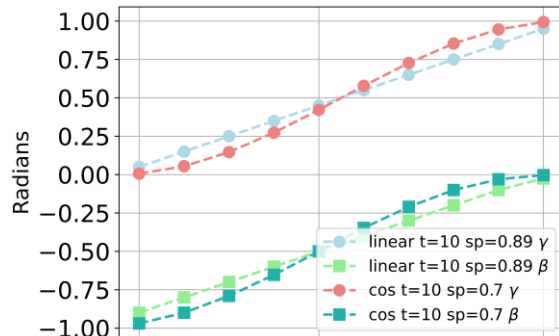


Where to start?

Initial parameters $p > 1$

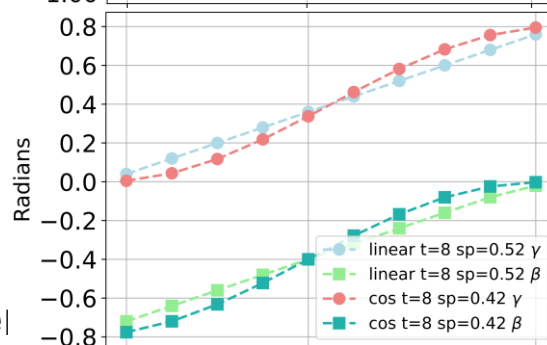
Where to start?

- Annealing parameters [Sack et al. [arXiv:2101.05742](https://arxiv.org/abs/2101.05742) **[quant-ph]**]
 - Linear
 - Cosine (from seeing what it trained to)
- Annealing time t becomes a hyperparameter

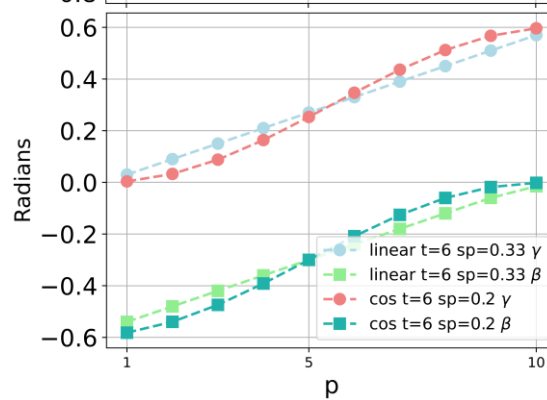


Lattice size:

(2,2)



(3,2)



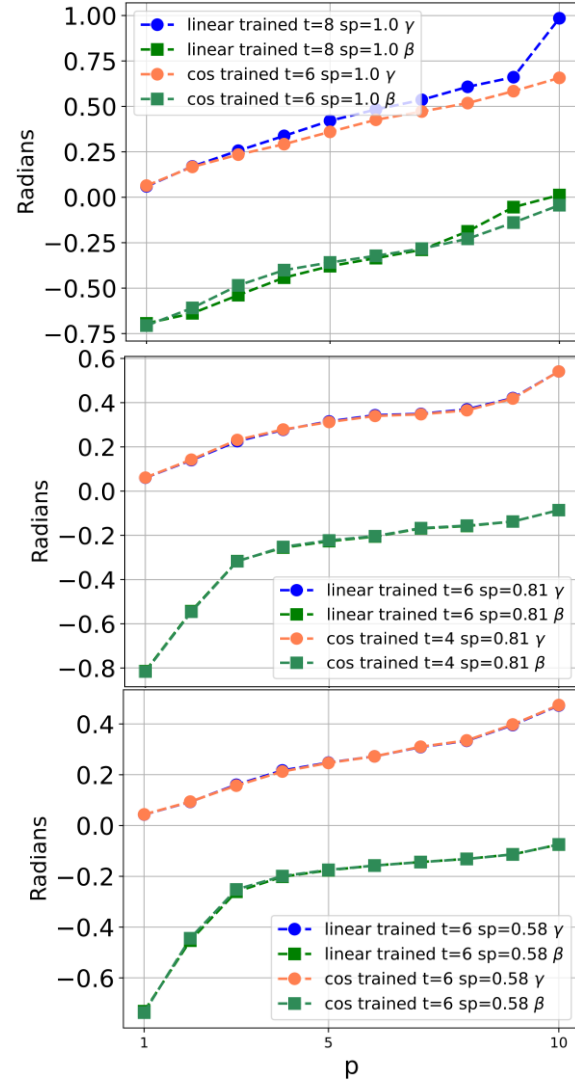
(3,3)



Initial parameters $p > 1$

Where to start?

- Train for 100 steps with Adam optimiser (gradient descent).
- Finds same minima.
- Gives a suggestion of what the best annealing schedule could be.



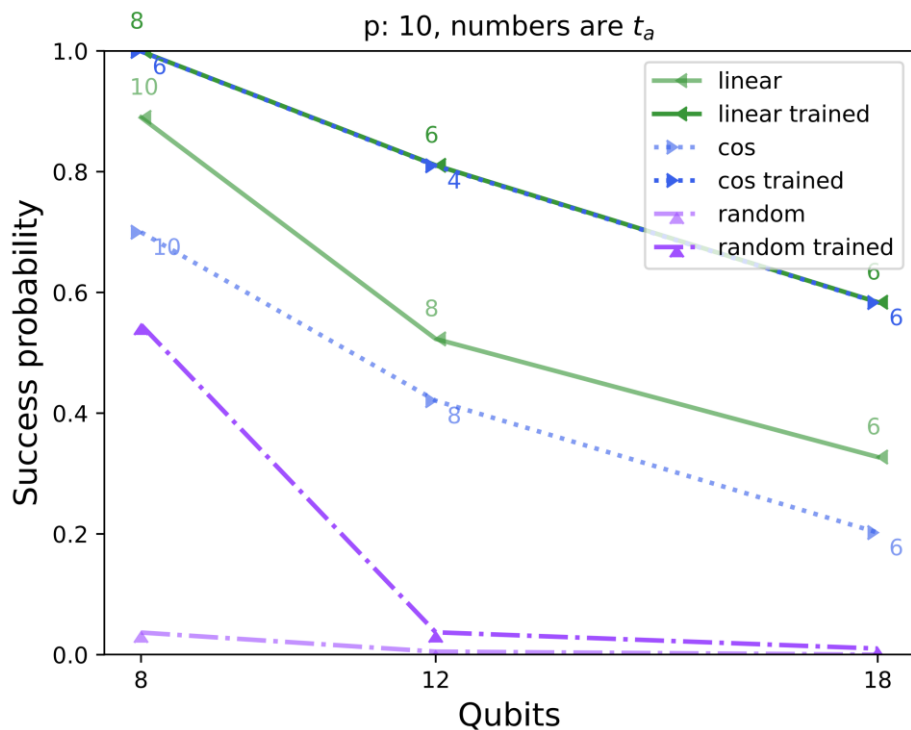
Lattice size:
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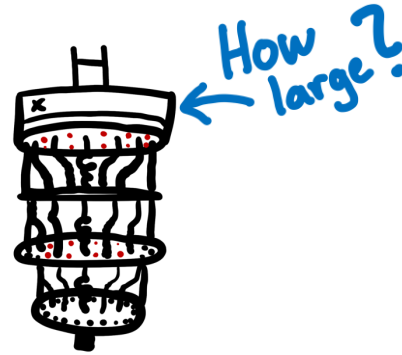
Larger lattices needs more qubits and thereby harder to optimise.



From current proofs of principle to future practical implementations

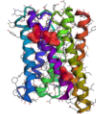
Resources in a quantum computer

- Resources:
 - Number of qubits
 - Connectivity of the qubits
 - Number of gates
- Protein models:
 - Side-chain conformation-based model
 - HP-Lattice model
 - Turn-based
 - Coordinate-based
- Bit strings encodings:
 - One-Hot
 - Binary
 - BUBinary

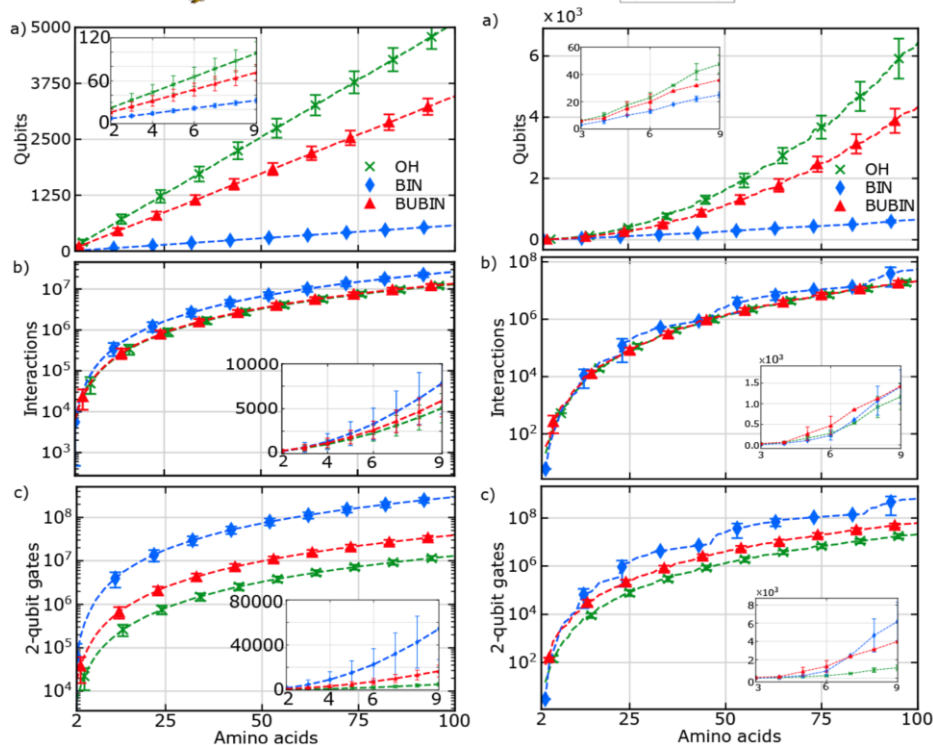
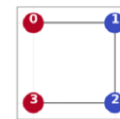


Decimal	One-hot	Binary	BUBinary _{g=3}
0	10000	000	00 01
1	01000	001	00 10
2	00100	010	00 11
3	00010	011	01 00
4	00001	111	10 00

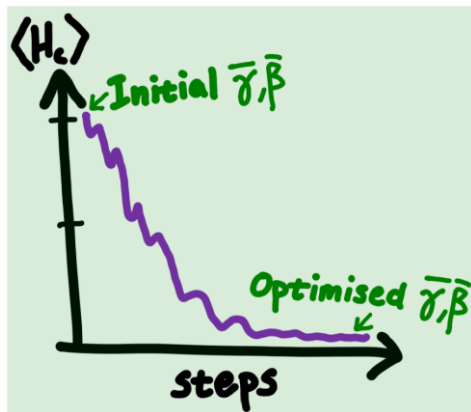
Resources in a quantum computer



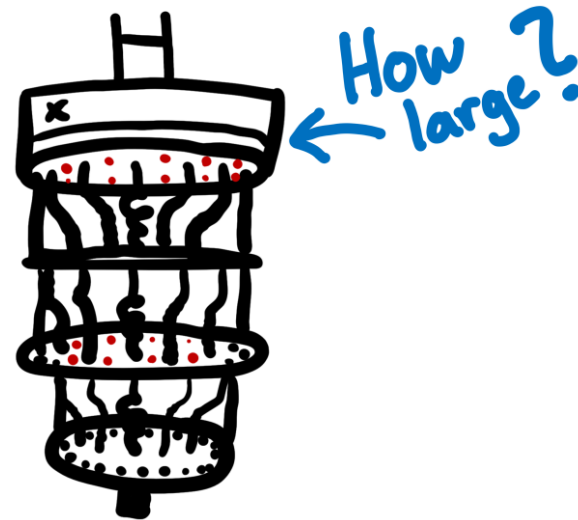
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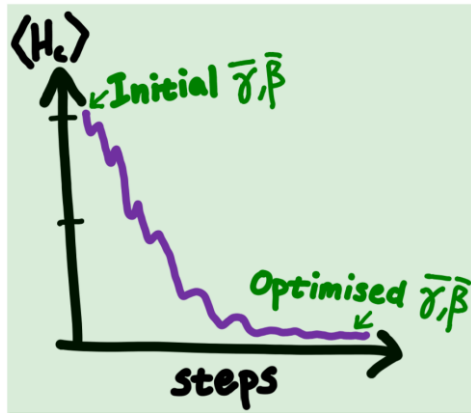
Summary



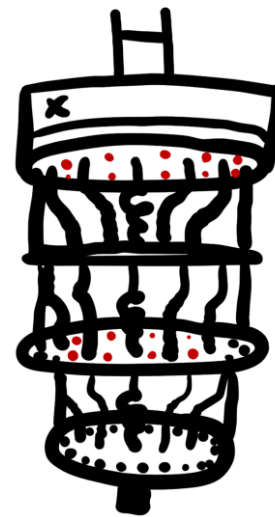
Where to start?



Summary



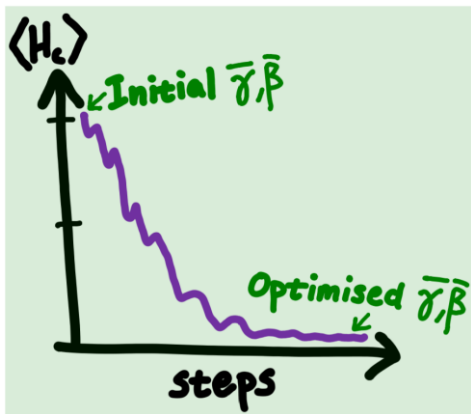
Where to start?



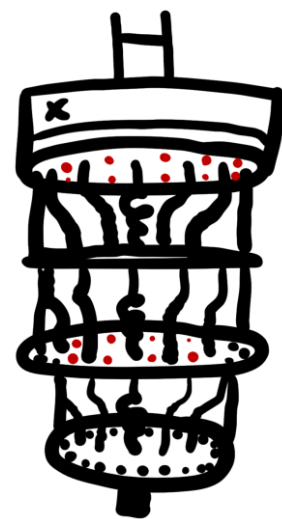
How large?

Annealing parameters

Summary



Where to start?



How large?

Very large

Annealing parameters

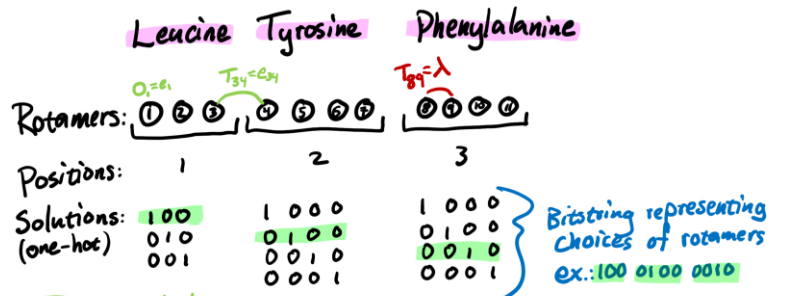


CHALMERS



Protein folding simulations

- Rotamer model




T_{jk} : Two body interaction energy between rotamer j & rotamer k

O_i : one body interaction energy for rotamer i


λ : penalty for choosing more than one rotamer per position
set to high enough = 500

Summarise all contributing energies for chosen rotamers:
 $E_{(1000100010)} = O_1 + O_2 + O_{10} + T_{15} + T_{1,10} + T_{5,10}$

From code to function

DNA 

mRNA **GCAUUGUUC**

Amino Acid Sequence 

Course-grained model
Hydrophobic & Polar beads on a Lattice

Simulations

Classical packing

Quantum packing

Unpacked \Rightarrow High energy

What is used now

Faster?

Packed \Rightarrow Lowest energy



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Comparison with quantum annealing: Soft suppression

