

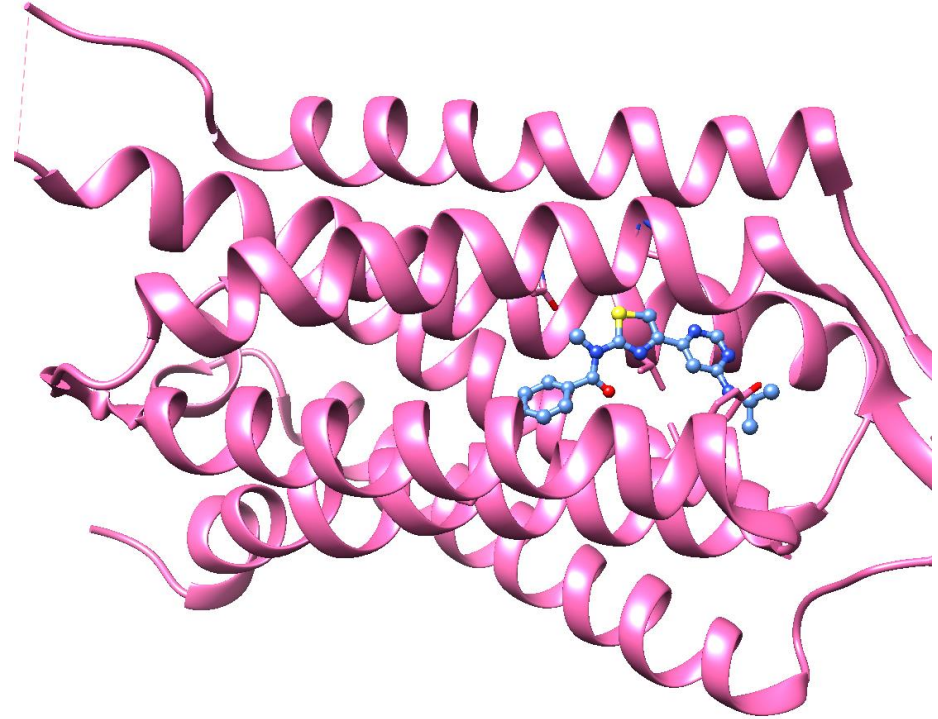
Quantum sea - Classifying water molecules and sodium ions in protein structures

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Protein is also a molecule.

- Even though protein shows incredible functions, but it is still a molecule.
- Understanding the physics behind protein would help to understand its function.

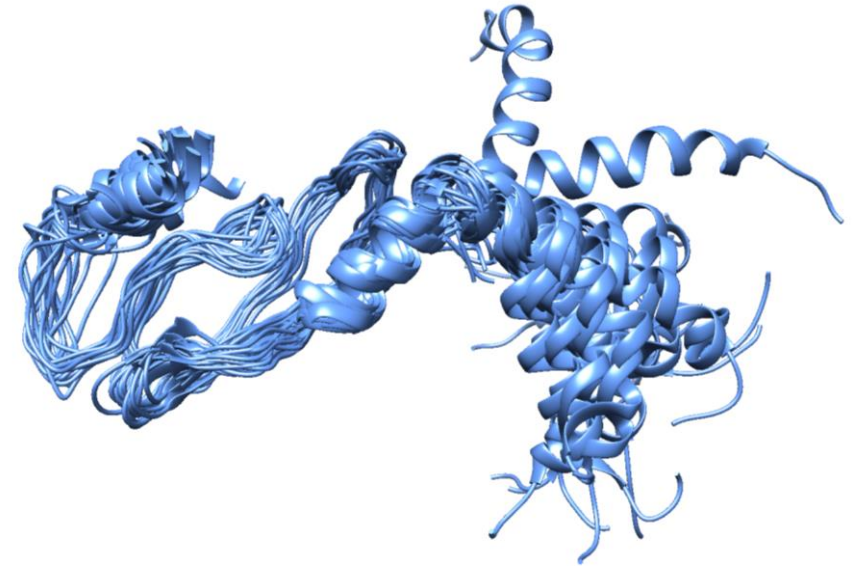


GPCR in complex with a negative allosteric modulator (PDB ID: 4OR2)

Understanding physics behind the protein would help to know interactions / dynamics of the protein.

Why we need quantum computer?

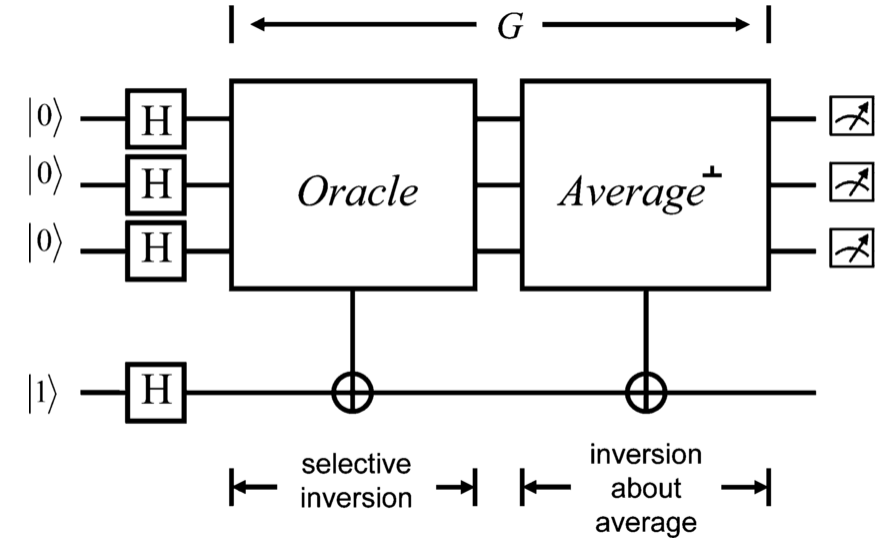
- Interaction of the protein is governed by Gibbs free energy.
 - To know Gibbs free energy, we should know the entropy term.
 - It means, we should know every possible state of the protein. Quite exponential!
- Maybe we need new method which is exponentially faster than classical ones!



Protein could have a lot of structural states.
(PDB ID: 2L27, NMR structure)

However, It's bit early.

- Correct algorithm for predicting free energy of the protein...
 - Would use full superposition like Grover search...?
 - Actually we don't have an algorithm yet!
- Fidelity / # of qubits are not enough for the prediction... yet!
 - Variational Quantum Eigensolver, Quantum Machine learning is available though...



Ju, Yi-Lin & Tsai, I-Ming & Kuo, Sy-Yen. (2007).
10.1109/TCSI.2007.907845.

Performance Benchmarks [†]			
Qubits		Average Fidelity	Best Fidelity
Single-qubit gates on		Single-qubit gates	Single-qubit gates
79 Qubits		>99%	>99.97%
Two-qubit gates on all pairs up to		Two-qubit gates	Two-qubit gates
11 Qubits		>98%*	>99.3%*
Minimum Fidelity		Coming Soon: 32 Qubits	
Single-qubit gates		We are currently gathering detailed data on our latest system, which features a capacity of 32 fully-connected qubits and world-leading algorithmic performance.	
>99%		more about our latest breakthrough →	
Two-qubit gates			
>96%*			

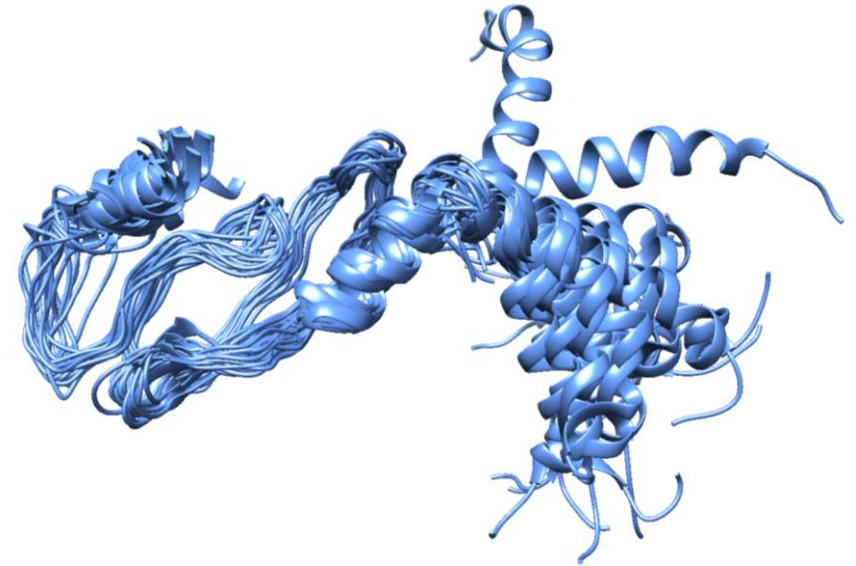
It's state-of-the-art, but we need more!
(From IONQ's website.)

Lots of limitations

- Limitations of quantum computer
- Limitations of time (5 days)
- Limitations of myself
 - I think I'm still a beginner in QC area. (sorry!)
 - Scoring 7500 pts in QHack coding challenge might not enough...
- In this presentation, I'll try to solve toy problem.
 - With Quanyvolutional Neural Network

The toy problem: Classifying H_2O / Na^+

- X-ray crystallography:
 - The method for obtaining high-res structure of a protein
 - Uses diffraction of X-ray due to electrons in the protein
 - small molecules, atoms or ions with the same number of electrons are likely to produce similar peaks.
 - H_2O : 10 electrons, Na^+ : 10 electrons
- However...
 - H_2O : 0 net charge / Na^+ : positive net charge
 - H_2O binding structure \neq Na^+ binding structure

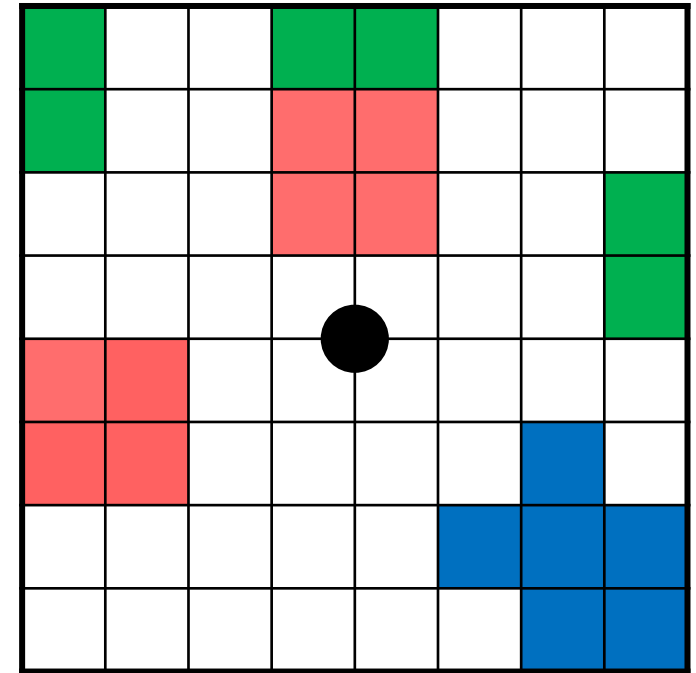


Please forget this NMR model. I will use X-ray crystallographic models only.

The toy problem: Classifying H_2O / Na^+

- The problem in this project:
 - Input: Voxelized 3D image of the structure of C,N,O atoms from proteins or other compounds exclude water, where H_2O / Na^+ exists at the center.
 - Size of the input: A cube size of 16\AA and grid spacing of 0.5\AA .
 - Output: which one exists at the center, Water, or sodium ions?

Example



Carbon

Oxygen

Nitrogen

Water molecule or sodium ion

The toy problem: Classifying H₂O / Na⁺

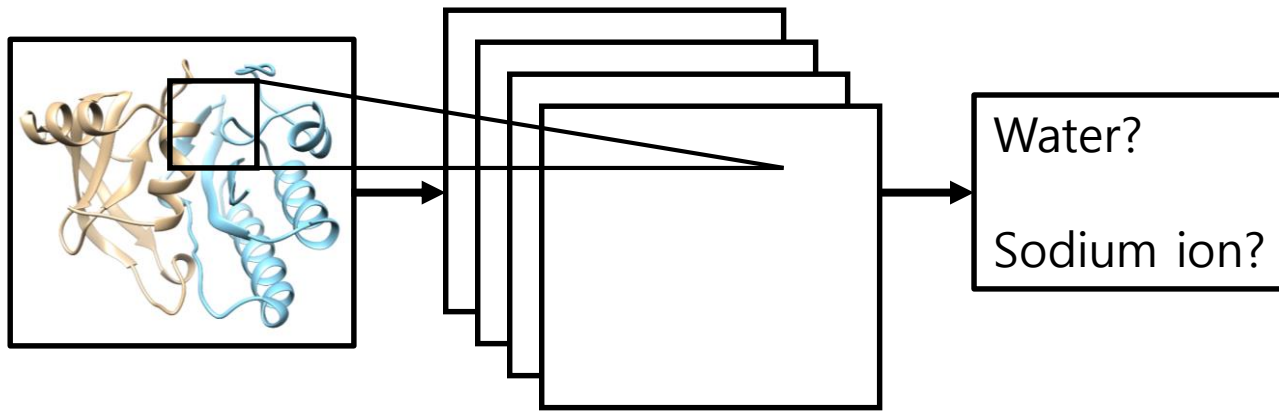
- Training / Validation set:
 - Training set: protein structures nearby 400 water molecules and 400 sodium ions, gathered from PDBBind v2019 refined set.
 - To train rotational invariance, 100 rotations were done for each structure (total 80000 structures. 800 structures per epoch)
 - (Inputs for epoch N == Inputs for epoch N+100)

The toy problem: Classifying H₂O / Na⁺

- Training / Validation set (cont.):
 - Validation set: protein structures nearby 54 water molecules and 54 sodium ions, gathered from PDBind v2019 refined set.
 - Yes, this set is not big enough and it contains some low resolution structures too.
 - No additional R-free, B-factor cutoff were applied
 - Need larger set for sodium ions. (This is the major reason of small set size.)

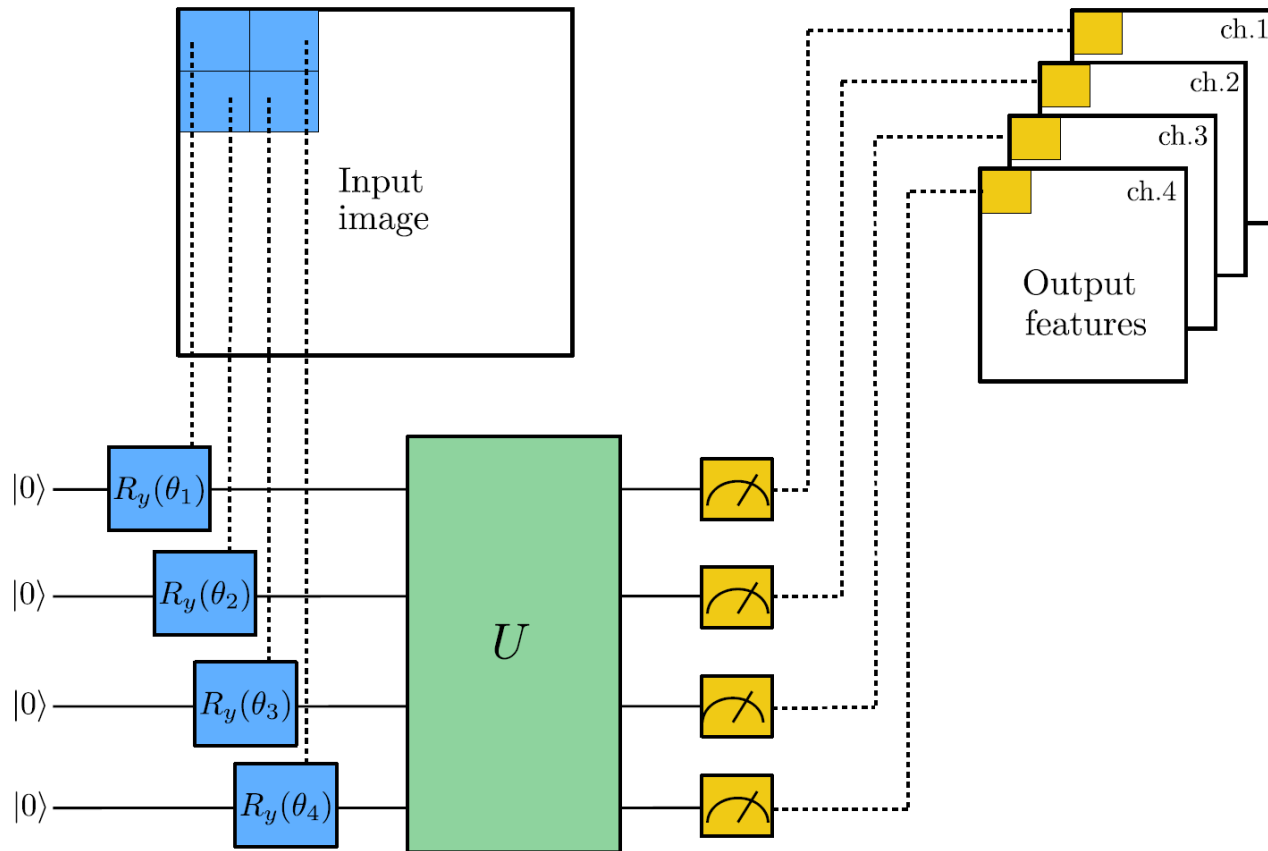
Pattern recognition for protein structures

- One simple way: using convolutional neural network



- And Quenvolutional neural network will be used for QML version!

Quanvolutional neural network

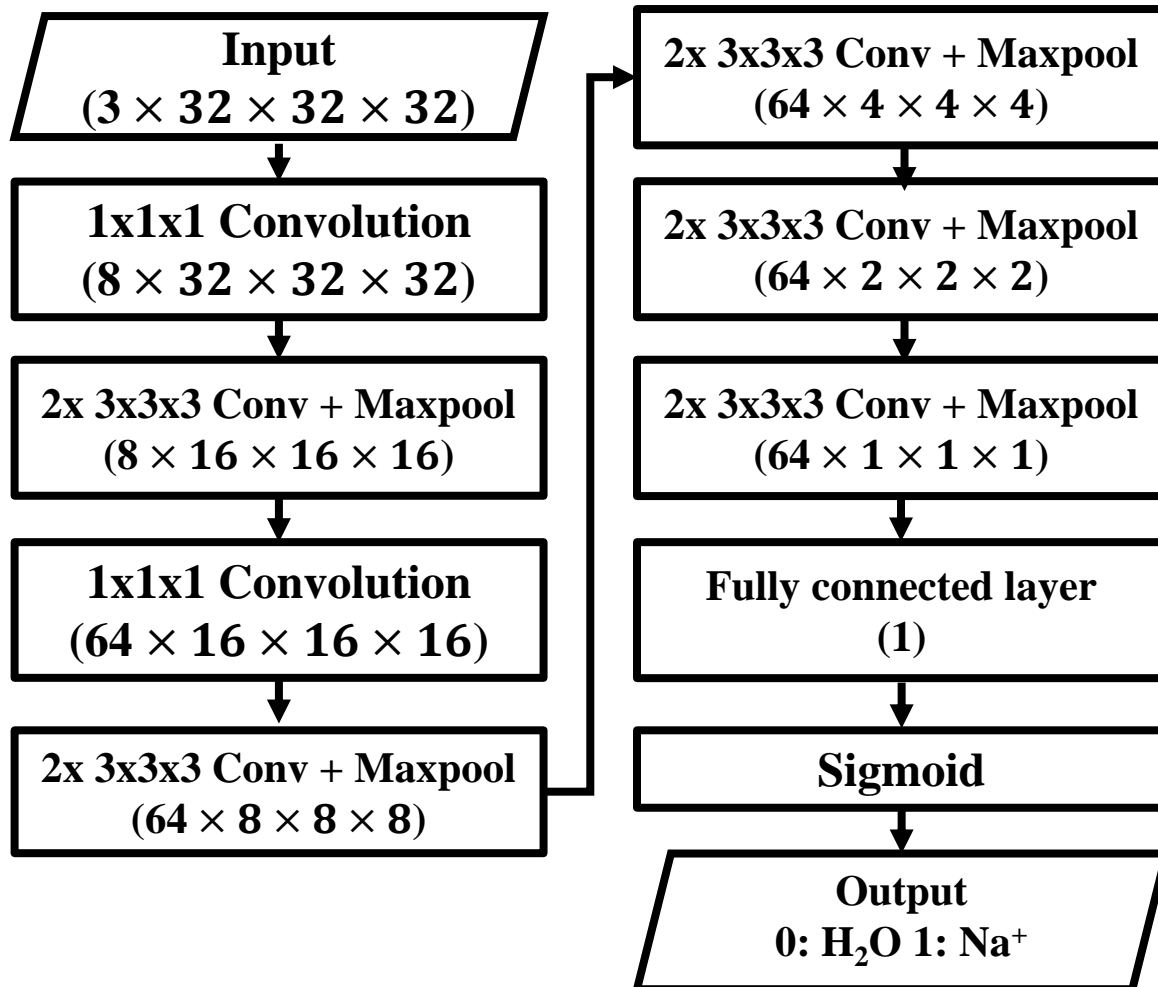


From pennylane's tutorial:

https://pennylane.ai/qml/demos/tutorial_quanvolution.html

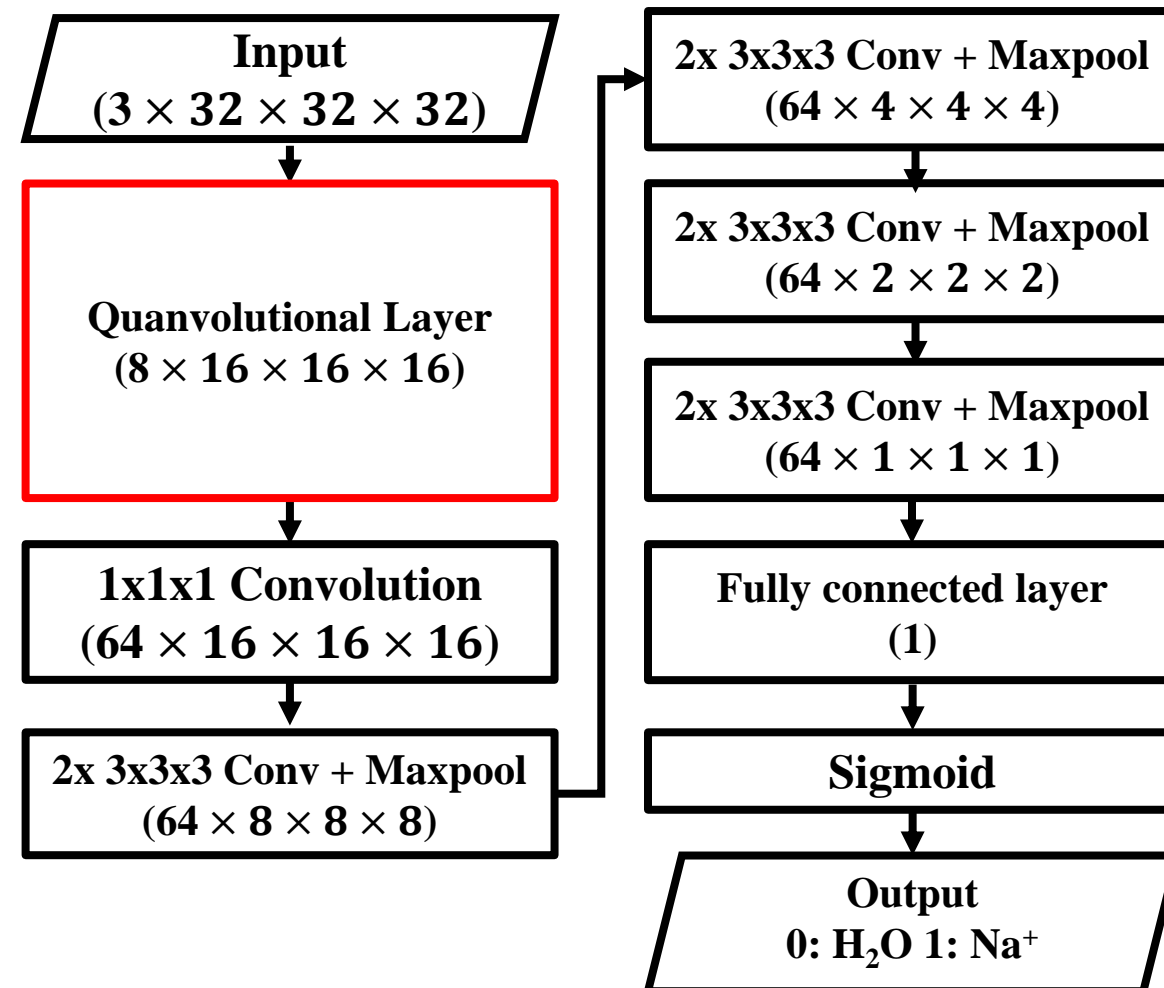
Networks used in this project (1/3)

CNN:



Networks used in this project (2/3)

Quanvolutional Neural Network:

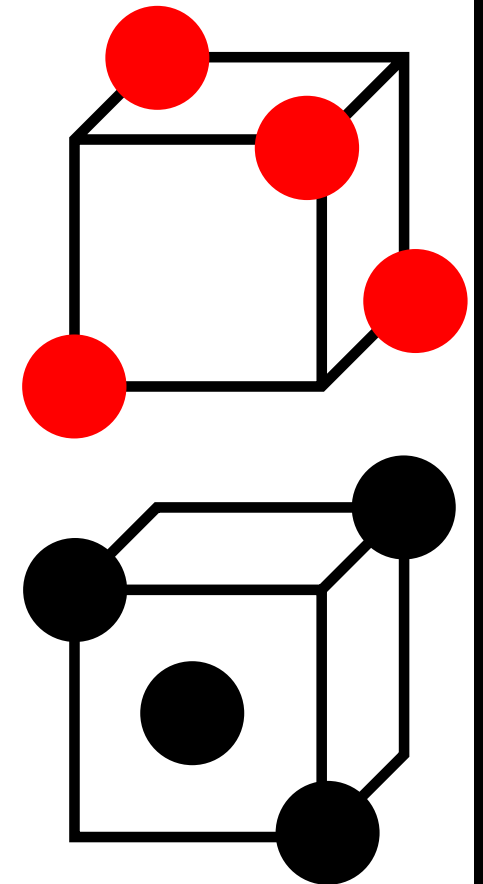


Quanvolutional Layer:

of wires: 4
(To reduce wires,
two quanvolutions
were done.)

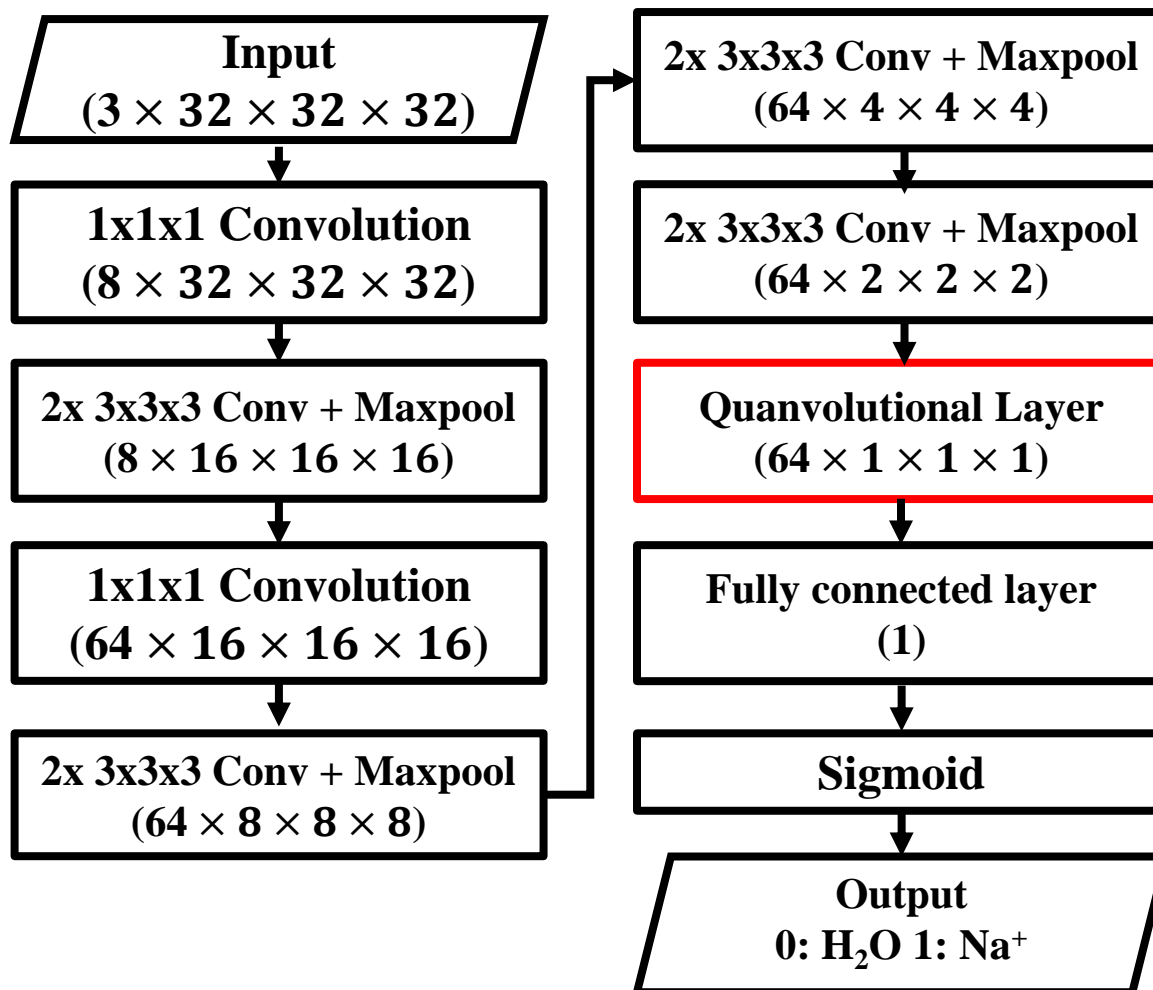
Quantum Circuit:
0. Starts with $|0\rangle$
1. RX ($\pi \cdot O$ density)
2. RY ($\pi \cdot N$ density)
3. RZ ($\pi \cdot C$ density)
4. Randomlayer (
circuit layer:2.
rotations: 4)

Measurement: $\langle Z \rangle$



Networks used in this project (3/3)

Trainable Qanvolutional Neural Network:



Quanvolutional Layer:

of wires: 4

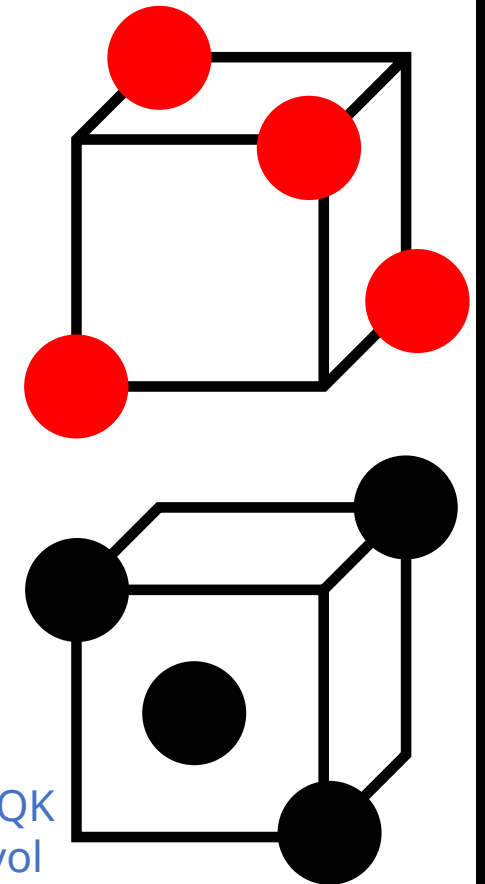
Quantum Circuit:
0. Starts with $|0\rangle$

1. RY ($\pi \cdot \text{input value}$)

2. Randomlayer (
circuit layer:2.
rotations: 4,
Trainable)

Measurement: $\langle Z \rangle$

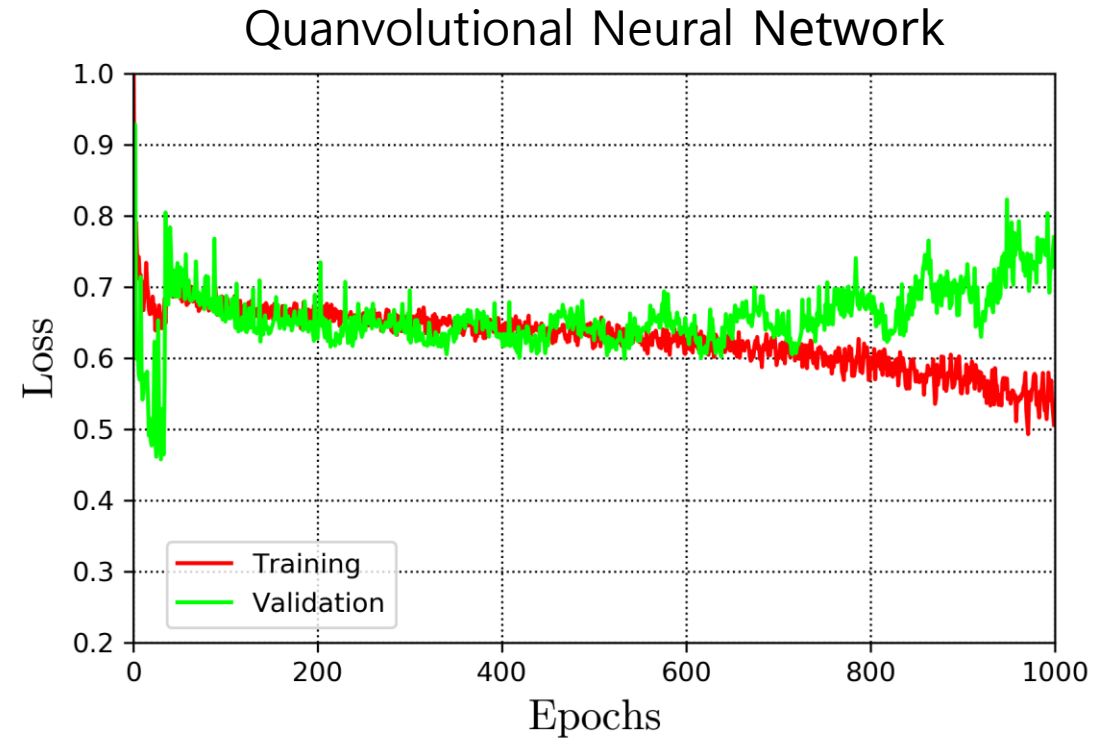
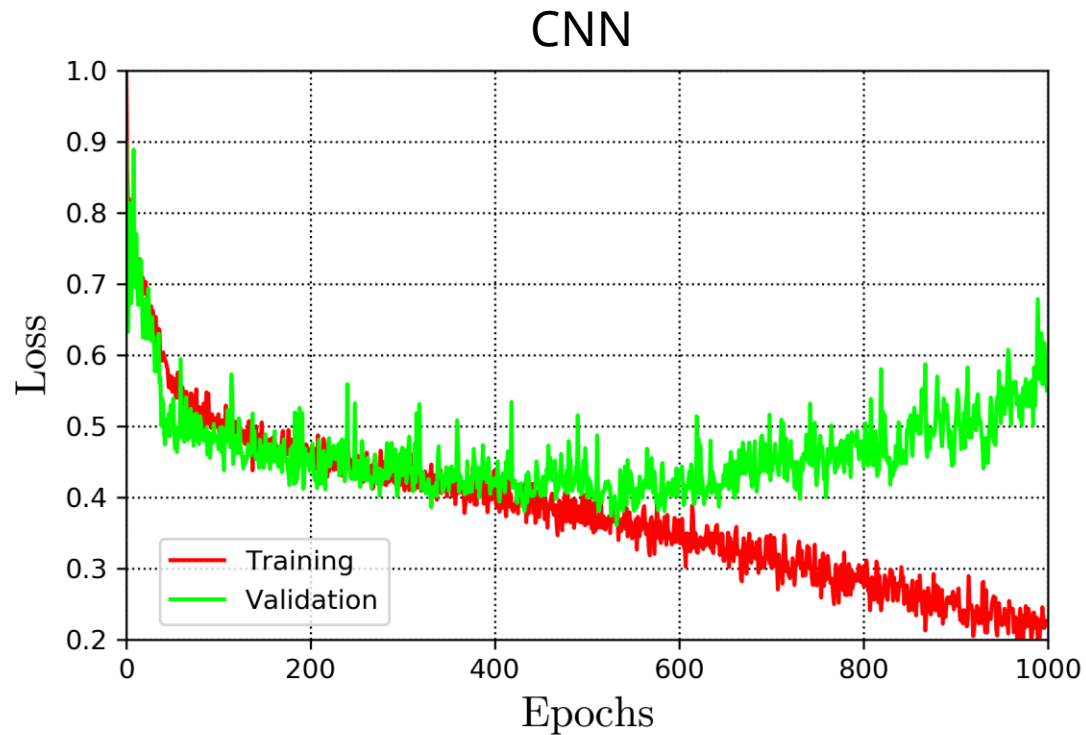
<https://github.com/PlanQK/TrainableQuantumConvolution>



Loss functions / Optimizers

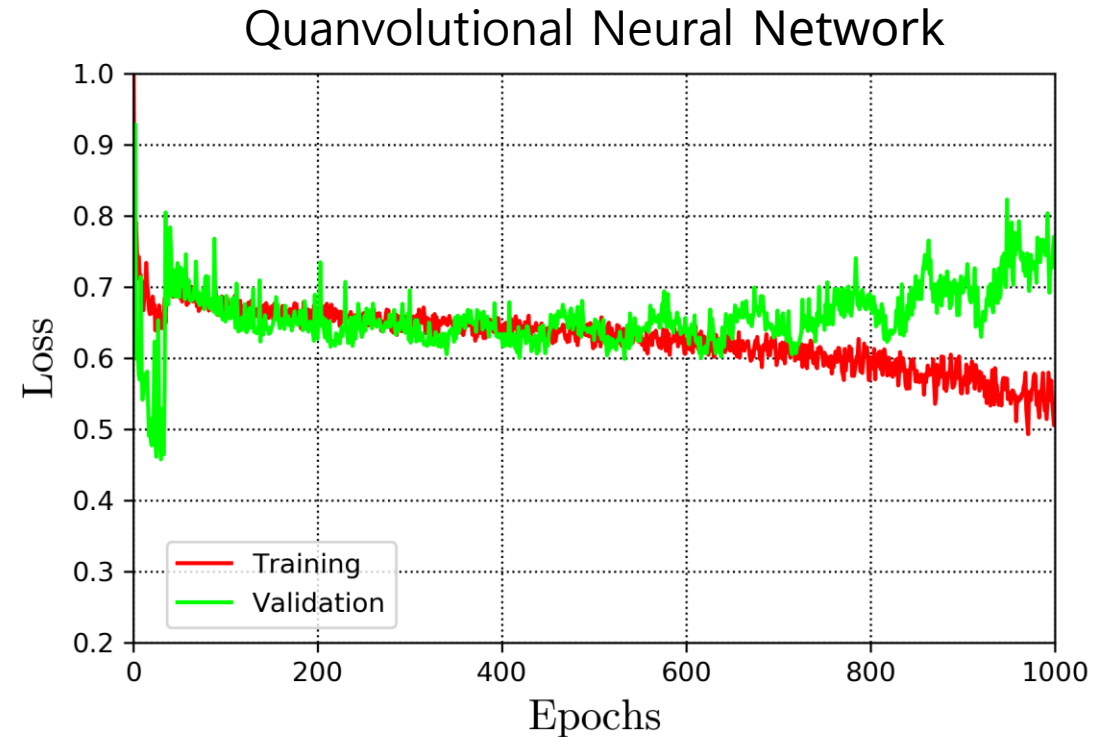
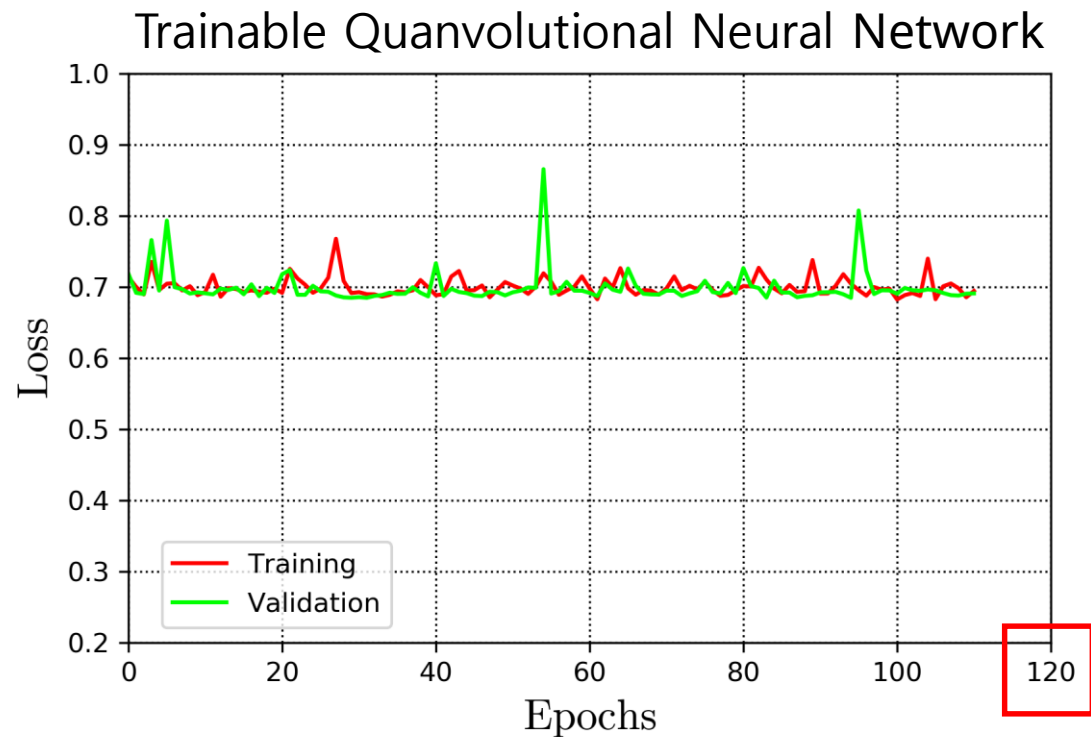
- Loss function: Cross Entropy loss (Batchsize = 4)
- Optimizer: Adam optimizer
 - CNN / QUANV : learning rate = 0.0001
 - Trainable QUANV : learning rate = 0.03

Results – Loss (1/2)



(maybe) Due to limited amount of rotations(=100) in training set,
Both CNN and QUANV shows overtraining after 400 epoch.

Results – Loss (2/2)



Trainable Qunvolutional Neural Network was not trained well,
even though learning rate was higher than other two methods.

(Maybe I need to learn more about optimizers in Quantum Machine Learning.)

Results – Validation set accuracy

	Overall accuracy	Water accuracy	Sodium ion accuracy
CNN - 400 epochs (Not overtrained yet)	81.5% (88 / 108)	85.2% (46 / 54)	77.8% (42 / 54)
CNN - 1000 epochs (Overtrained)	77.8% (84 / 108)	87.0% (47 / 54)	68.5% (37 / 54)
QUANV - 400 epochs (Not overtrained yet)	66.7% (72 / 108)	68.5% (37 / 54)	64.8% (35 / 54)
QUANV - 1000 epochs (Overtrained)	61.1% (66 / 108)	64.8% (35 / 54)	57.4% (31 / 54)
Trainable QUANV (111 epochs)	55.6% (60 / 108)	27.8% (15 / 54)	83.3% (45 / 54)

Conclusion

- Machine learning can specify H_2O / Na^+ !
 - From CNN's accuracy, which is about 80% !
- However, quanvolution based method showed worse accuracy.
 - 55.6% for trainable quanv, 61~67% for non-trainable quanv
 - Maybe different network design, loss function, optimization method would be necessary to show higher performance.
 - But, still better than random guessing!

What can be done further?

- Prepare better training / test set
 - Larger and high-resolution (low R-free, B-factor, etcetc) set
 - Use more atom types rather than using C, N, O only.
- Use better optimization method for quantization, or try to use QGCNN
 - Embedding will be done for nearby atoms, rather than nearby voxels

What can be done further? (cont.)

- Try to apply rotational equivariance concept in the network
 - Most of computation were consumed for learning rotation!
 - Building 100 rotated input structure for each target, training 1000 epochs...
 - SE(3)-CNN-like network would be helpful for this problem.
 - What could be QML-version of SE(3)-CNN?
- And the most important one:
 - Try to think about the method about free E estimation with quantum computer – This is the true problem!!

Thanks for reading this presentation!

Acknowledgements:

- Seoklab (<https://seoklab.org>)
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- IBM Quantum (<https://quantum-computing.ibm.com/>)
- BEMANI SOUND TEAM