Protein Folding

2D MJ Lattice model on D-Wave Quantum Annealing Hardware

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Use Conventional Monte Carlo

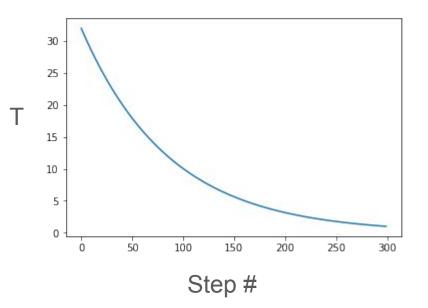
Simulated Annealing

Methods Simulated Annealing (Conventional MC)

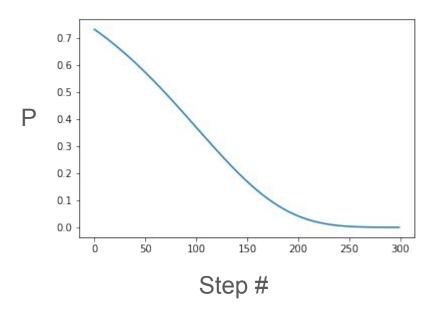
- Define a schedule for annealing temperature T
- Randomly choose i-th residue r_i
- Perform random walk, with respect to r_(i-1)
 - \circ Keep residue path directions for r_i with j > i
- Compute the change in energy dE = E E'
 - o E' and E are the energies before and after the step is taken
- Accept step if exp(-dE/T) > random.uniform(0, 1)
 - Note that $dE \le 0 \rightarrow accept$ always

Methods Simulated Annealing (Conventional MC)

Annealing Schedule



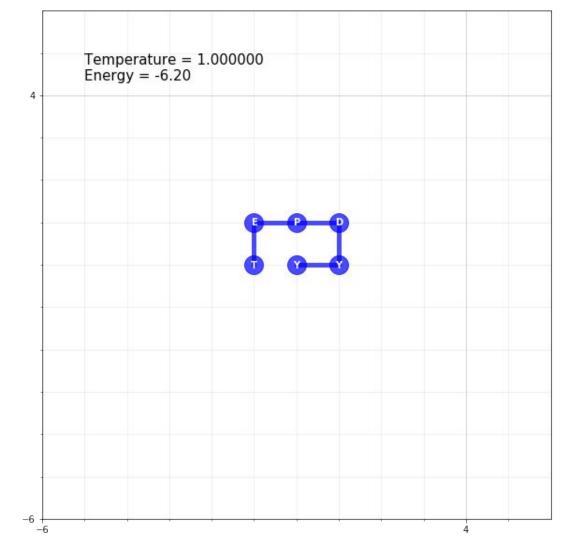
Probability of accepting dE = +10



Results

Simulated Annealing (Conventional MC)

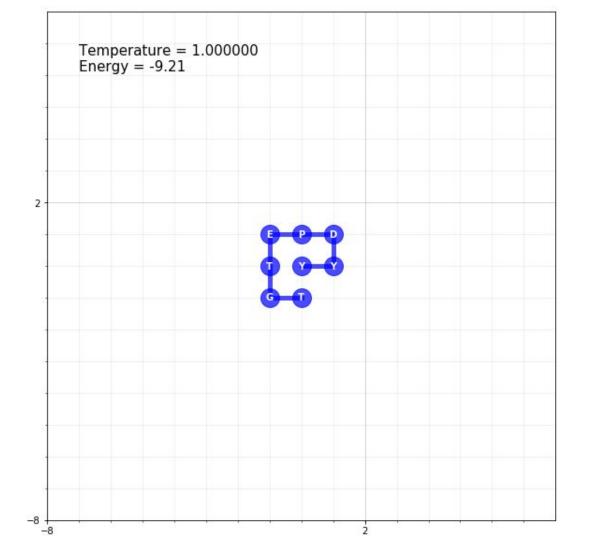
67 out of 360 (18.6%) in lowest energy conformation



Results

Simulated Annealing (Conventional MC)

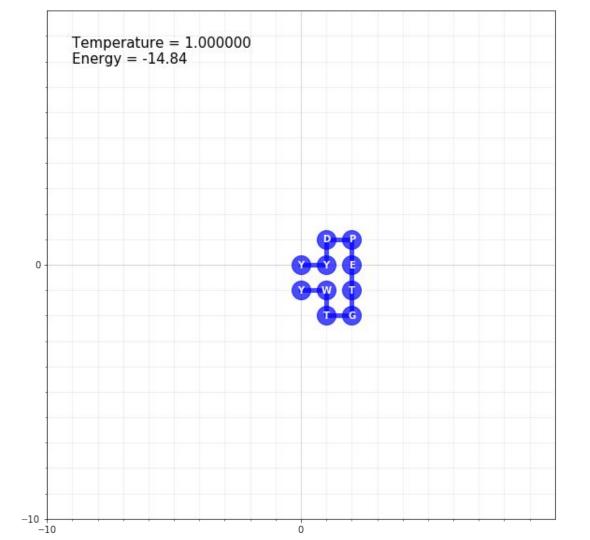
22 out of 360 (6.1%) in lowest energy conformation



Results

Simulated Annealing (Conventional MC)

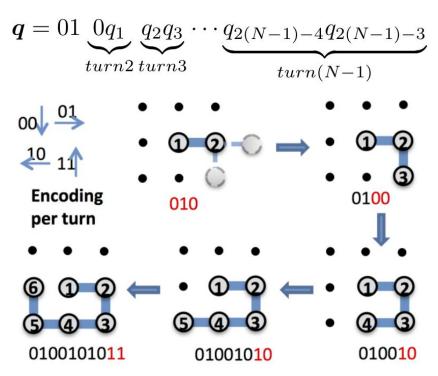
5 out of 360 (1.4%) in lowest energy conformation



Simulated annealing with qbit model: Turn Ancilla Encoding

Babbush, R., Perdomo-Ortiz, A., O'Gorman, B., Macready, W., and Aspuru-Guzik, A. (2013). Construction of energy functions for lattice heteropolymer models: a case study in constraint satisfaction programming and adiabatic quantum optimization. arXiv preprint arXiv:1211.3422v2

Babbush, R. et al. (2013). arXiv preprint arXiv:1211.3422v2



Babbush, R. et al. (2013). arXiv preprint arXiv:1211.3422v2

$$E(\mathbf{q}) = E_{back}(\mathbf{q}) + E_{overlap}(\mathbf{q}) + E_{pair}(\mathbf{q})$$

- Construct energy functions
 - Penalize bad conformations
 - Favor (or penalize) contact between residues
 - Use Miyazawa-Jernigan interaction potentials
- Optimization problem: minimize objective function E(q)

Babbush, R. et al. (2013). arXiv preprint arXiv:1211.3422v2

$$E_{back}(\mathbf{q}) = \lambda_{overlap} (q_1 q_2 + q_2 q_3 - 2q_1 q_2 q_3) + \lambda_{overlap} \sum_{i=2}^{2N-8} E_{back} (q_i q_{i+1} q_{i+2} q_{i+3}) [(i+1) \text{mod} 2]$$

$$E_{back}\left(q_{i}q_{i+1}q_{i+2}q_{i+3}\right) = \lambda_{overlap}\left(2q_{i}q_{i+2} - q_{i} - q_{i+2}\right)\left(2q_{i+1}q_{i+3} - q_{i+1} - q_{i+3}\right)$$

Babbush, R. et al. (2013). arXiv preprint arXiv:1211.3422v2

$$E_{overlap}\left(\boldsymbol{q}\right) = \sum_{i=1}^{N-4} \sum_{j=i+4}^{N} \left[\left(1+i-j\right) \operatorname{mod} 2 \right] \gamma_{ij} \qquad \text{with} \quad \gamma_{ij} = \lambda_{overlap} \left[2^{\mu_{ij}} - g_{ij} - \alpha_{ij} \right]^2$$

$$\forall g_{ij} \ge 1 \,\exists \, \alpha_{ij} : 2^{\mu_{ij}} - g_{ij} - \alpha_{ij} = 0$$

hence
$$2^{\mu_{ij}} - g_{ij} - \alpha_{ij} \ge 1 \,\forall \, \alpha_{ij}$$
 if and only if $g_{ij} = 0$

- $g_{ij} \rightarrow$ Manhattan distance between i-th and j-th residues
- α_{ij} \rightarrow Some number in decimal representation, with $0 \le \alpha_{ij} \le 2^{\mu_{ij}} 1$
- μ_{ij} \rightarrow Number of qbits used for a_{ij} 's binary representation

Babbush, R. et al. (2013). arXiv preprint arXiv:1211.3422v2

$$E_{pair}(\boldsymbol{q}) = \sum_{i=1}^{N-3} \sum_{j=i+3}^{N} \omega_{ij} J_{ij} (2 - g_{ij})$$
 $arphi_{ij} = \omega_{ij} J_{ij} (2 - g_{ij})$
 $arphi_{ij} = J_{ij} ext{ if and only if } g_{ij} = 1 \wedge \omega_{ij} = 1$

- J_{ij} ightharpoonup Miyazawa-Jernigan interaction potential between i-th and j-th residues
 - Note that J_{ij} < 0 for all possible pairwise interactions, hence if gij > 2 then $φ_{ij}$ becomes positive, penalization that is easily removed by setting $ω_{ij}$ = 0
 - Only pairs with odd relative positions along the backbone can be in contact, we set J_{ii} = 0 for the rest
- ω_{ij} Ancillary bit: a switch which is only "on" without incurring an energy penalty if two amino acids are interacting (g_{ii} = 1)

Methods Simulated Annealing (Ancilla Encoding MC)

- Define a schedule for annealing temperature T
- Randomly choose i-th "qbit" q_i
- Perform qbit flip
- Compute the change in energy dE = E E'
 - o E' and E are the energies before and after the step is taken
- Accept flip if exp(-dE/T) > random.uniform(0, 1)
 - \circ dE ≤ 0 \rightarrow accept always

Methods Simulated Annealing (Ancilla Encoding MC)

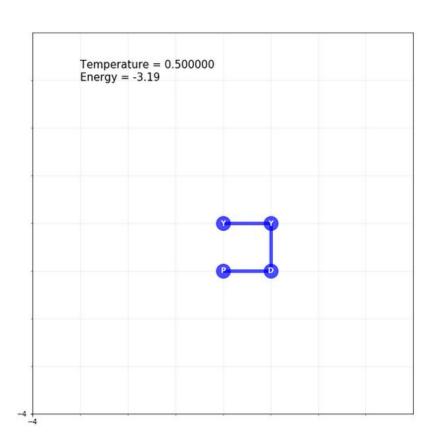
The energy (4 residue protein)

$$E = 20.0q_0q_1q_2q_3 - 10.0q_0q_1q_2 - 10.0q_0q_1q_3 + 5.0q_0q_1 - 10.0q_0q_2q_3 + 12.76q_0q_2q_6 + 5.0q_0q_3 + 12.76q_0q_4q_6 - 12.76q_0q_6 - 10.0q_1q_2q_3 + 5.0q_1q_2 + 12.76q_1q_3q_6 + 12.76q_1q_5q_6 - 12.76q_1q_6 + 20.0q_2q_3q_4q_5 - 10.0q_2q_3q_4 - 10.0q_2q_3q_5 + 10.0q_2q_3 - 10.0q_2q_4q_5 + 12.76q_2q_4q_6 + 5.0q_2q_5 - 12.76q_2q_6 - 10.0q_3q_4q_5 + 5.0q_3q_4 + 12.76q_3q_5q_6 - 12.76q_3q_6 + 5.0q_4q_5 - 12.76q_4q_6 - 12.76q_5q_6 + 22.33q_6$$

Results Simulated Annealing (Ancilla Encoding MC)

4 residue protein

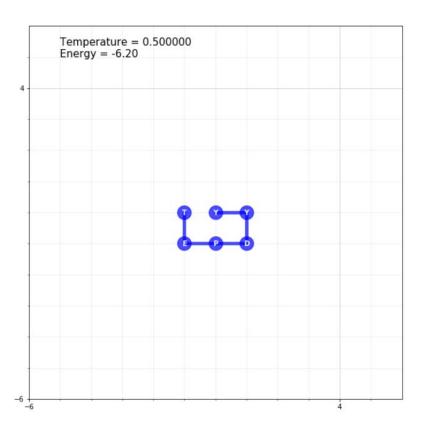
625 out of 720 (86.8%) in lowest energy conformation



Results Simulated Annealing (Ancilla Encoding MC)

6 residue protein

3 out of 720 (0.4%) in lowest energy conformation

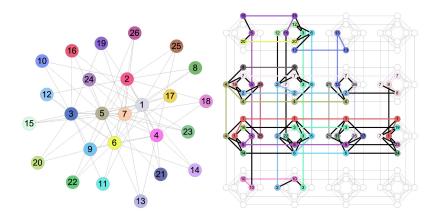


Adapting the problem

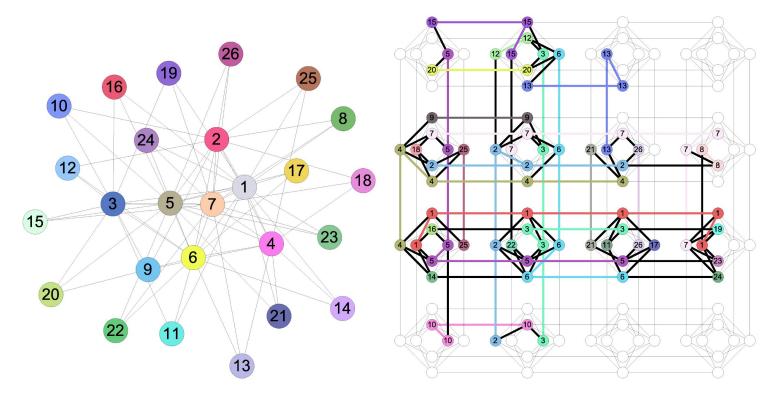
So it fits in D-Wave's Hardware with Chimera Architecture

Methods Order reduction and D-Wave Minor-Embedding

- Our energy expression has terms with up to degree 4
 - We need to introduce ancillary qbits to build equivalent expression of order 2
- A qbit in our model may need be coupled with many other qbits
 - Qbit connectivity is limited
 - Qbit chains need to be introduced to build equivalent interaction graph

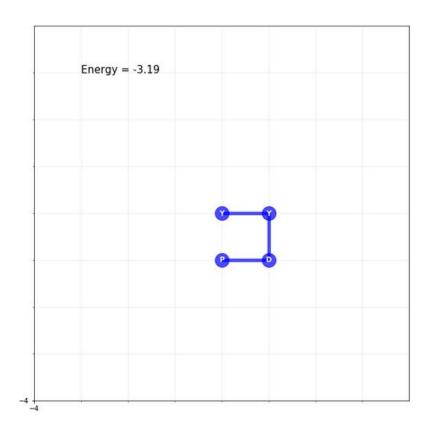


Methods D-Wave Minor-Embedding



```
# Now make sure an embedding can be found
problem = nx.Graph()
for k, v in dict(bqm.linear).items():
    problem.add node(k)
for k, v in dict(bqm.quadratic).items():
    problem.add edge(*k)
num cores = 12
embedding list = Parallel(n jobs=num cores)(delayed(find embedding)(problem, solver G) for jobid in range(10*num cores))
assigned gbits = np.array([len(sum(emb.values(), [])) if len(emb) > 0 else np.nan for emb in embedding list])
assert bool(sum(assigned qbits[~np.isnan(assigned qbits)])), "No embedding has been found"
print(np.sort(assigned gbits[~np.isnan(assigned gbits)]))
embedding = embedding list[np.nanargmin(assigned gbits)]
all assigned qbits = sum(embedding.values(), [])
print(f"Using {len(all assigned qbits)}/{solver.properties['num qubits']} qbits")
[1330, 1342, 1354, 1355, 1356, 1362, 1364, 1365, 1367, 1375, 1376, 1380,
 1381. 1387. 1388. 1391. 1394. 1399. 1400. 1402. 1403. 1405. 1405. 1405.
 1407. 1409. 1412. 1413. 1416. 1417. 1418. 1418. 1419. 1420. 1422. 1423.
 1424. 1425. 1425. 1426. 1426. 1426. 1426. 1426. 1427. 1432. 1433. 1434.
 1435. 1437. 1437. 1438. 1439. 1444. 1446. 1450. 1454. 1455. 1459. 1459.
 1460. 1461. 1463. 1464. 1464. 1466. 1472. 1476. 1479. 1481. 1494. 1496.
 1499. 1500. 1500. 1509. 1518. 1521. 1523. 1550. 1571.]
Using 1330/2048 gbits
```

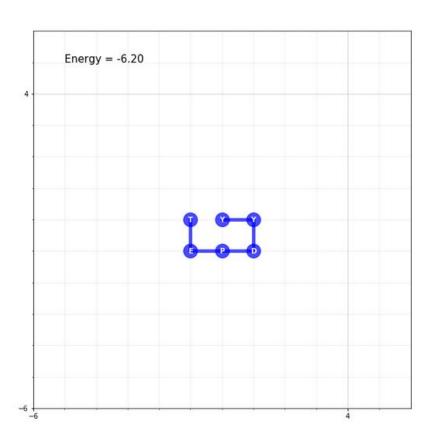
```
solver = DWaveSampler(solver="DW 2000Q 5")
solver G = nx.Graph(solver.edgelist)
sampler = FixedEmbeddingComposite(solver, embedding=embedding)
response = sampler.sample(bqm spin, num reads=num reads,
                          annealing time=20,
                          num spin reversal transforms=2,
                          postprocess='optimization',
                          answer mode='raw')
```



	energy	count		
0	-0.075758	1700		

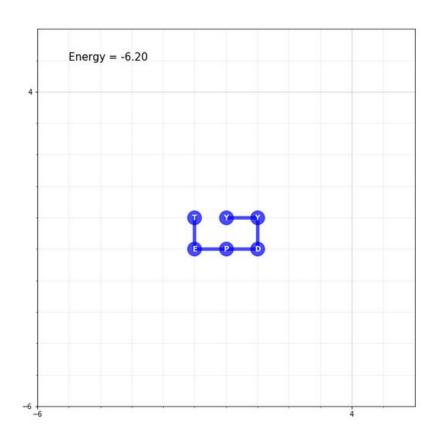
- 170 instances in single embedding
 - o 1190 qbits used
- 10 reads
- QPU time used: 24 ms

100% in lowest energy conformation



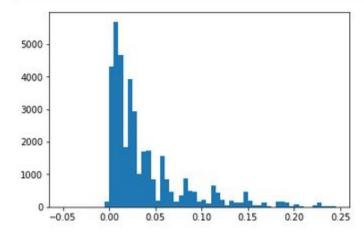
- 7 instances in single embedding
 - o 1330 qbits used
- 10000 reads
- QPU time used: 3170 ms

6 out of 70000 (0.00009%) in lowest energy conformation



	state	isvalid	energy	Hb	Но	Hi	count
0	0101011011100111100	True	-1.391382e-03	0	0	-6.20	6
1	1111010011101110110	True	-1.301616e-03	0	0	-5.80	3
2	1001010011101110110	True	-1.301616e-03	0	0	-5.80	6
3	0100001001100111001	True	-1.119838e-03	0	0	-4.99	15
4	0001011001101110101	True	-1.079443e-03	0	0	-4.81	10
5	0100000001101101000	True	-7.158887e-04	0	0	-3.19	8
6	0100001001100111000	True	-7.158887e-04	0	0	-3.19	10
7	0101010011101101000	True	-7.158887e-04	0	0	-3.19	1
8	0101011011100111000	True	-7.158887e-04	0	0	-3.19	6
9	0100010001100011000	True	-7.158887e-04	0	0	-3.19	8
10	0101000011100011000	True	-7.158887e-04	0	0	-3.19	9
11	1111010011101110100	True	-6.754937e-04	0	0	-3.01	2
12	0001011001101110100	True	-6.754937e-04	0	0	-3.01	9

```
plt.hist(all_sbsener[all_sbsvald], [-0.05 + 0.005*i for i in range(60)])
plt.show()
```



Code available

https://github.com/argearriojas/2dlattice-protfold

References

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- Miyazawa Jernigan (1996) Residue-Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading. https://doi.org/10.1006/jmbi.1996.0114
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 https://arxiv.org/abs/1811.00713