

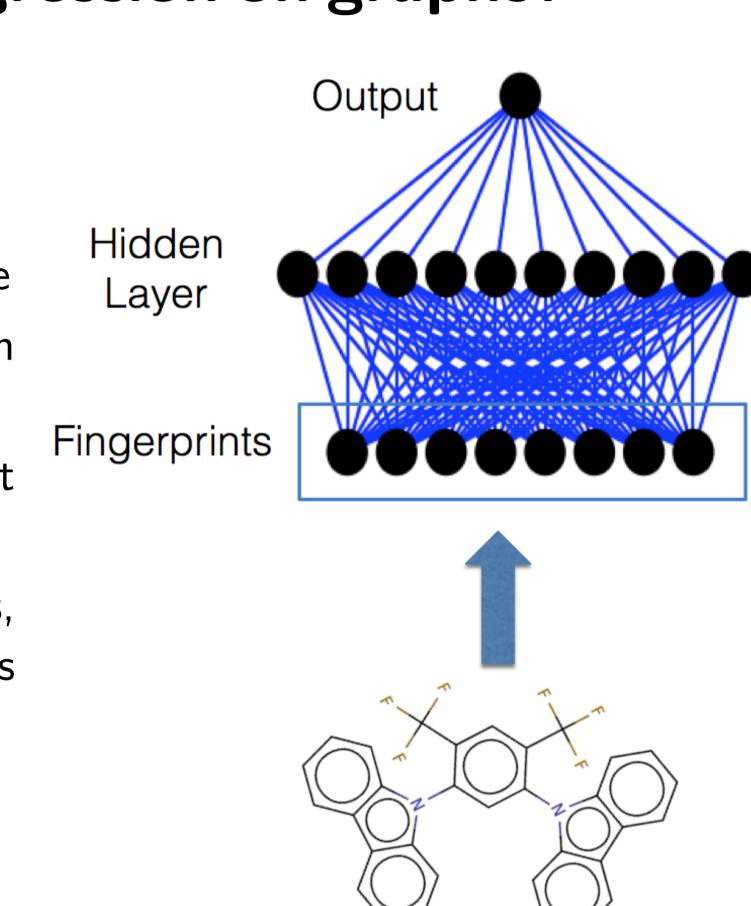
# Convolutional Networks on Graphs for Learning Molecular Fingerprints



David Duvenaud\*, Dougal Maclaurin\*, Jorge Aguilera-Iparraguirre

## How to do regression on graphs?

- Input can be any size or shape
- Hard to turn into fixed-length vector
- In our case, graphs represent molecules
- Applications to photovoltaics, organic LEDS, flow batteries and pharmaceuticals

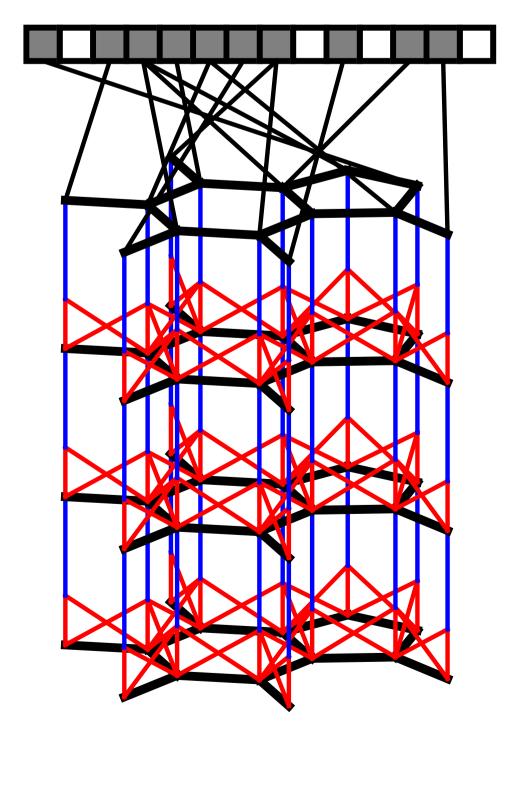


## Circular fingerprints

- Maps variable-sized molecular graph to fixed-length binary vector
- Binary features indicate presence of substructures

Can be efficiently computed using local operations:

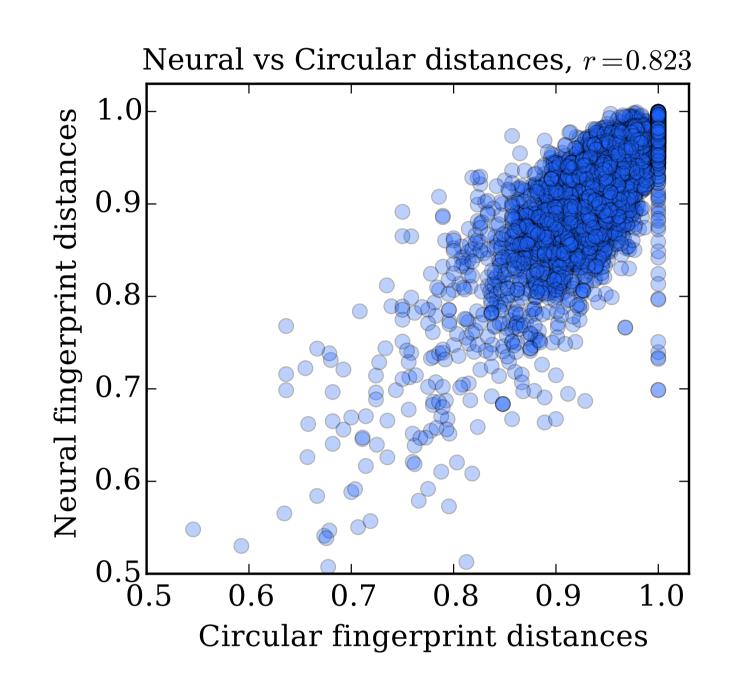
- At each layer, hash the features of each atom and its neighbors/bonds
- More layers correspond to increasing radius of substructures
- Interpret each hash as integer and set that entry to one



Was state-of-the-art for large-scale regression and classification.

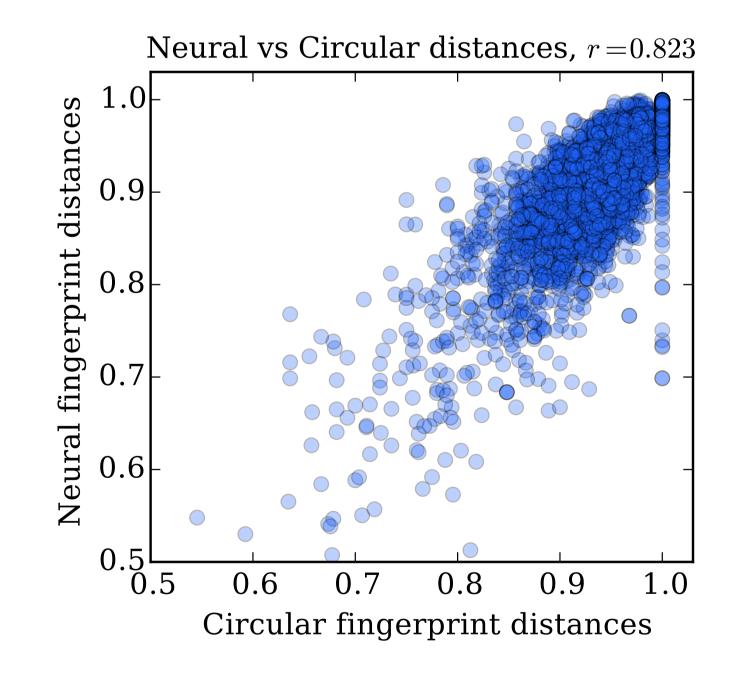
## Learning Curves - la vs lb

Comparison of learning



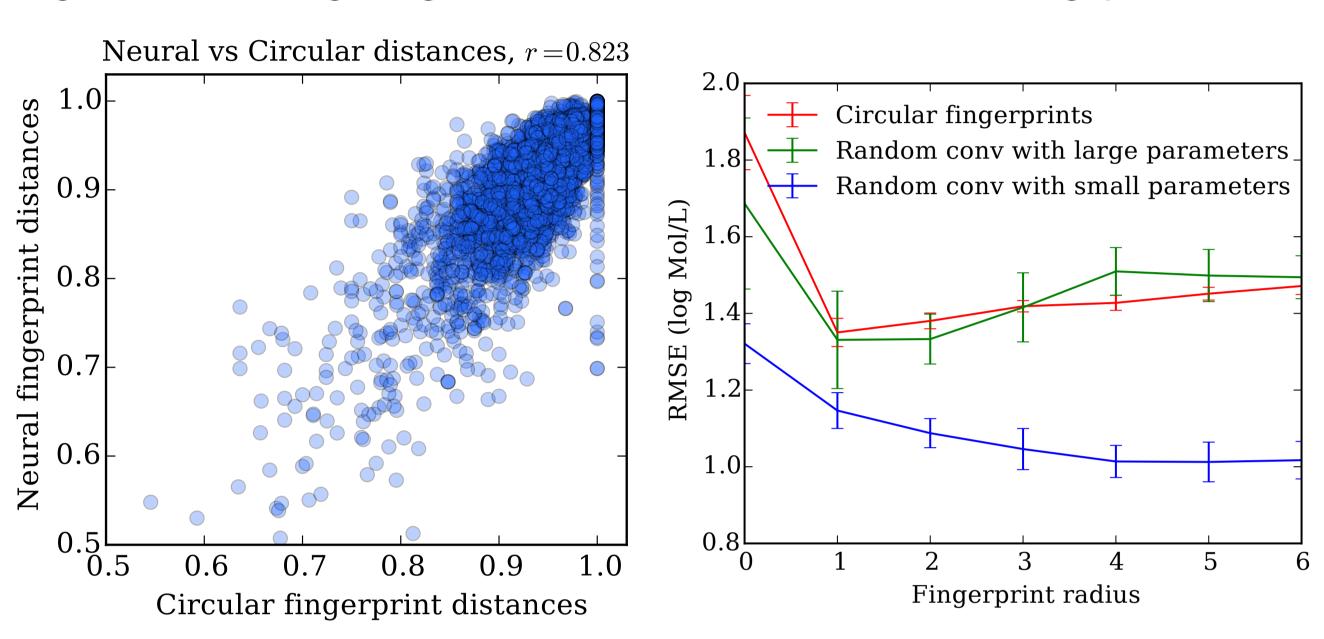
#### Visualisation of learned manifolds

Comparison of learning



### Full VB

Large random weights give similar behavior to circular fingeprints:

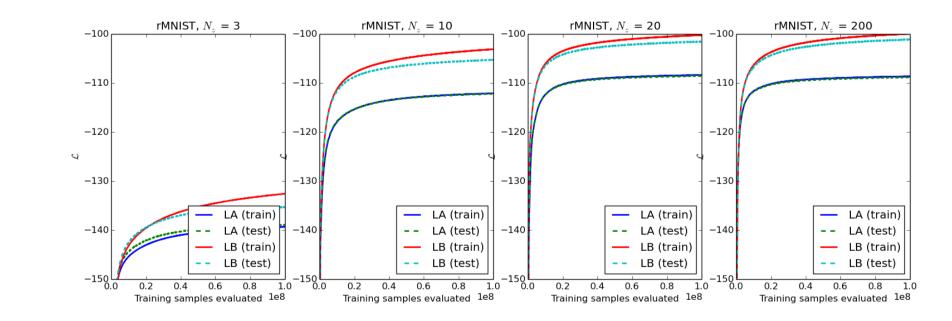


Small random weights already much better than circular fingerprints! Can do even better by optimizing for given task.

## Architecture experiments

We tested various set-up of the autoencoder

- Increasing the depth of the
- encoderDifferent activations
- Different activations



#### Conclusion

- Can learn graph features end-to-end!
- Works on other types of graphs too
- Code at github.com/HIPS/neural-fingerprint
- Autodiff package that works on standard Numpy code: github.com/HIPS/autograd