

Neural Network Model Chemistries

RIKEN 3/25/2017

John Parkhill

Department of Chemistry and Biochemistry, Notre Dame

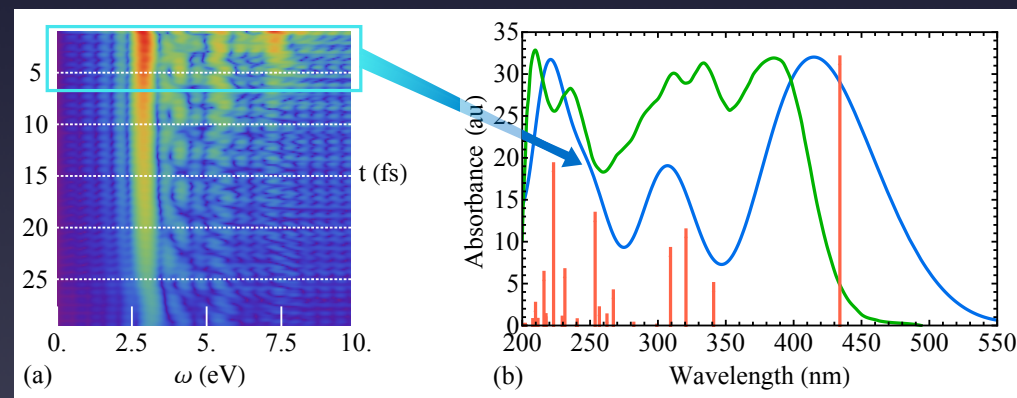
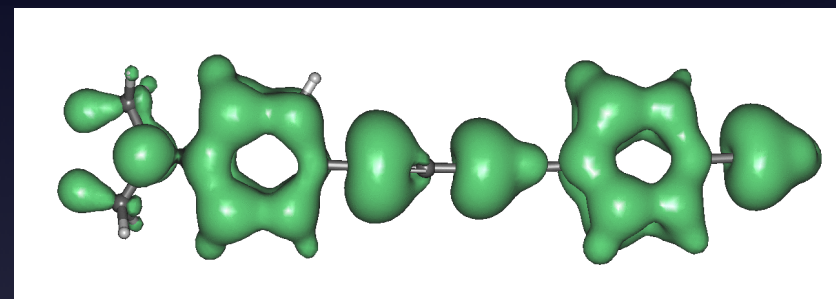
Parkhill Group

5 Students (K Yao)

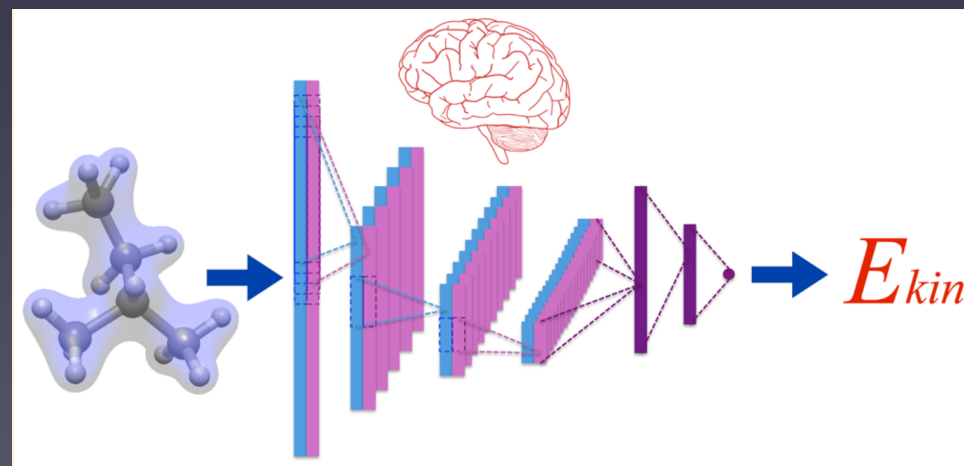
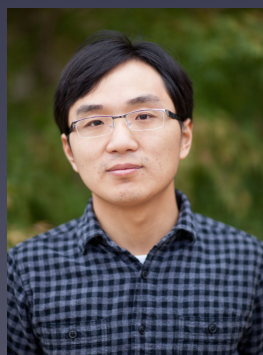
Research Areas:

Non-equilibrium realtime
quantum electronic dynamics.

$$\frac{d}{dt}\gamma_p = \frac{1}{2}\{\gamma_s\gamma_t V(s)_{st}^{pr} V(t)_{pr}^{st} \eta_p \eta_r + \gamma_s\gamma_t V(s)_{pr}^{st} V(t)_{st}^{pr} \eta_p \eta_r - \gamma_p\gamma_t V(s)_{rs}^{pt} V(t)_{pt}^{rs} \eta_r \eta_s - \gamma_p\gamma_t V(s)_{pt}^{rs} V(t)_{rs}^{pt} \eta_r \eta_s\}$$

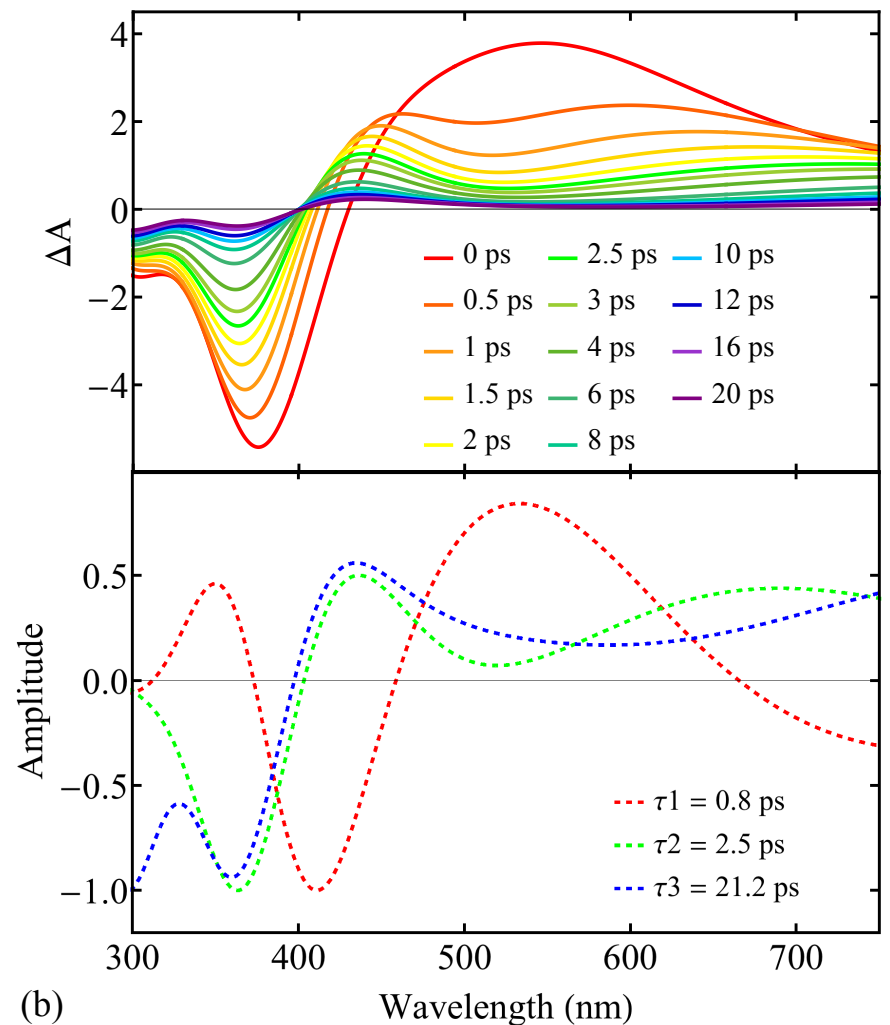
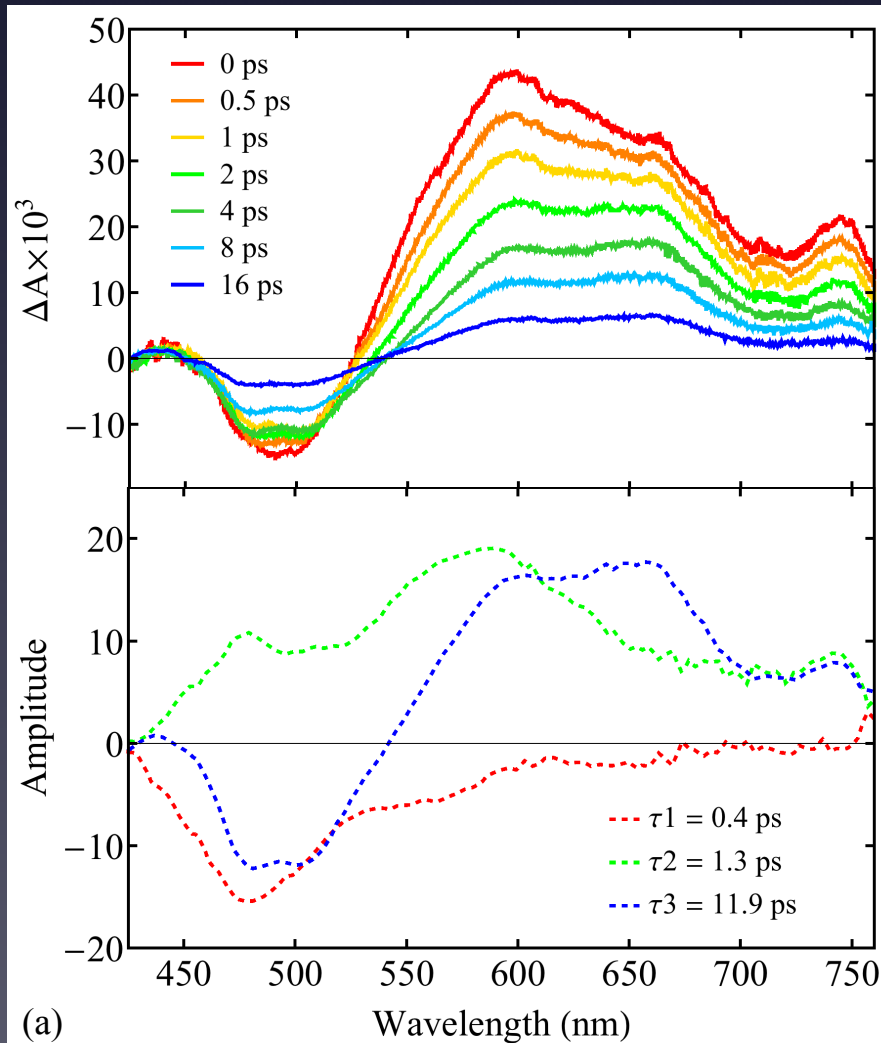
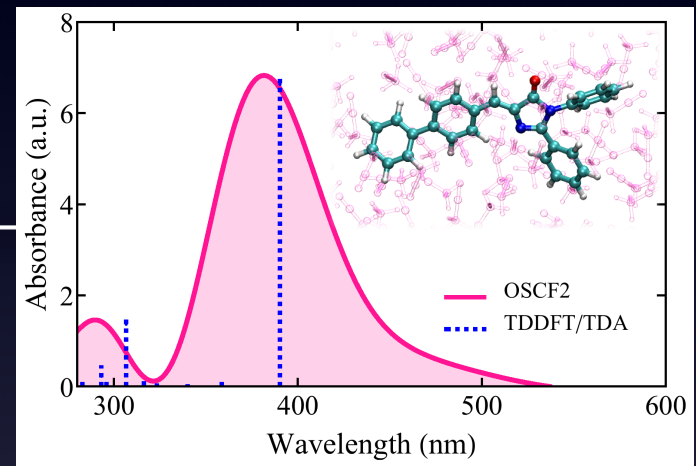


Applications of Neural
Networks to electronic
structure theory.



Realtime Spectra

Realtime Transient Abs. spectra
(Expt, Vauthey left)



Begging for Breakthroughs

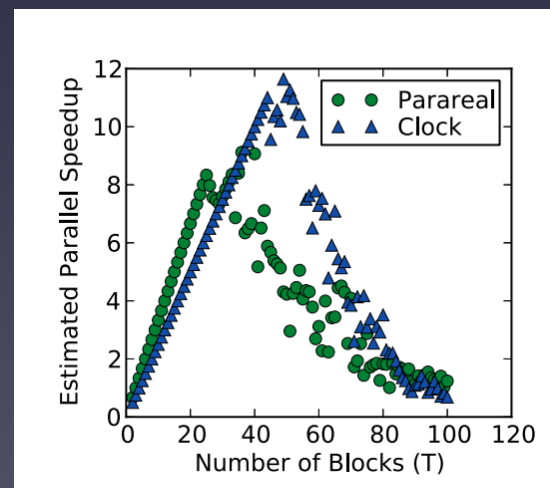
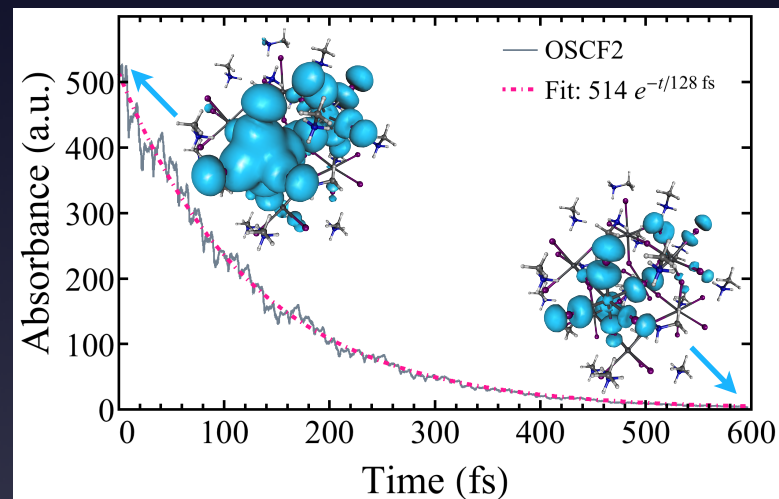
Electronic timescale

$\sim 4 \times 10^{-4}$ fs

1 ps = 10^7 fock builds

114 days at 1 build/second

Dynamics is sequential
and parallelization in time
is weak.



Feynman's clock, a new variational principle, and parallel-in-time quantum dynamics

Jarrod R. McClean^a, John A. Parkhill^b, and Alán Aspuru-Guzik^{a,1}

^aDepartment of Chemistry and Chemical Biology, Harvard University, Cambridge, MA 02138; and ^bDepartment of Chemistry, University of Notre Dame, South Bend, IN 46556

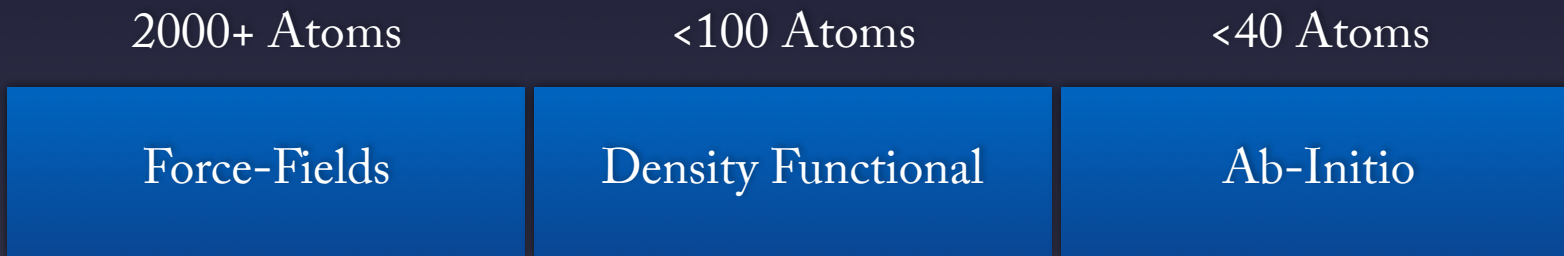
Edited by Frank A. Wilczek, Center for Theoretical Physics, Cambridge, MA, and approved August 20, 2013 (received for review April 29, 2013)

We introduce a discrete-time variational principle inspired by the quantum clock originally proposed by Feynman and use it to write generalize the Feynman clock into a time-embedded discrete variational principle (TEDVP) that offers additional insight

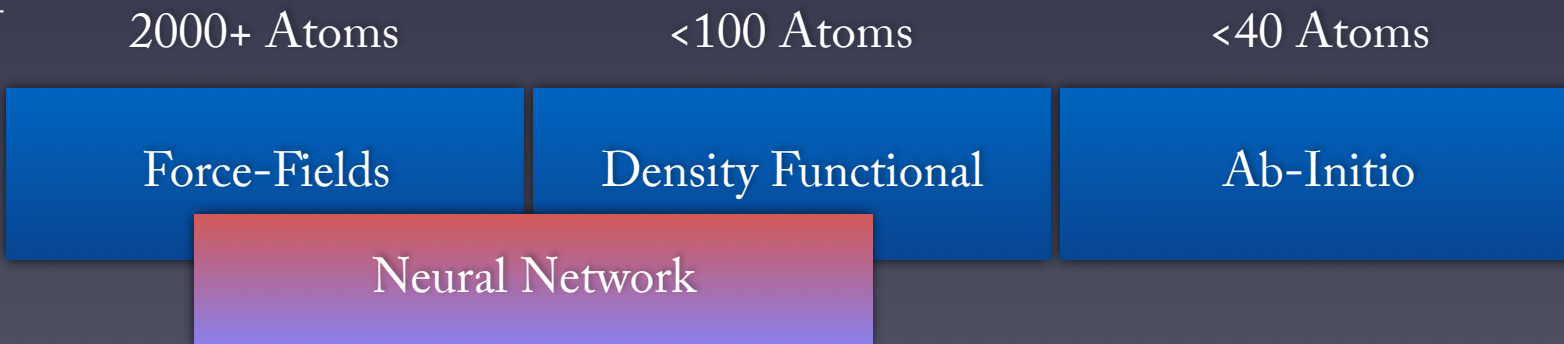
3 Models

- Orbital Free DFT
- Neural Networks + Many Body Expansion.
- A Diatomics in Molecules NN

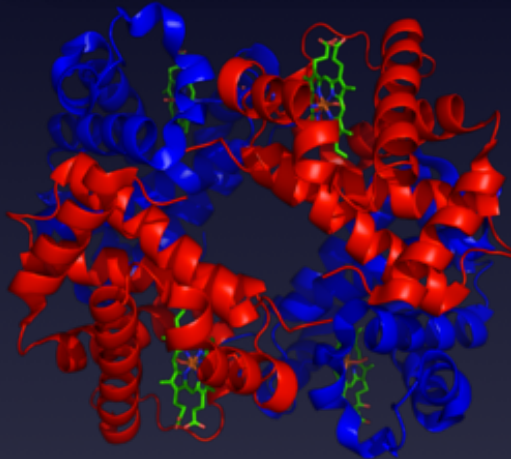
Today



Soon



Orbital Free DFT

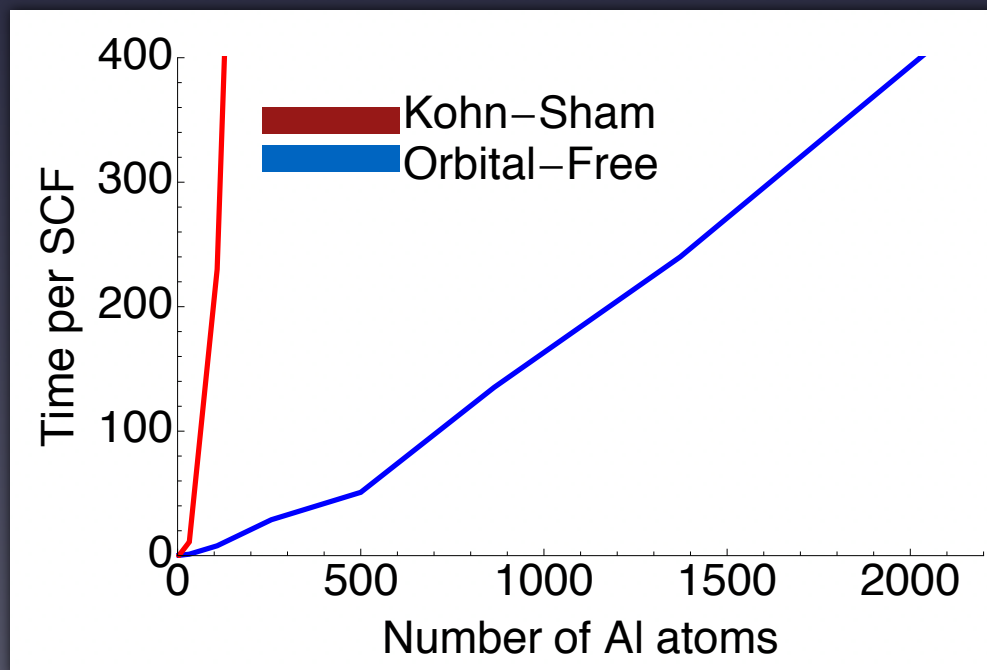


Hemoglobin : 16000 Daltons
~ 16000 orbitals vs Limit of Most KS ~ 3000

With orbital free-DFT you only need 1 orbital, and get a 10x speedup.

But you must know a mysterious ‘functional’ which maps the density to kinetic energy....

$$E_{\text{kin}} = \int T(n(r)) dr$$



PRL 108, 253002 (2012)

PHYSICAL REVIEW LETTERS

week ending
22 JUNE 2012

Finding Density Functionals with Machine Learning

John C. Snyder,¹ Matthias Rupp,^{2,3} Katja Hansen,² Klaus-Robert Müller,^{2,4} and Kieron Burke¹

¹Departments of Chemistry and of Physics, University of California, Irvine, California 92697, USA

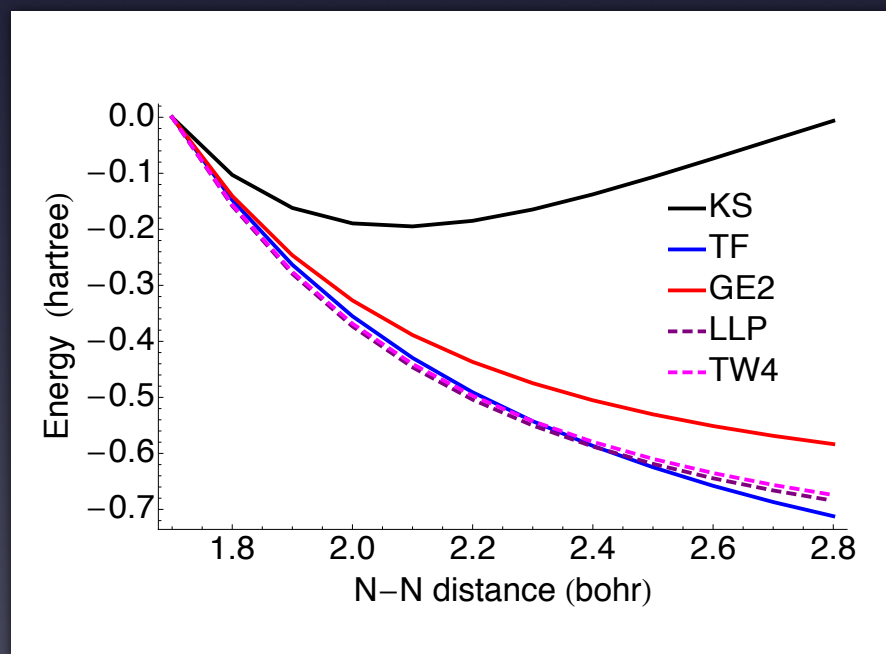
²Machine Learning Group, Technical University of Berlin, Berlin 10587, Germany

³Institute of Pharmaceutical Sciences, Eidgenössische Technische Hochschule Zürich, Zürich 8093, Switzerland

⁴Department of Brain and Cognitive Engineering, Korea University, Anam-dong, Seongbuk-gu, Seoul 136-713, Korea
(Received 16 December 2011; published 19 June 2012)

Chemistry Starts in the 4th digit.

$$T_{\text{GGA}} = \int \tau_{\text{TF}}(n(r)) F \left(\frac{|\nabla n(r)|}{n(r)^{3/4}} \right)$$



Accuracy ~ 1 %

No shell structure

No Bonding !

A Kohn-Sham Kinetic Energy Density

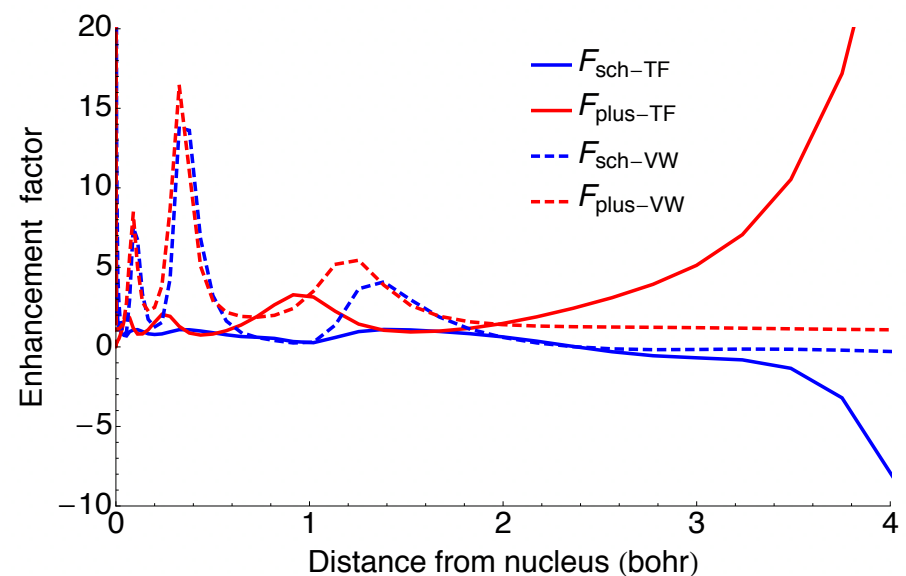
$$T = \int F(\rho(r), \rho(r_1), \rho(r_2), \dots) t_{TF(VW)}(\rho; r) dr$$

Local kinetic energy $t_{plus} = \frac{1}{2} \sum_{i=1}^N |\nabla \phi_i(r)|^2$ $t_{sch} = -\frac{1}{2} \sum_{i=1}^N \phi_i^*(r) \nabla^2 \phi_i(r)$

Thomas Fermi and
Von Weisacker

$$T_{TF} = \int C_{TF} \rho^{5/3} dr \quad T_{VW} = \frac{1}{8} \int \frac{|\nabla \rho|^2}{\rho} dr$$

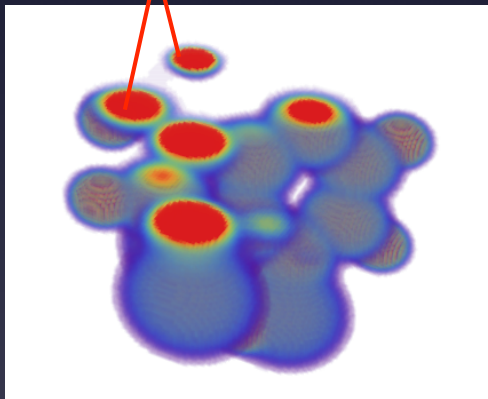
- Four types of F
- They all display the shell structure
- TF based F diverge at long distance, while VW based converge



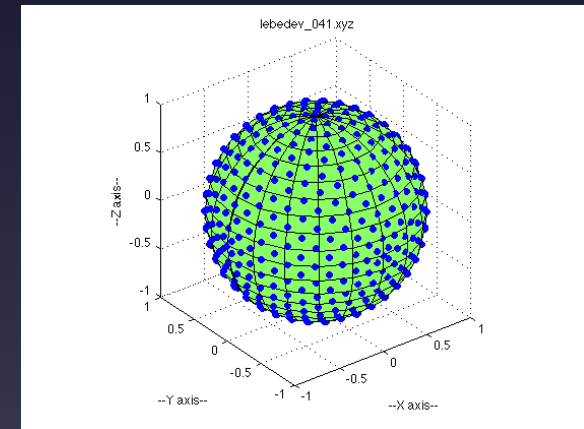
CNN version 0.1

Pseudo 2-d input motivated by computational limitations

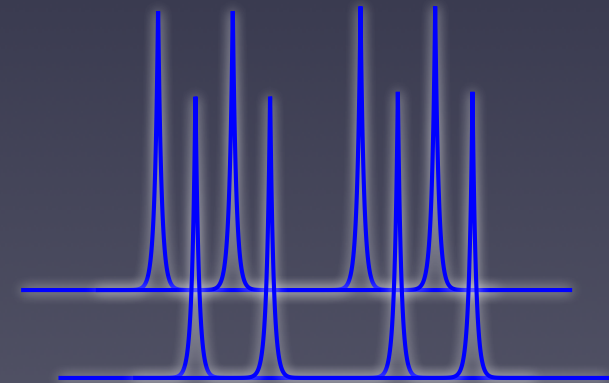
quadrature point



Density along lines fed into convolutional neural network.



- ~1 million quadrature points per atom.
- ~2000 inputs per quadrature point.
- ~Barely tractable

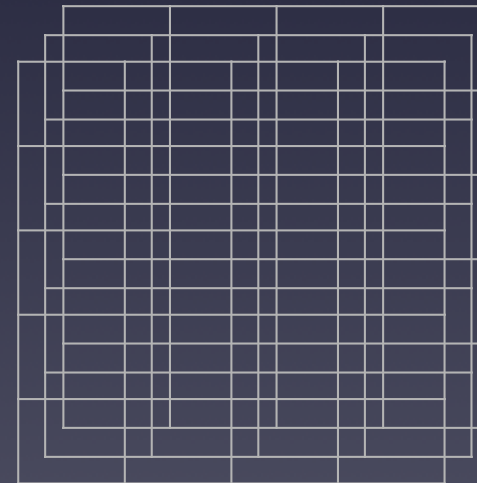
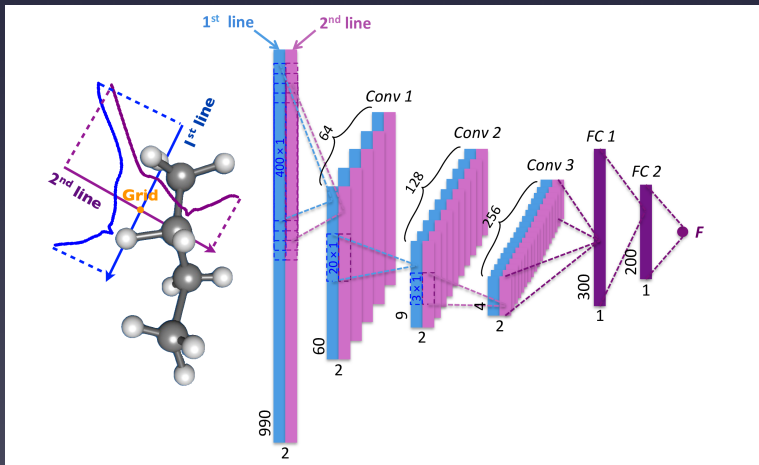


Our Network

$$T\{n(r)\} = \int F\{n(r), r'\} \tau_{tf}(r') dr' \quad \tau_{TF} = \frac{3}{10} (3\pi^2)^{5/3} n(r)^{2/3} dr$$

~4000 samples per grid point
 10^6 samples per atom

Future thoughts:
 3D Convolutional Networks
 Basis sets

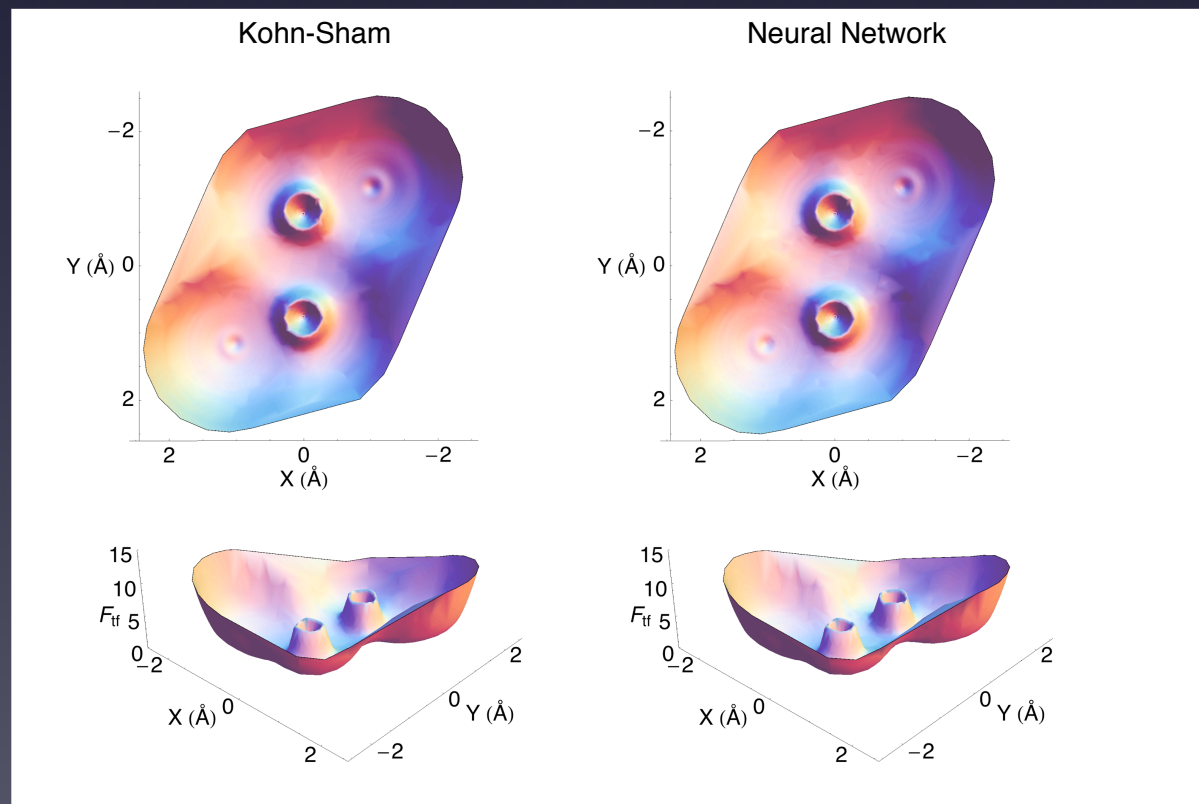


$$y_{mn}^i = f(b^i + \sum_{a=0}^{a=p} \sum_{b=0}^{b=q} y_{(m+a)(n+b)}^{i-1} w_{ab}^{i-1,i}) \quad f(x) = \max(0, x)$$

Finding a functional

Learn F as a function of $n(r)$, given as a slice of the surface.

$$T\{n(r)\} = \int F\{n(r), r'\} \tau_{tf}(r') dr'$$



The shape of the error

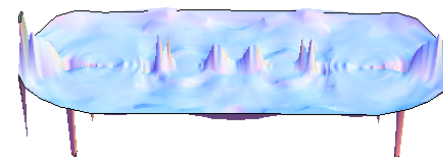
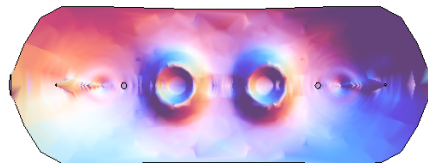
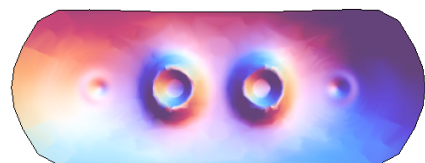
Enhancement Factor in C-C bonding plane

Accurate (KS)

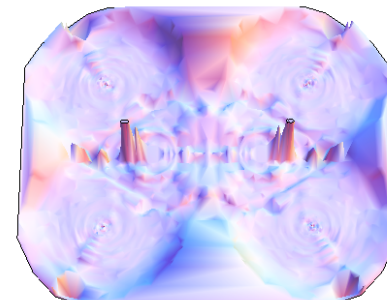
Neural Net

Error(NN-KS)

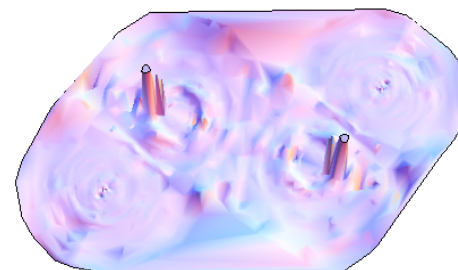
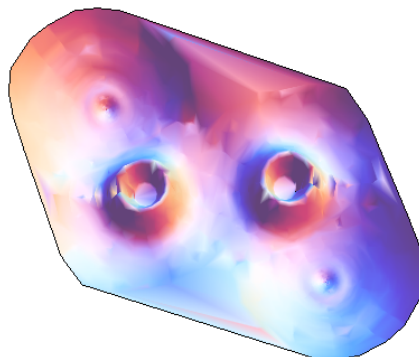
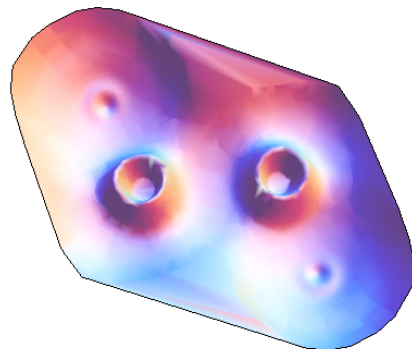
C_2H_2



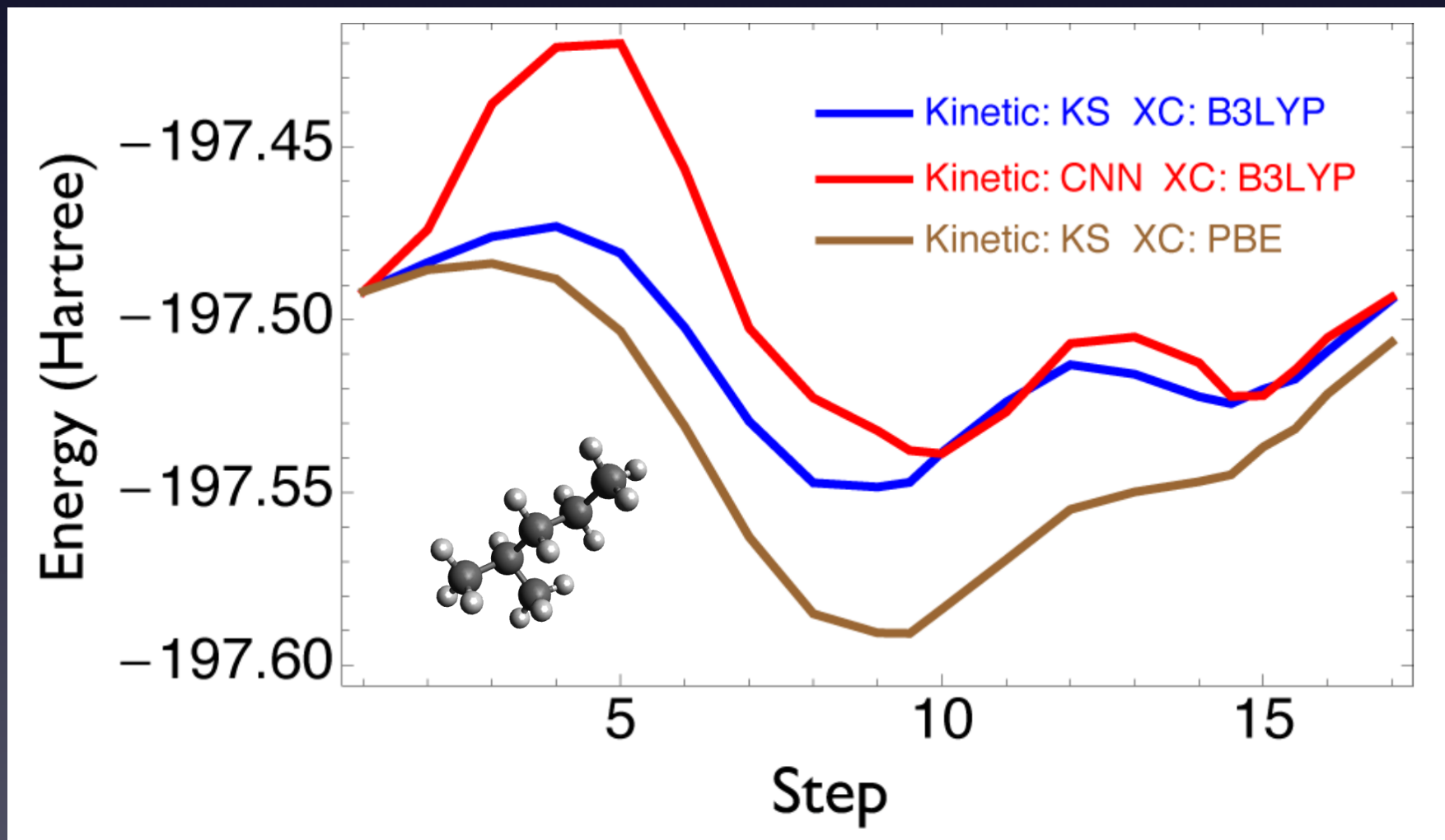
C_2H_4



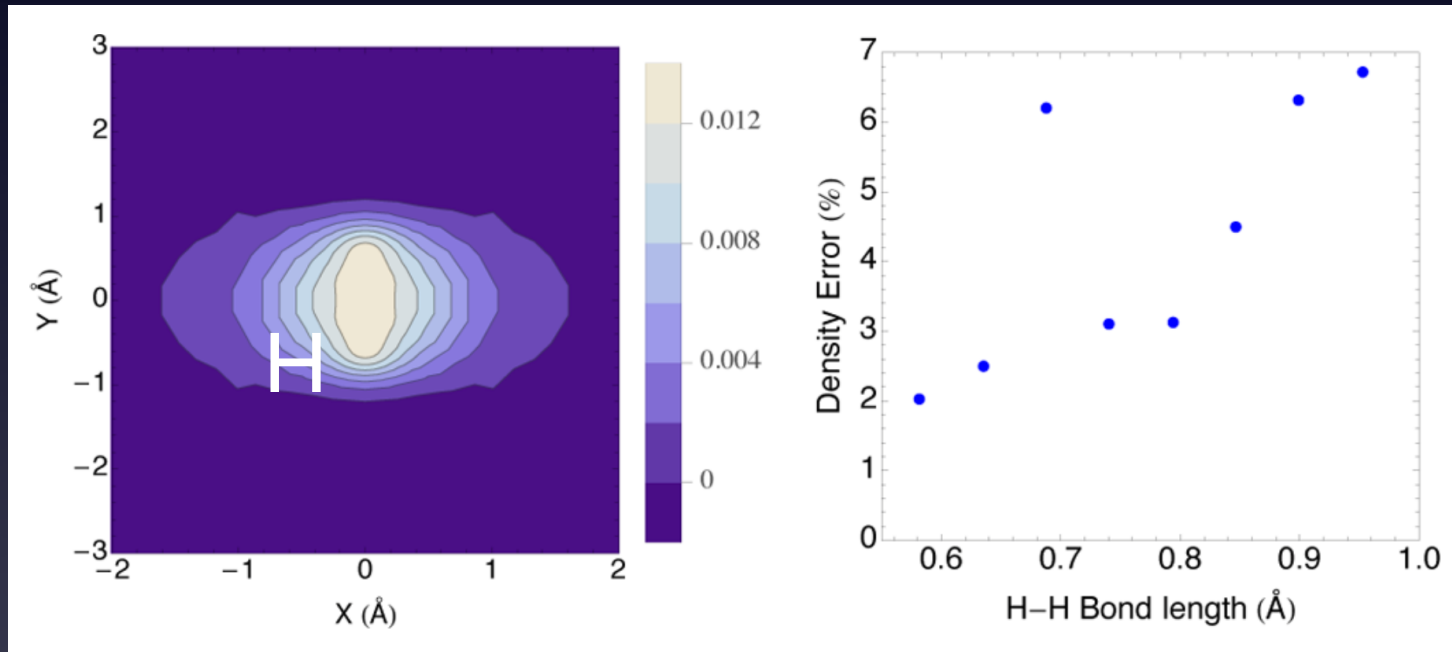
C_2H_6




Reproducing Potential Energy Surfaces



Self-Consistent Densities.



Errors of the NN's optimal density in Hydrogen

 **cuda-convnet**
High-performance C++/CUDA implementation of convolutional neural networks

[Project Home](#) [Wiki](#) [Issues](#) [Source](#)

Summary [People](#)

Project Information

★ Starred by 360 users
[Project feeds](#)

Code license
[New BSD License](#)

Labels
Machinelearning,

Note July 18, 2014:

- I've released an update to cuda-convnet, called [cuda-convnet2](#). The two main new features are faster training and support for multi-GPU training.

This is a fast C++/CUDA implementation of convolutional (or more generally, feed-forward) neural network connectivity and network depth. Any directed acyclic graph of layers will do. Training is done using the backpropagation algorithm. Fermi-generation GPU (GTX 4xx, GTX 5xx, or Tesla equivalent) required.

Getting Serious.

- Better Density inputs.
- Gradients (which require tight integration between electronic structure and the NN).
- Some architecture for training data

PYSCF

TensorMol



The screenshot shows the GitHub repository page for `jparkhill / TensorMol`. At the top, it displays repository statistics: 7 watchers, 9 stars, and 0 forks. Below this is a navigation bar with links for Code, Issues (0), Pull requests (0), Projects (0), Wiki, Pulse, Graphs, and Settings. The repository description is "Tensorflow + Molecules = TensorMol" with a link to <http://blogs.nd.edu/parkhillgroup>. Below the description, it shows repository statistics: 448 commits, 3 branches, 0 releases, 4 contributors, and GPL-3.0 license. At the bottom, there are buttons for "Branch: master", "New pull request", "Create new file", "Upload files", "Find file", and "Clone or download". The latest commit is by `jeherr` with the message "transformer clean up and cabbage" and a commit hash of `55ce7a8` from 2 days ago.

What is TensorMol

A set of chemical routines
(90% python 10% C++) on top of

TensorFlow™

Capabilities:

- Behler-Parrinello, Many Body etc.
- Various network types (FC, Convolutional, 3d)
- A variety of digesters: (Coulomb, Symmetry Functions, Radial*Spherical Harmonics)
- A variety of outputs (energy, force, probability)
- Some gradients.
- Integration with PYSCF for Ab-initio energies, Coulomb integrals etc.

A Heretical Model

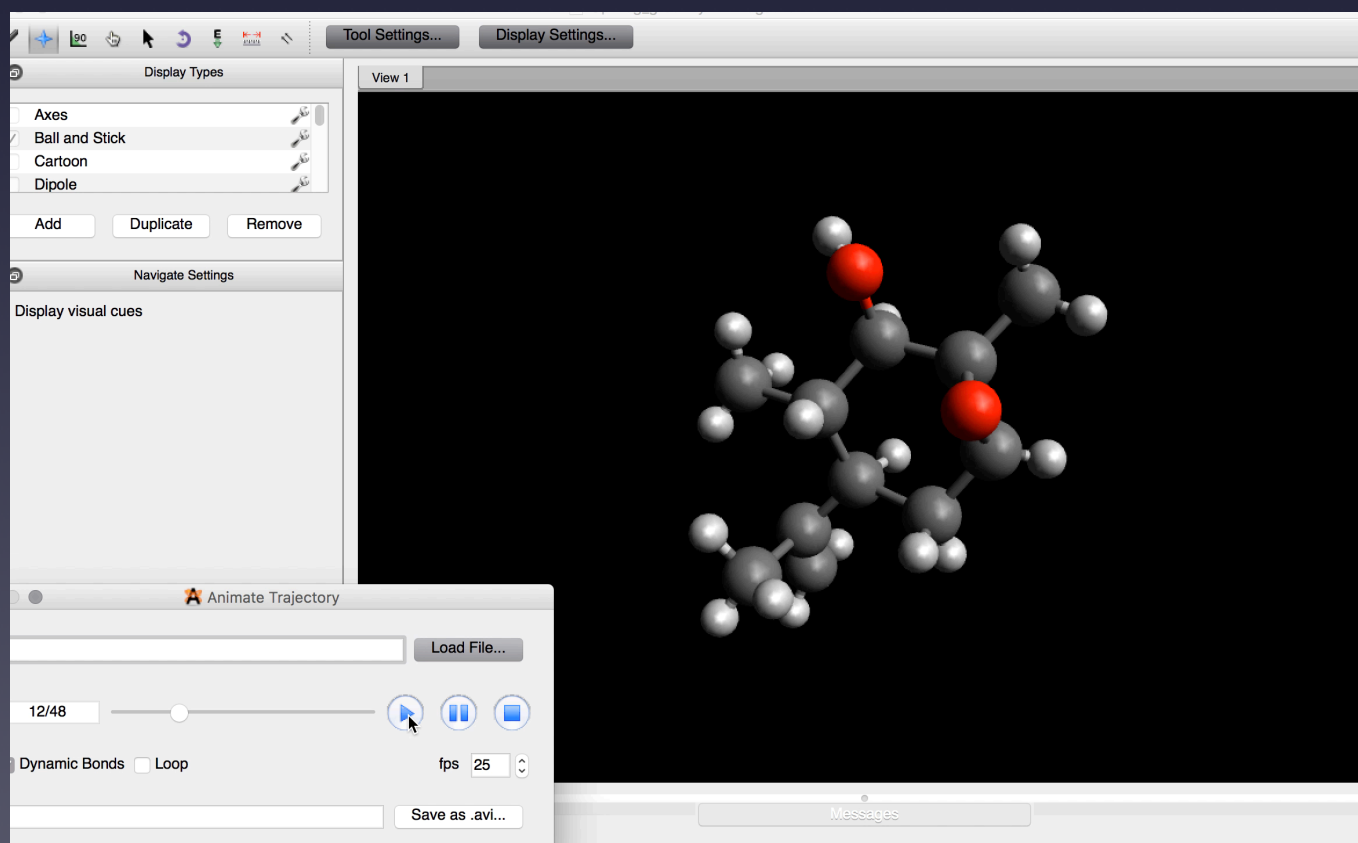
Take some crystal structures, define a Gô type potential. Sample its normal modes, and learn its force. Then optimize other molecules

```
a=MSet("OptMols")
a.ReadXYZ("OptMols")
c=a.DistortedClone(60)
b=a.DistortAlongNormals()
TreatedAtoms = b.AtomTypes()
# 2 - Choose Digester
d = Digester(TreatedAtoms, name_="GauSH",OType_ ="Force")
# 4 - Generate training set samples.
tset = TensorData(b,d)
tset.BuildTrain("OptMols_NEQ",TreatedAtoms) # generates dataset numpy arrays for each atom.
tset2 = TensorData(c,d)
tset2.BuildTrain("OptMols_NEQ",TreatedAtoms,True) # generates dataset numpy arrays for each atom.
tset = TensorData(None,None,"OptMols_NEQ_GauSH",None,6000)
manager=TFManage("",tset,True,"fc_sqdiff") # True indicates train all atoms

test_mol = a.mols[0]
print "Orig Coords", test_mol.coords
test_mol.Distort()
print test_mol.coords
print test_mol.atoms
manager=TFManage("OptMols_NEQ_GauSH_fc_sqdiff",None,False)
optimizer = Optimizer(manager)
optimizer.Opt(test_mol)
```

A Heretical Model

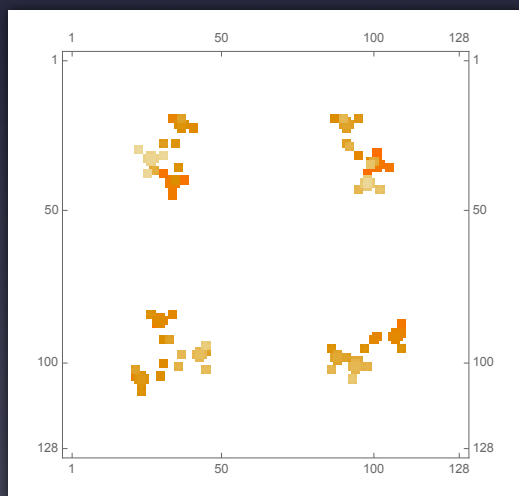
Take some crystal structures, define a Gô type potential. Sample its normal modes, and learn its force. Then optimize other molecules



Physical Inputs with Invariance

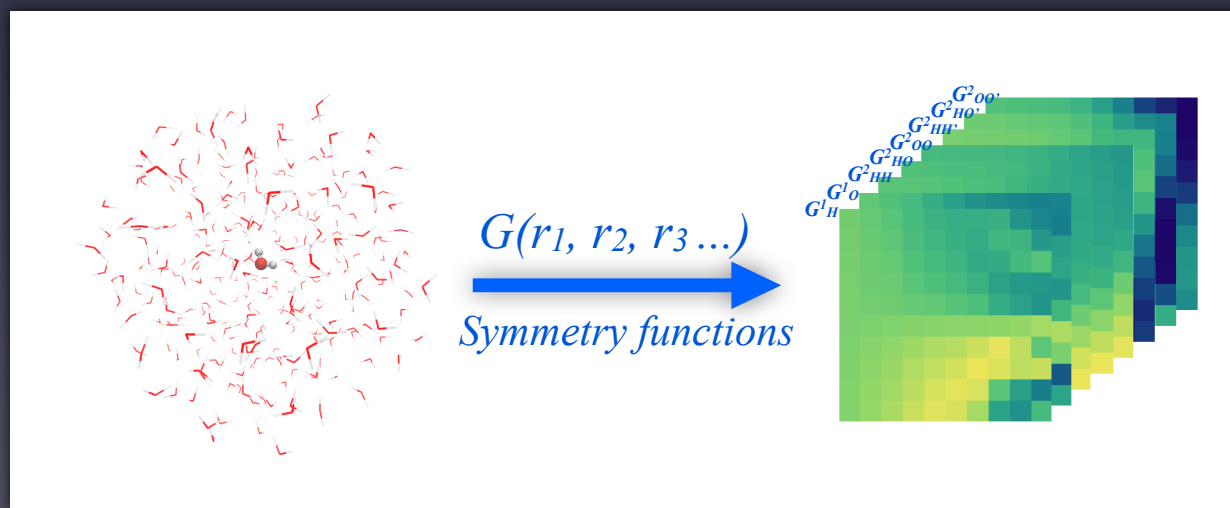
How to parameterize a molecule with invariances and retain invertibility?
How to express atomic number differences avoiding separate channels.

Depth Map



Coulomb Matrix?
Sorted by distance or atomic number?

Symmetry Functions?

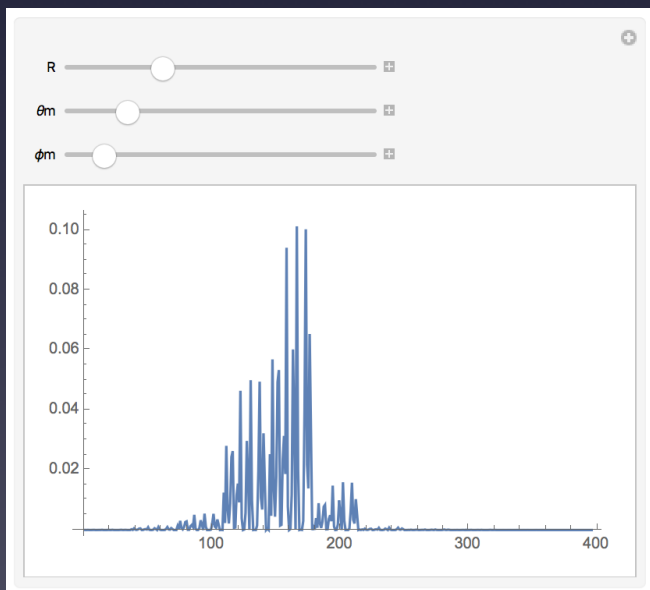


Physical Inputs with Invariance

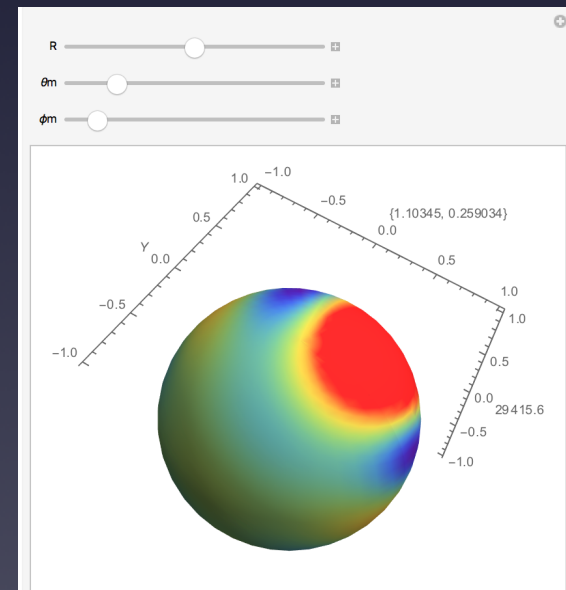
$$f_{nlm}(x, y, z) = R_n Y_{l,m}$$

$$R_n = e^{-(r-r_0)^2 / (2\sigma^2)}$$

Embedded Space

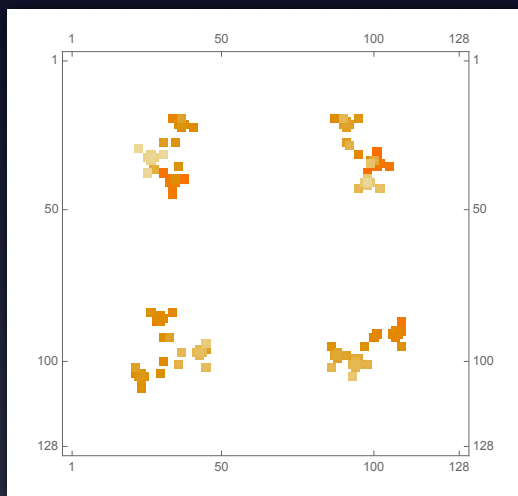


Real Space

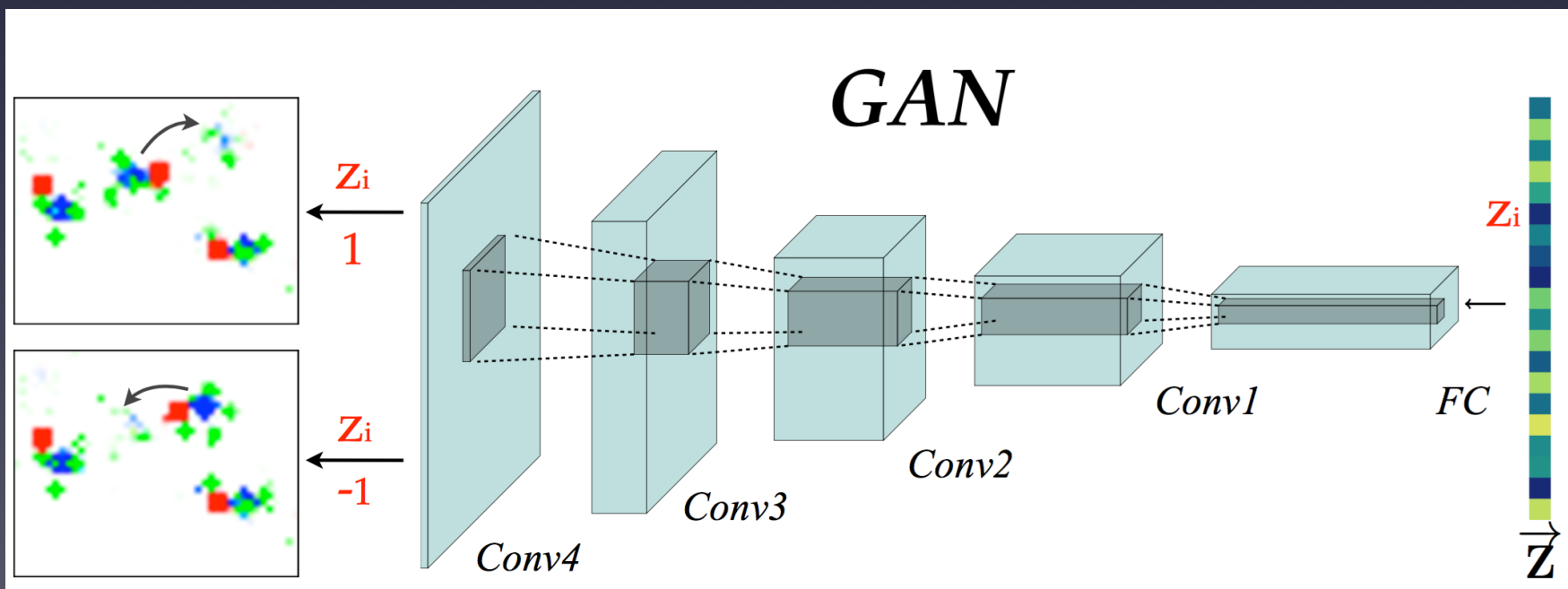


This embedding is reversible! can go between geometry and embedded geometry reversibly.

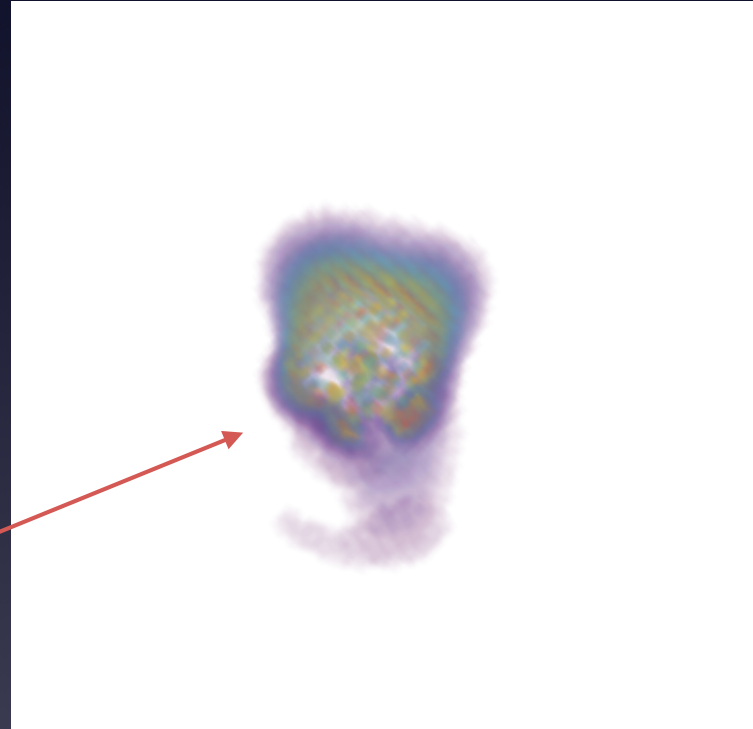
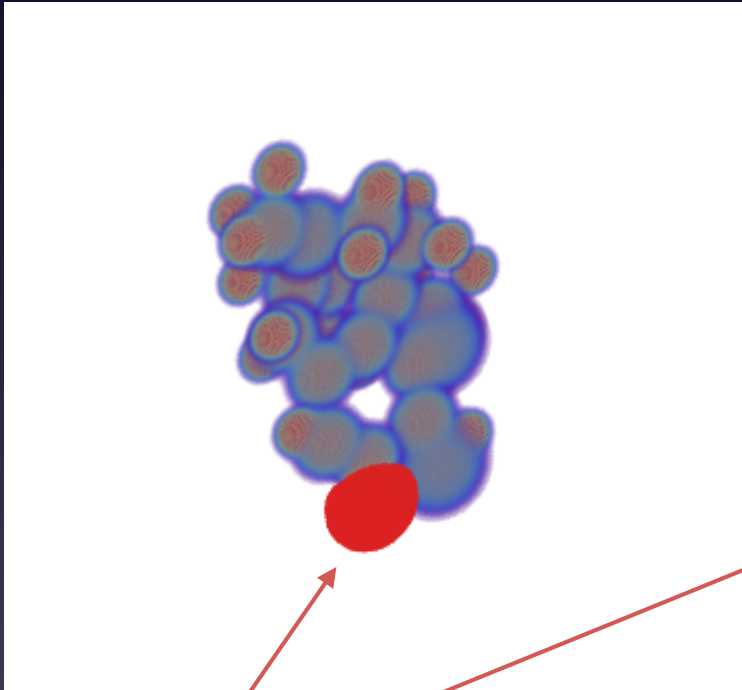
Generative Adversarial models.



Depth of field map for an MD trajectory of 3 methanols
A way to create a set of nonlinear modes to sample chemical space.



My personal favorite



Embedding for this atom

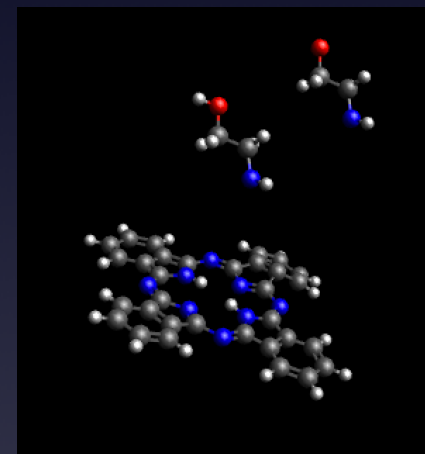
$$|rlm\rangle = \sum_{\text{atoms}} f_r(x, y, z) Y_m^l(x, y, z) * (\text{Atm.Number})$$

Partitioning of the energy.

Behler-Parinello

$$E = \sum_{\text{Atoms}} E_{\text{atom}}$$

Back propagates
atom networks for each
element with only 1 energy



Many Body Expansion

$$E = \sum_{\text{Molecules}} E_{\text{mol}} + \sum_{\text{pairs}} E_{\text{pair}} + \dots$$

Uses separate monomer
dimer etc. training data

Diatomics-in-molecules NN

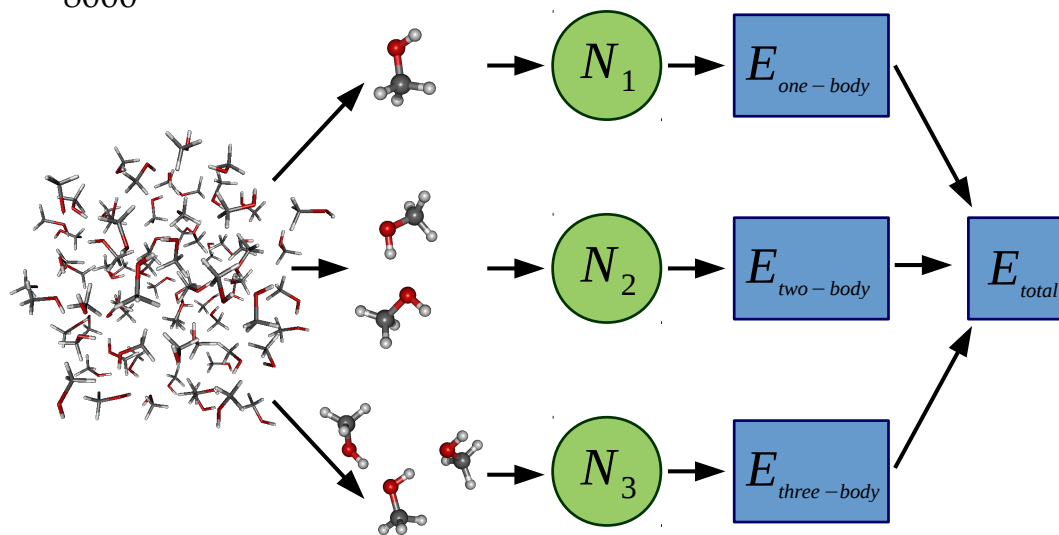
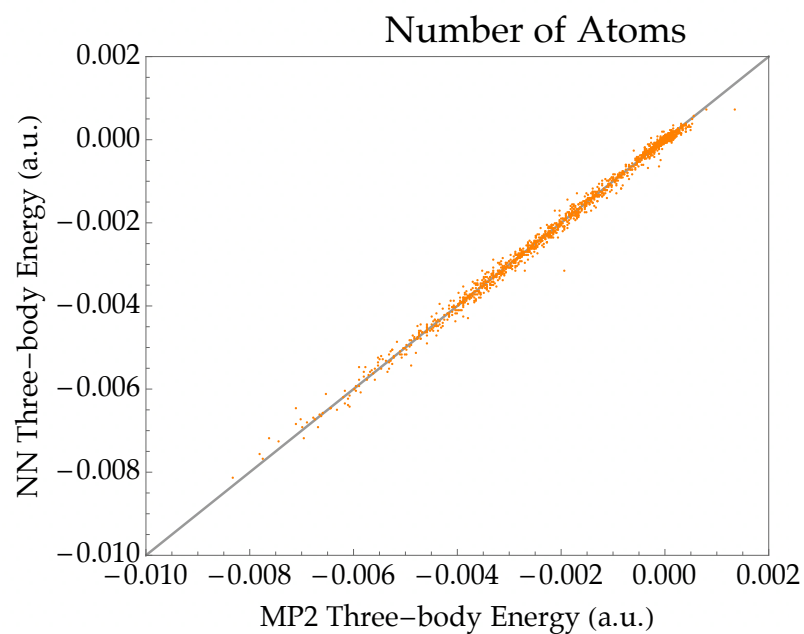
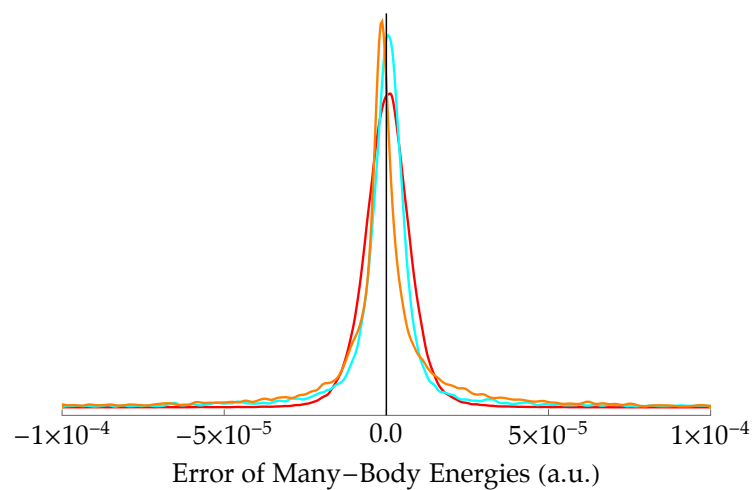
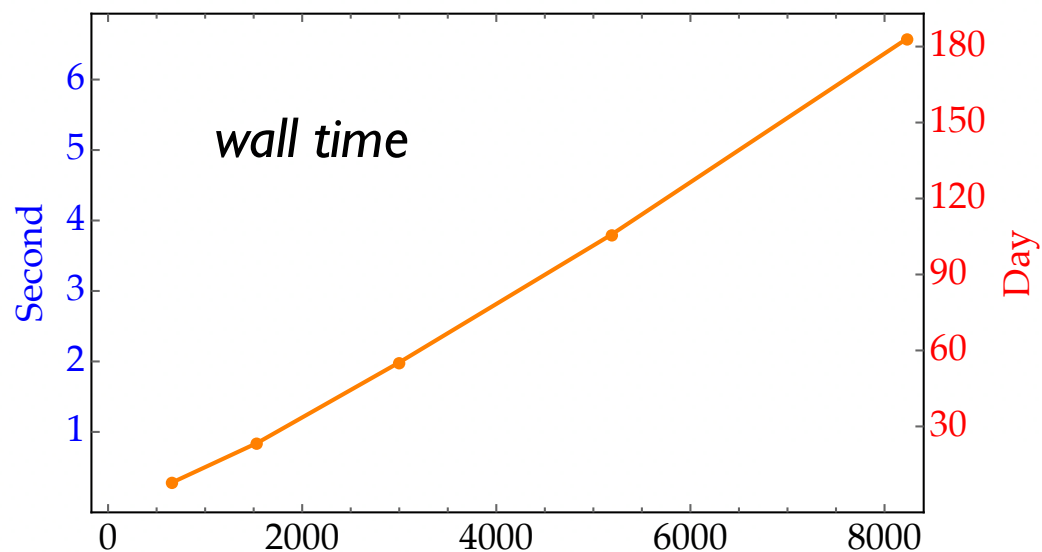
$$E = \sum_{\text{Bonds}} E_{\text{bond}}$$

Like Behler-Parinello but
bond energies vary less

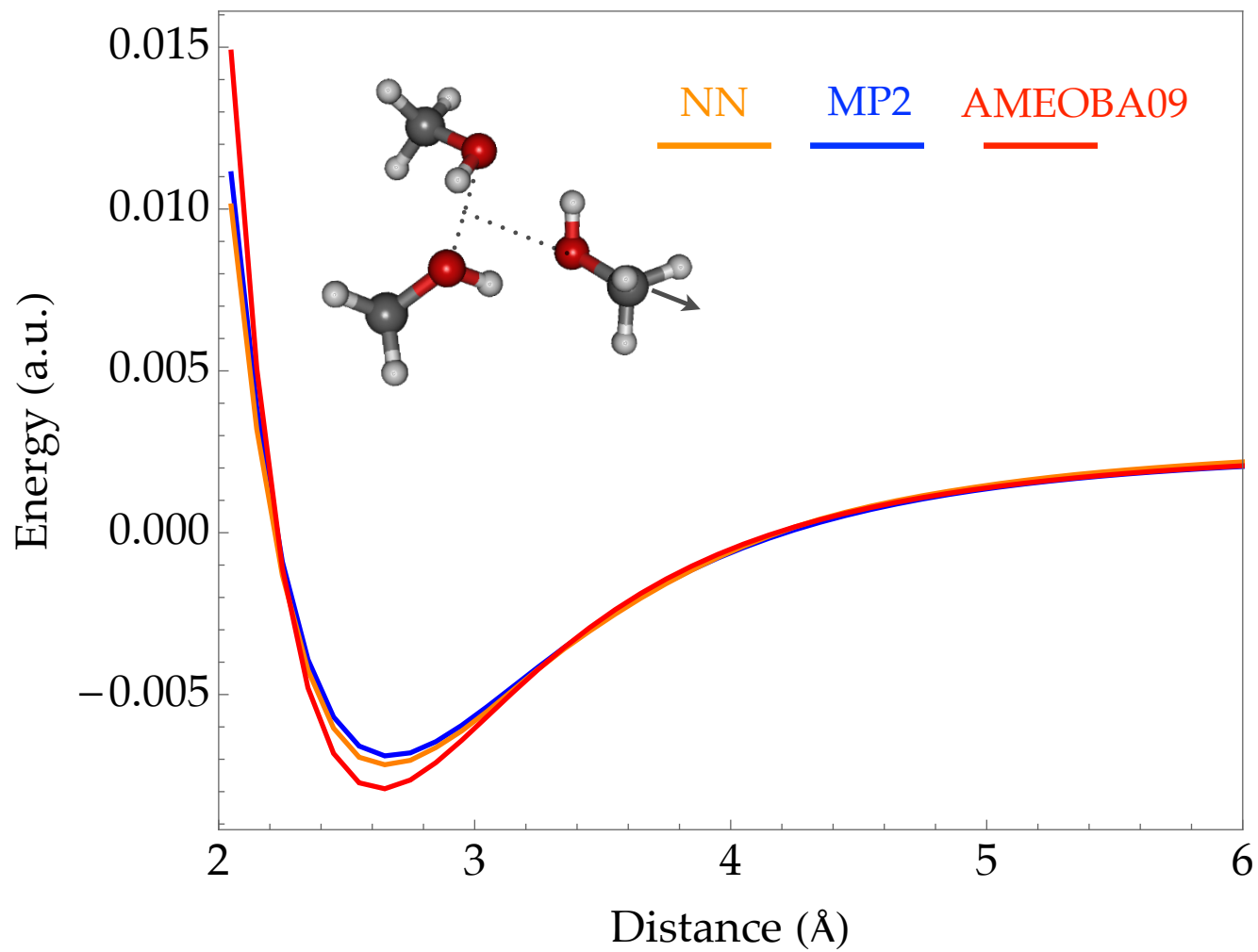
Neural Network PESs

NN-MP2 MBE

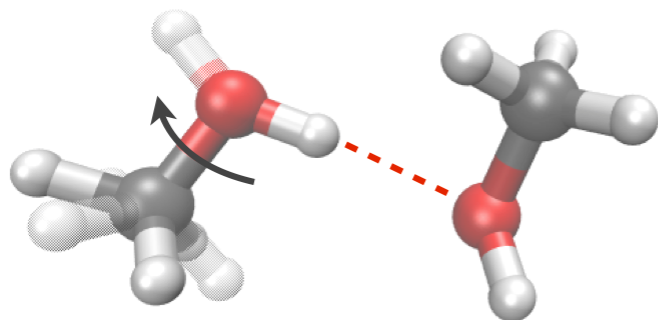
RI-MP2 MBE



Cluster accuracy

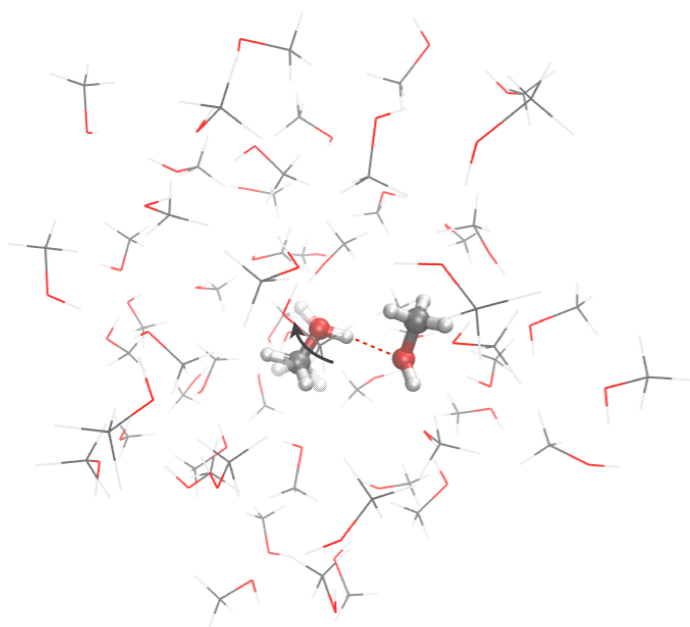


Cluster accuracy



$$\Delta E_{MP2-MBE} = 5.6$$

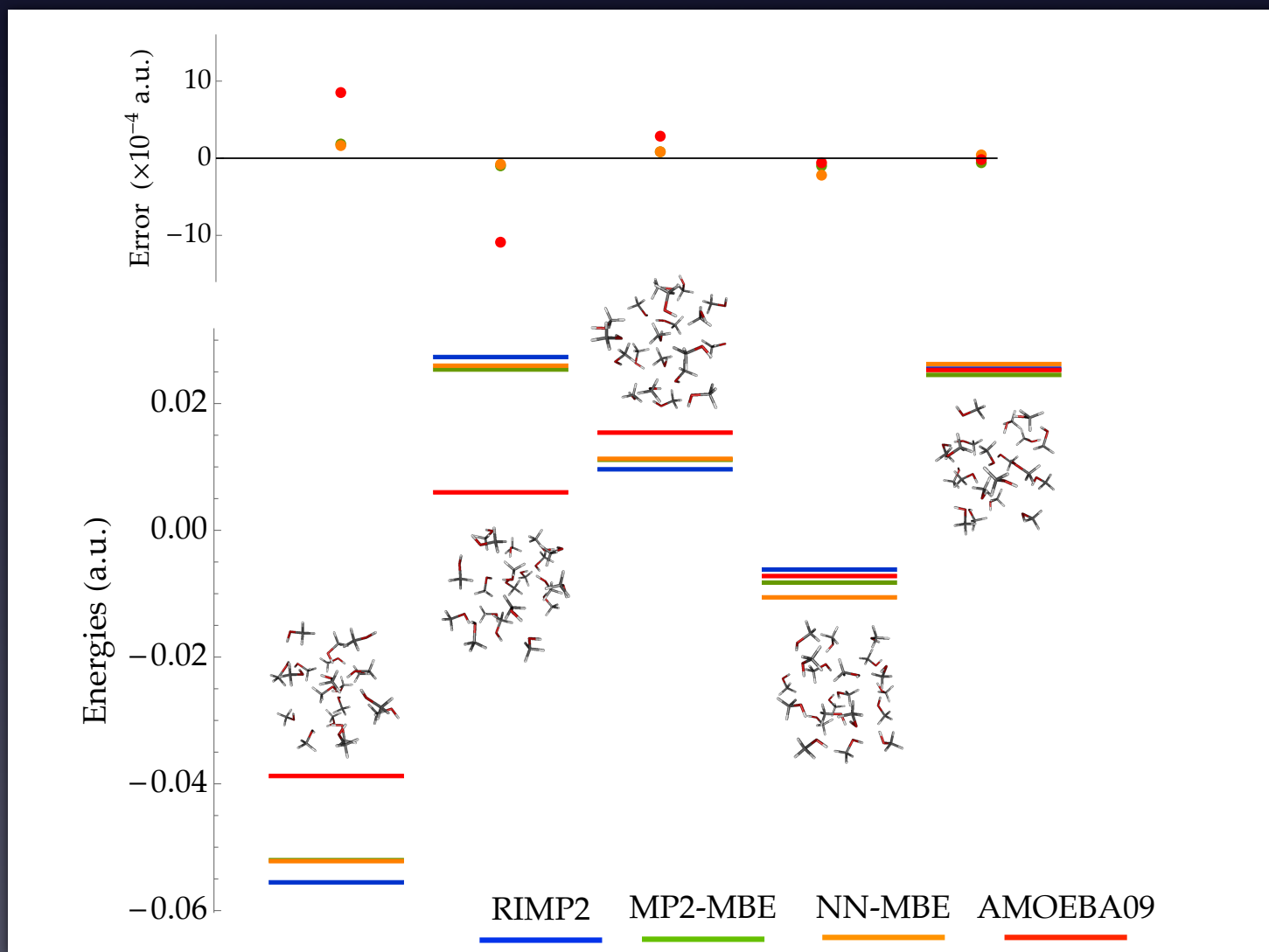
$$\Delta E_{NN-MBE} = 5.8$$



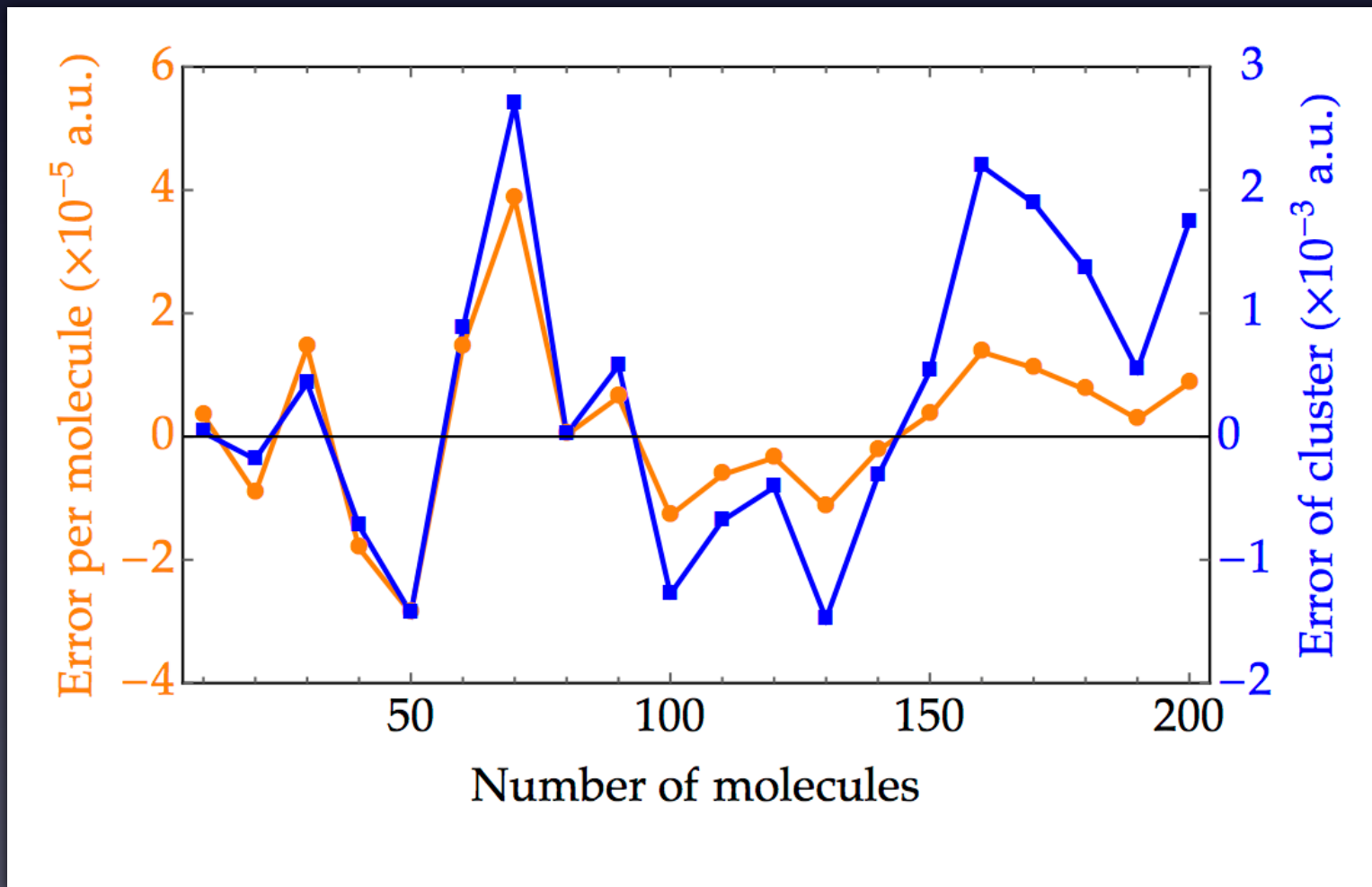
$$\Delta E_{MP2-MBE} = 13.3$$

$$\Delta E_{NN-MBE} = 14.6$$

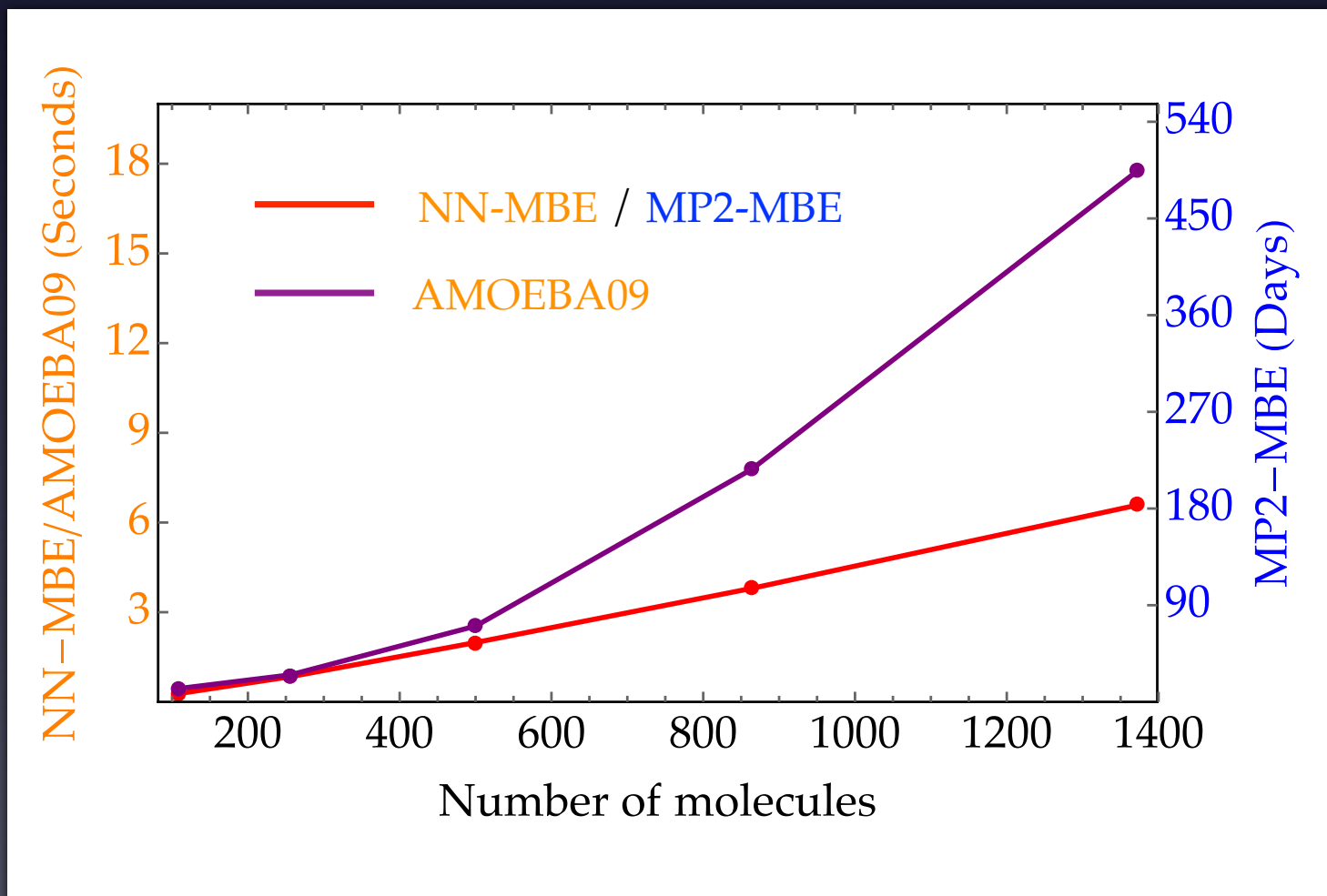
Cluster accuracy



Cancellation of errors in large clusters



Polarizable FF's on notice.

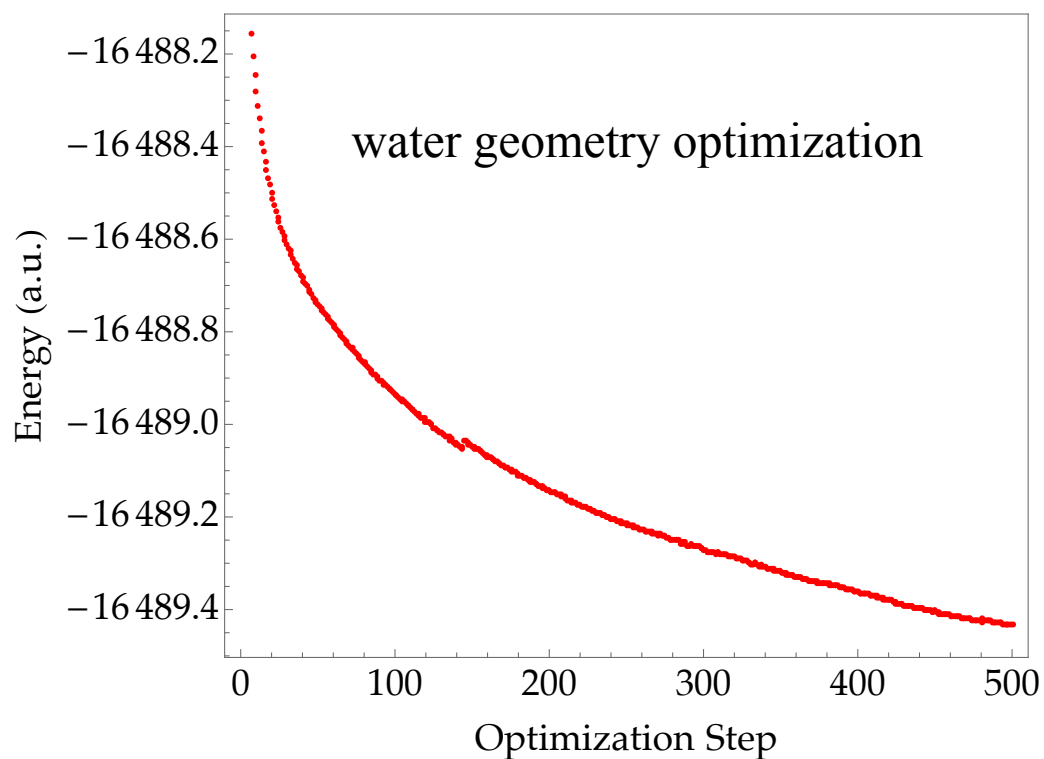
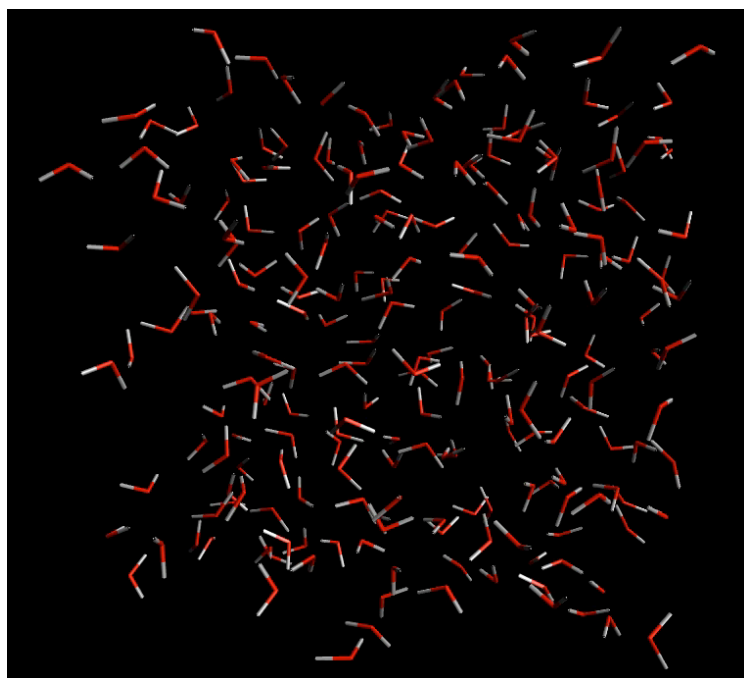


Forces

$$F(R_n) = \frac{\partial E_{total}}{\partial R_n} = \sum_{i=1}^{i_{max}} \frac{\partial E_i}{\partial R_n} = \sum_{i=1}^{i_{max}} \sum_j \frac{\partial E_i}{\partial D_j} \frac{\partial D_j}{\partial R_n}$$

Provided by TensorFlow

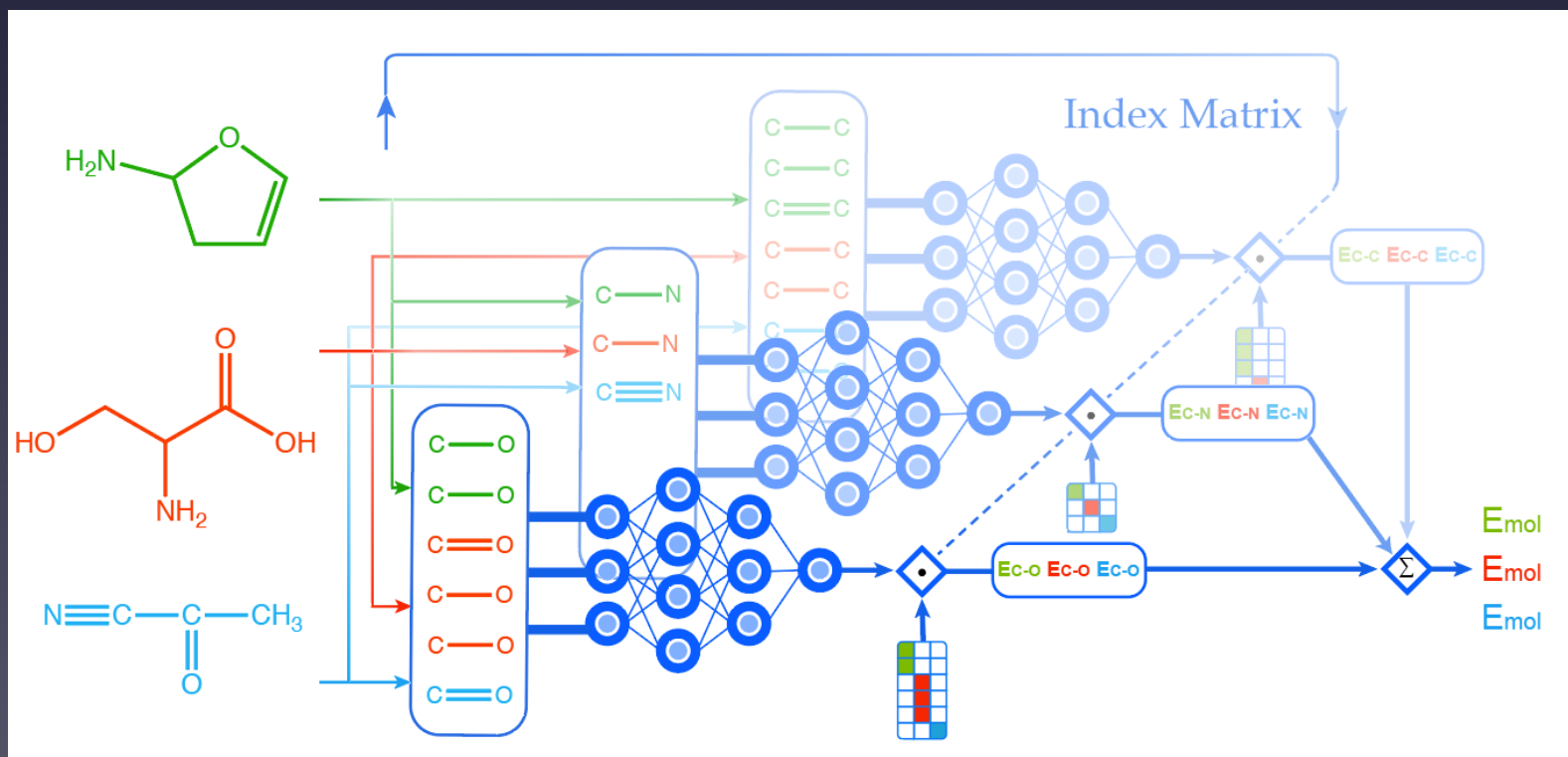
We Code



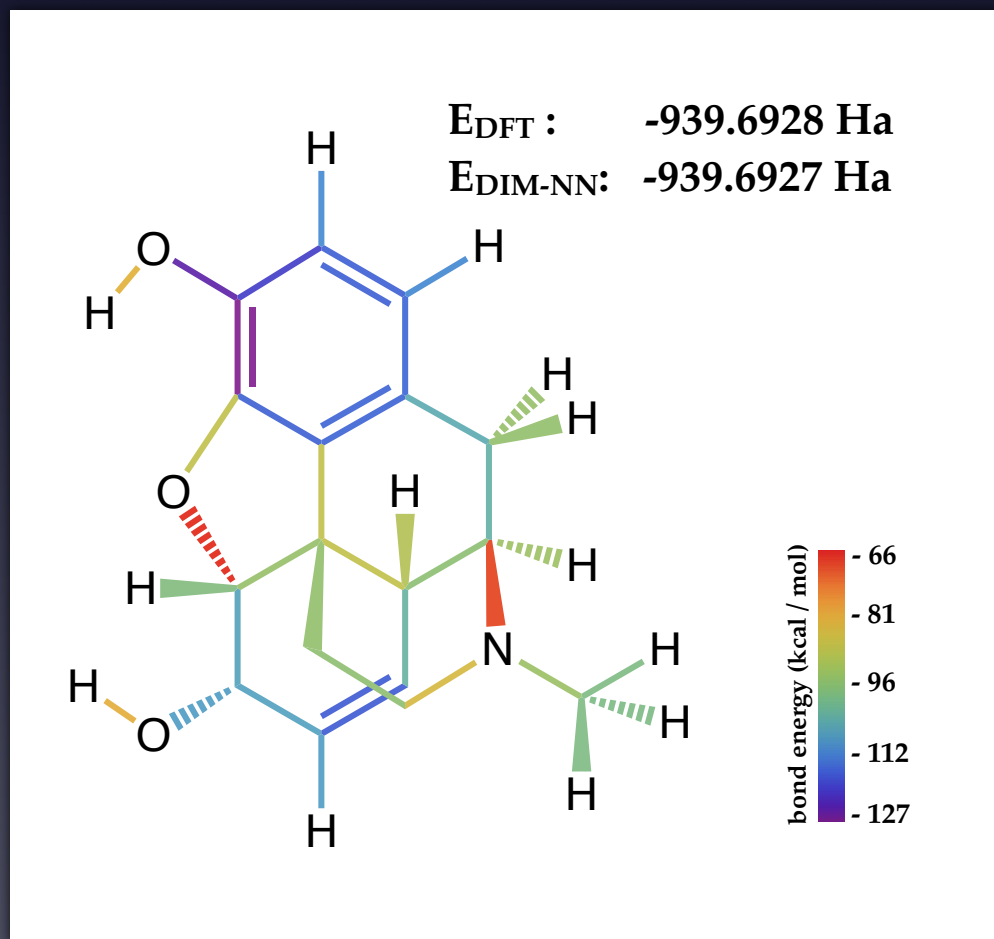
DIM-NN

Expresses the total molecular energy as a sum of bonds

- Only requires total energy training data
- Networks for each bond type

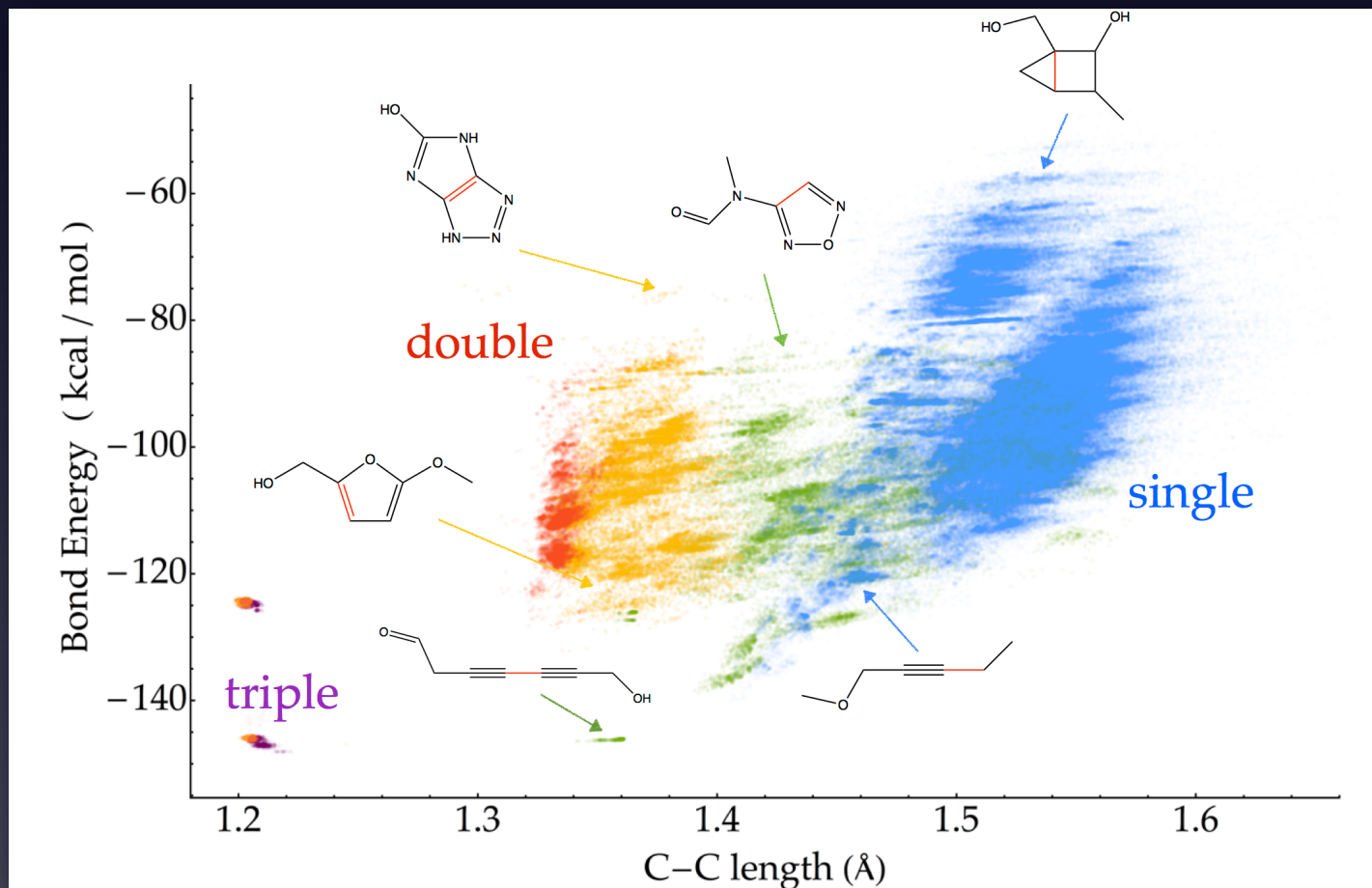


Accurate total energies.



Similar errors for
vitamin B12, D3 etc...

The Space of Carbon Carbon Bonds



700,000 Carbon Carbon bond energies.

A Synthetic Chemist



Seth Brown University of Notre Dame, South Bend

Chemical Thermodynamics, Chemical Kinetics, Catalysis

il 35.13

TensorMOL

Case #	Chemist	Neural Network	NBO
1	 <chem>C#CC</chem> \rightarrow <chem>C#CC</chem>	44.73	0.0123
2	 <chem>CC(=C)C</chem> \rightarrow <chem>CC(=O)C</chem>	-40.50	-0.0294
3	 <chem>COC</chem> \rightarrow <chem>COC=O</chem>	-24.57	-0.0010
4	 <chem>C1CCOC1</chem> \rightarrow <chem>C1CO1</chem>	23.87	0.0097
5	 <chem>C12CC3C(C1)N(C2)C3=O</chem> \rightarrow <chem>C12CC3C(C1)N(C2)C3=O</chem>	-17.19	-0.0096
6	 <chem>CC(=O)C</chem> \rightarrow <chem>CC=O</chem>	-16.49	-0.0103
7	 <chem>CC(O)C</chem> \rightarrow <chem>CC(N)C</chem>	14.23	0.0020
8	 <chem>C1=CC=CC=C1</chem> \rightarrow <chem>C1=CC=CC=C1</chem>	11.88	1.6500
9	 <chem>C=CC</chem> \rightarrow <chem>C=CC</chem>	11.00	-0.0044
10	 <chem>COC1=CC=CC=C1</chem> \rightarrow <chem>COC1=CC=CC=C1</chem>	10.68	-0.0016

Conclusions

Because of GPU dependencies and large datasets required, the most powerful ML PES methods are not in common use in chemistry
They will be soon.

Over the next year TensorMol and several other packages will appear where users can “Roll their own” ML-PES’s with minimal effort.
These will compete heavily with DFT

The domain of chemical space which can be explored in a weekend is about to exponentially increase.

THANKS!