



UNC
ESELMAN
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ML4MS Workshop @ Aalto
May 10, 2019

Learning Quantum Chemistry with Neural Networks



@olexandr

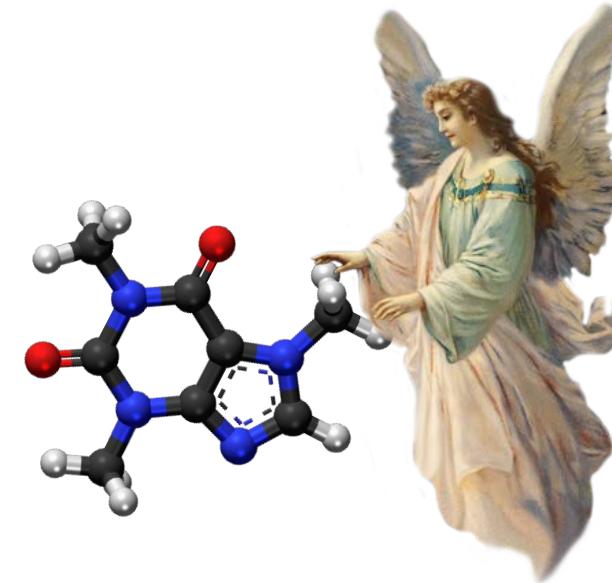
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olexandr@unc.edu

<http://olexandrisayev.com>

The Ultimate Dream of a Computational Chemist



Challenges:

- system complexity
- length scale
- time scale
- model accuracy

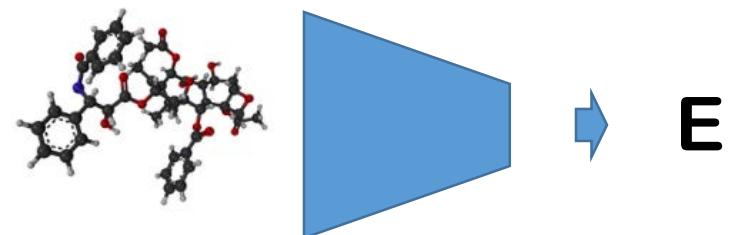
Quantum Mechanics 101

$$\hat{H}\psi = E\psi$$

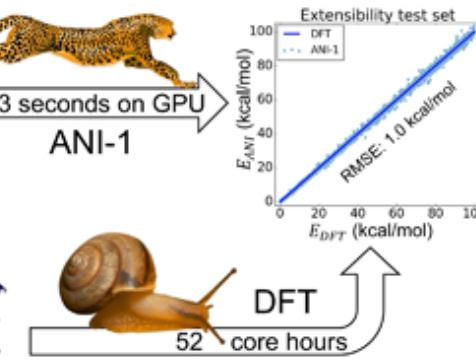
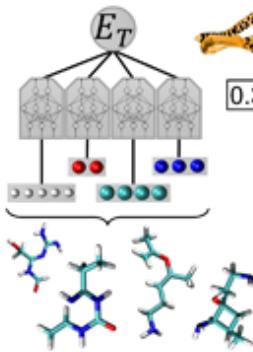
The Schrodinger equation was discovered in 1926 by Erwin Schrodinger, an Austrian theoretical physicist. It is an important equation that is fundamental to quantum mechanics.



$$E = f(R_{\text{vector}})$$



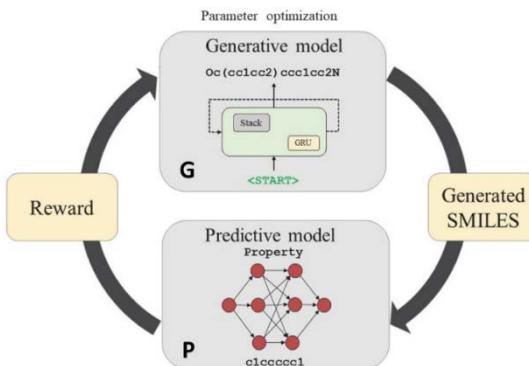
J. Chem. Phys. **2018**, *148*, 241733



Chem. Sci., **2017**, *8*, 3192-3203



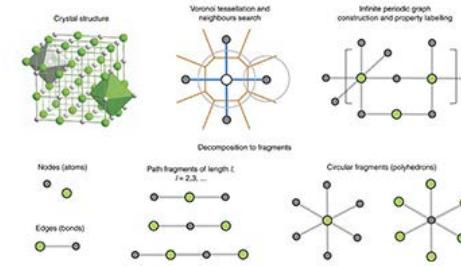
J. Phys. Chem. Lett., **2018**, *9* (16), pp 4495–4501



ACS Med. Chem. Lett. **2018**, *9*, 1065–1069

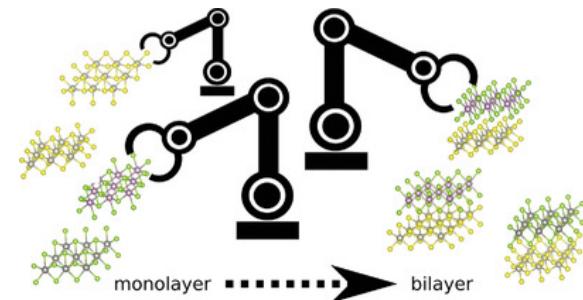
Science Advances, **2018**, *4* (7), eaap7885

Chem. Mater., **2015**, *27*, 735-742.

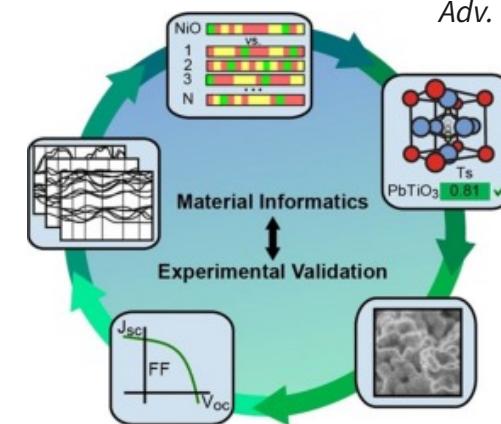
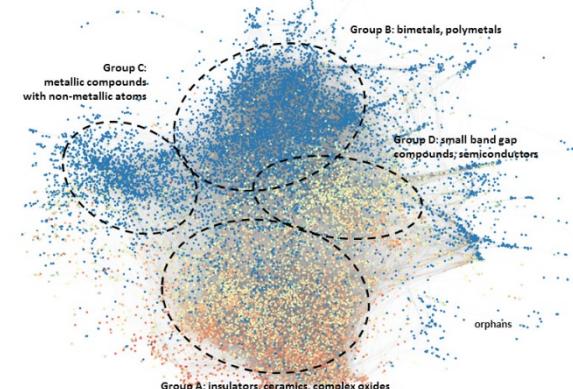


Nature Commun. **2017**, *8*, 15679

Comp. Mater. Sci., **2018**, *152*, 134-145

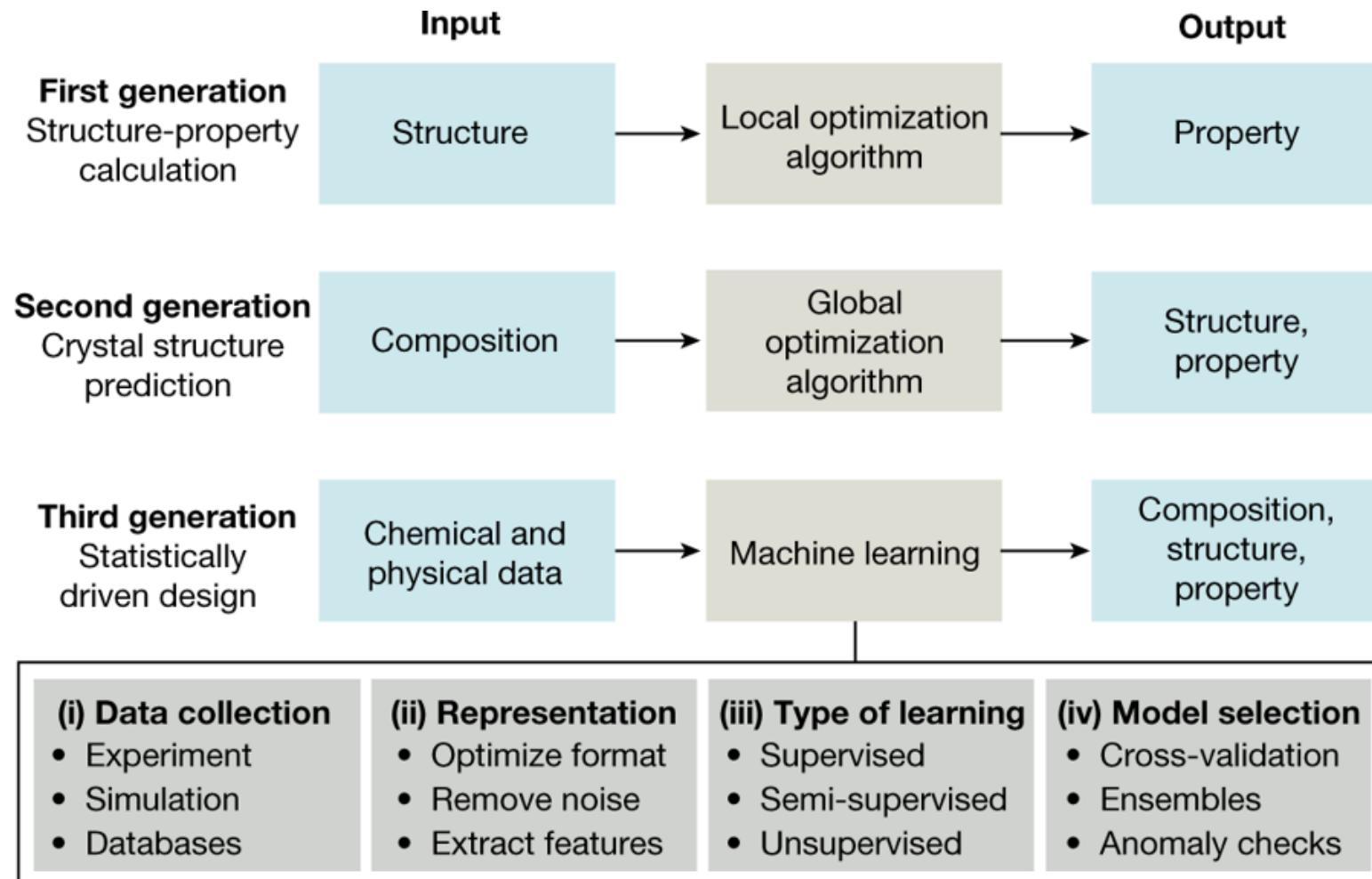


Adv. Theory Simul., **2019**, *2*: 1800128



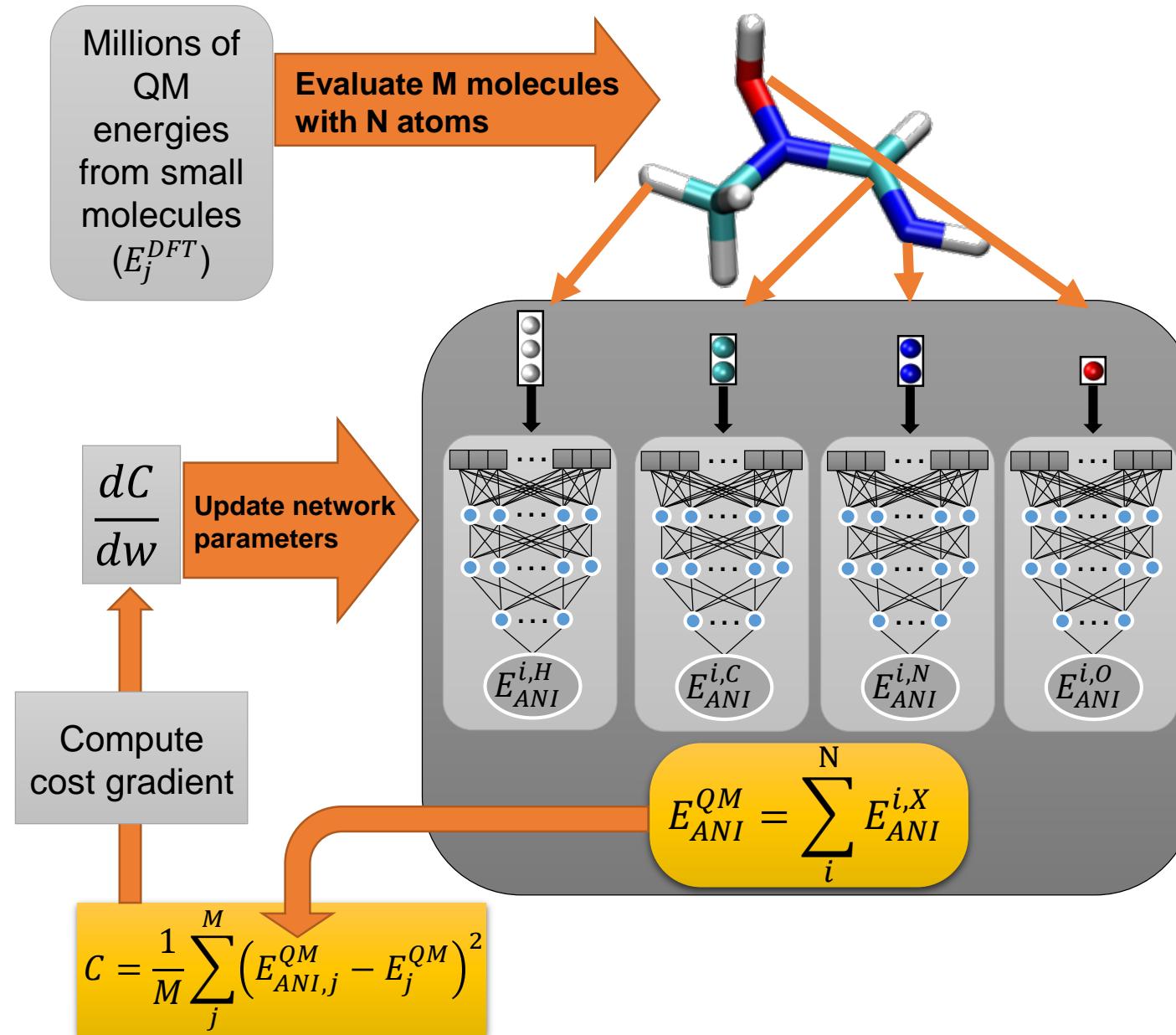
Materials Discovery, **2017**, *6*, 9-16

Evolution of statistical modeling applications in computational chemistry



Butler KT, Davies DW, Cartwright H, Isayev O, Walsh A Machine learning for molecular and materials science. *Nature*, **559**, 547–555 (2018). DOI: 10.1038/s41586-018-0337-2

Neural Network molecular potential - training



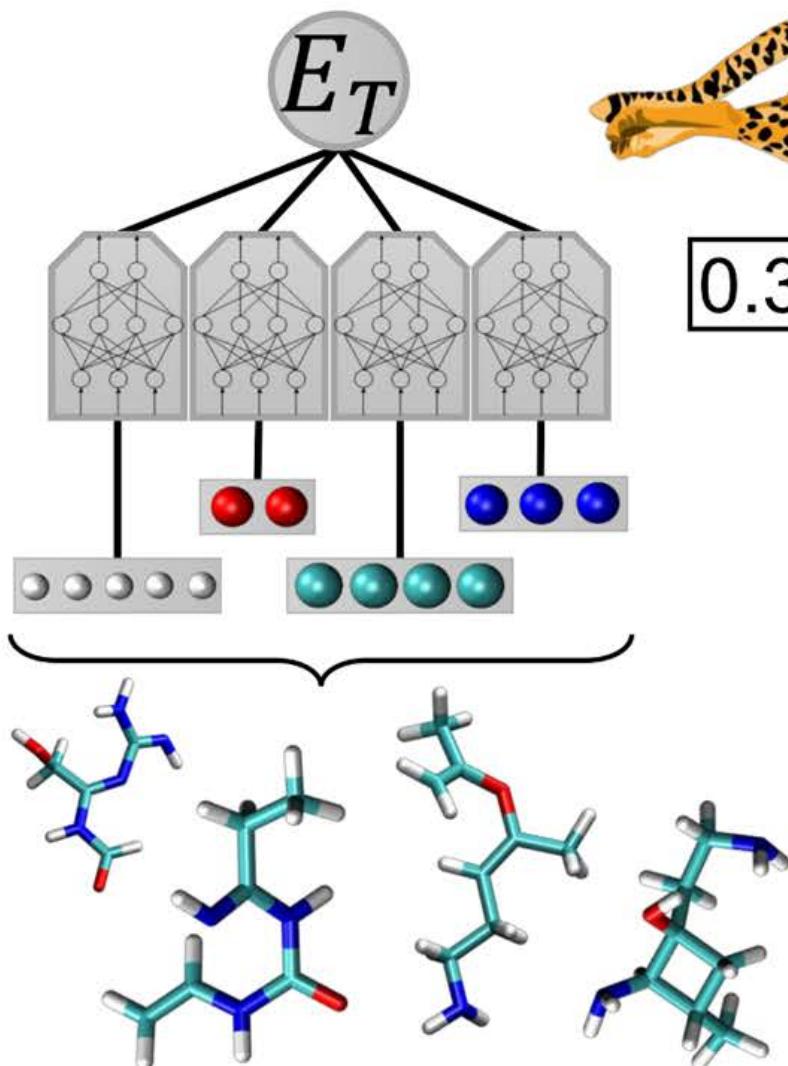
Neural Networks are
not Magic!

Currently available:
CHNOSCl

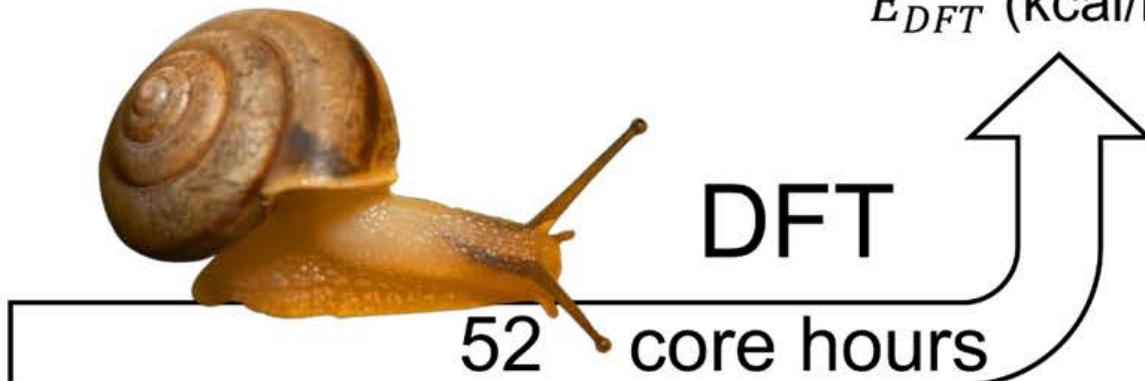
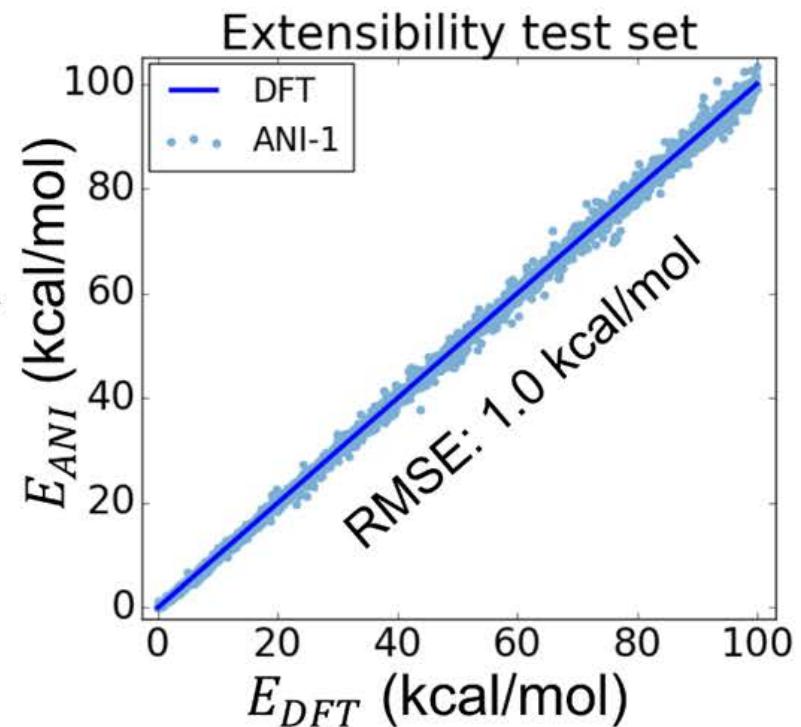
P, Si, Br, I, ...
in progress

ω B97x/DZ (TZ soon)

ANI Deep Neural Network



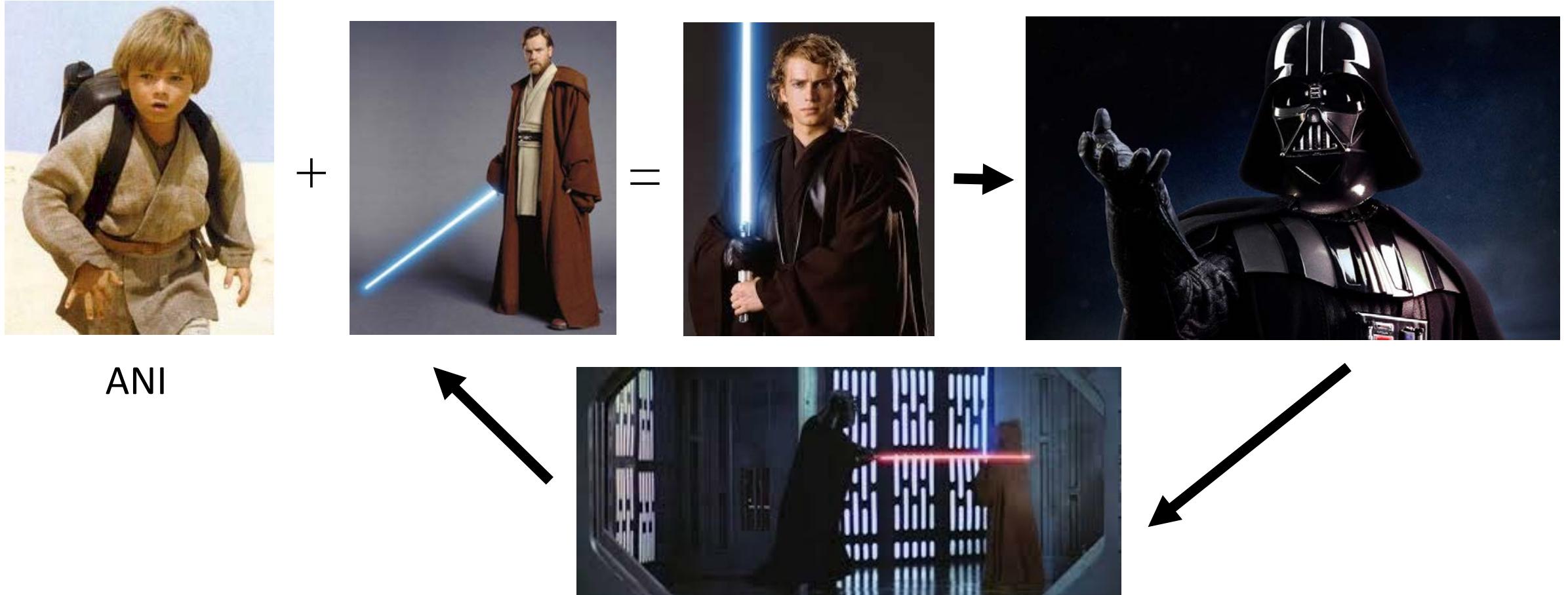
0.3 seconds on GPU
ANI-1



ANAKIN-ME

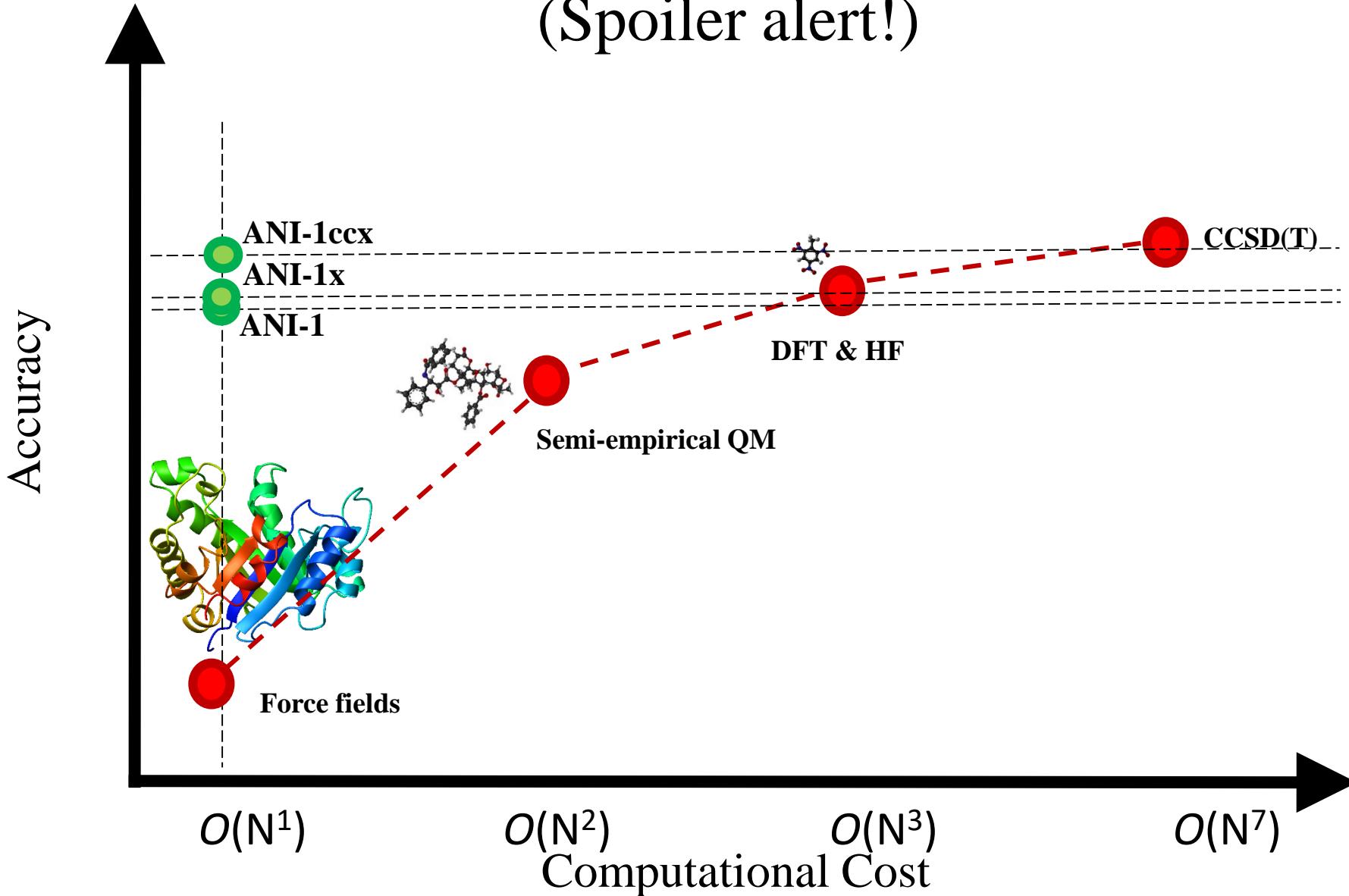
Accurate NeurAl networK engINe for Molecular Energies

We want to train a padawan network to become a DFT jedi master



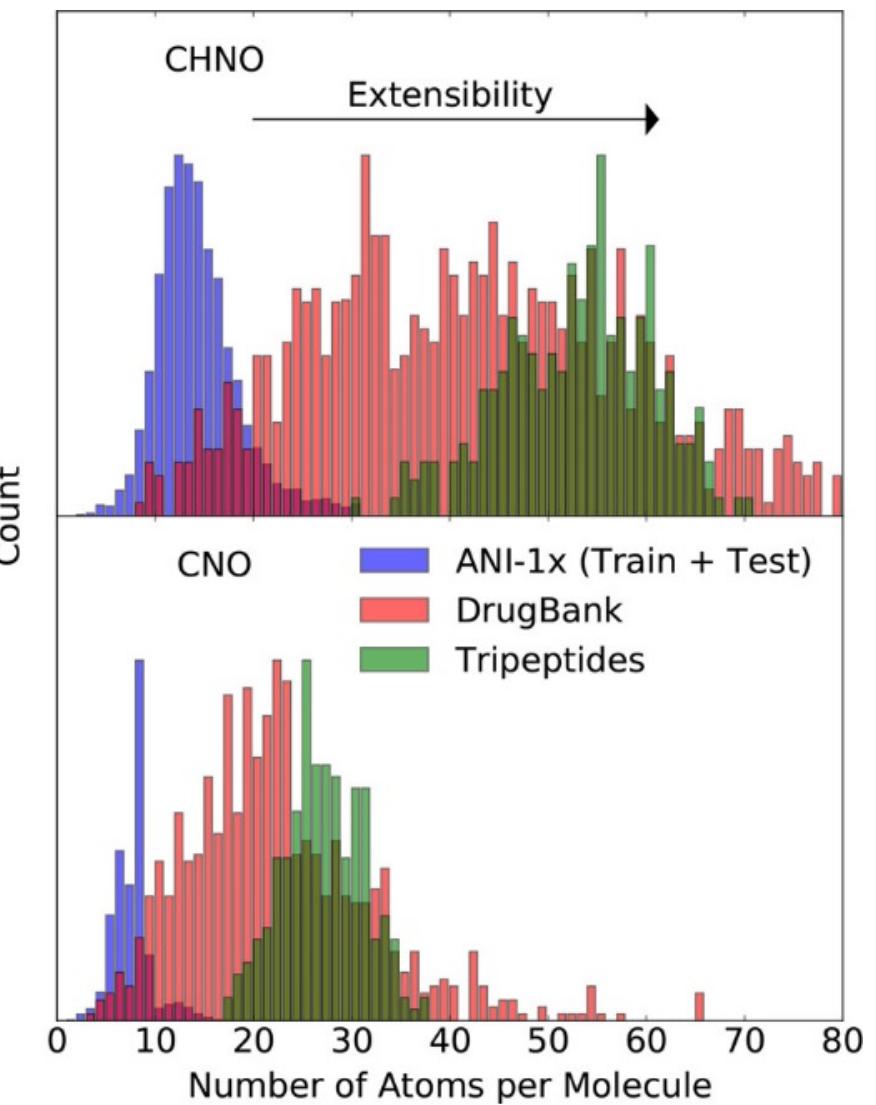
Where do we fit?

(Spoiler alert!)



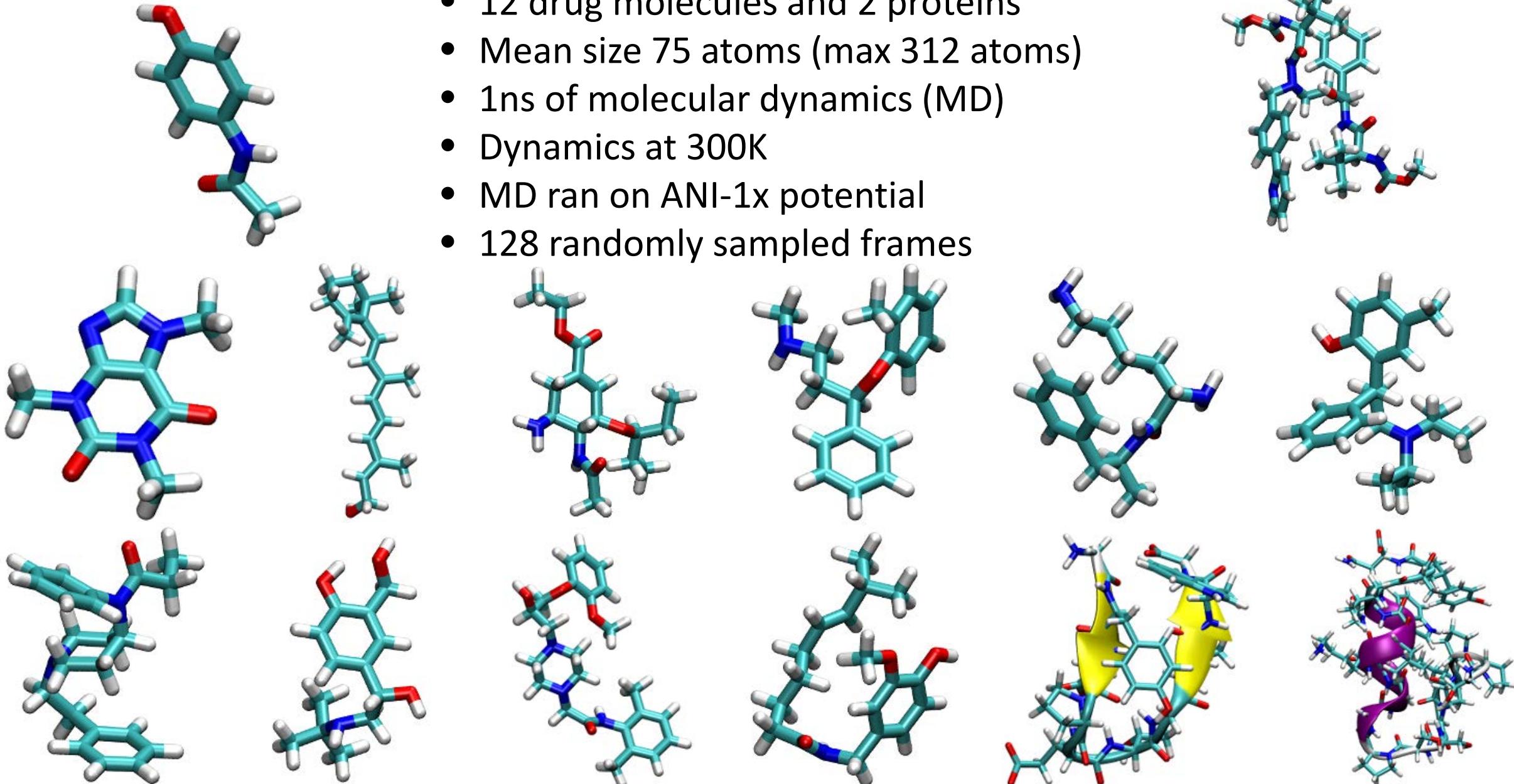
What do you need?

- ANI requires **TONS** of data
 - For ANI-1 we run ~20M DFT data points @ wB97x/DZ.
 - Available to anyone!
 - Molecules with 1 to 8 heavy atoms from the GDB database
 - Out-of-equilibrium geometry sampling with NMS, MD
- Train network on a fraction of available data, validate on independent data
- Test on ‘**known sizes**’ (Molecules with \leq # max heavy atoms per molecule in training set)
 - Interpolation
- Test on ‘**unknown sizes**’ (Molecules larger than any in the training set)
 - Extrapolation



ANI-MD Benchmark // COMP6

- 12 drug molecules and 2 proteins
- Mean size 75 atoms (max 312 atoms)
- 1ns of molecular dynamics (MD)
- Dynamics at 300K
- MD ran on ANI-1x potential
- 128 randomly sampled frames

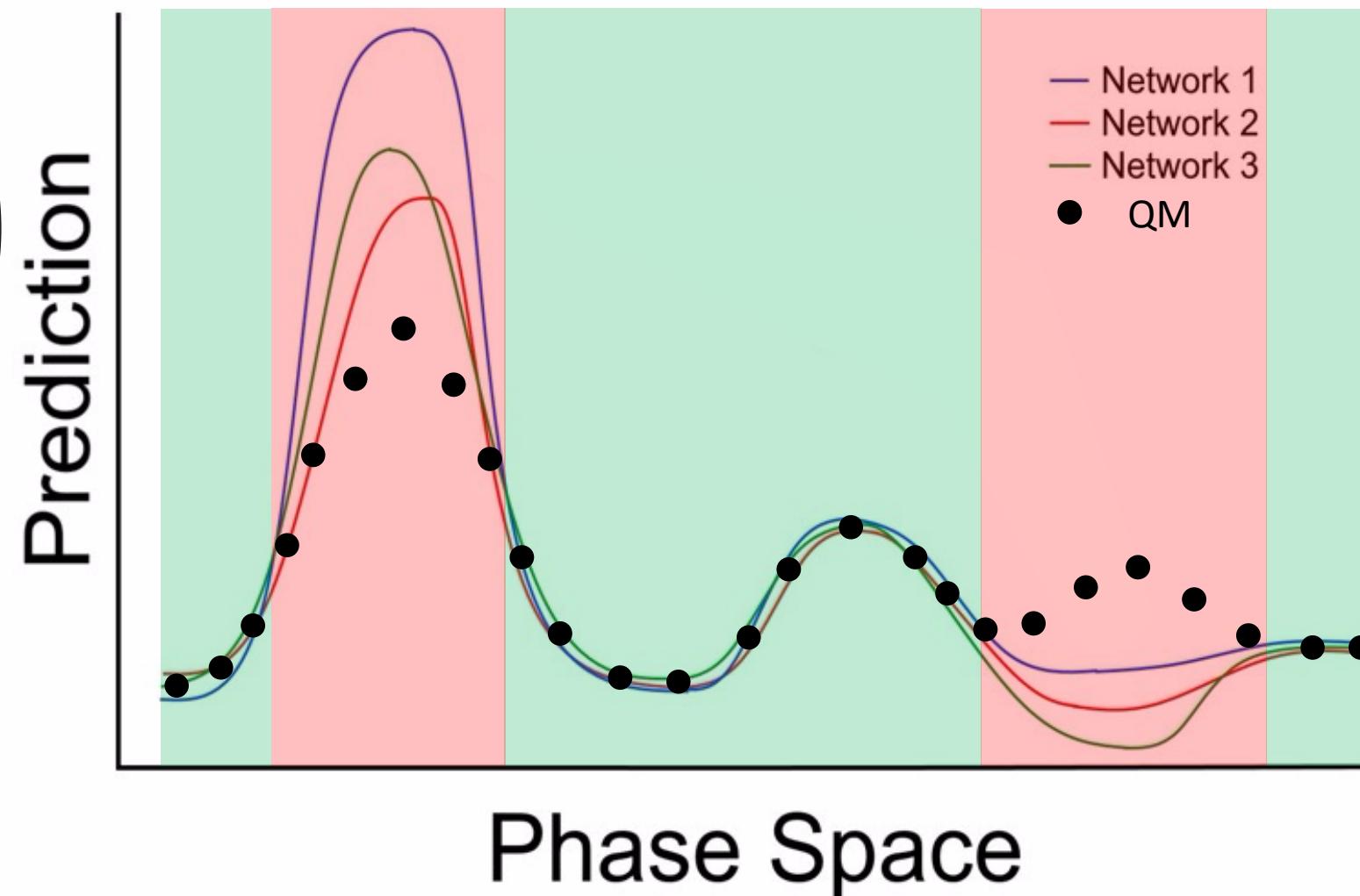


Can we predict when the model is wrong?

Ensemble
disagreement
can drive data
generation

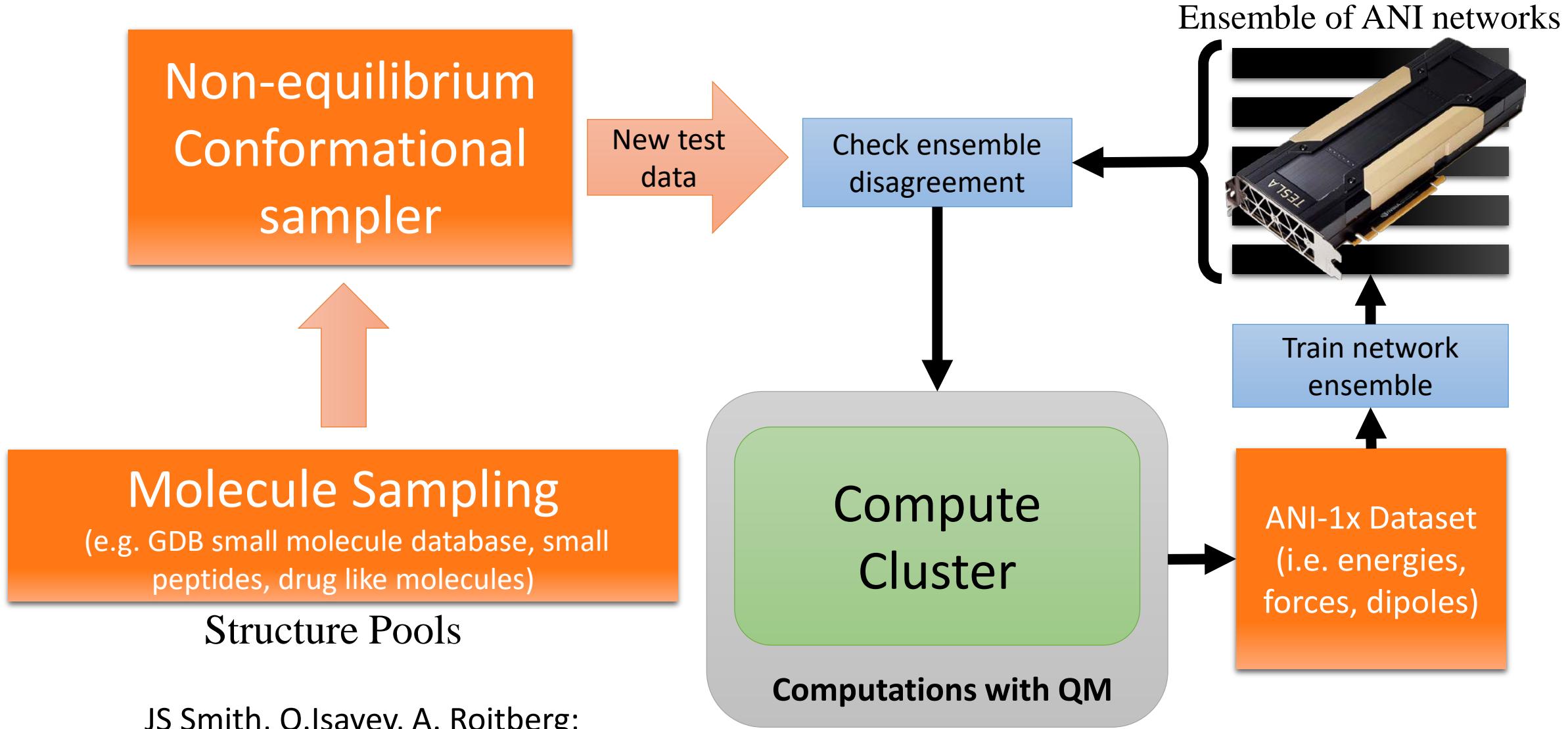
Good data
coverage

Bad data
coverage

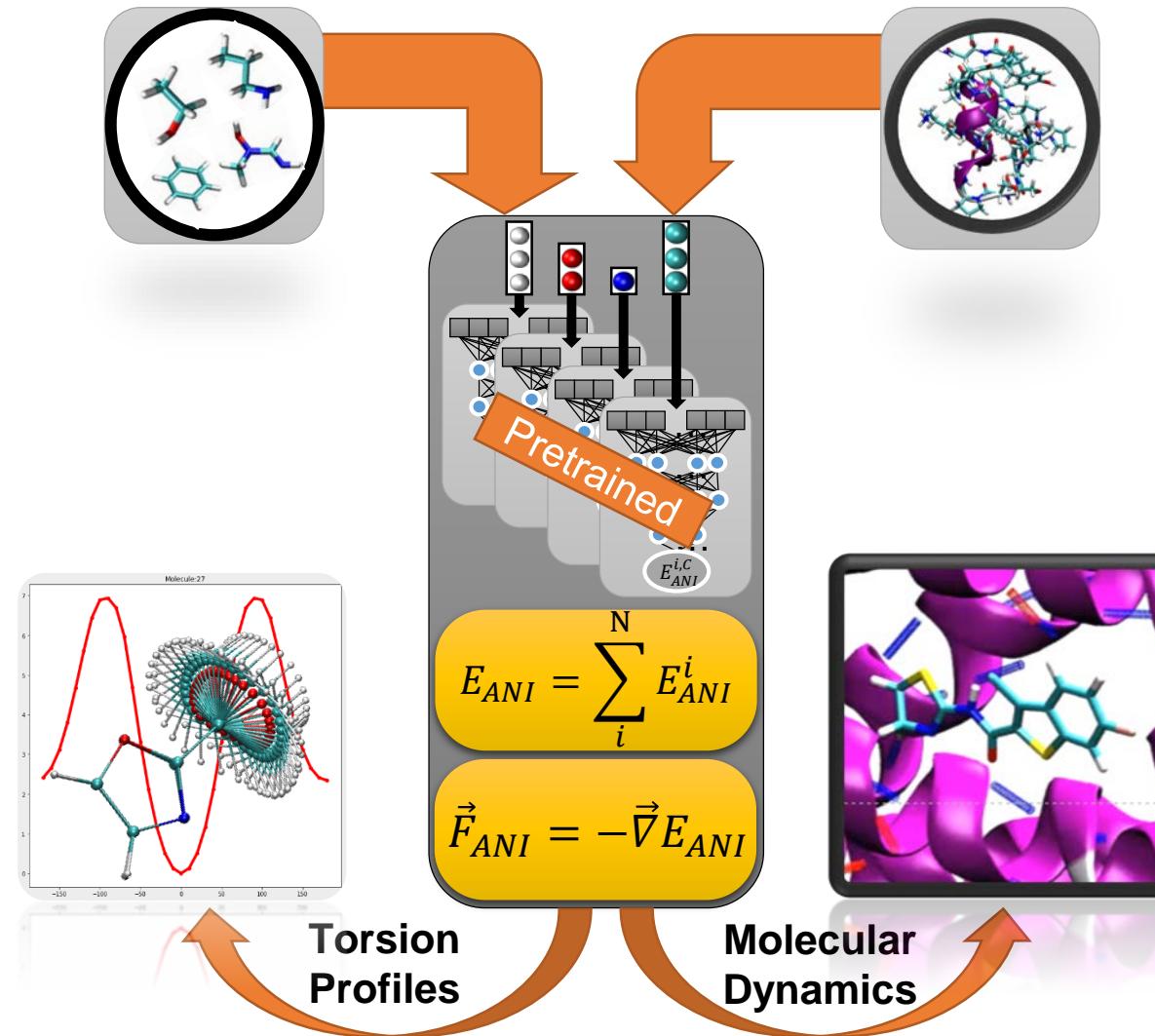


Active Learning - The Big Picture

An automated and self-consistent data generation framework

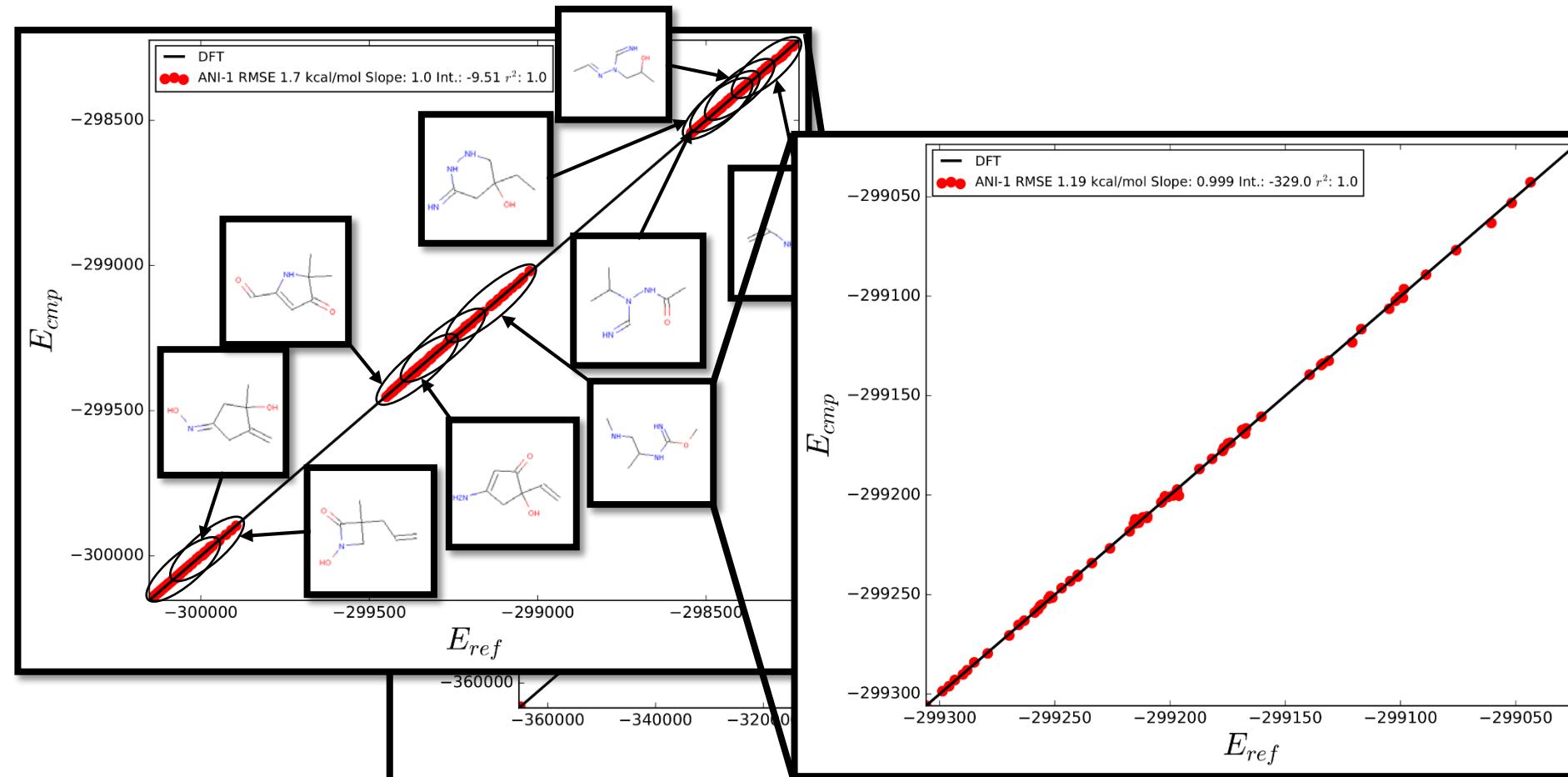


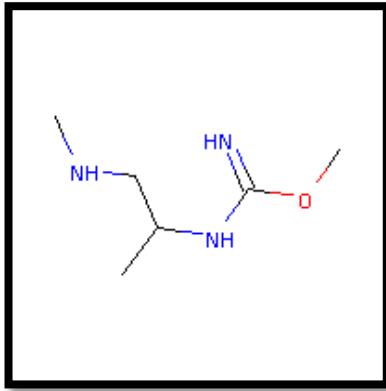
ANI molecular potential - application



Total energy correlation for ANI-1 vs. DFT

(External test of 131 molecules with 10 heavy atoms, 8200 total molecules + conformations) [units: kcal/mol]





73 total **test** structures

10 Heavy atoms

25 Total atoms

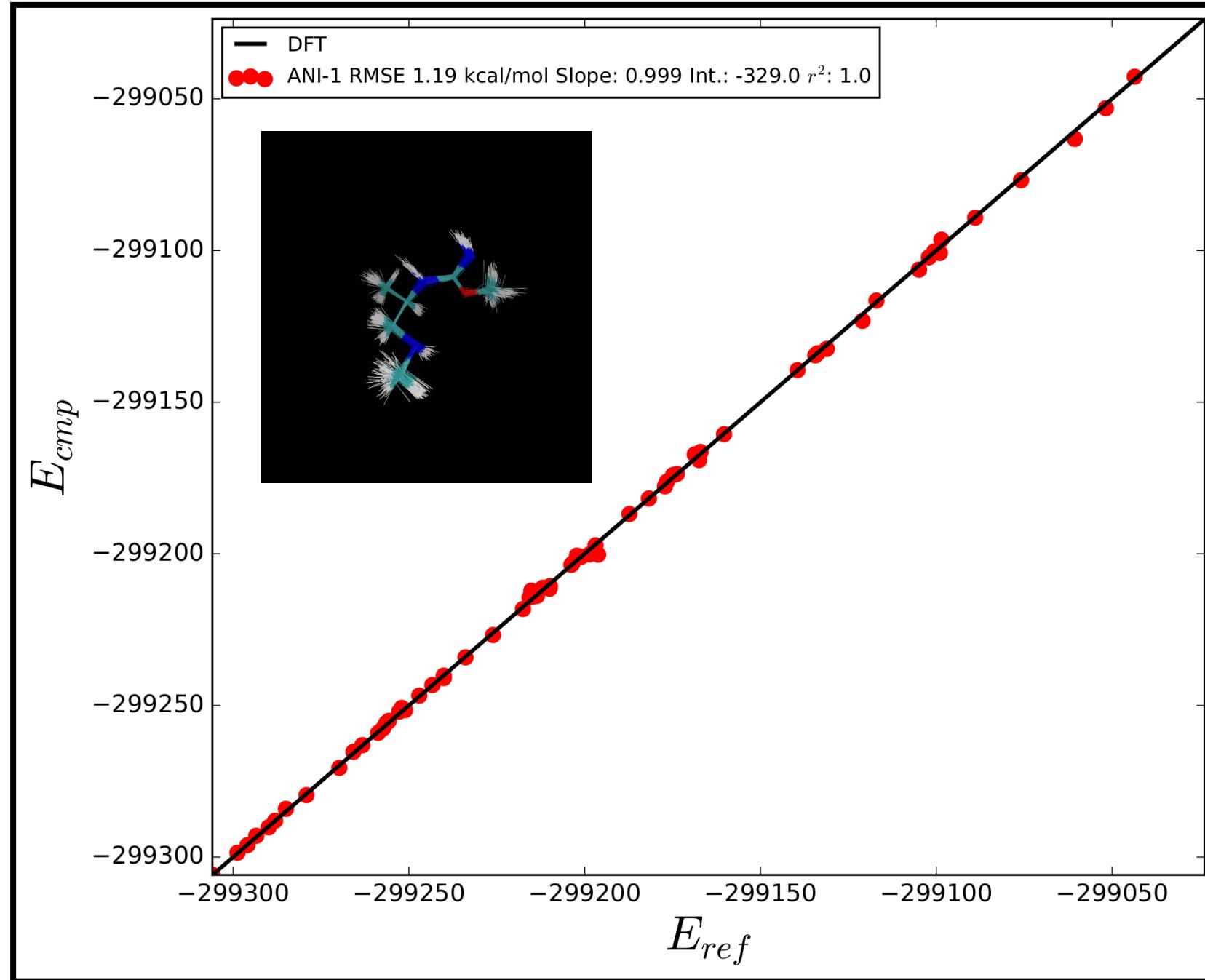
RMSE: 1.2 kcal/mol

(0.048 kcal/mol/atom)

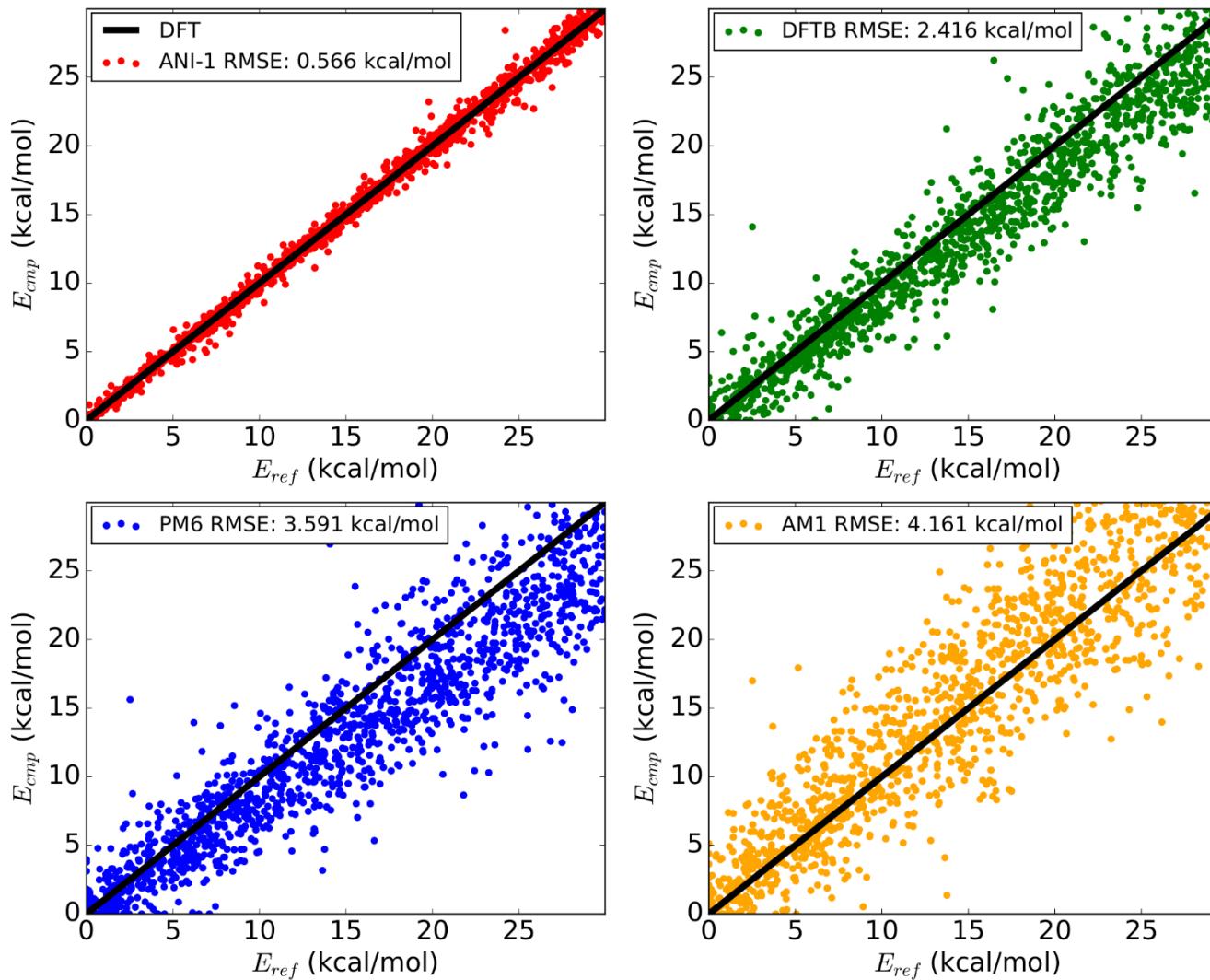
DFT time: 1143.11s

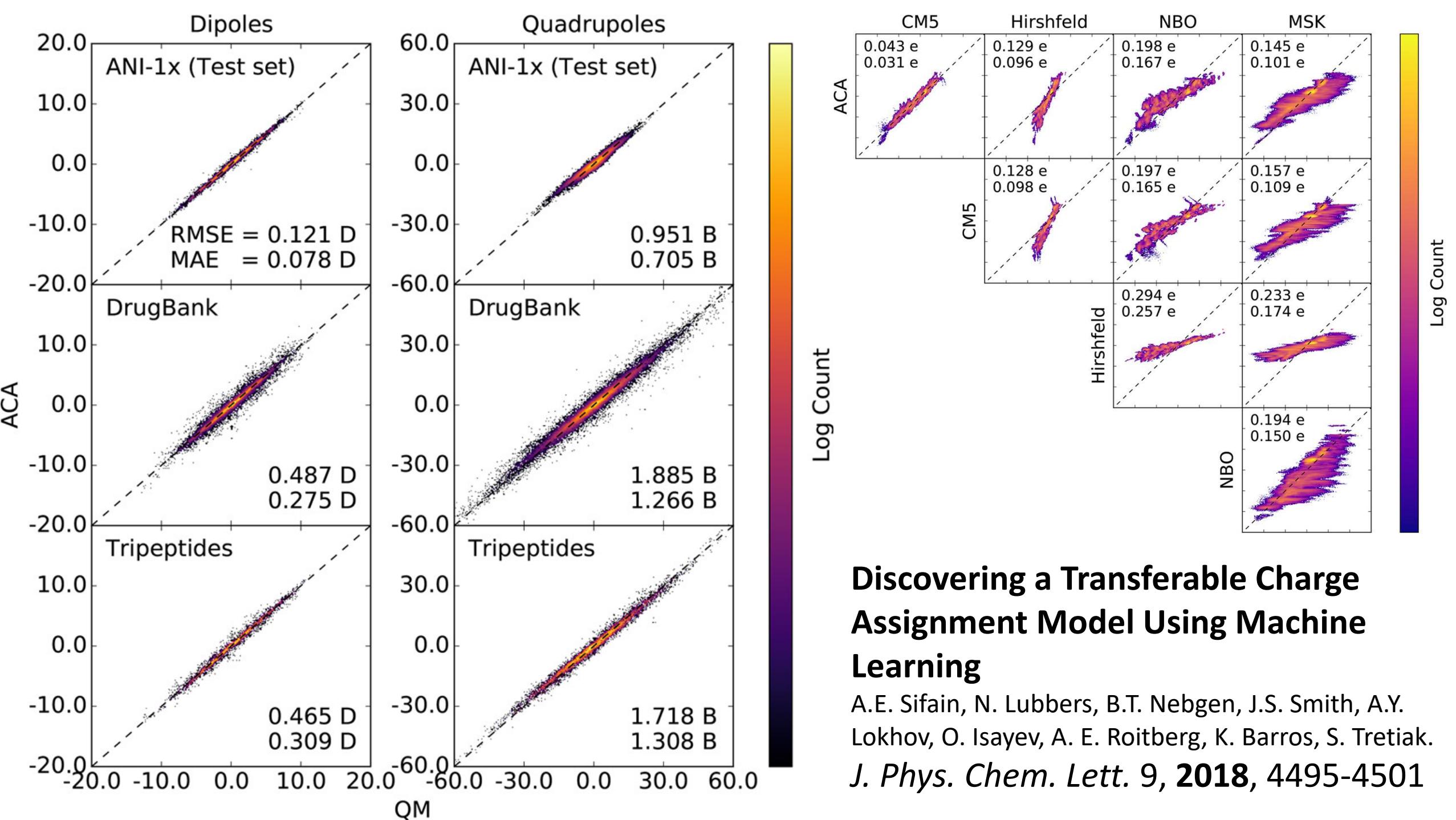
ANI time: 0.0032s

357,000x speedup!

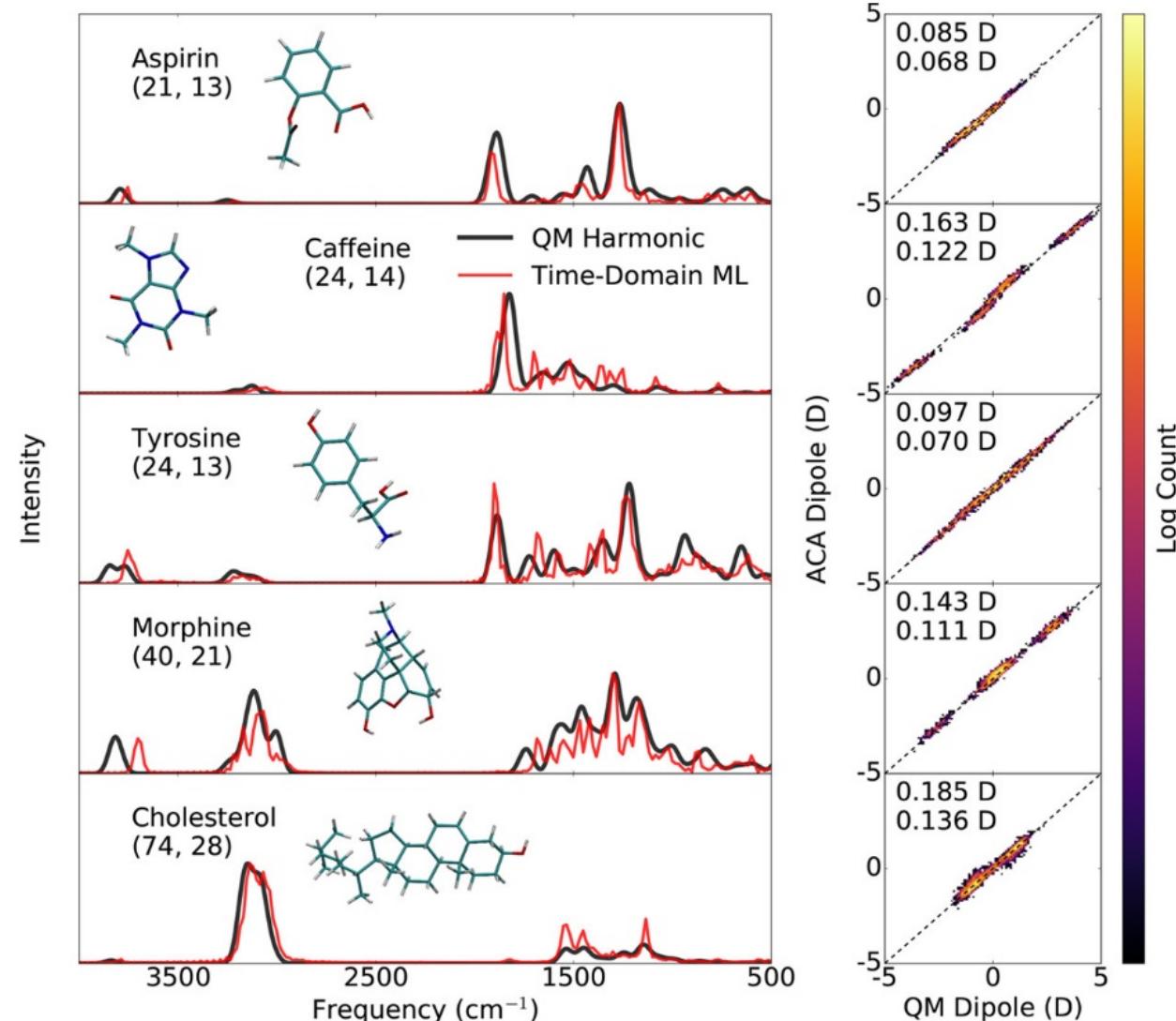


Relative Energy correlation (30kcal/mol)

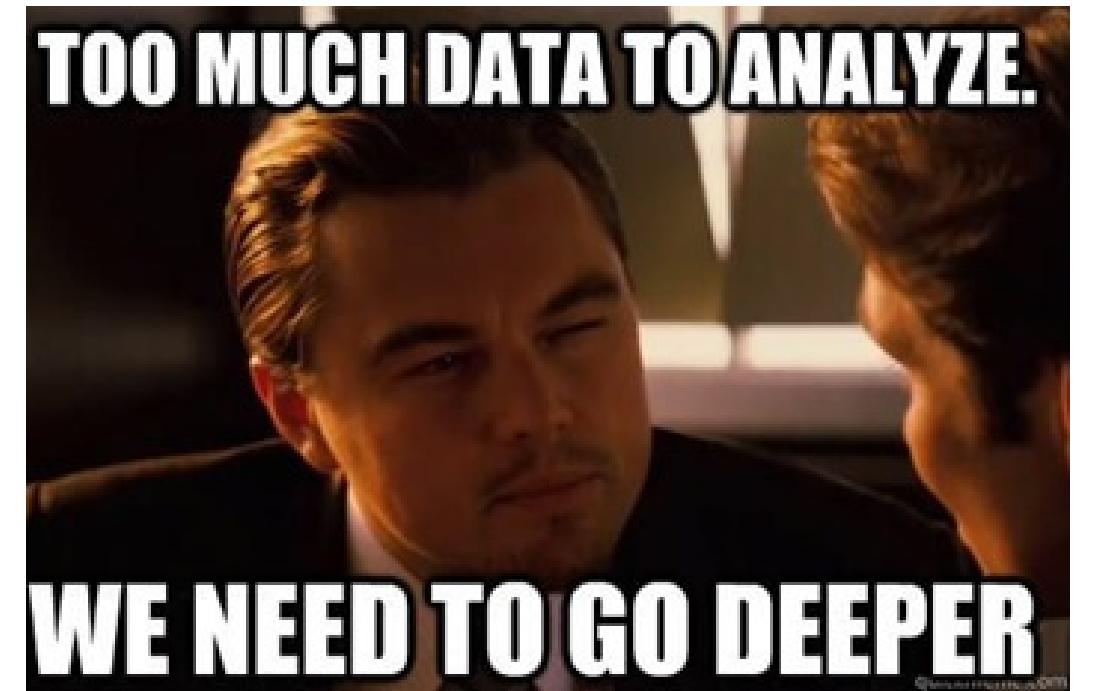




Accurate IR spectra simulation with time-domain ML

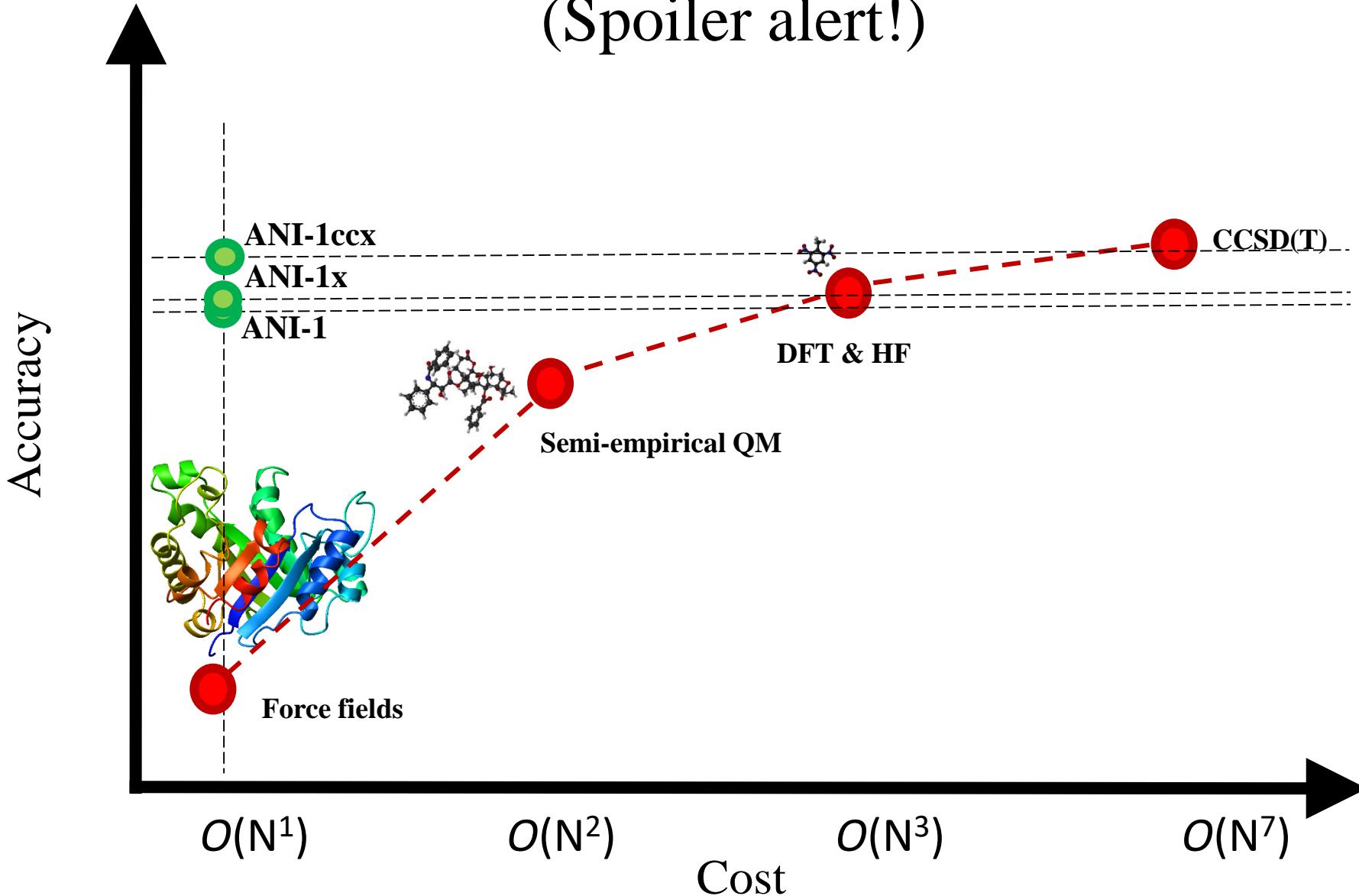


Can we go beyond DFT?



Where do we fit?

(Spoiler alert!)



High Throughput CSDT(T)/CBS

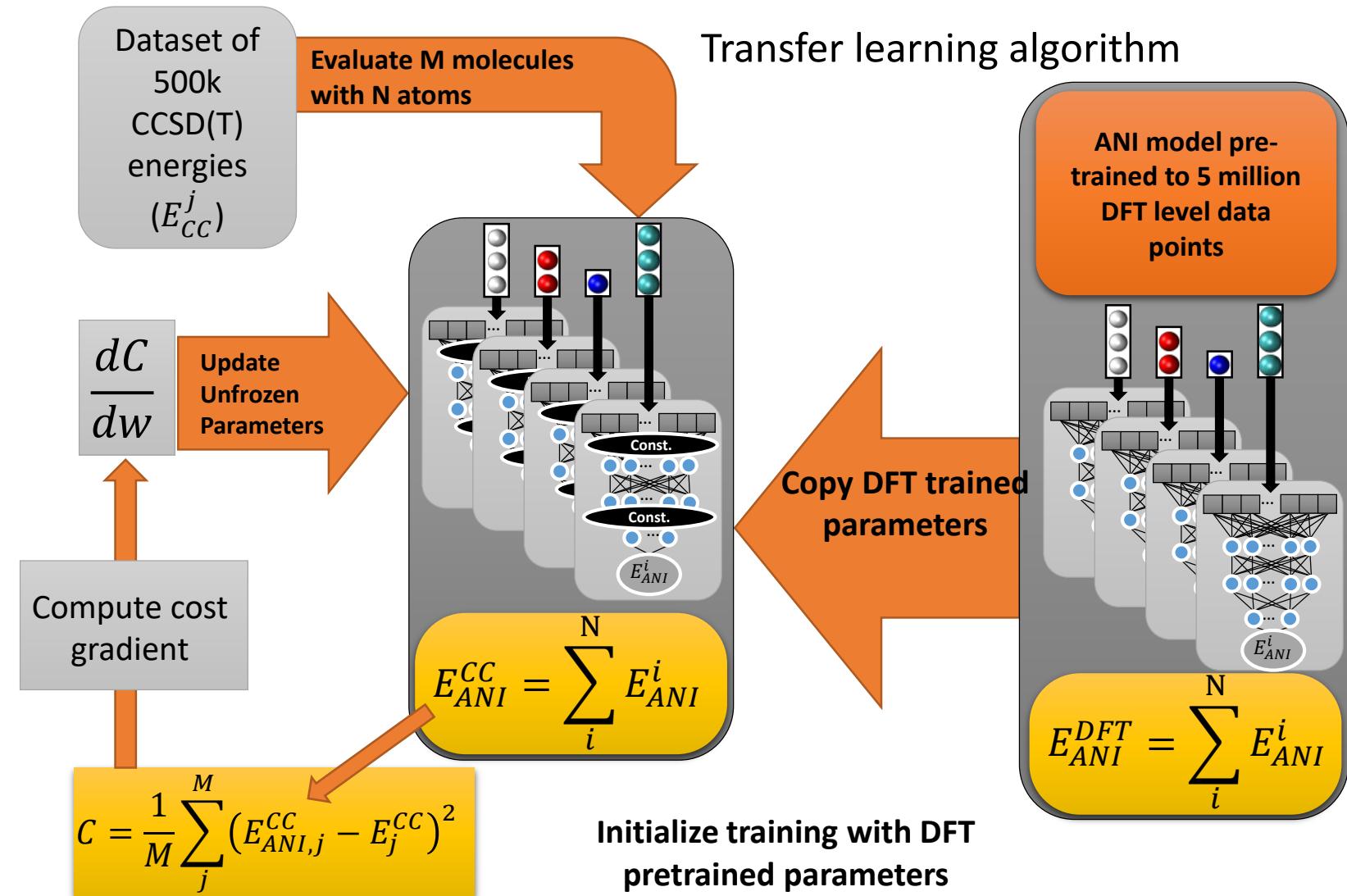
	CPU-core hours		Mean absolute deviation from CCSD(T)-F12 (kcal/mol)	
	Alanine (13 atoms)	Aspirin (21 atoms)	S66	W4-11
CCSD(T)/CBS	9.13	427.00	0.03	1.31
CCSD(T)*/CBS (this work)	1.44	7.44	0.09	1.46

$$E_{total}^{CBS} \approx E_{HF}^{CBS} + E_{MP2}^{CBS} + \left(E_{CCSD(T)}^{cc-pVTZ} - E_{MP2}^{cc-pVTZ} \right)$$

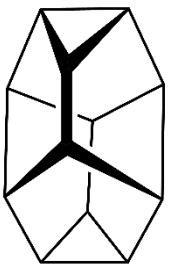
$$E_{CCSD(T)}^{cc-pVTZ} \approx E_{Normal-DPLNO-CCSD(T)}^{cc-pVTZ} + \left(E_{Tight-DPLNO-CCSD(T)}^{cc-pVDZ} - E_{Normal-DPLNO-CCSD(T)}^{cc-pVDZ} \right)$$

Transferring knowledge of CCSD(T)/CBS

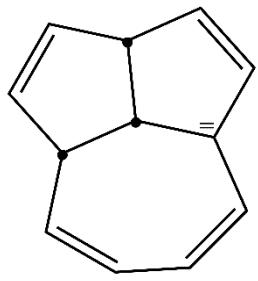
- Regenerate 10% of ANI-1x training data (0.5M of 5M)
- For high-level reference we use CCSD(T)/CBS accurate QM model
- We only retrain 60k of 400k neural network parameters
- Results show clear improvement over DFT trained model
- New models are **exceeding the DFT** in accuracy



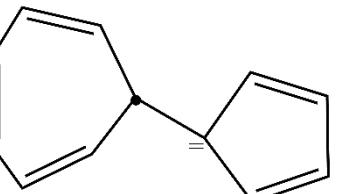
Hydrocarbon reaction energy benchmark, DFT vs CCSD(T)



E1 (1)



E2 (22)



E3 (31)

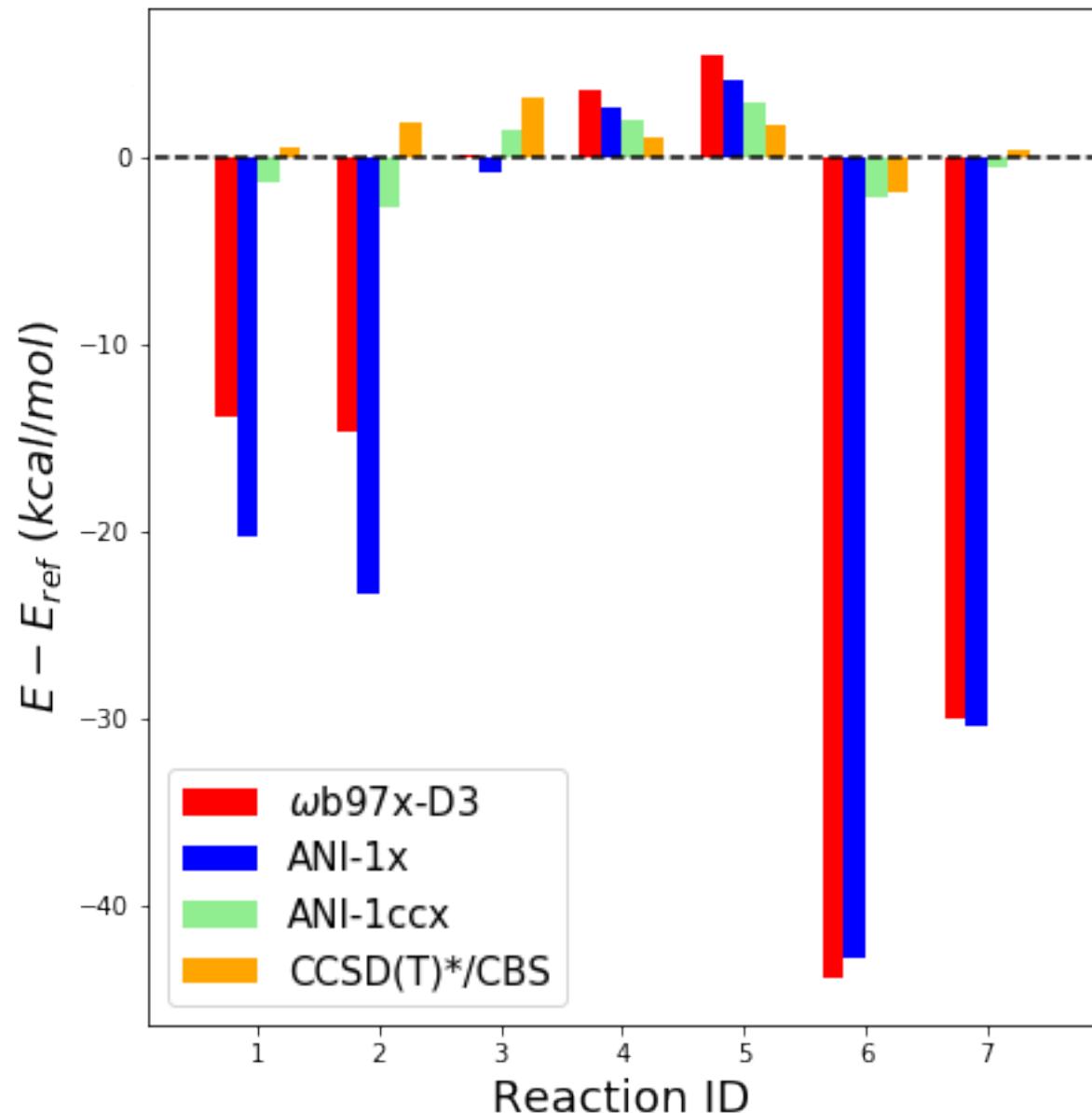
E4
(Bicyclo[2.2.2]octane)

Units: kcal/mol

Reaction	Ref.	ANI-1ccx	CCSD(T)*/ CBS	ANI-1x	ω b97x
1) E1 → E2	14.3	15.6	13.8	34.6	28.2
2) E1 → E3	25.0	27.7	23.1	48.3	39.7
3) Octane-a → Octane-b	1.9	0.4	-1.3	2.7	1.7
4) $4CH_4 + C_6H_{14} \rightarrow 5C_2H_6$	9.8	7.9	8.7	7.2	6.2
5) $6CH_4 + C_8H_{18} \rightarrow 7C_2H_6$	14.8	11.9	13.1	10.8	9.3
6) Adamantane → $3CH_4 + 2C_2H_2$	194.0	196.2	195.9	236.8	238.0
7) E4 → $3CH_4 + 2C_2H_2$	127.2	127.8	126.9	157.7	158.0

Reference data: Peverati, R.; Zhao, Y.; Truhlar, D. G., *J. Phys. Chem. Lett.* **2011**, 2 (16), 1991–1997.

Benchmark HC7



Can we go beyond
simple energies?

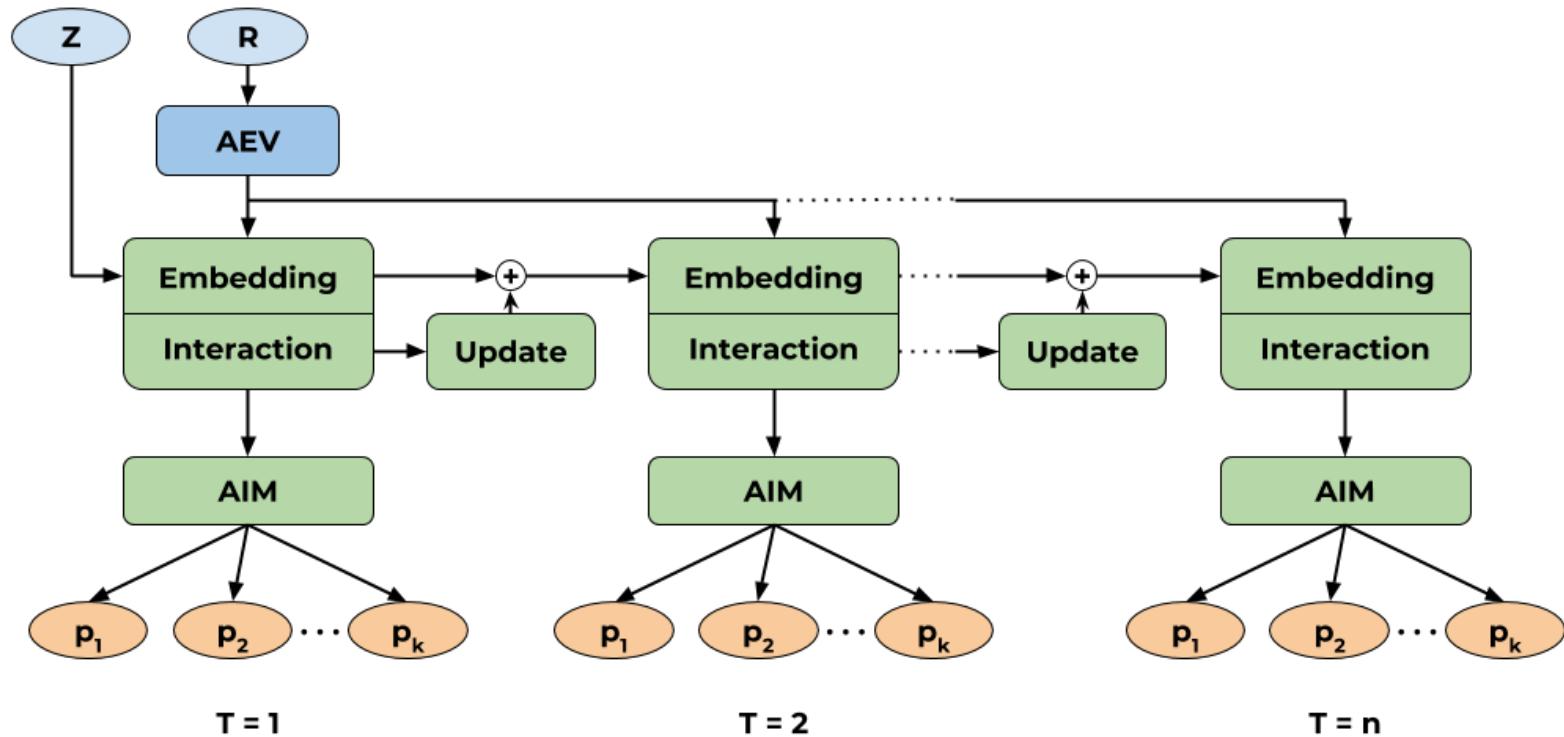


Rethinking Network Architecture: AIMNet

Atoms-in-molecules neural net

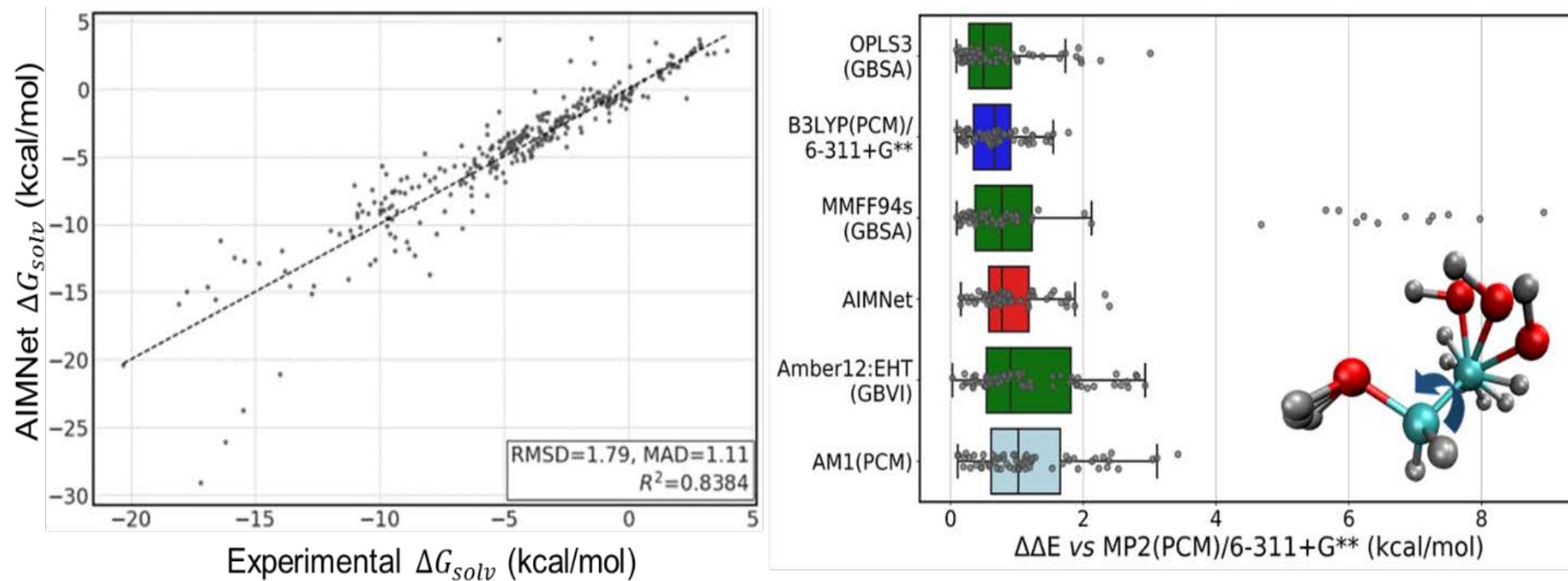
Iterative “SCF-like” update for
better accuracy and
Long range interactions

Multimodal and
multi-task learning: gas phase
energy, charges, atomic
volumes, continuum solvent
(SMD) Correction



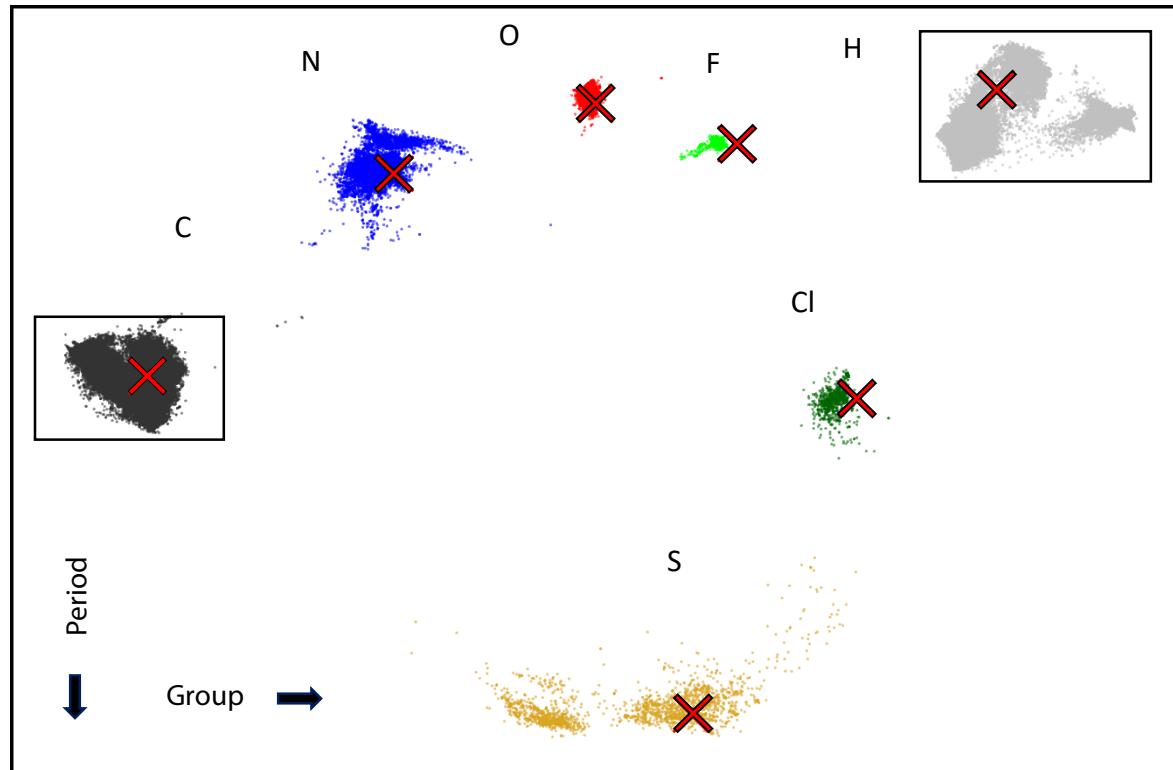
Deep NN network, AIMNet with $T=3$:
33 hidden layers, $\sim 1M$ parameters

Fast & Accurate Solvation Free Energies with AIMNet

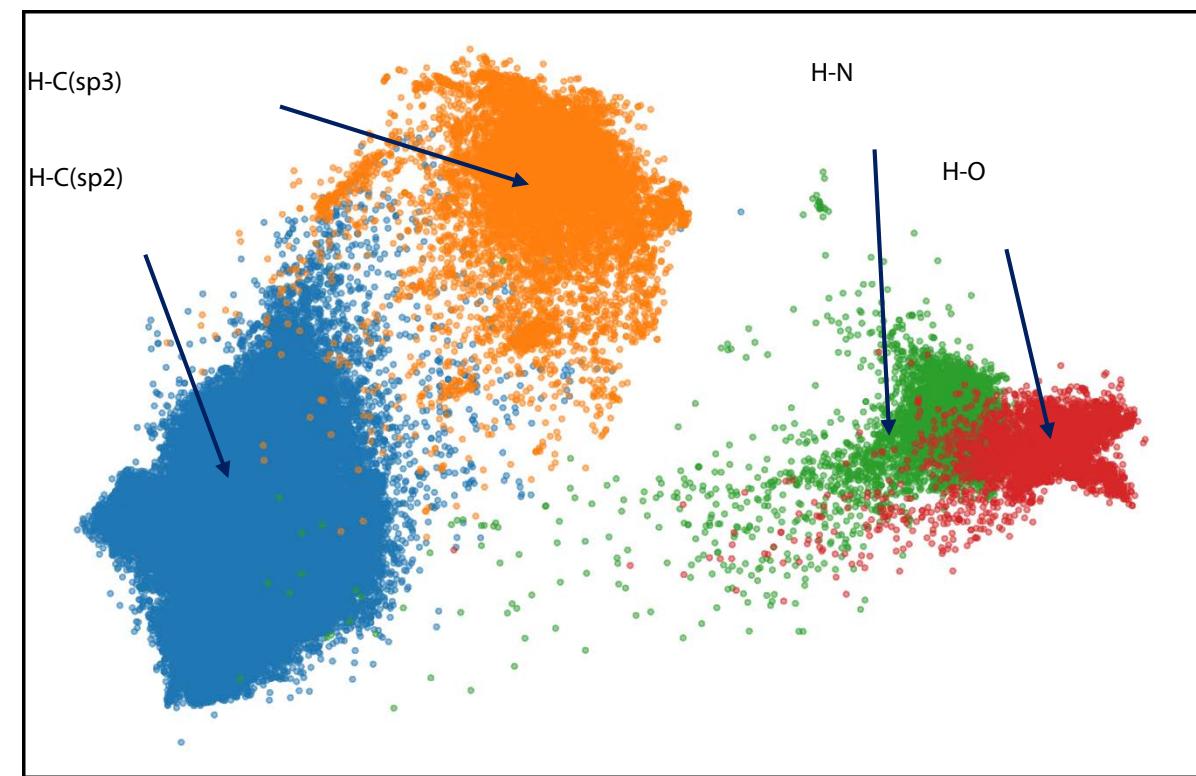
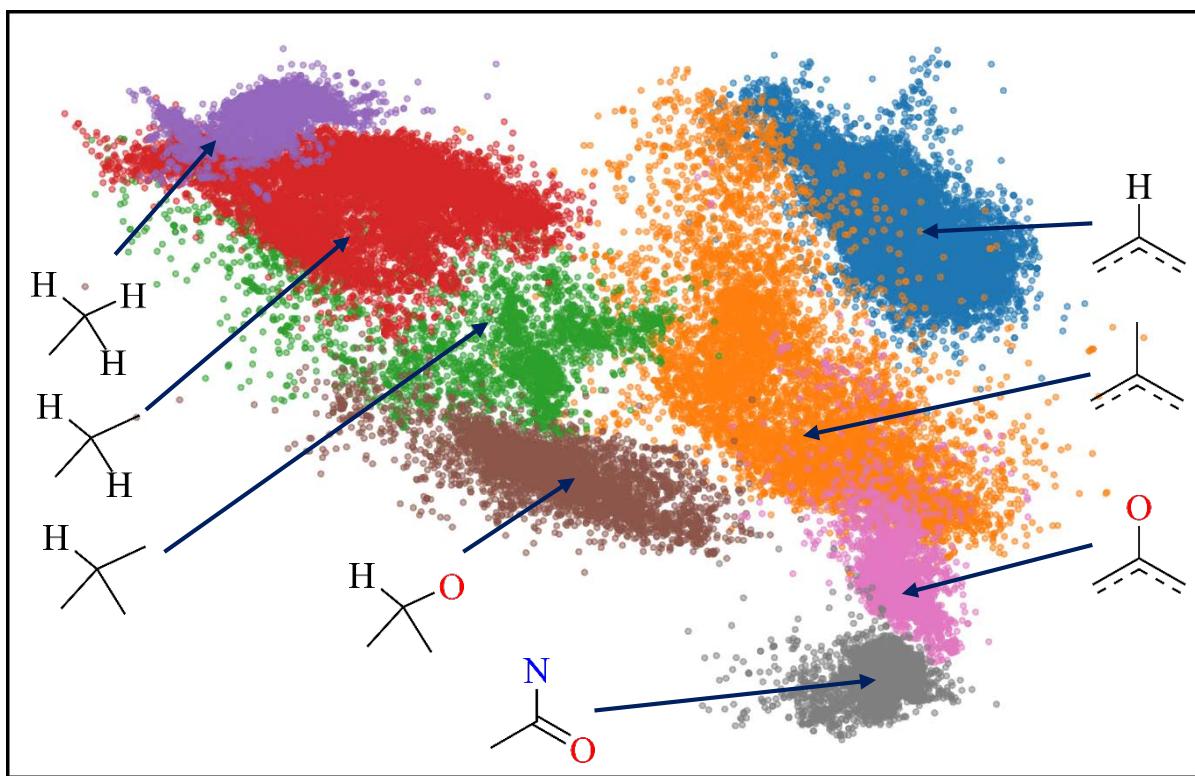


a) Experimental versus predicted with AIMNet solvation free energies (kcal/mol) for 414 neutral molecules from MNSol database. b) performance of AIMNet and other solvation models on torsion benchmark of Sellers et al.

Nature of Learned Atomic Embeddings

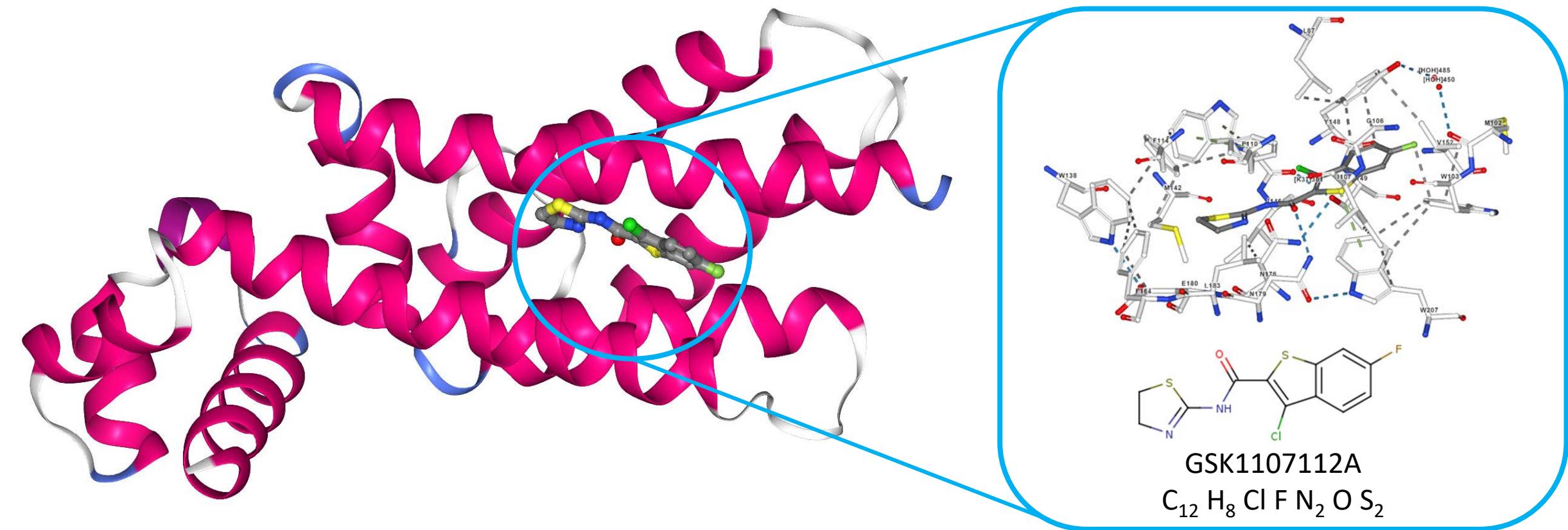


Example of Carbon and Hydrogen



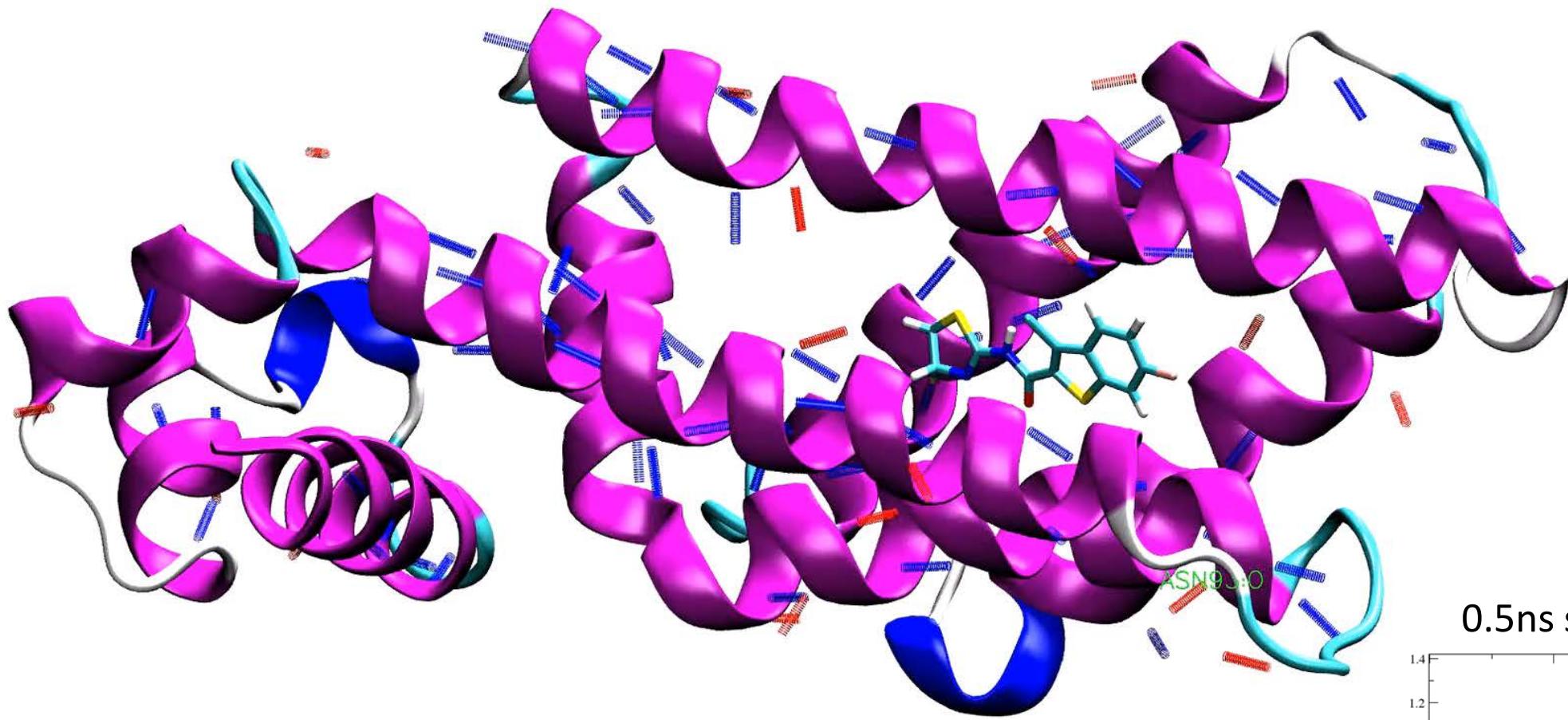
Major future developments

Toward Realistic Macromolecular Simulations

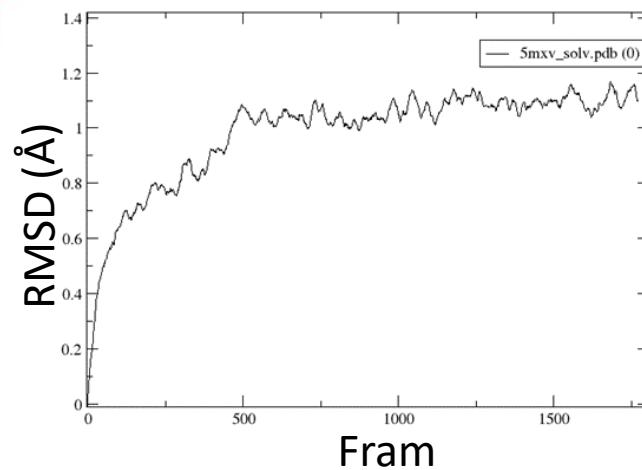


Mycobacterium tuberculosis (5MXV) in explicit water
Simulated with ANI-2 (CHNOSFCI)

- ~35K atoms
- Explicit water
- No ions
- S, F and Cl in ligand

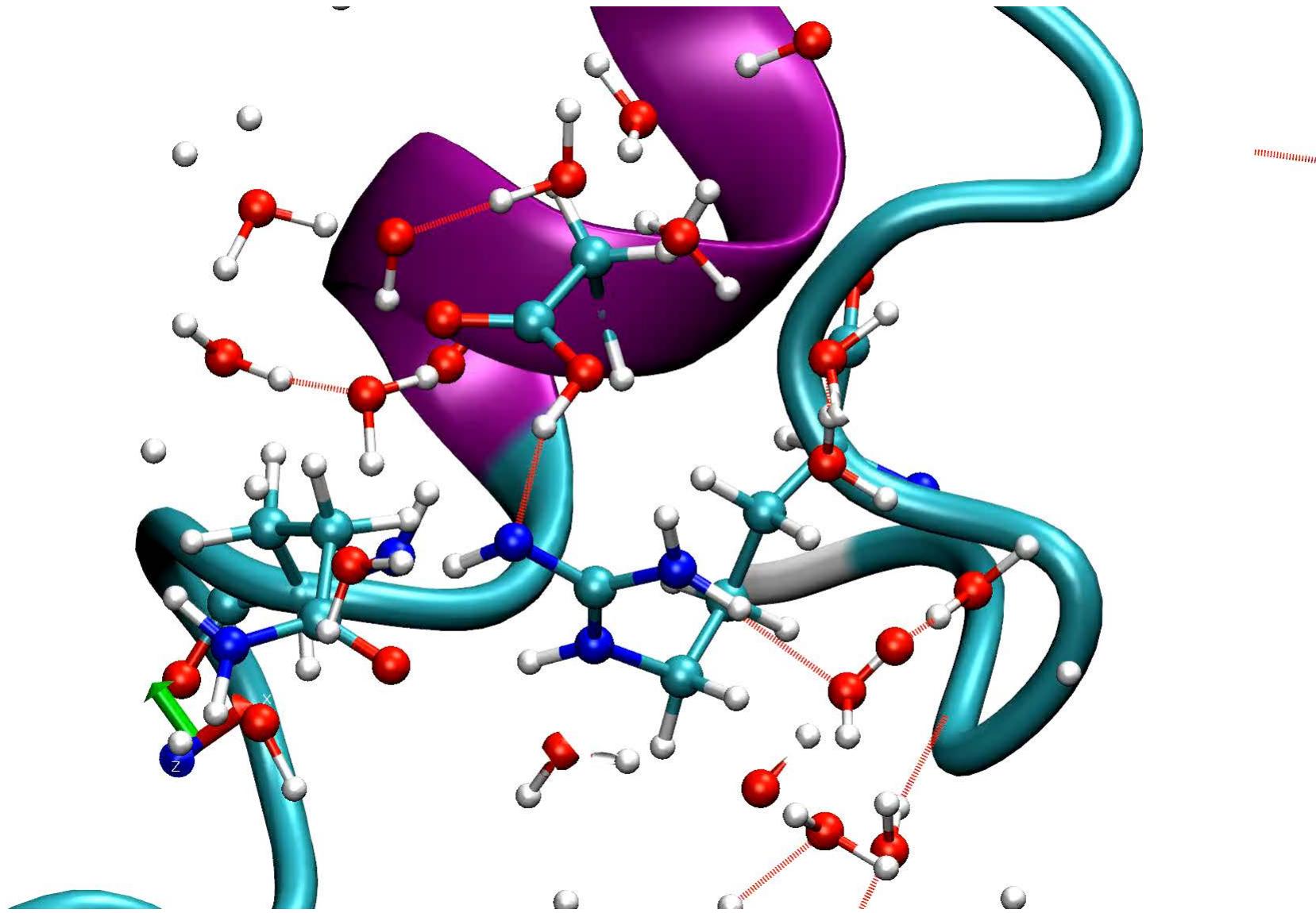


0.5ns simulation time

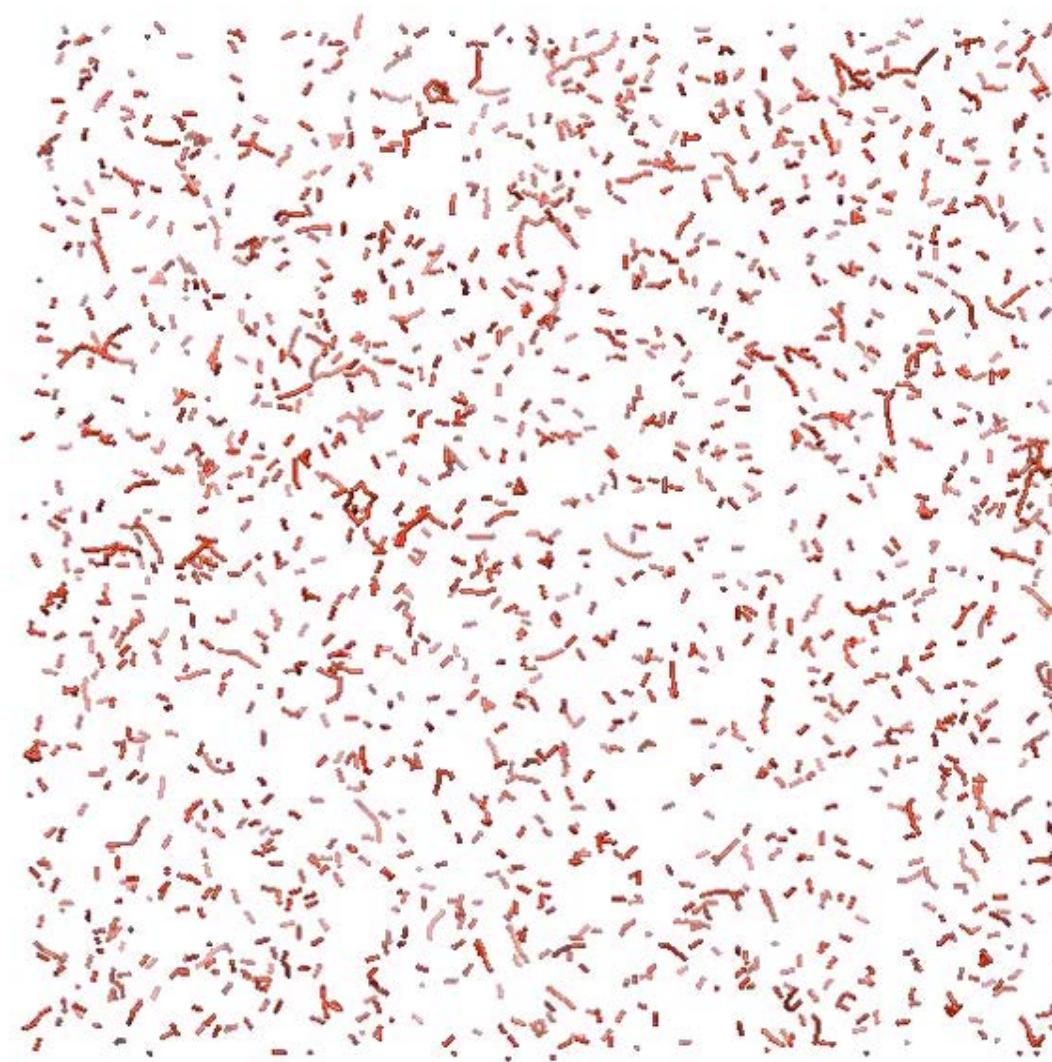


Timings for a 5x ensemble prediction for ANI-2x

GPU	ANI-2x time per step	Total time per step	Steps per day
Tesla V100	297ms	317ms	272k



Simulation of Complex Chemical Reactions



<https://youtu.be/DRVMH5u8EA0>

Carbon nanoparticles/sheets nucleation [4000 atoms in 60Å box at 2500K, 5ns MD simulation]

Use the ANI-1x potential:

ANI-1x interfaced to ASE Python library

Available at: https://github.com/isayev/ASE_ANI

ANI-1x implementation in PyTorch

Available at: <https://github.com/aqm/torchani>

Coming soon to AMBER, OpenMM & LAMMPS

Use the ANI-1 dataset:

ANI-1: A data set of 20M off-equilibrium DFT calculations for organic molecules

Sci. Data, 2017, 4, 170193 DOI: 10.1038/sdata.2017.193

ANI Data set Python library

Available at: https://github.com/isayev/ANI1_dataset

Users:

academic labs:

- Stanford (Vijay Pande)
- U Pitt (Geoff Hutchison)
- CMU MSE (Noa Marom)
- USF
- NCSU
- Barcelona
- Helsinki
- Tel Aviv

Government labs, companies etc.



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HPC Computing:

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