

Hydrogen Bonding: *Ab Initio* Accuracy From Fast Interatomic Gaussian Approximation Potentials 22nd August 2018

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Introduction

- Gaussian Approximation Potential (GAP)
 - A short introduction
 - Practical example
 - Ab initio accuracy without electrons
- The Hydrogen Bond Model
 - How GAPs are applied
- Results
 - Accuracy of the model
 - Speed-up
 - Improvements for the model



B3LYP/def2-SVP



B3LYP/def2-SVP



- Input from an *ab-initio* calculation:
 - Cartesian Coordinates
 - Energy Values
 - Force Values
- Representation of geometry
 - Invariant with respect to permutational, rotational, reflectional and translational symmetry
- Smooth Overlap of Atomic Positions (SOAP)
 - Finite cut-off
 - Complicated environments
 - Size of the system does not matter
- Interatomic potential fit using Gaussian Processes
 - Gaussian Approximation Potential (GAP)





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B3LYP/def2-SVP



ΔE is the relative energy value (compared to the conformation with the lowest energy value)

GAP for Methanol

- How to explore the PES (obtain data points)
 - Molecular dynamics simulation
 - Single point calculations of MD snapshots

New DFT Data DFT

 ΔE is the relative energy value

12 Degrees of Freedom!

 ΔE is the relative energy value

GAP for Methanol

- How to explore the PES (obtain data points)
 - Molecular dynamics simulation
 - Single point calculations of MD snapshots
- Training and testing
 - 100 initial points
 - 1000 points for testing



12 Degrees of Freedom!

Training with 9 Points

 ΔE is the relative energy value

GAP for Methanol

- How to explore the PES (obtain data points)
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12 Degrees of Freedom!

Training with 32 Points

 ΔE is the relative energy value

GAP for Methanol

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 - Single point calculations of MD snapshots
- Training and testing
 - 100 initial points
 - 1000 points for testing
- 46 training points

• 1000 Points



12 Degrees of Freedom!

Testing the GAP

- Complicated PES
 - 25 degrees of freedom
 - Hydrogen bond
 - Wide range of conformations



- Complicated PES
 - 25 degrees of freedom
 - Hydrogen bond
 - Wide range of conformations
 - $0 3.5 \times 10^{92}$
 - $0 2.4 \times 10^{5}$





 ΔE is the relative energy value

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• Simplifications



- Complicated PES
 - 25 degrees of freedom
 - Hydrogen bond
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10 000 Points For Testing



• 1500 Training Points

 ΔE is the relative energy value



• Form a fragment based system



- Form a fragment based system
- Hydrogen bond energy
 - Methanol molecules
 - Methanol dimer



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 - Train potential with E_{HB}
- Advantages
 - More accurate
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Image created with the SeeSAR^m module of StarDrop^m.

Summary

- Hydrogen bonding model ab initio accuracy using GAPs
 - Error (RMSE): 1.2 kJ mol⁻¹
 - Time gain: 120 seconds (DFT), 0.02 seconds (GAP)



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Average Error: 0.54 kJ mol⁻¹, RMSE: 0.66 kJ mol⁻¹, Maximum Error: 1.28 kJ mol⁻¹



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- Applicability
 - Other dimers
 - E.g.

methanol : formaldehyde methanol : formic acid anion methanol : primary amine methanol : formic acid, formic acid : formic acid, primary amine : primary amine

- GAPs have a wide range of applications
- Any level of theory can be used with GAPs

- Über potential
 - Additional dimers found in and between drug molecules and proteins
 - More charged species
 - Combine atom types
 - Reduce the amount of dimers
- Additional interactions
 - Complex dimers
 - Third monomer
- Predict errors of the model

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