

Machine learning the Born-Oppenheimer potential energy surface: from molecules to materials

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Engineering Laboratory

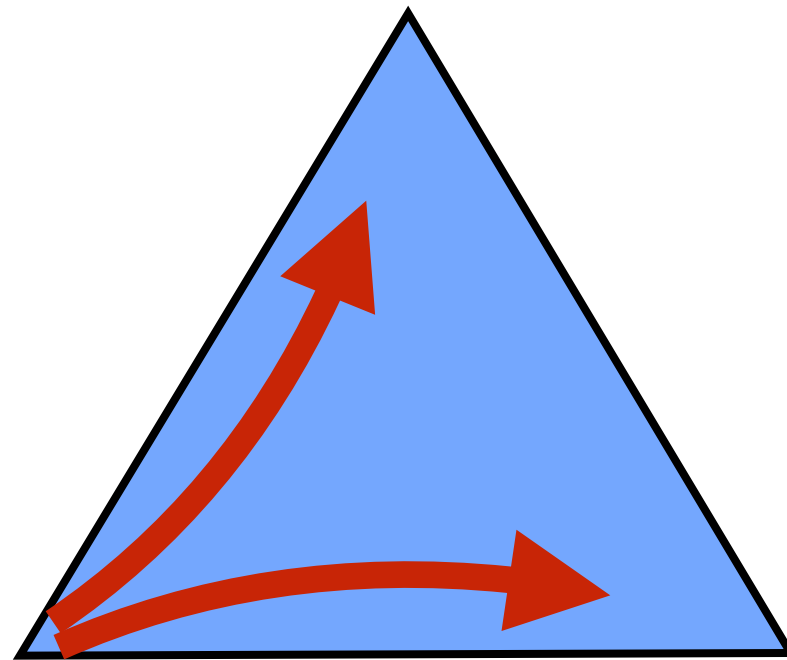


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Interatomic potentials for molecular dynamics

Transferability
biomolecular
force fields
(biochemistry)

AMBER
CHARMM
AMOEBA
GROMACS
OPLS
...



Accuracy
small molecules
in gas phase
(quantum chemistry)

Bowman
Szalewicz
Paesani
...

Reactive
solid state
materials
(physics & materials)

Tersoff
Brenner
EAM
BOP
...

Ingredients

- **Representation** of atomic neighbourhood \longrightarrow smoothness, faithfulness, continuity
- **Interpolation** of functions \longrightarrow flexible but smooth functional form, few sensible parameters
- **Database** of configurations \longrightarrow predictive power non-domain specific

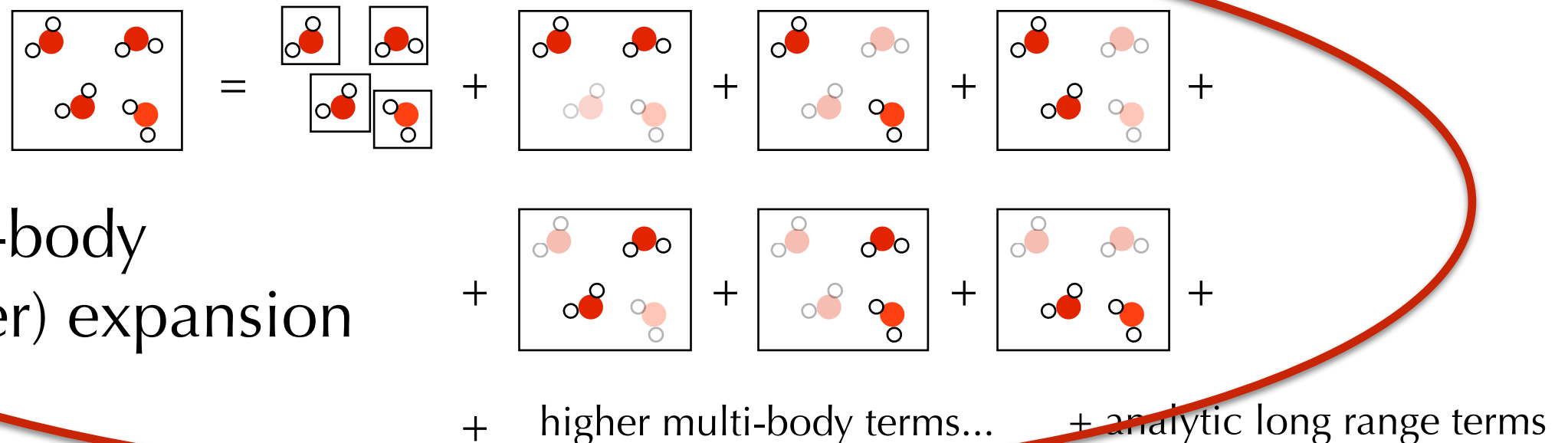
Interpolating the solution of an eigenproblem

$$-i\hbar \frac{\partial \Psi}{\partial t} = \mathcal{H} \Psi \quad \mathcal{H}_{\text{el}} = \frac{1}{2} \sum_i \nabla_{r_i}^2 + \sum_{ij} \frac{Z_j(-1)}{|R_j - r_i|} + \sum_{ij} \frac{1}{|r_i - r_j|}$$

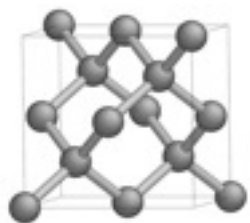
Lowest eigenstate: $E_0 \equiv V_{\text{el}}(R_1, R_2, \dots)$ has **spatial locality**

Weak

Many-body
(cluster) expansion



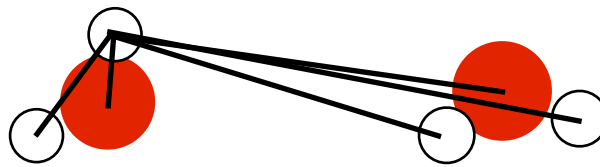
Strong



$$E = \sum_i \varepsilon(q_1^{(i)}, q_2^{(i)}, \dots, q_M^{(i)}) + \text{analytic long range terms}$$

q_i are **descriptors** of local atomic neighbourhood

Parametrisation of the H₂O dimer



- Standard representation:
6 atoms \Rightarrow 15 interatomic distances : $x = \{r_{ij}\}$
- Symmetrize kernel function:

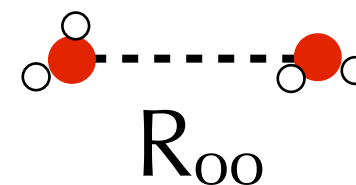
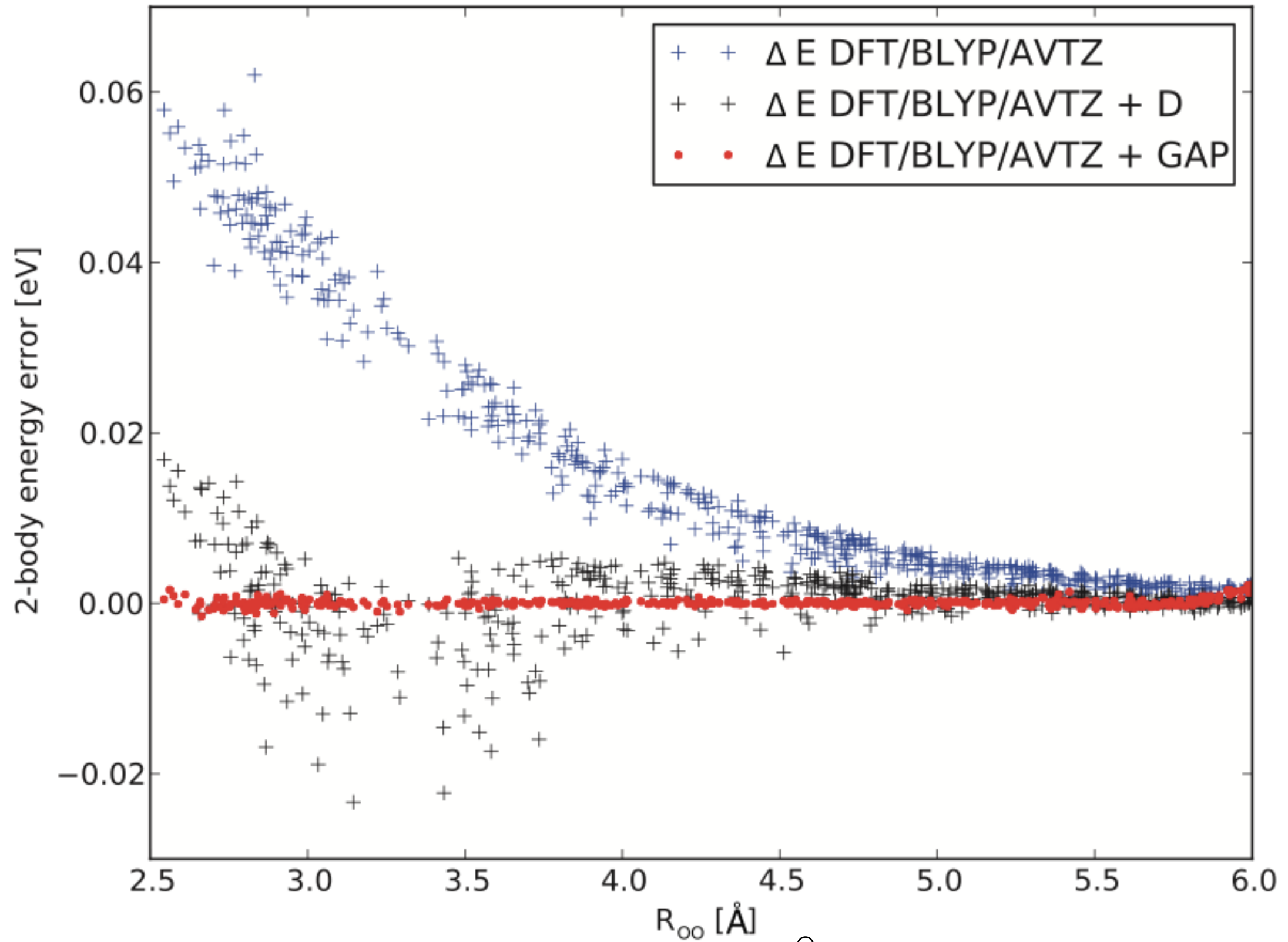
$$\tilde{K}(x, x') = \sum_{p \in S} K(p(x), x')$$

S : symmetry group of molecules

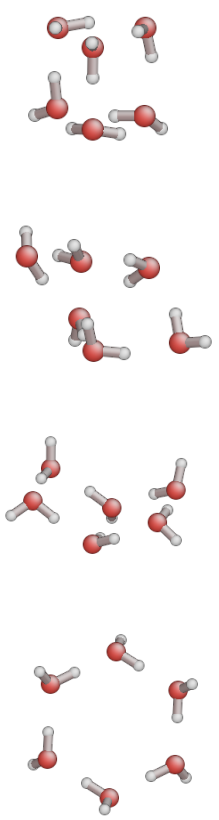
- Use analytic forces if available:

$$K'(x, x') = \frac{\partial}{\partial x} K(x, x')$$

H2O dimer corrections



Water hexamers - relative energies - no ZPC



CCSD(T)	BLYP	DMC	Bowman	BLYP+GAP
0.00	0.00	0.00	0.00	0.00
0.24	-0.59	0.33	0.46	0.15
0.70	-2.18	0.56	2.39	0.52
1.69	-2.44	1.53	4.78	1.77

[kcal / mol]

(B3LYP optimised
geometries from
Tschumper)

GAP error < 0.03 kcal/mol / H₂O

Ice polymorphs

Relative energies

[meV / H ₂ O]	Expt	DMC \pm 5	PBE0+vdW ^{TS}	BLYP+GAP \pm 3
Ih	0	0	0	0
II	I	-4	6	-5
IX	4		3	-3
VIII	33	30	76	30

error < 0.15 kcal/mol / H₂O

Ice polymorphs

Absolute binding energies

[meV / H ₂ O]	Expt	DMC ±5	PBE0+vdW ^{TS}	BLYP+GAP ±3
I _h	610	605	672	667
II	609	609	666	672
IX				
VIII	577	575	596	637

BLYP+GAP overbinds *uniformly* by ~ 60 meV
⇒ 3-body terms!

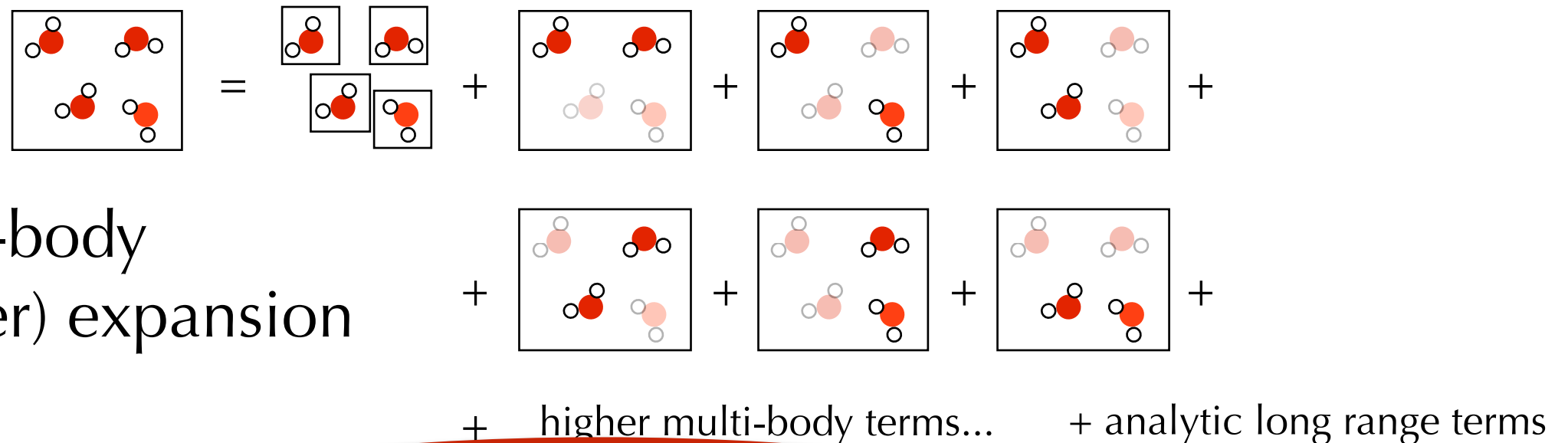
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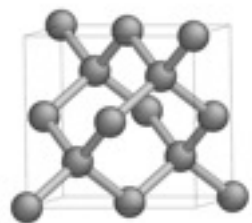
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Weak

Many-body
(cluster) expansion



Strong

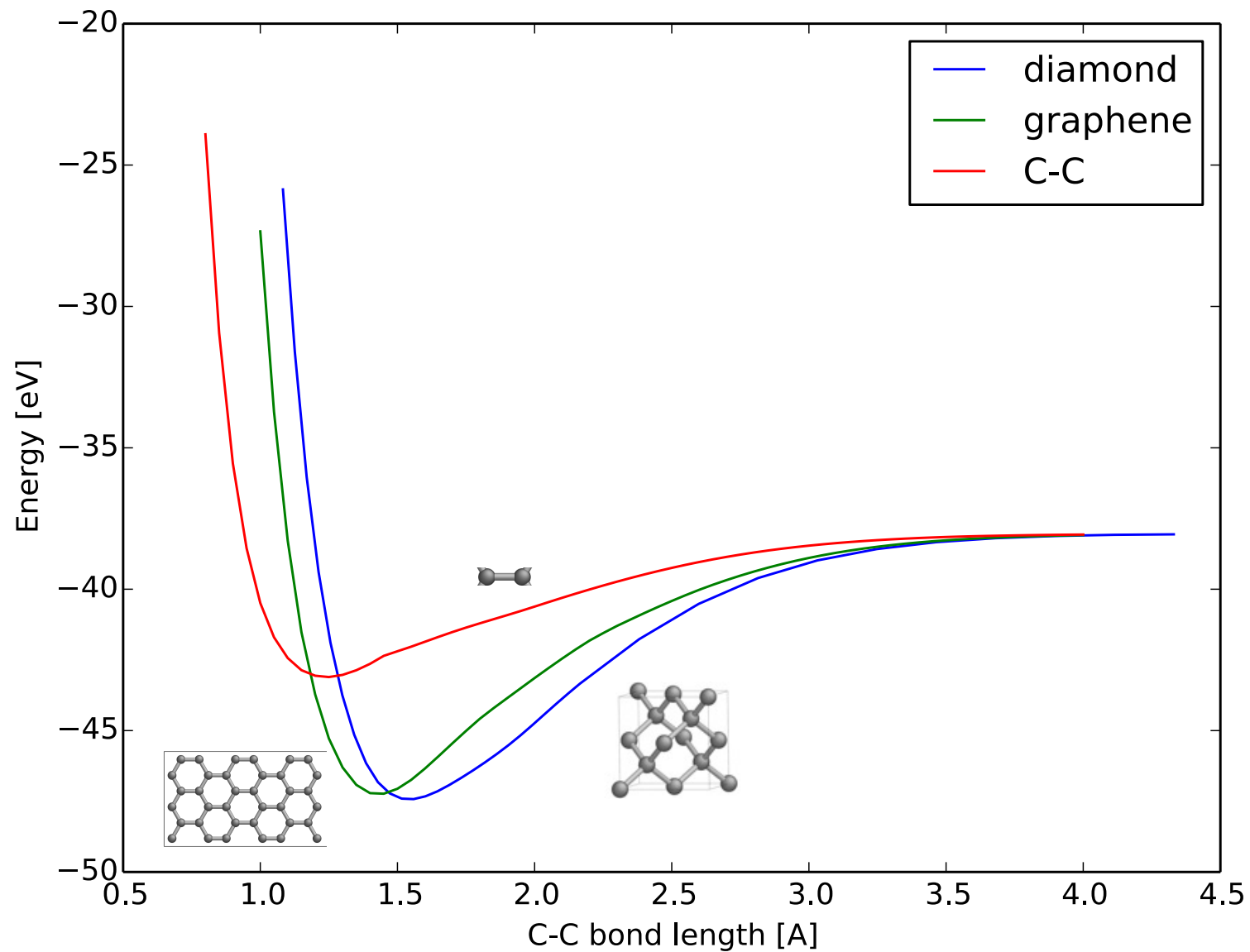


$$E = \sum_i \varepsilon(q_1^{(i)}, q_2^{(i)}, \dots, q_M^{(i)}) + \text{analytic long range terms}$$

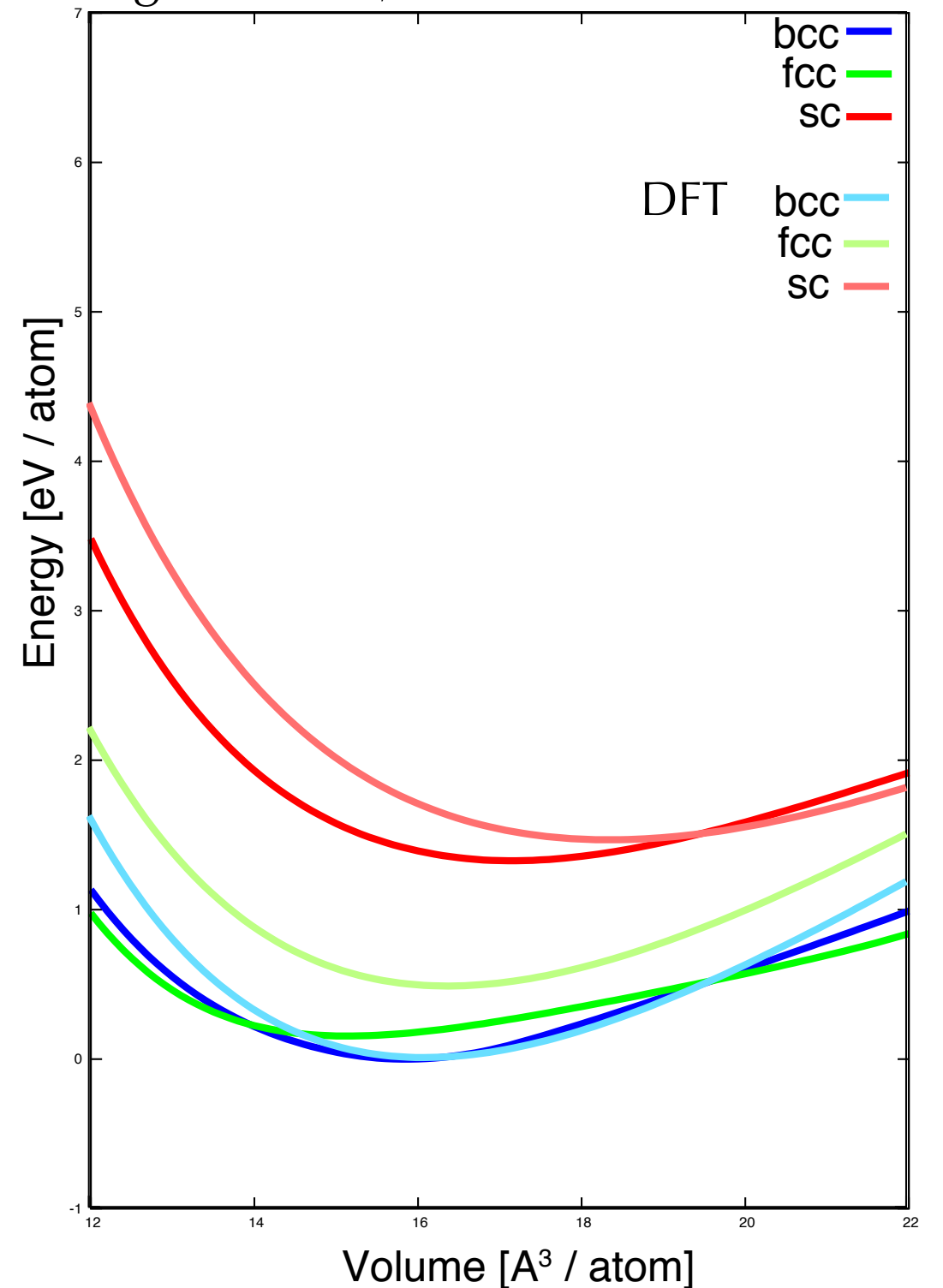
q_i are **descriptors** of local atomic neighbourhood

Quantum mechanics is many-body

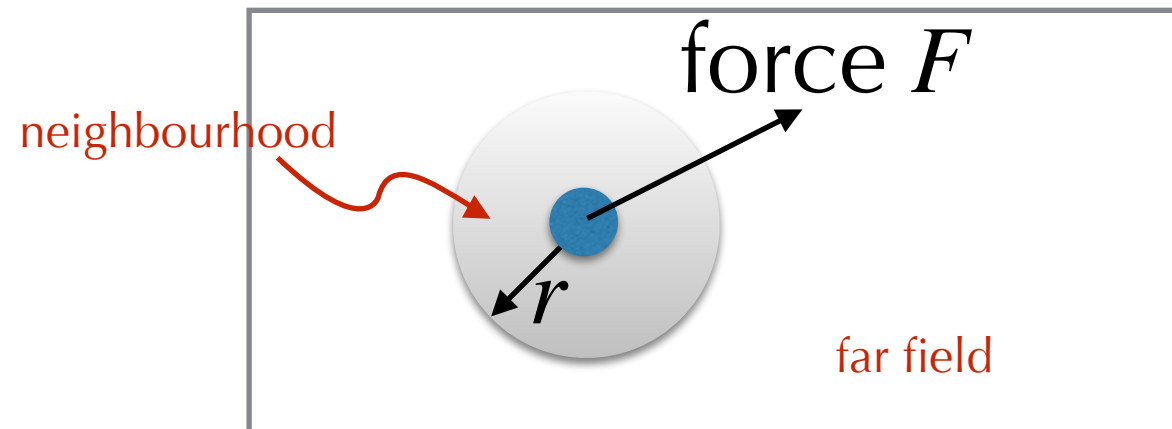
Carbon: tight binding



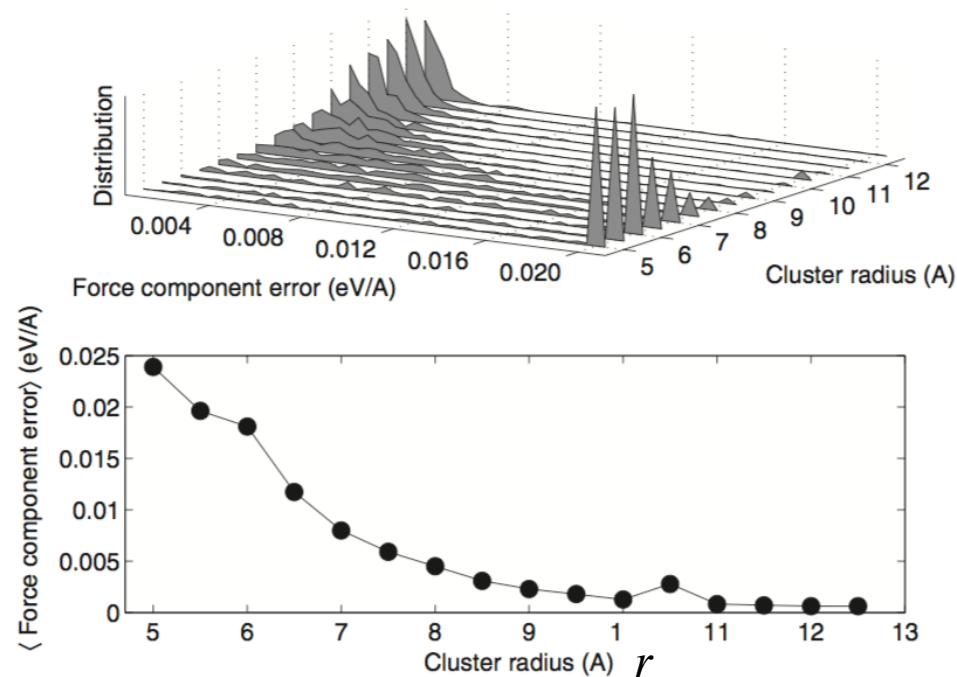
Tungsten: DFT, Embedded Atom Model



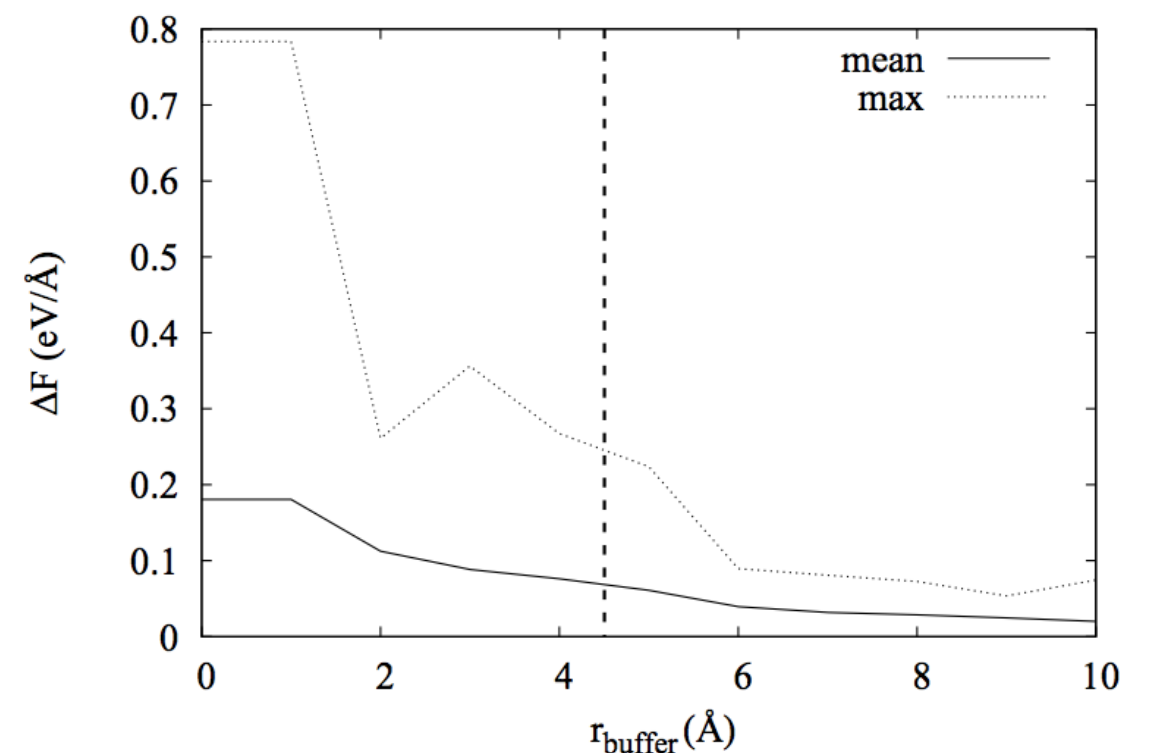
Quantum mechanics has some locality



Force errors around
Si self interstitial



Force errors around
O in water with QM/MM



Is there a finite range atomic energy function that gives the correct total energy and forces?

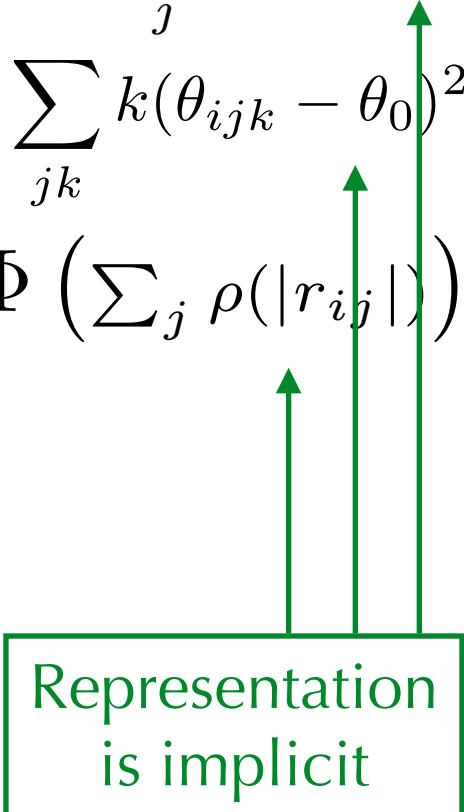
$$V_{\text{el}}(R_1, R_2, \dots) \approx \sum_i^{\text{atoms}} \varepsilon(R_1 - R_i, R_2 - R_i, \dots) + \frac{1}{2} \sum_{ij} \hat{L}_i \hat{L}_j \frac{1}{R_{ij}} + \frac{q_i q_j}{|R_{ij}|^6}$$

Finite range atomic energy function

$$L_i = q_i + \mathbf{p}_i \cdot \nabla_i + \dots$$

Traditional ideas for functional forms

- Pair potentials: Lennard-Jones, RDF-derived, etc.
- Three-body terms: Stillinger-Weber, MEAM, etc.
- Embedded Atom (no angular dependence)
- Bond Order Potential (BOP)
Tight-binding-derived attractive term with
pair-potential repulsion
- ReaxFF: kitchen-sink + hundreds of parameters

$$\varepsilon_i = \frac{1}{2} \sum_j V_2(|r_{ij}|) + \sum_{jk} k(\theta_{ijk} - \theta_0)^2$$
$$\varepsilon_i = \Phi \left(\sum_j \rho(|r_{ij}|) \right)$$


Representation is implicit

These are NOT THE CORRECT functions.
Limited accuracy, not systematic

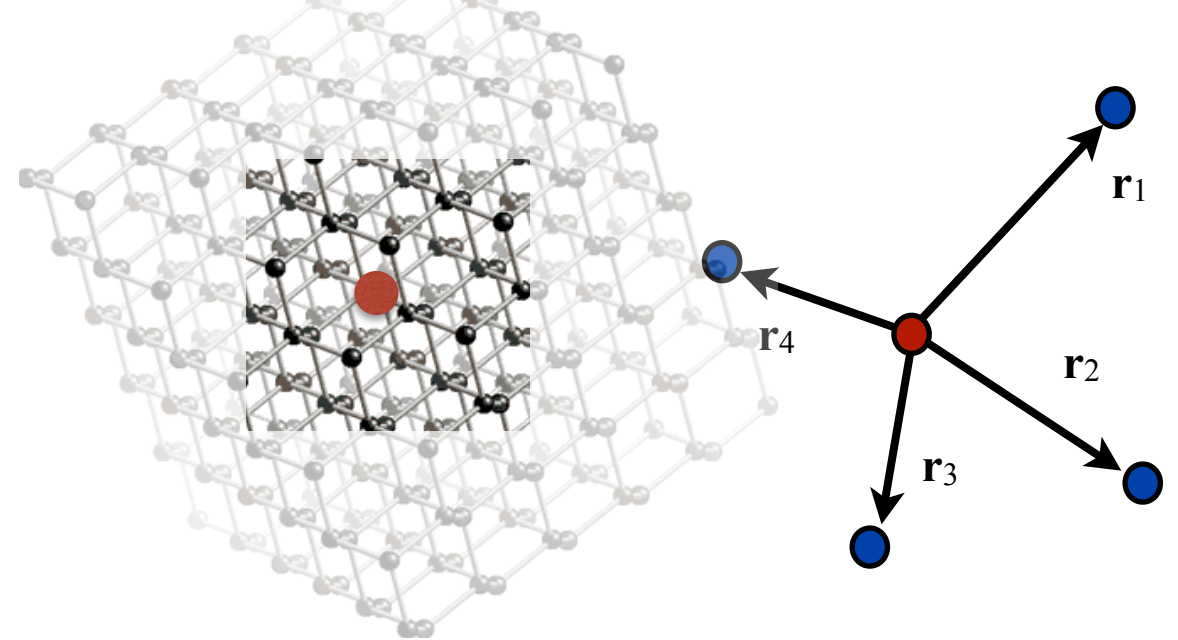
given by
GOAL: potentials ~~based on~~ quantum mechanics

Representing the atomic neighbourhood in strongly bound materials

- What are the arguments of the atomic energy ε ?

Need a representation, i.e. a coordinate transformation

$$\{\mathbf{r}_i\} \rightarrow \mathbf{q}$$

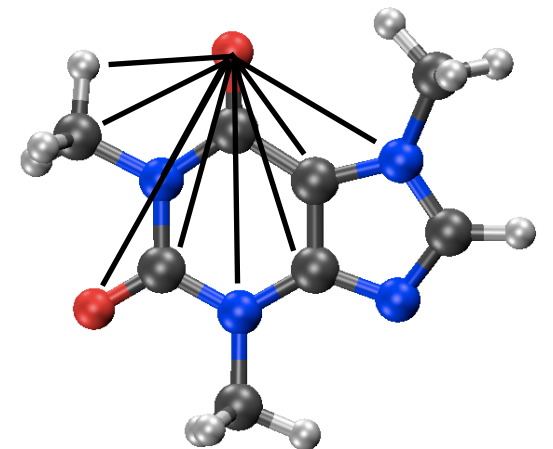


- Exact symmetries:
 - Global Translation
 - Global Rotation
 - Reflection
 - Permutation of atoms
 - Faithful: different configurations correspond to different representations
 - Continuous, differentiable, and smooth (i.e. slowly changing with atomic position) (“Lipschitz diffeomorphic”)
- Rotational invariance by itself is easy: $\mathbf{q} \equiv R_{ij} = \mathbf{r}_i \cdot \mathbf{r}_j$ (Weyl)
 - Complete, but not invariant permutationally
 - Not continuous with changing number of neighbours

Matrix of interatomic distances

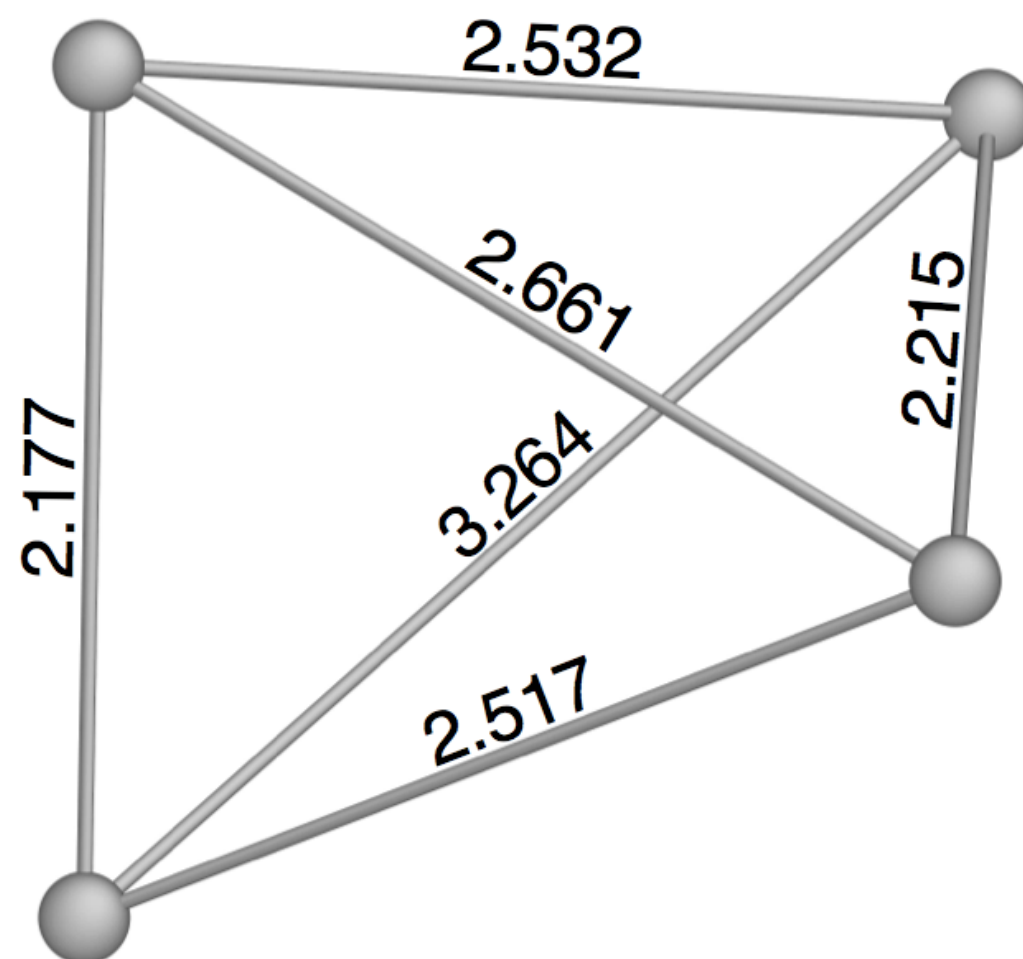
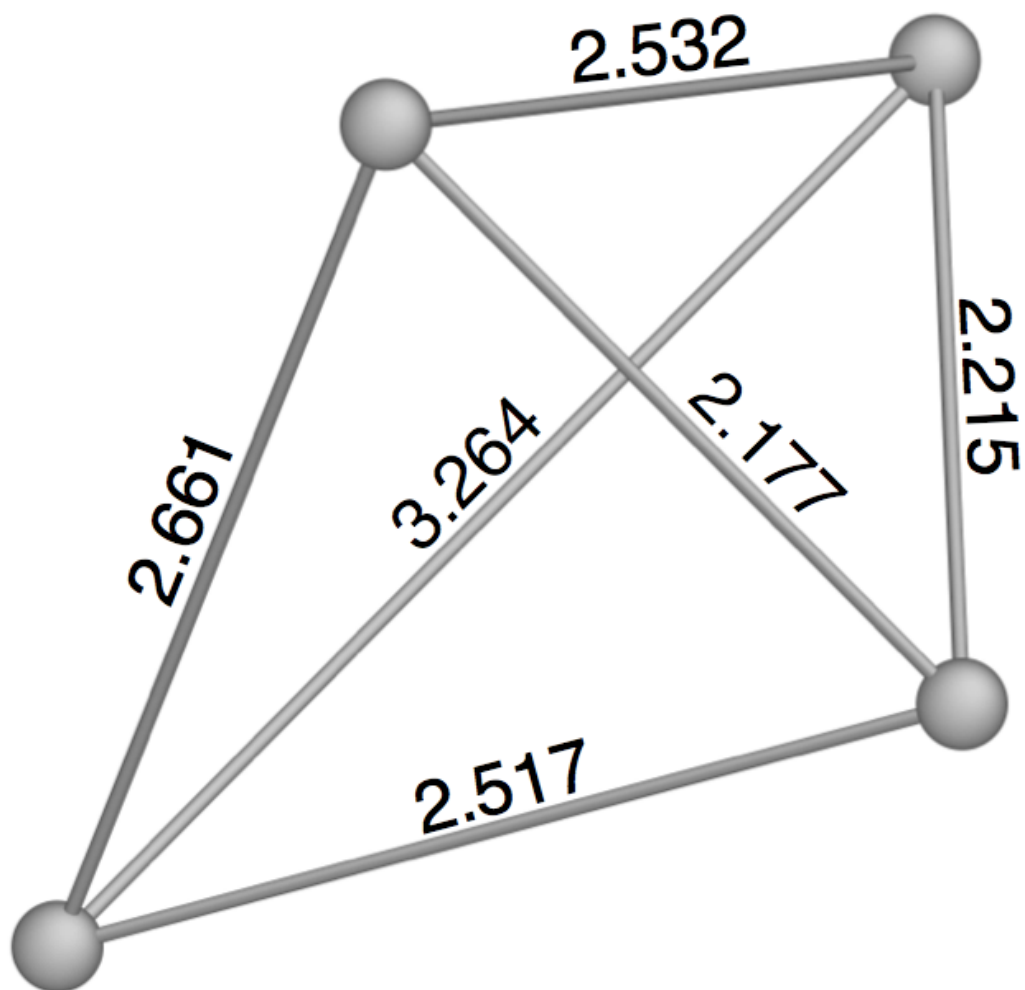
- Equivalent to Weyl matrix

$$\begin{bmatrix} \mathbf{r}_1 \cdot \mathbf{r}_1 & \mathbf{r}_1 \cdot \mathbf{r}_2 & \cdots & \mathbf{r}_1 \cdot \mathbf{r}_N \\ \mathbf{r}_2 \cdot \mathbf{r}_1 & \mathbf{r}_2 \cdot \mathbf{r}_2 & \cdots & \mathbf{r}_2 \cdot \mathbf{r}_N \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{r}_N \cdot \mathbf{r}_1 & \mathbf{r}_N \cdot \mathbf{r}_2 & \cdots & \mathbf{r}_N \cdot \mathbf{r}_N \end{bmatrix}$$



- Rotationally invariant: no alignment needed
- Permutation problem: Weyl matrix is not permutation invariant

Drop atom ordering ?



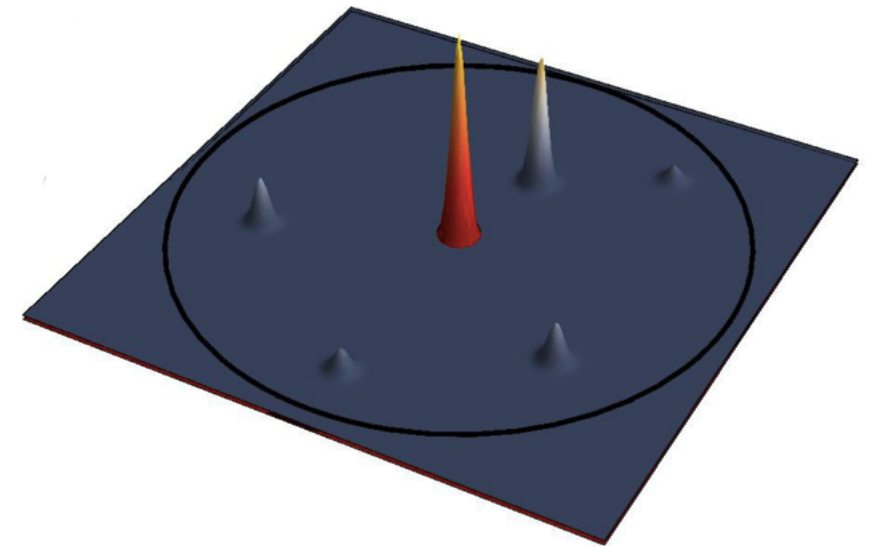
Not unique!

Atomic neighbour density function

$$\varepsilon(\mathbf{r}_1 - \mathbf{r}_i, \mathbf{r}_2 - \mathbf{r}_i, \dots) \equiv \varepsilon[\rho_i(\mathbf{r})]$$

$$\rho_i(\mathbf{r}) = s\delta(\mathbf{r}) + \sum_j \delta(\mathbf{r} - \mathbf{r}_{ij}) f_{\text{cut}}(|\mathbf{r}_{ij}|)$$

$$\rho(r, \theta, \phi) = \sum_{n=1}^{\infty} \sum_{l=0}^{\infty} \sum_{m=-l}^l c_{l,n}^m g_n(r) Y_l^m(\theta, \phi)$$



- Translation ✓
- Permutation ✓
- Need rotationally invariant features of $\rho(\mathbf{r})$

Rotational Invariance

$$\rho(\hat{\mathbf{r}}) = \sum_{lm} c_{lm} Y_{lm}(\hat{\mathbf{r}})$$

$$\begin{aligned} \rho(\hat{R}\hat{\mathbf{r}}) &= \sum_{lm} c_{lm} Y_{lm}(\hat{R}\hat{\mathbf{r}}) = \sum_{lm} c_{lm} \sum_{m'} D_{mm'}^l(\hat{R}) Y_{lm'}(\hat{\mathbf{r}}) \\ &= \sum_{lm'} \left(\sum_m D_{mm'}^l c_{lm} \right) Y_{lm'}(\hat{\mathbf{r}}) \end{aligned}$$

Transformation
of coefficients:

$$\mathbf{c}_l \xrightarrow{\hat{R}} \mathbf{D}^l \mathbf{c}_l$$

- Wigner matrices are unitary:

$$\mathbf{D}^{-1} = \mathbf{D}^\dagger$$

- Construct invariants:

$$p_l = \mathbf{c}_l^\dagger \mathbf{c}_l \rightarrow \left(\mathbf{c}_l^\dagger \mathbf{D}^{l\dagger} \right) (\mathbf{D}^l \mathbf{c}_l) = \mathbf{c}_l^\dagger \mathbf{c}_l$$

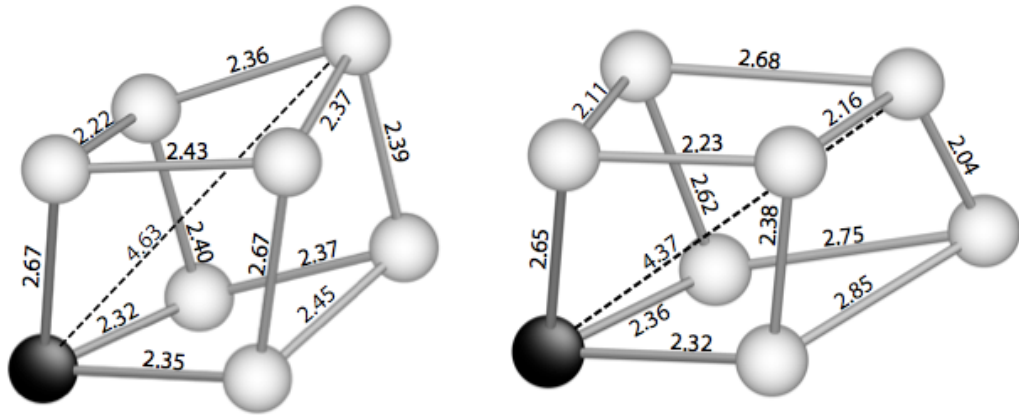
- Equivalent to Steinhardt bond order Q_2 , Q_4 , Q_6 ... parameters
- Higher order invariants possible, (generalisation of Steinhardt W)

First few terms of power spectrum for 3 atoms

$$\begin{aligned}p_0 &= \frac{9}{4\pi} \\p_1 &= \frac{3}{4\pi} \left(\sum_{jk} \cos \theta_{ijk} + 3 \right) \\p_2 &= \frac{5}{4\pi} \left(\frac{3}{2} \sum_{jk} \cos^2 \theta_{ijk} + 6 \right) \\p_3 &= \frac{7}{4\pi} \left(\frac{5}{2} \sum_{jk} \cos^3 \theta_{ijk} - \frac{3}{2} \sum_{jk} \cos \theta_{ijk} + 3 \right) \\p_4 &= \frac{9}{16\pi} \left(\frac{35}{2} \sum_{jk} \cos^4 \theta_{ijk} - 15 \sum_{jk} \cos^2 \theta_{ijk} + 13 \right)\end{aligned}$$

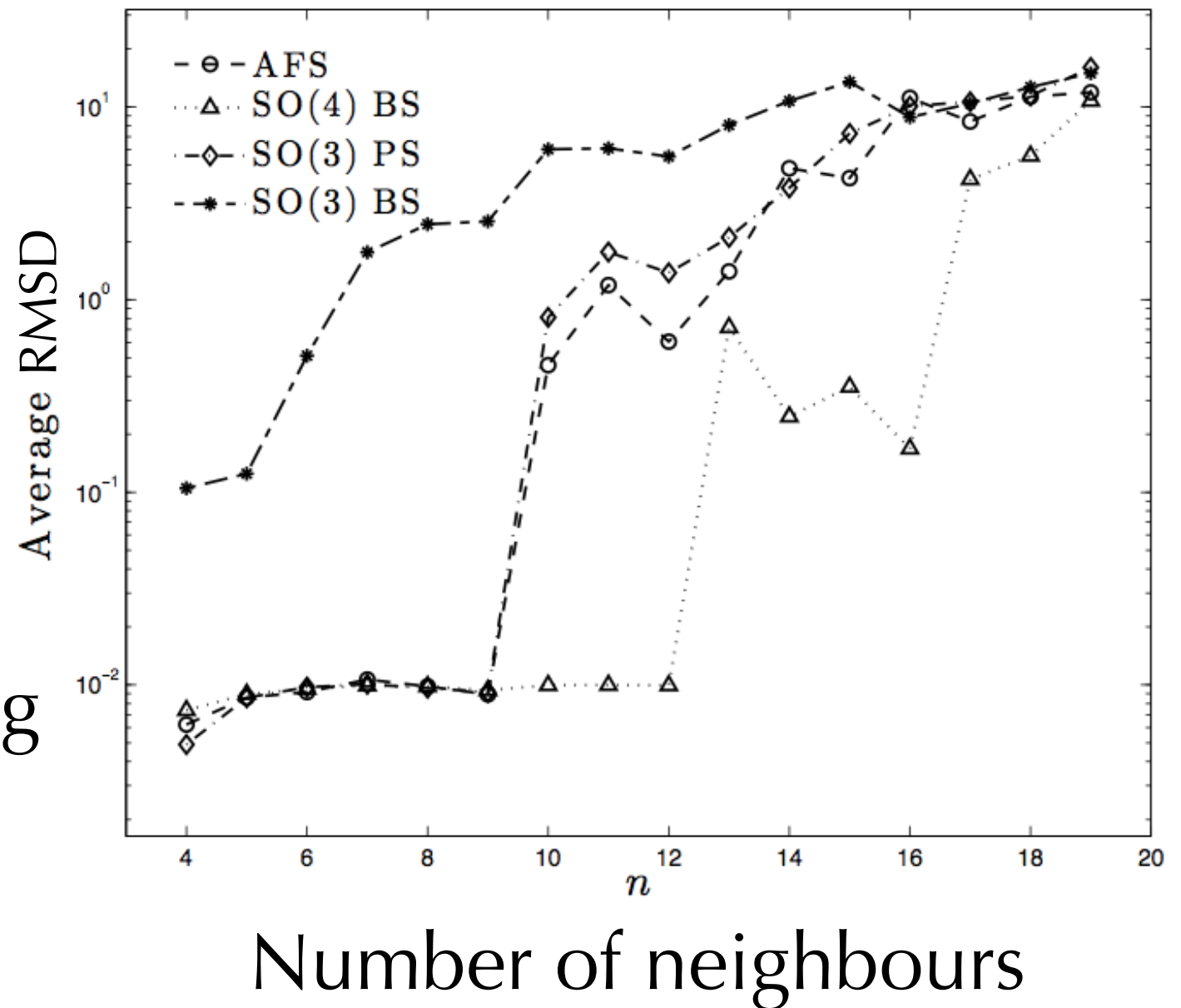
- Polynomials of Weyl invariants
- Highly oscillatory for large l : *not smooth*
- Different l channels uncoupled

Uniqueness: environment reconstruction tests



1. Select target configuration
2. Randomise neighbours
3. Try to reconstruct target by matching descriptors

Error in distinguishing

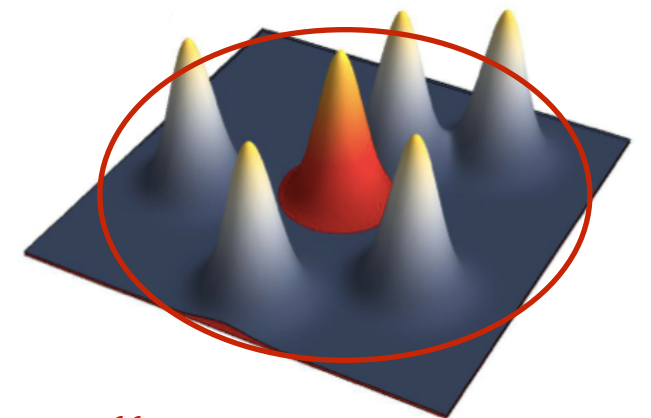


Construct smooth similarity kernel directly

$$\rho_i(\mathbf{r}) = \sum_j \exp(-|\mathbf{r} - \mathbf{r}_{ij}|^2 / 2\sigma^2) = \sum_j \sum_{lm} c_{nlm}^{(i)j} g_n(r) Y_{lm}(\hat{\mathbf{r}})$$

- Overlap integral

$$S(\rho_i, \rho_{i'}) = \int \rho_i(\mathbf{r}) \rho_{i'}(\mathbf{r}) d\mathbf{r},$$



cutoff: compact support

- Integrate over all 3D rotations:

$$k(\rho_i, \rho_{i'}) = \int \left| S(\rho_i, \hat{R}\rho_{i'}) \right|^2 d\hat{R} = \int d\hat{R} \left| \int \rho_i(\mathbf{r}) \rho_{i'}(\hat{R}\mathbf{r}) d\mathbf{r} \right|^2$$

- After LOTS of algebra: SOAP kernel

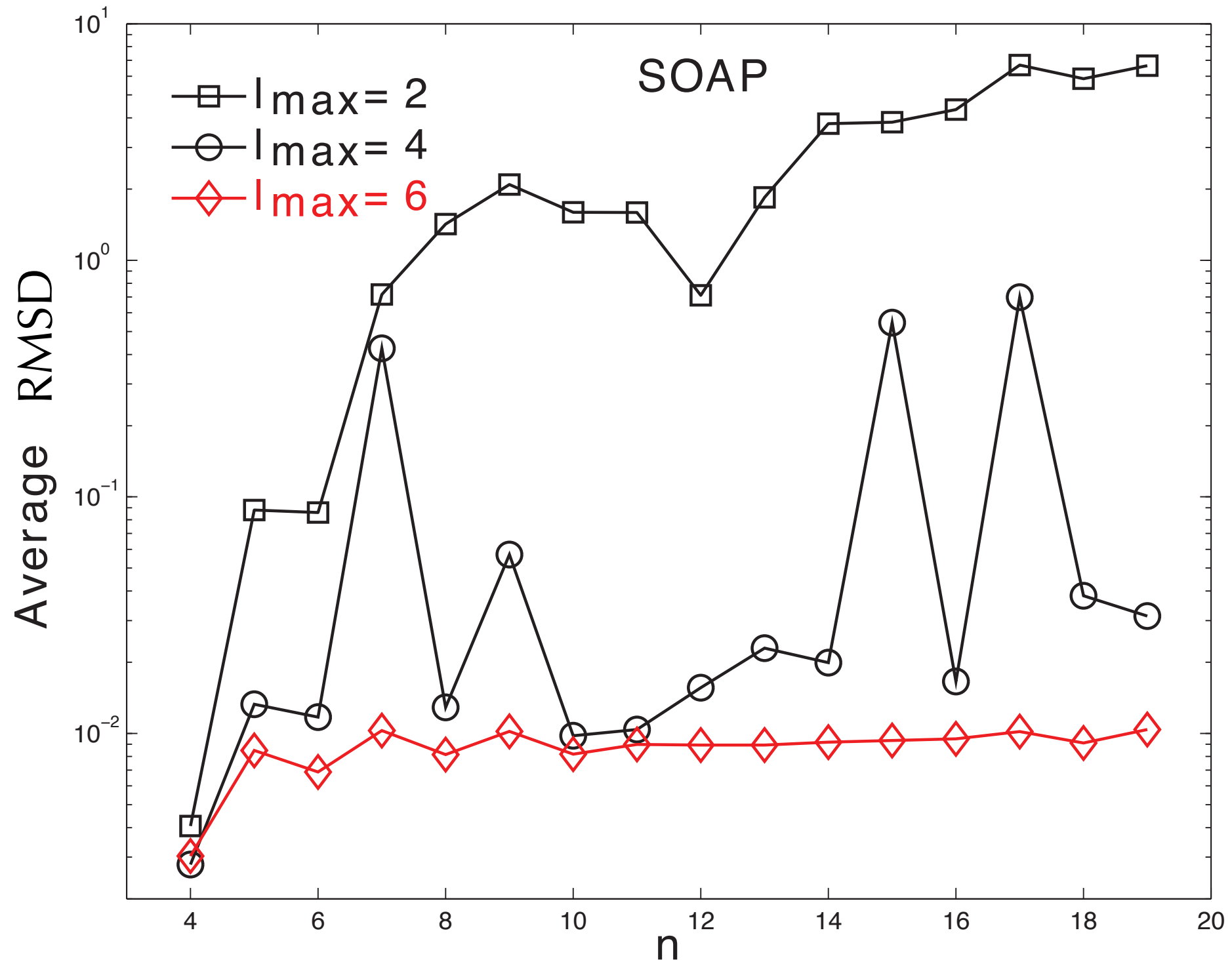
$$k(\rho_i, \rho_{i'}) = \sum_{n,n',l} p_{nn'l}^{(i)} p_{nn'l}^{(i')}$$

$$p_{nn'l} = \mathbf{c}_{nl}^\dagger \mathbf{c}_{n'l}$$

$$K(\mathbf{q}, \mathbf{q}') \propto |k(\rho, \rho')|^\xi$$

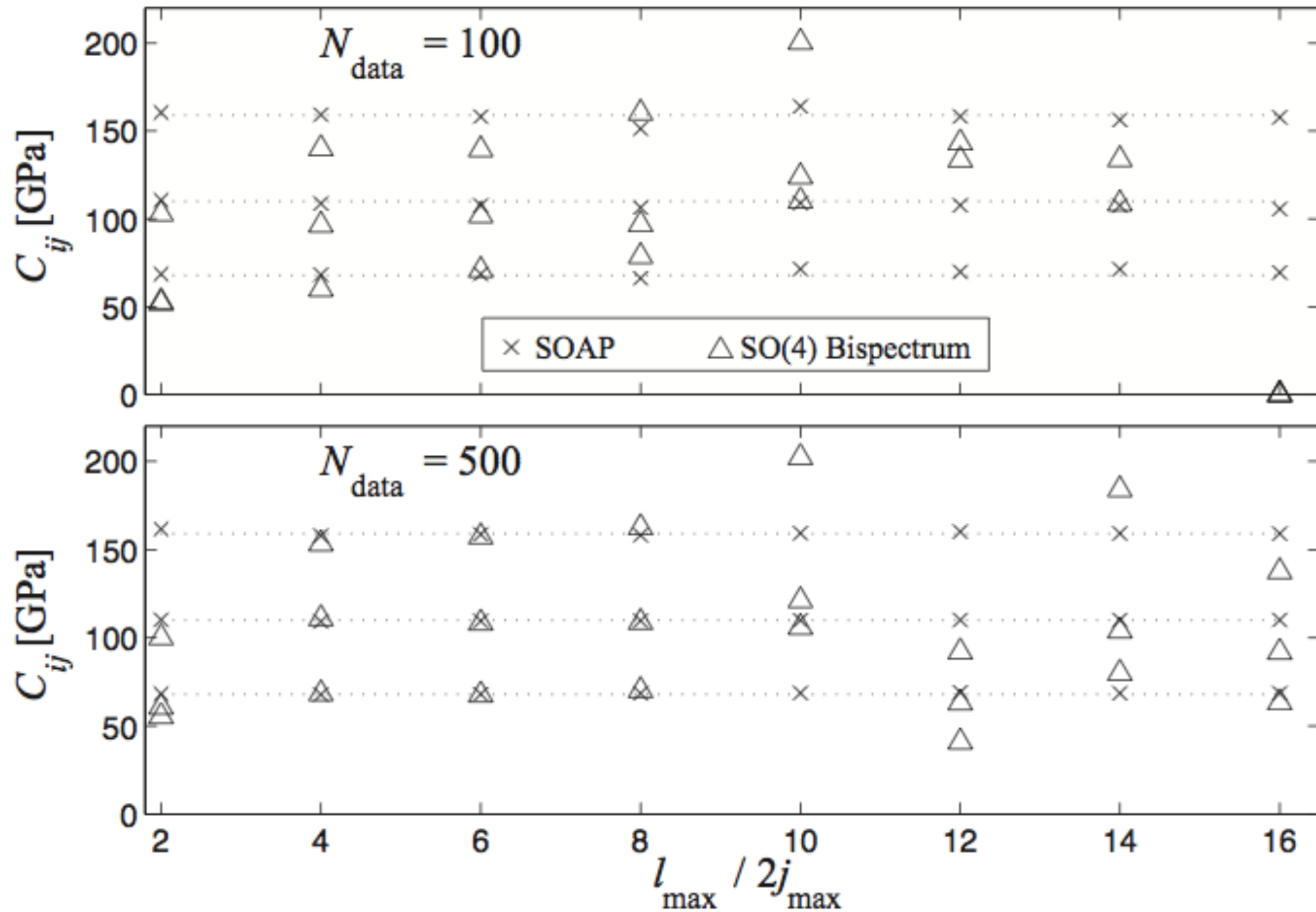
Smooth Overlap of Atomic Positions (SOAP)

Error in distinguishing



Number of neighbours

Stability of fit: elastic constants of Si



Order of angular momentum expansion

How to generate databases?

- Target applications: **large systems**
- Capability of full quantum mechanics (QM): **small systems**

QM MD on “representative” small systems:

sheared primitive cell → elasticity

large unit cell → phonons

surface unit cells → surface energy

gamma surfaces → screw dislocation

vacancy in small cell → vacancy

vacancy @ gamma surface → vacancy near dislocation

Iterative refinement

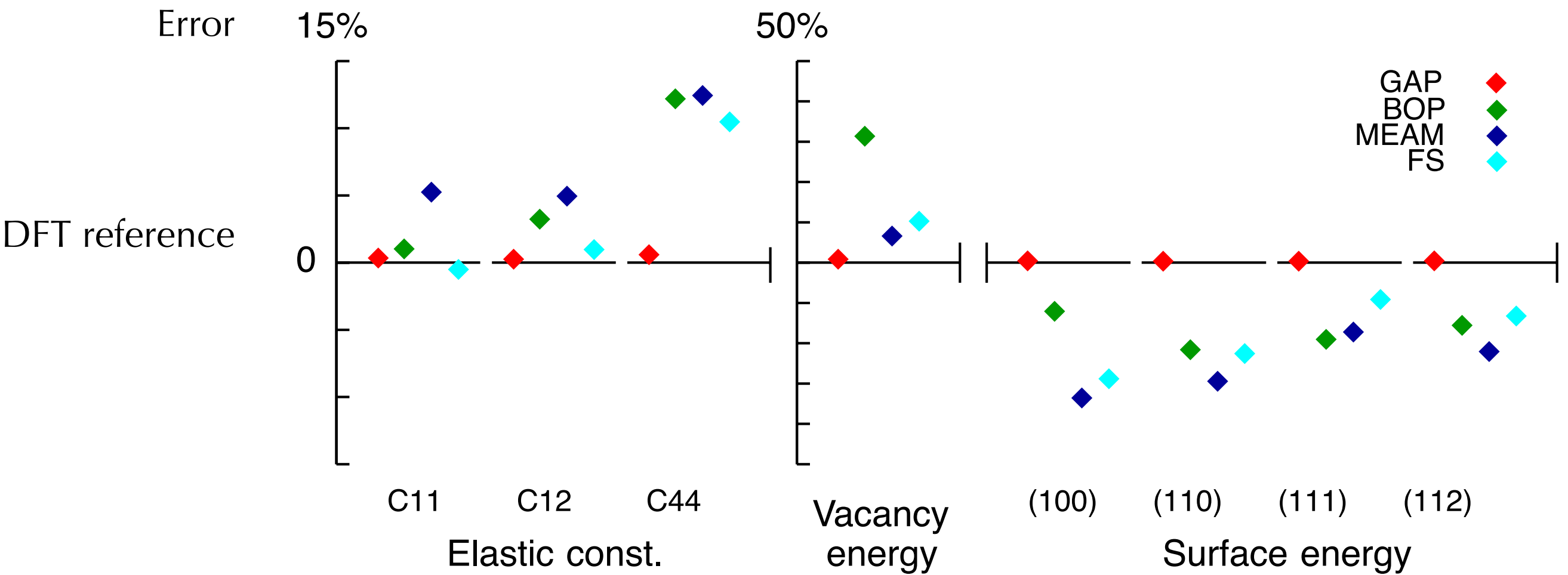
1. QM MD → Initial database

2. Model MD

3. QM → Revised database

What is the acceptable validation protocol?
How far can the domain of validity be extended?

Existing potentials for tungsten

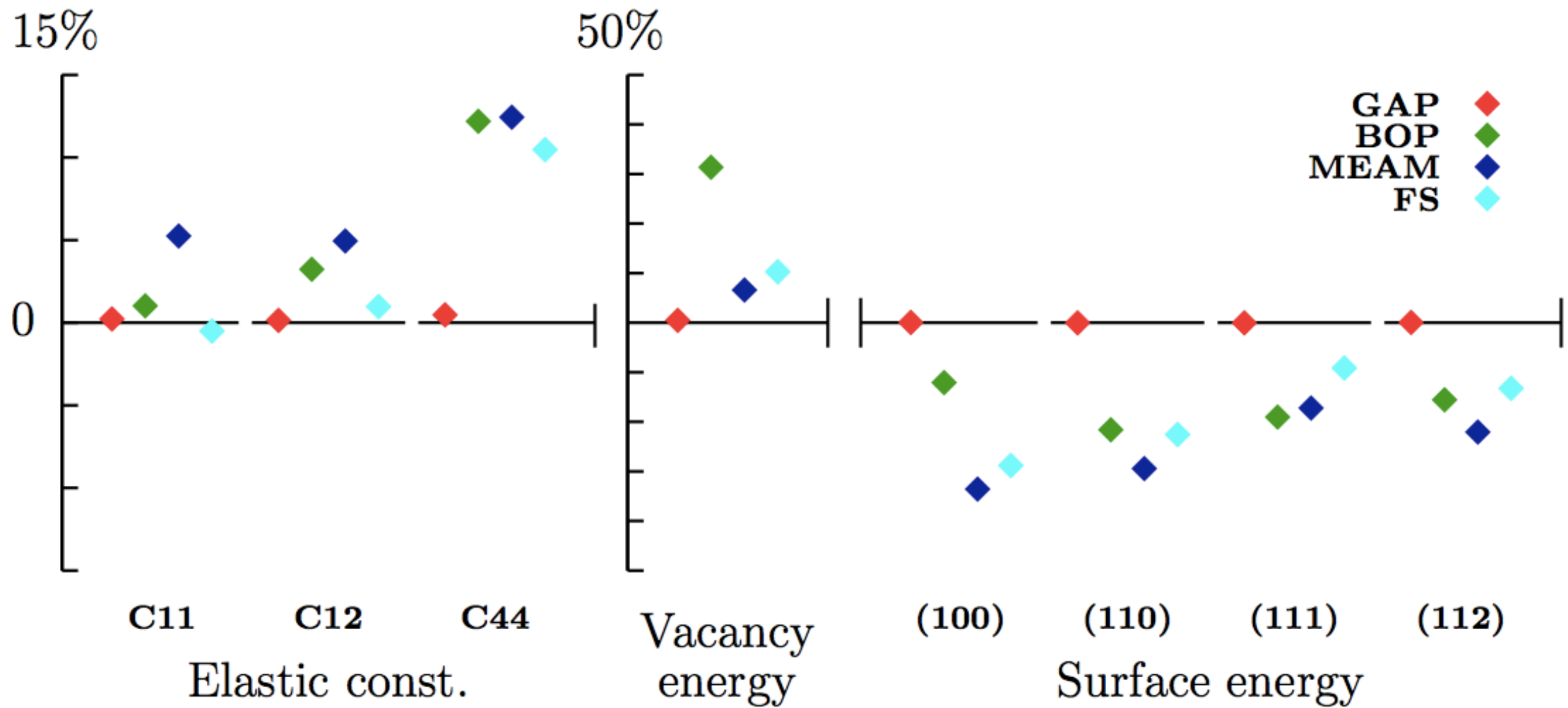


Building up databases for tungsten (W)

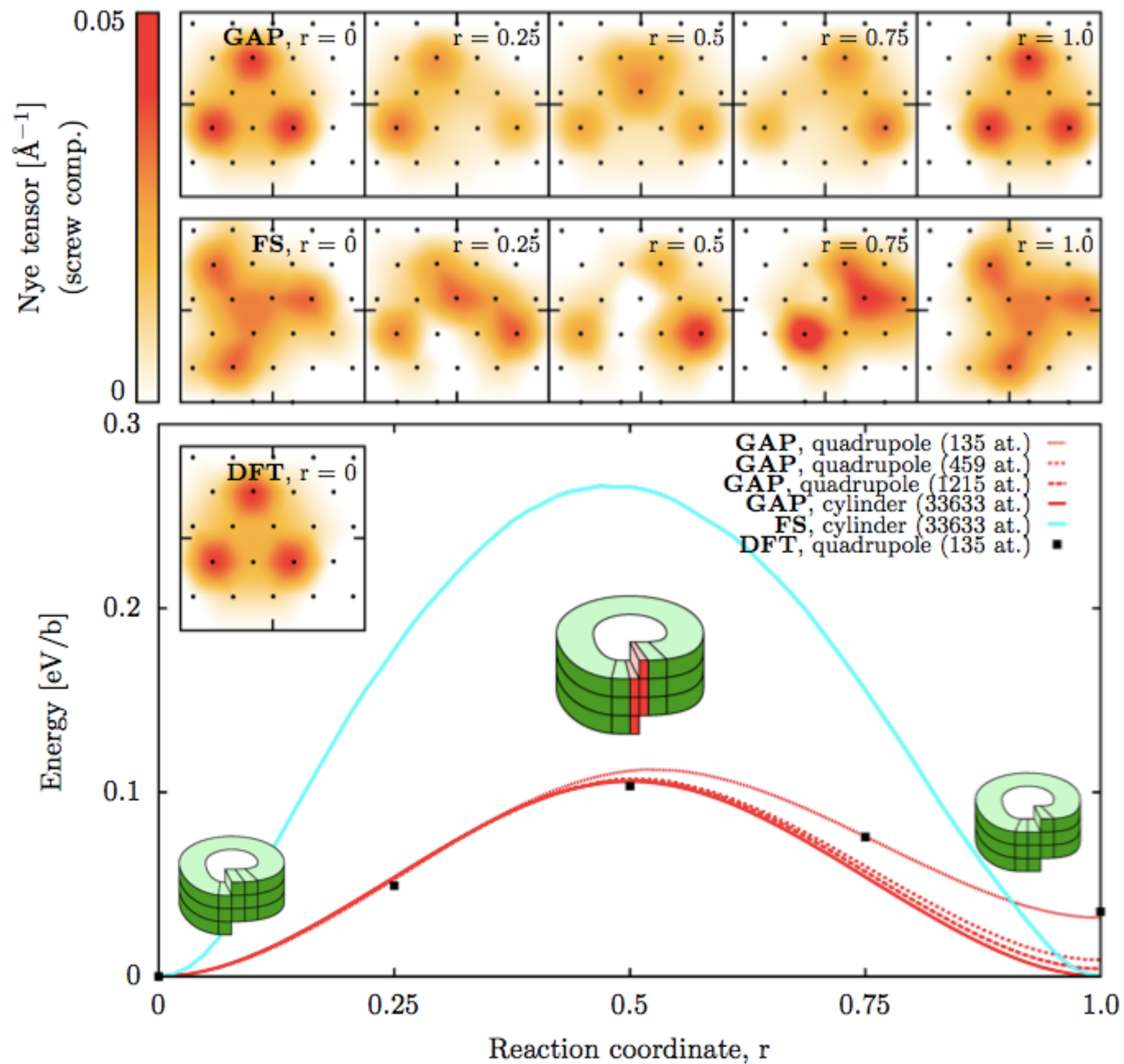
Database:			Computational cost ^a [ms/atom]	Elastic constants ^b [GPa]	Phonon spectrum ^b [THz]	Vacancy formation ^c [eV]	Surface energy ^b [eV/Å ²]	Dislocation structure ^d [Å ⁻¹]	Dislocation-vacancy binding energy [eV]	Peierls barrier [eV/b]
GAP ₁ :	2000 × primitive unit cell with varying lattice vectors		24.70	0.623	0.583	2.855	0.1452	0.0008		
GAP ₂ :	GAP ₁ + 60 × 128 atom cell		51.05	0.608	0.146	1.414	0.1522	0.0006		
GAP ₃ :	GAP ₂ + vacancy in: 400 × 53 atom cell, 20 × 127 atom cell		63.65	0.716	0.142	0.018	0.0941	0.0004		
GAP ₄ :	GAP ₃ + (100), (110), (111), (112) surfaces 180 × 12 atom cell (110), (112) gamma surfaces 6183 × 12 atom cell		86.99	0.581	0.138	0.005	0.0001	0.0002	-0.960	0.108
GAP ₅ :	GAP ₄ + vacancy in: (110), (112) gamma surface 750 × 47 atom cell		93.86	0.865	0.126	0.011	0.0001	0.0002	-0.774	0.154
GAP ₆ :	GAP ₅ + $\frac{1}{2}\langle 111 \rangle$ dislocation quadrupole 100 × 135 atom cell		93.33	0.748	0.129	0.015	0.0001	0.0001	-0.794	0.112

^a Time on a single CPU core of Intel Xeon E5-2670 2.6GHz, ^b RMS error, ^c formation energy error, ^d RMS error of Nye tensor over the 12 atoms nearest the dislocation core, cf. Figure 2.

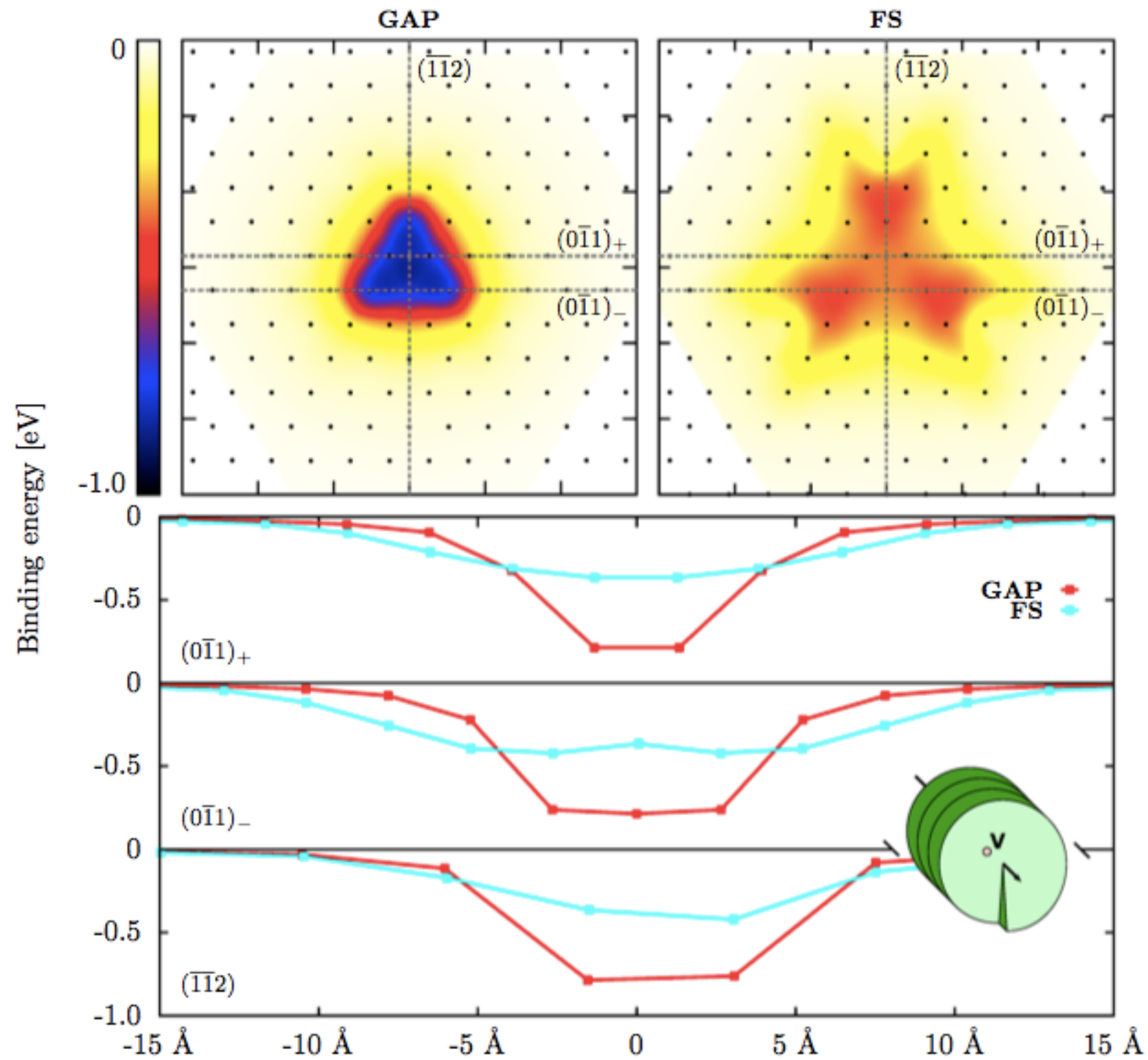
Improvement for tungsten (W)



Peierls barrier for screw dislocation glide



Vacancy-dislocation binding energy



(~100,000 atoms in 3D simulation box)

Outstanding problems

- Accuracy on database \longrightarrow accuracy in properties?
- Database contents \longrightarrow region of validity ?
- Alloys - permutational complexity? Chemical variability?
- Systematic treatment of long range effects
- Electronic temperature