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Quantum Simulations on Nano-Structured Materials

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Nano-structured materials

To understand their formation processes & properties/functions at the atomistic level, FP simulation methods based on DFT are an ideal tool.

Surface dynamics (DFT/ Hybrid)

(i) Diffusion of F on Si(111) : Si-F complex diffusion
(ii) Adsorption of O2 on Si(001) : Energy dissipation
(iii) Atomic structure of AFM tip apex

Large nano-structured systems

- (i) PW electronic structure codes : shallow impurity in Si
- (ii) Linear scaling algorithms:
 - (a) Surface nano-structures; Ge cluster on Si(001)
 - (b) Bio-molecules: DNA

Transport through molecular junctions (NEGF)

- (i) p-stacked systems: styrene wires on H/Si(001)
- (ii) Molecular sensors: iron-porphyrin
- (iii) Molecular switch: biphenyl dithiol

Photochemical reaction (RTP-TDDFT)

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Redox reaction

(i) RuO4: $RuO_4^{-}(aq) + H_2O(l) + e^{-} --> [RuO_3(OH)_2]^{2-}(aq)$





Diffusion of F on Si(111)



Surface diffusion which depends on diffusing Si density has not been observed so far. The diffusion mechanism in atomic scale is not clarified.



Diffusion of F on Si(111)

Y. Fujikawa, et. al. : J. Chem. Phys. 129, 234710 (2008)





Diffusion of Si-F complex





Adsorption of O2 on Si(111): hybrid method

How the adsorption/reaction energy is used for the formation of the final adsorption geometry.



N. Takahashi, T. Ohno: Surf. Sci. 602, 768 (2008)

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AFM tip apex: hybrid method

How does the atomic protrusion exists at the AFT tip apex?





Shallow Impurity in Si

Conventional PW electronic structure code parallelized for Earth Simulator









First-Principles Order-N methods





O(N) DFT code CONQUEST (I)





O(N) DFT code CONQUEST (II)

Efficient on parallel machines

- Vector parallel, RISC-based, PC clusters
- Diagonalisation with ScaLapack (not O(N))
- **CONQUEST** can employ various methods having different accuracies.
 - Full DFT:
 - optimization of support functions is performed.
 - SCF and density matrix minimization are also performed.
 - SC-AITB (self-consistent ab initio TB):
 - Fixed support functions (ex. single-ζ)
 - NSC-AITB (non-self-consistent ab-initio TB):
 - Harris-Foulkes energy functional + superposition of atomic charge
 - (Semi-empirical TB) by DensEl





h3



Ge 3D hut cluster on Si(001)





Ge 3D hut cluster on Si(001)

O. E. Shklaev et al., PRL 94, 176102 (2005)



FIG. 3. Contributions to the formation energy of an isolated Ge {105} pyram.dal island versus size (L). (a) ΔE^{relax} (dotted lines) and ΔE^{relat} (solid line) along with the {100} and {105} contributions to ΔE^{uurf} (dashed lines); (b) ΔE^{torm} for various edge energies, σ^{edge} , in eV/Å.

 $E_{form} = E_{relax} + E_{surf} + E_{edge}$

- E_{relax}: relaxation by the 3D structure (calculated by Finite Element method.)
- E_{surf}: surface energy, usually unfavorable for 3D structure (calculated by DFT)
- E_{edge}: energy of the edges (difficult to calculate. A parameter in this work.)



FIG. 2. Ge (100) and (105) surface energies (per unit area of deformed surface) versus biaxial strain. Triangles denote (105) results from Ref. [5]. Circles, squares, and diamonds are (100) results obtained in this work for $p(2 \times 2)$ and $p(2 \times 2)$ based 2×6 and 2×8 DVL reconstructions, respectively. Solid lines highlight the surface energy for the stable reconstruction of a given orientation.



FIG. 1 (color). Isolated {105} pyramidal hat island on Si(100). colored according to one-half the trace of the calculated *in-plane* surface strain fields (see text for discussion).



Si(001)表面上Geクラスター:構造安定性



To determine the stability and size of the hut cluster,

- effects of boundary, ridge, top
- effect of distortion from {105} planes
- effect of the finite surface area may be also important.

"DFT calculations on the entire hut cluster systems are desirable. "

order-N method



Results: bulk Ge - calculation condition -





Method: strategy for Ge/Si(001)

h8





strained Ge(105): accuracy of various methods

Surface energy of type-I strained Ge(105) surface

Method	Surface energy (meV/Å ²)			
semi-empirical	74.3	DensEl		
NSC-AITB	76.5			
SC-AITB	81.5	CONOUEST		
full DFT(blip, R _{reg} =3.85 Å)	83.5	CONQUEST		
full DFT(blip, R _{reg} =4.23 Å)	74.8			
planewave	70.0	STATE		

NSC-AITB is reasonably accurate. Reliable calculation conditions have been determined. (for surface energy, we need large R_{reg})



Ge 'hut' cluster on Si(001) - system size -





Ge 'hut' cluster on Si(001): NSC-AITB

Structure optimization







Stability: Ge/Si(001)-2xN vs 3D hut cluster





- Accuracy and calculation condition for order-N calculations on Ge/Si(001) have been investigated by the study on the strained Ge(105) surfaces.
- Order-N DFT calculations with structure optimization are now possible for Ge/Si(001) 23,000-atom systems. (within NSC-AITB level)
- Ge hut 3D islands are more stable than Ge 2xN structure when the coverage of Ge is more than 3.
- Our results suggest that the initial emergence of 3D Ge hut clusters is determinde mainly by energetics, and that kinetic effects do not need to be considered.



O(N) DFT calculations on DNA systems using CONQUEST

T. Otsuka, T. Miyazaki, T. Ohno, D. R. Bowler and M. J. Gillan, J. Phys.: Cond. Matter, 20, 294201 (2008)

- 1. Pseudo Atomic Orbitals
- 2. Exchange-correlation functional
- 3. O(N) method by Density matrix minimisation
 - single DNA base
 - **DNA base pairs**
 - **DNA** + water molecules



Bio-materials: DNA

Bio-materials: Proteins, DNA, et. al. One of the important targets of O(N) calculations



Parameterized interaction model Transferability for different environments ? Interaction between bio- and inorganic materials

Quantum mechanical modeling is required







adenine thymine

guanine cytosine

Can describe base pairs properly?

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Pseudo Atomic OrbitalsSZ: single-ζDZP: double-ζ with polarization functionExchange-correlation functionalLDA, GGA-PBEO(N) method by Density matrix minimizationsingle DNA baseDNA base pairsDNA + water molecules
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Structure optimization: single DNA bases (A, C, G, T)









Structure optimization: DNA base pairs (A-T, G-C)

■ Binding energy (eV)

With Counterpoise correction for basis set superposition error (BSSE)

	CONQUEST		Gaussian03			Ref. (a)		
	LDA	PBE	SVWN5	PBE	B3LYP	MP2	RI-MP2	CCSD(T) corrected
basis	D	ZP	cc-pVDZ		CBS			
A-T	-1.11	-0.64	-1.05	-0.60	-0.50	-0.48	-0.67	-0.67
G-C	-1.84	-1.20	-1.77	-1.15	-1.05	-0.94	-1.22	-1.25

•PBE results are very close to RI-MP2 results •PBE looks good for hydrogen bonds! Extrapolated value of MP2 results with respect to the increase of basis sets

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Application to DNA systems

DNA (1WQZ) : by Neutron Diffraction Measurements

•Hydrating water molecules were generated by AMBER.
•Snapshot of MD after the equilibrium by AMBER.

• DNA:	634 atoms
• Mg ²⁺ :	9 atoms
• Total H ₂ O:	932 molecules
	= 2796 atoms
• Total # of atoms:	3439 atoms







CQ on DNA systems

Hydrogen bond distances of G-C pair

SZ (single zeta) calculations on

- DNA (+Mg) without water molecules : 643 atoms
- DNA (+Mg) with hydrating water molecules: 3439 atoms



L matrix cutoff dependence of total energy



without H₂O: diag. vs order-N

 → convergence from R_L = 16.0
 the error is 1.7 mHartree/(643 atoms)

 with H₂O → convergence is same behavior at RL=16.0 bohr the error is 3.5 mHartree/ (3439 atoms) at RL=18.0 borh

the error is 0.64 mHartree/ (3439 atoms)



CQ on DNA systems: Summary

- CONQUEST calculations on single DNA bases agree with those by other codes (Gaussian, VASP).
- PBE is accurate to represent hydrogen bonds in A-T and G-C pairs.
- O(N) calculations using DMM technique is extremely accurate on DNA systems.
 - Error = 0.64 mHartree/3439 atoms at R_L = 18.0 bohr



Molecular Electronics



NH₂+

θ=180°

NO₂



Non-Equilibrium Green's Function method (NEGF)





Transport: benzene dithiol molecule (BDT)





Dependence of the conduction of a BPD molecule on the dihedral angle between the phenyl rings and its application to a nano-rectifier

H. Kondo, J. Nara, H. Kino, and T. Ohno, J. Chem. Phys. 128, 064701 (2008)





Transport: biphenyl dithiol molecule (BPD)





Molecular Rectifier

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Molecular Rectifier: End-group dependence



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Molecular Rectifier: End-group dependence





Molecular Sensor





Iron-porphyrin (FeP)





•Ion porphyrin (FeP) is an important molecule in biological systems.

•the basic unit of many proteins and enzymes

•a planar molecule with one Fe atom chelated at the center of a porphyrin cycle.

•its derivatives display a surprising variety of biological functions, acting as carriers

of metabolic species (O2) and signal transmitters (NO), as well as redox centers.

•Fe plays a central role in molecular recognition and chemical selectivity of FeP.

•FeP will be used in the design of chemical sensors such as an electronic nose/tongue.

Investigate whether the adsorption of molecules can be detected by the electronic transport?



Molecular sensor: iron-porphyrin (FeP)





Dependence on junction geometry



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Molecular orbitals: FeP



NIMS

Transport property: iron-porphyrin (FeP)



平成21年2月25日

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Adsorption geometries of XO on FeP





Molecular orbitals: XO adsorbed FeP

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Transport: XO adsorbed FeP





Transport: XO adsorbed FeP





Possibility of Molecular Sensing





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Advanced Simulation Technology for Innovation of Nano-Scale Materials



