CHIMIA
CHIMIA 2015, Volume 69
ISSN 0009-4293
www. chimia.ch

SCS
Swiss Chemical
Society

Supplementa to Issue 7-8/2015

SCS Fall Meeting 2015

Oral Presentation Abstracts Session of Computational Chemistry

September 4, 2015
Ecole Polytechnique Fédérale de Lausanne (EPFL)
http://scg.ch/fallmeeting/2015

Swiss Chemical Society
Haus der Akademien
Postfach
3001 Bern
Switzerland
info@scg.ch
www.scg.ch

Challenges of Electronic Structure Calculations: Hamiltonian Gadgets with Reduced Resource Requirements

S. Kais[1,2]

[1]Qatar Environment and Energy Research Institute, Doha, Qatar, [2]Department of Chemistry and Physics, Purdue University, USA

The exact electronic structure calculations of atoms and molecules on classical computers generally scale exponentially with the size of the system. Using quantum computers, the computational resources required to carry out the simulation are polynomial. I will present two related approaches to electronic structure: The quantum circuit model, and the adiabatic quantum computing model . Application of the adiabatic model of quantum computation requires efficient encoding of the solution to computational problems into the lowest eigenstates of a Hamiltonian that supports universal adiabatic quantum computation. Experimental systems, such as the D-wave machine and others, are typically limited to restricted forms of two-body interactions. Therefore, universal adiabatic quantum computation requires a method for approximating quantum many-body Hamiltonians up to arbitrary spectral error using at most two-body interactions. I will discuss the Hamiltonian Gadgets with reduced resource requirements for electronic structure calculations and present open problems in the field and future applications.

Addressing the selection bias: Genetically optimized molecular data sets to train machine learning models of atomization enthalpies

N. Browning[1], R. Ramakrishnan[2], O. Lilienfeld[2], U. Röthlisberger[1]*

[1]EPF Lausanne, [2]University of Basel

A comprehensive and chemically accurate exploration of the entire space spanned by all synthetically tractable molecules is severely limited by the computational cost of quantum mechnical (QM) methods. In previous works by Matthias Rupp et al. [1] and Raghunathan et al. [2], non-linear regression machine learning was used to augment approximate QM methods, thereby allowing the prediction of expensive, yet far more accurate methods with a fast yet inaccurate baseline level of theory. The training of molecular models based on supervised learning requires large data sets which exemplify the map from chemical structure to molecular property in a representative manner. Ordinarily, these examples are drawn at random from previously generated subspaces of chemical space. In this work we introduce the application of genetic algorithms (GAs) to the optimization of machine learning through the intelligent generation of training sets. Specifically, we optimize the selection of molecules which represent a large chemical space through a reduction in mean absolute error (MAE) of predicting enthalpies of atomisation. These optimised training sets can then be used for highly accurate predictions of molecular properties for significantly larger molecular sets.

[1] Matthias Rupp, Alexandre Tkatchenko, Klaus-Robert Muller, O. Anatole von Lilienfield, *Phys. Rev. Lett.*, **2012**, 108**,** 058301**.** Raghunathan
[2] Ramakrishnan, Pavlo O. Dral, Mathias Rupp, O. Anatole von Lilienfield, *J. Chem. Theory Comput.*, **2015**, 11, 2087-2096.

Tunneling and Parity Violation in Trisulfane (HSSSH): An Almost Ideal Molecule for Detecting Parity Violation in Chiral Molecules

C. Fabri[1], L. Horny[1], M. Quack[1]*

[1]Physical Chemistry, ETH Zurich, CH-8093 Zurich, Switzerland

Measuring the parity-violating energy difference $\Delta_{\text{pv}}E$ between enantiomers of chiral molecules by spectroscopy is one of the frontiers of highest resolution molecular spectroscopy and a considerable challenge, which so far has not been met with success [1-5]. Over the last decade, considerable progress has been made in the accurate theoretical description of molecular parity violation [6-8], its possible implications for the origin of molecular chirality and biomolecular homochirality, and its role in the stereomutation dynamics of chiral molecules [1-5]. Accurate theoretical predictions of molecular parity violation importantly assist in a search for the most suitable molecular system. At the same time, tunneling must be studied for candidate molecules, as $\Delta_{\text{pv}}E$ has to be substantially larger than $\Delta E_{\pm}$ (the tunneling splitting for the symmetrical case).

In this work we investigate the stereomutation tunneling process in the HSSSH molecule. We report calculations of the parity-violating potential and the ground-state tunneling splitting employing different one- and two-dimensional vibrational Hamiltonians. Our computations utilized the quasi-adiabatic channel reaction path Hamiltonian method [9], the general rotational-vibrational GENIUSH program package [10] and our recently developed coupled-cluster singles and doubles linear response (CCSD-LR) approach [8] to electroweak quantum chemistry. We report that the ground-state tunneling splitting (for the symmetrical case) is substantially smaller than the parity-violating energy difference. This is the consequence of high interconversion barriers, complex tunneling reaction path and the presence of the three heavy sulphur atoms. Therefore the dynamics of chirality in HSSSH is dominated by *de lege* symmetry breaking [11] and HSSSH is an ideal candidate for the experiment proposed in [2] to measure $\Delta_{\text{pv}}E$, for which the basic experimental capabilities have been demonstrated in our laboratory recently [12].

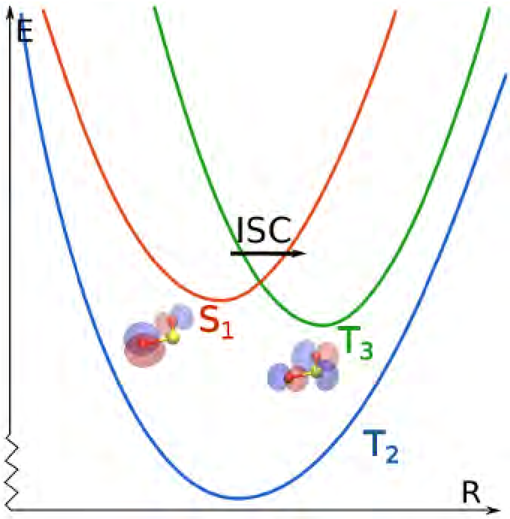
[1] M. Quack, Fundamental Symmetries and Symmetry Violations from High Resolution Spectroscopy, in Handbook of High-resolution Spectroscopy, edited by F. Merkt and M. Quack, (John Wiley Sons, Ltd., Chichester, New York, 2011), pp. 659-772.
[2] M. Quack, *Chem. Phys. Lett.* **1986**, 132, 147-153.
[3] M. Quack, *Angew. Chem. Intl. Ed. (Engl.)* **1989**, 28, 571-586.
[4] M. Quack, *Angew. Chem. Intl. Ed. (Engl.)* **2002**, 41, 4618-4630.
[5] M. Quack, J. Stohner, M. Willeke, *Ann. Rev. Phys. Chem.* **2008**, 59, 741-769.
[6] A. Bakasov, T. K. Ha, M. Quack, *J. Chem. Phys.* **1998**, 109, 7263-7285.
[7] R. Berger, M. Quack*, J. Chem. Phys*. **2000**, 112, 3148-3158.
[8] Ľ. Horný, M. Quack, *Mol. Phys.* ***2015***, DOI: 10.1080/00268976.2015.1012131.
[9] B. Fehrensen, D. Luckhaus, M. Quack, *Chem. Phys.* **2007**, 338, 90-105.
[10] A. G. Császár, C. Fábri, T. Szidarovszky, E. Mátyus, T. Furtenbacher , G. Czakó, *Phys. Chem. Chem. Phys.* **2012**, 14, 1085-1106.
[11] C. Fábri, Ľ. Horný, M. Quack, to be published.
[12] P. Dietiker, E. Miloglyadov, M. Quack, A. Schneider, G. Seyfang, *Proc. of the 49th SASP* **2014**, 152.

Molecular Dynamics with inter-system crossing and nonadiabatic effects

F. Franco de Carvalho[1], I. Tavernelli[2]

[1]Centre européen de calcul atomique et moléculaire, [2]IBM Research Zurich

Last year we rigorously derived a method for the computation of spin-orbit coupling (SOC), using the Breit-Pauli SOC hamiltonian, within linear-response time-dependent functional density theory (LR-TDDFT) [1] and implemented it in the software package CPMD [2].
SOC is the effect that allows for a molecule to go from a singlet to a triplet state, a phenomenon known as inter-system crossing (ISC). Said phenomenon is important in several photochemical/photophysical systems, including organic and inorganic photosensitizers, organic light-emitting diodes and several organic reactions (e.g. hydrogen abstraction in ketones).
Thanks to our method, we have been able to include ISC in our ab-initio molecular dynamics program, in which we use a Landau-Zener-like theory in order to simulate ISC.
This means we are now in a position to give a complete description of nonradiative decay pathways in photochemical systems, including large ones, thanks to our use of LR-TDDFT.
In fact, we have succesfully described the excited states dynamics of gas phase SO2, liquid SO2 (using a QM-MM) and graphene nanoflakes, including both ISC and nonadiabatic effects [3].



[1] F. Franco de Carvalho, Basile FE Curchod, Thomas J. Penfold, Ivano Tavernelli. J. Chem. Phys. **140**, 144103 (2014); dx.doi.org/10.1063/1.4870010
[2] CPMD, copyright IBM 1990-2008, copyright MPI für Festkörperforschung Stuttgart, 1997-2001
[3] Enrico Tapavicza, Ivano Tavernelli, and Ursula Rothlisberger, Phys. Rev. Lett. 98, 023001,DOI: http://dx.doi.org/10.1103/PhysRevLett.98.023001

Local density fitting within a Gaussian and plane waves approach

D. Golze[1], J. Hutter[1]*, M. Iannuzzi[1]*

[1]University of Zurich

The computationally most expensive step in construction of the Kohn-Sham (KS) matrix is the evaluation of the Coulomb matrix. The latter requires the calculation of two-electron integrals with the characteristic $O(N^4)$ problem. Baerends *et al.* [1] introduced a local resolution of identity approach (LRI), where the atomic pair densities are approximated by an expansion in one-center fit functions reducing the scaling order to $O(N^3)$.
In this work, the LRI technique was adapted for usage in a Gaussian and plane waves (GPW) approach and implemented in the CP2K program [2,3] package. The fitted density is employed for evaluation of Coulomb as well as exchange-correlation potential. The construction of the KS matrix in GPW scales already linearly with respect to system size since the plane wave expansion of the density is exploited to solve the Poisson equation in Fourier space. The combination of a local basis and an auxiliary basis set of plane waves leads to an $O(N)$ process for the evaluation of the Coulomb matrix. Using LRI, improvements are expected for the calculation of the grid-dependent terms. The prefactor for building the KS matrix is reduced resulting in a system-dependent speed-up. Furthermore, the scalability of the grid-based calculation and integration of the potential with respect to number of CPUs can be simplified and improved. Results regarding timings and scalability are presented for liquid water demonstrating that a speed-up of the SCF step by a factor of at least three can be expected for large and medium-sized systems. The accuracy of the LRI approach is assessed by reaction energies and structural properties for a broad range of systems.

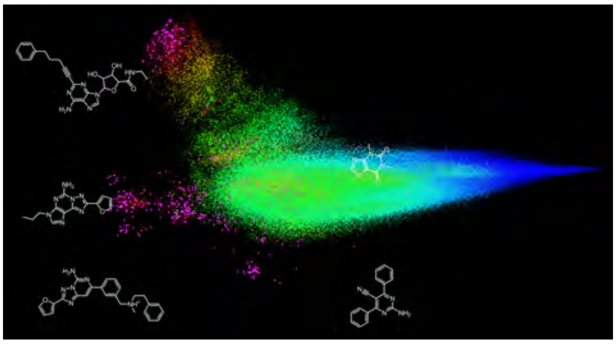
[1] E.J. Baerends, D.E. Ellis, P. Ros, *Chem. Phys.*, **1973**, 41
[2] J. Hutter et al., *WIREs: Comput. Mol. Sci.*, **2014**, 4, 15
[3] The CP2K developers group, CP2K is freely available from: http://www.cp2k.org

Interactive Similarity Maps for Visualization of High Dimensional Chemical Spaces

M. Awale[1], J.-L. Reymond[1]*

[1]University of Bern

Database visualization methods provide support to drug discovery projects by facilitating rapid understanding of the content of chemical space and enabling the comparative analysis of chemical libraries. Here, we report a non-linear projection method that create 2D-maps of high-dimensionality fingerprint spaces with high coverage of data variability in which local relationships between compounds are preserved. The method consists in the computation of a similarity fingerprint composed of the similarity values computed with respect to a set of reference molecules, followed by the projection of this similarity space by principal component analysis. The computation can be parallelized and is therefore suitable for very large databases. When the reference molecules are chosen at random the 2D-maps provide a global insight into database. In an another implementation of the method, the reference molecules are chosen to be a sets of active compounds for one or more targets, resulting in 2D-maps illustrating the structure-activity landscape of the active sets. The method is exemplified by the generation of 2D-maps for ChEMBL using six property spaces namely: 42-D molecular quantum numbers (MQN), 34-D smiles fingerprint (SMIfp), 20-D shape fingerprint (APfp), 55-D pharmacophore fingerprint (Xfp), 1024 bit long daylight type substructure (Sfp) and extended connectivity fingerprint (ECfp4). This is particularly appealing for the Xfp, Sfp and ECfp4, which otherwise cannot be projected in low dimensions. Activity focused 2D-maps of ChEMBL were generated using each of the 101 sets of bioactive compounds available in Enhanced Directory of Useful Decoys database (eDUD), as reference sets. An internet portal (http://www.gdbtools.unibe.ch:8080/PORTAL.v2) automatically generates such maps in relation to user-defined reference molecules and is available for visualizing drug optimization projects and their relationship to other known bioactive compounds.



1. Medina-Franco, J. L.; Martinez-Mayorga, K.; Giulianotti, M. A.; Houghten, R. A.; Pinilla, C., Visualization of the Chemical Space in Drug Discovery. *Curr. Comput.-Aided Drug Des.* **2008,** 4, (4), 322-333.
2. Garrity, G. M.; Lilburn, T. G., Mapping taxonomic space: an overview of the road map to the second edition of Bergey's Manual of Systematic Bacteriology WFCC Newsl. **2002,** 35, 5-15.
3. Awale, M.; van Deursen, R.; Reymond, J.-L., MQN-Mapplet: Visualization of Chemical Space with Interactive Maps of DrugBank, ChEMBL, PubChem, GDB-11, and GDB-13. *J. Chem. Inf. Model.* **2013,** 53, (2), 509-518.
4. Schwartz, J.; Awale, M.; Reymond, J. L., SMIfp (SMILES fingerprint) Chemical Space for Virtual Screening and Visualization of Large Databases of Organic Molecules. *J. Chem. Inf. Model.* **2013,** 53, (8), 1979-1989.
5. Awale, M.; Reymond, J.-L., Atom Pair 2D-Fingerprints Perceive 3D-Molecular Shape and Pharmacophores for Very Fast Virtual Screening of ZINC and GDB-17. *J. Chem. Inf. Model.* **2014,** 54, (7), 1892-1907.
6. Rogers, D.; Hahn, M., Extended-Connectivity Fingerprints. *J. Chem. Inf. Model.* **2010,** 50, (5), 742-754.

Addressing the Rare Event Sampling problem with the PINS and SA-MC Methods : studying Structure and Dynamics of the Myoglobin protein

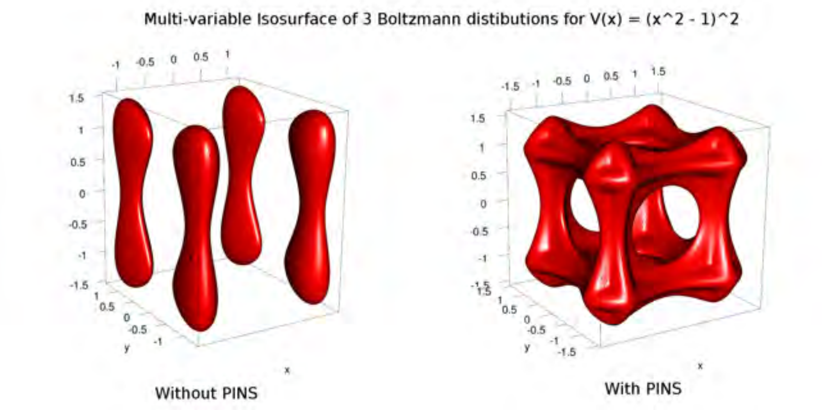
F. Hédin[1], N. Plattner[2], J. D. Doll[3], M. Meuwly[1]*

[1]University of Basel, [2]Freie Universtität Berlin , [3]Brown University, Providence, RI, USA

Molecular Dynamics (MD) and Monte Carlo methods (MC) are widely used in computer simulations for understanding biological processes. Although the computational resources are continously increasing, many biological processes cannot be adequately observed, as they usually occur on time scales which are several orders of magnitude higher than the usual MD simulation step. Such processes are also a limitation for MC simulations which are not time related, as the probabilty of sampling such rare configurations is low, thus making the rare event sampling problem a challenging task.

The PINS (Partial Infinite Swapping [1,2]) method, based on the Parallel Tempering / Replica Exchange algorithms, uses a symmetrization strategy for combining probability distributions at different temperatures, so that they become more higly connected and then easier to sample than the original ones (see Fig. below for a simple double-well potential example, from [1]).

The SA-MC (Spatial Averaging MC [3,4,5]) method, extending the MC Metropolis algorithm, uses a different approach where a set of modified probability distributions is generated and distributed in the configuration space around the original one, by following a Normal law distribution.


Multi-variable Isosurface of 3 Boltzmann distibutions for V(x) = (x^2 - 1)^2

Without PINS

With PINS

We decided to apply both the PINS and SA-MC methods to the study of the Myoglobin protein, an oxygen-binding member of the globins family, found in the tissues of vertebrates. Previous studies (ref [6] and others) found several stable cavities in which the binding ligand diffuses before reaching the Fe atom, with an average residence time estimated between 1 ns for pocket Xe3 and 53 ns for pocket Xe1. Such slow diffusion processes are thus good candidates for rare event sampling methods.

[1] N. Plattner et al., *JCP*, **2011**, 135, 134111, DOI: 10.1063/1.3643325
[2] N. Plattner et al., *JCTC*, **2013**, 9, 4215-4224, DOI: 10.1021/ct400355g
[3] J. D. Doll et al, *JCP*, **2009**, 131, 104107, DOI: 10.1063/1.3220629
[4] N. Plattner et al., *JCP*, **2010**, 133, 044506, DOI: 10.1063/1.3458639
[5] F Hédin et al., *JCTC*, **2014**, 10, 4284-4296, DOI: 10.1021/ct500529w
[6] Bossa et al., *Biophys. Jounal*, **2005**, 89, 465-474, DOI:10.1529/biophysj.104.055020

Accelerating Quantum Instanton Calculations of Kinetic Isotope Effects

K. Karandashev[1], J. Vanicek[1]*

[1]EPF Lausanne

While computing rate constants for reactions that exhibit strong quantum effects, running quantum dynamics can be avoided by a combination of Feynmann path integral formalism and Quantum Instanton approximation, that reduce the quantum problem to a classical one in a space of increased dimensionality [1]. Thermodynamic integration with respect to mass further simplifies computation of Kinetic Isotope Effects, allowing to use only efficient Monte Carlo integration procedures [2]. We accelerate these calculations using higher order Boltzmann operator splittings, which allow faster convergence to the exact quantum result [3], and virial estimators, which decrease the statistical error and hence the Monte Carlo simulation length needed for a given precision [4, 5]. We also improve the accuracy of the calculations by modifying procedures for thermodynamic integration and dividing surfaces' optimization. The improvements are tested on the model $H+H_2$ rearrangement and CH_4+H reaction [6].

1. Takeshi Yamamoto and William H. Miller, *J. Chem. Phys.* **2004**, 120, 3086.
2. Jiri Vanicek, William H. Miller, Jesus F. Castillo, and F. Javier Aoiz, *J. Chem. Phys*. **2005**, 123, 054108.
3. Alejandro Perez and Mark E. Tuckerman, *J. Chem. Phys*. **2011**, 135, 064104.
4. Sandy Yang, Takeshi Yamamoto, and William H. Miller, *J. Chem. Phys*. **2006**, 124, 084102.
5. Jiri Vanicek and William H. Miller, *J. Chem. Phys.* **2007**, 127, 114309.
6. Karandashev Konstantin and Jiri Vanicek, in preparation.

First principles based crystal structure prediction from alchemical coupling

A. Solovyeva[1], A. von Lilienfeld[1,2]

[1]Institute of Physical Chemistry, Department of Chemistry, University of Basel, Switzerland , [2] Argonne Leadership Computing Facility, Argonne National Laboratory, USA.

The prediction of stable crystalline phases remains an outstanding challenge for atomistic simulations
despite recent progress made. We explore the applicability of fictitious "alchemical" paths that couple
different chemical compositions for various crystal structure symmetries.
The alchemical changes are predicted using first order perturbation theory within
linearly coupled Hamiltonians connecting reference to target system [1,2].
We studied the prediction of formation energies, equilibrium lattice constants, and bulk moduli of
pristine and doped alkali chloride structures including Caesium chloride, rock-salt, and zinc blende symmetries.
We find that the electronic perturbation induced by transmutating
one alkali element into another cancels to such a degree that reasonable
property predictions can be made for the target system - at negligible computational overhead [3].

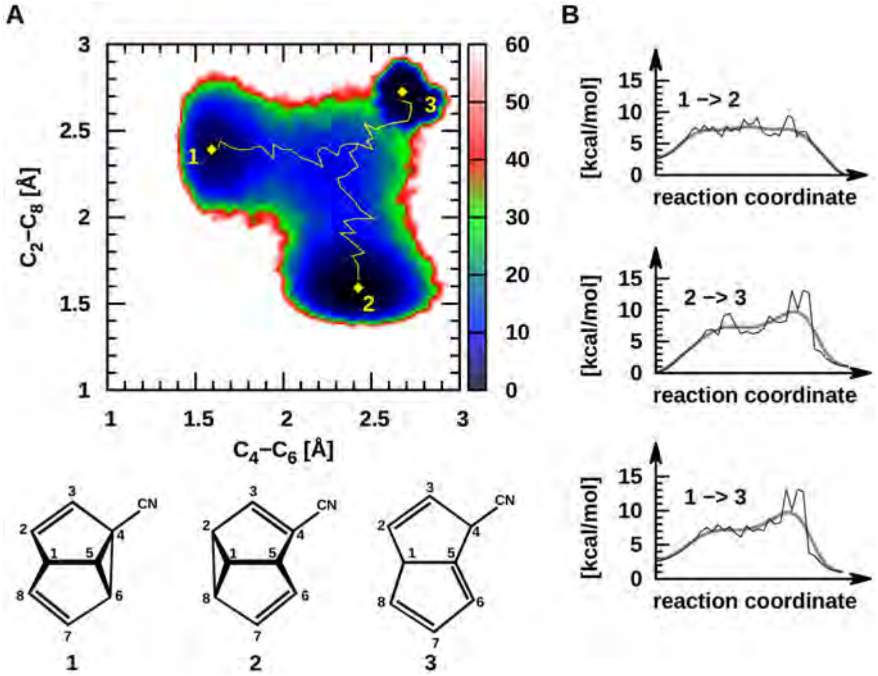
[1] R. P. Feynman, *Phys. Rev.* 56 (1939) 340.
[2] O. A. von Lilienfeld, *J. Chem. Phys.* 131 (2009) 164102.
[3] A. Solovyeva, O. A. von Lilienfeld, in preparation (2015)

Beyond Static Structures: Putting Forth REMD as a Tool to Solve Problems in Computational Organic Chemistry

R. Petraglia[1], A. Nicolai[1], M. Wodrich[1], M. Ceriotti[1], C. Corminboeuf[1]*

[1]EPF Lausanne

Computational studies of organic systems are frequently limited to static pictures that closely align with textbook style presentations of reaction mechanisms and isomerization processes. Of course, in reality chemical systems are dynamic entities where myriad molecular conformations exist on incredibly complex potential energy surfaces (PES). Here, we borrow a computational technique essentially used in the context of biological simulations together with empirical force fields and apply it to organic chemical problems. Replica-exchange molecular dynamics (REMD) permits thorough exploration of the potential energy surface. We report meaningful data obtained by combining REMD with density functional tight binding (DFTB), thereby establishing the required accuracy necessary to analyze small molecular systems. Through the study of four prototypical problems: isomer identification, reaction mechanisms, temperature-dependent rotational processes, and catalysis, we reveal new insights and chemistry that likely would be missed using standard electronic structure computations. The REMD-DFTB methodology at the heart of this study is powered by i-PI, which efficiently handles the interface between the DFTB and REMD codes.



[1] R. Petraglia, A. Nicolai, M. D. Wodrich, M. Ceriotti, C. Corminboeuf,*Journal of Computational Chemistry,*submitted.
[2] Y. Sugita, Y. Okamoto, *Chemical Physics Letters*,**1999,**314, 141-151.

Interface effects in the case of dry reforming – CO_2 activation on Ni-supported γ-Al_2O_3 and Ni-nanoparticles vs ideal Ni(111) surface

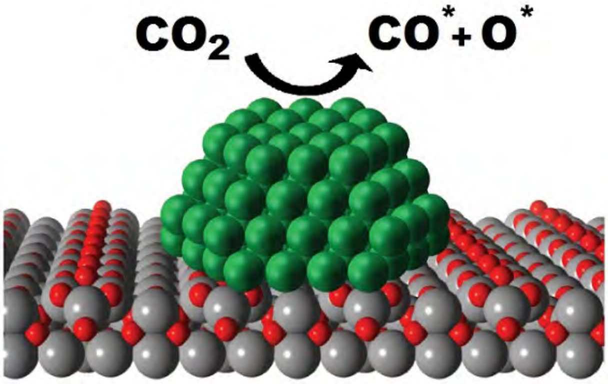
M. Silaghi[1], A. Comas-Vives[1], C. Copéret[1]*

[1]ETH Zurich

Significant increase of petrol demands open new routes for fuel production than from oil, such as natural gas reforming, through the gas-to-liquid process. Here, steam reforming is the major process for generating the syngas (H_2 and CO) in a ratio of R=3, required for the off-stream Fischer-Tropsch synthesis. However, since this ratio needs to be tuned, CO_2 reforming can be used to provide lower syngas compositions (R=1). In the case of dry reforming Ni-nanoparticles supported on γ-Al_2O_3 is the industrially most common catalytic system [1].

From the mechanistic point of view, several computational and experimental studies have improved the understanding of dry reforming. For instance, (i) CH_4 and CO_2 activation on Ni surfaces is surface sensitive, (ii) carbon whiskers formation occurs at steps and (iii) that CO_2 is negatively charged when adsorbed on them. Despite all the efforts devoted to understand the mechanism of dry reforming the evaluation of the whole reaction mechanism has just been partially addressed and more realistic metal/support systems need to be considered. Especially the computational studies so far lack in accounting for these beneficial support effects, which have been proven experimentally to play an important role in this complex reaction mechanism. In this sense, some studies have proposed that peripheric Ni atoms near the metal/support perimeter determine the catalytic activity and thus underlining the importance of the metal/support interface. Moreover, the effect of particle size and morphology has not yet clearly been addressed.

Therefore, the scope of the present study is to determine trends for CO_2 adsorption and activation on Ni-supported γ-Al2O3 systems with varying cluster sizes and morphologies by dint of periodic DFT calculations. These more realistic metal/support systems are then compared to gas phase cluster calculations and ideal Ni(111) surface.



[1] Pakhare Devendra; Spivey James, *Chemical Society Reviews*, **2014**, 43, 7813-7837.

Response time of quantum-chemical calculations during real-time reactivity explorations

A. C. Vaucher[1], M. Haag[1], M. Reiher[1]*

[1]ETH Zurich

Real-time quantum chemistry was invented as a tool for interactive and intuitive studies of chemical reactivity [1–4]. It relies on an exploration of the Born–Oppenheimer potential energy surface based on first principles in real time. An operator can study reactivity with the help of interaction devices that provide an instantaneous feedback upon manipulation of the molecular system. For example, haptic devices allow one to explore the potential energy surface by moving atoms while feeling the quantum chemical force acting on them.

We developed strategies for a reliable real-time exploration of the potential energy surface despite the delay caused by the execution of the iterative electronic structure calculations [5]. For example, second derivatives of the electronic energy facilitate an immediate guess of atomic forces for closely related molecular structures. For the application of self-consistent-field methods, schemes based on a propagation of the density matrix deliver approximated atomic forces without a fully converged solution of the Roothaan–Hall equations and can thus provide more frequent feedback.

[1] Konrad H. Marti, Markus Reiher, *J. Comput. Chem.*, **2009**, 30, 2010-2020.
[2] Moritz P. Haag, Markus Reiher, *J. Quantum Chem.*, **2013**, 113, 8-20.
[3] Moritz P. Haag, Markus Reiher, *Faraday Discuss.*, **2014**, 169, 89-118.
[4] Moritz P. Haag, Alain C. Vaucher, Maël Bosson, Stéphane Redon, Markus Reiher, *ChemPhysChem*, **2014**, 15, 3301-3319.
[5] Alain C. Vaucher, Moritz P. Haag, Markus Reiher, *in preparation*.

Orthogonality of embedded wave functions for different states in Frozen-Density Embedding Theory

A. Zech[1], F. Aquilante[1], T. A. Wesolowski[1]*

[1]Université de Genève

The Euler-Lagrange equations for the embedded wave function may lead to several solutions in Frozen-Density Embedding Theory (FDET) [1]. Following the Levy-Perdew theorems [2], other-than ground state solutions can be associated with excited states. Due to the dependency of the functional for the embedding potential on the embedded density (ρ_A), embedded wave functions for different electronic states are not orthogonal. In practical calculations where the density functional for the FDET embedding potential is approximated, the deviations from orthogonality might be enhanced. The orthogonality might be rigorously assured by means of using linearized functionals as proposed in our earlier work [3]. Linearization consists of using some reference density (ρ_A^{ref}) instead of a state-dependent ρ_A in the embedding potential and the addition of a self-consistency assuring term in the energy. The numerical values presented in this work concern local excitations in model chromophores non-covalently bound to the molecules in the environment. It is shown that practically the same excitation energies are obtained using either linearized (i.e. independent on ρ_A) and the conventional (non-linear, i.e. depending on ρ_A) functionals.

[1] Tomasz A. Wesolowski, *Phys. Rev. A*, **2008**, 77, 11444
[2] John P. Perdew, Mel Levy, *Phys. Rev. B*, **1985**, 31, 6264
[3] Tomasz A. Wesolowski, *J. Chem. Phys.*, **2014**, 140, 18A530