Loriano Storchi

HPC in Chemistry and in Physics

Contents

- Grid Computing
- Green's function and the ADC
- Relativistic DFT
- GRID force-field pKa prediction
- GPGPU and DSP
- Sphere packing for Dye-sensitized solar cells

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Grid Computing - Introduction

Grid

Single Machine

APPLICATIONS

OPERATING SYSTEM

HARDWARE

APPLICATIONS

MIDDLEWARE

HARDWARE (NETWORK + MACHINES)



LNCS, 2658, 297, (2003)





LNCS, 3980, 675 (2006)









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$$\begin{split} G_{pq}(\boldsymbol{\omega}) &= \sum_{n \in N+1} \frac{\langle \Psi_{0}^{N} | \hat{a}_{p} | \Psi_{n}^{N+1} \rangle \cdot \langle \Psi_{n}^{N+1} | \hat{a}_{q}^{+} | \Psi_{0}^{N} \rangle}{\boldsymbol{\omega} + E_{0}^{N} - E_{n}^{N+1}} \\ &+ \sum_{n \in N-1} \frac{\langle \Psi_{0}^{N} | \hat{a}_{q}^{+} | \Psi_{n}^{N-1} \rangle \cdot \langle \Psi_{n}^{N-1} | \hat{a}_{p} | \Psi_{0}^{N} \rangle}{\boldsymbol{\omega} + E_{n}^{N-1} - E_{0}} \end{split}$$

 $\boldsymbol{G}(\boldsymbol{\omega}) = \boldsymbol{G}^{-}(\boldsymbol{\omega}) + \boldsymbol{G}^{+}(\boldsymbol{\omega}) = \boldsymbol{x}^{+}(\boldsymbol{\omega} \boldsymbol{1} - \boldsymbol{\Omega})^{-1} \boldsymbol{x}$

The Dyson equation

$$G(\omega) = G^{0}(\omega) + G^{0}(\omega) \geq (\omega G(\omega))$$

$$\geq (\omega) = \geq (\infty) + M(\omega)$$
The ADC
$$M_{pq}(\omega) = U_{p}^{+}(\omega 1 - K - C)^{-1}U_{q}$$

$$= U_{q}^{(1)} + U_{q}^{(2)} + \dots \qquad C = C^{(1)} + C^{(2)} + \dots$$

U





The ADC(3) Matrix (with affinity reduction)

$$\boldsymbol{G}(\boldsymbol{\omega}) = \boldsymbol{G}^{-}(\boldsymbol{\omega}) + \boldsymbol{G}^{+}(\boldsymbol{\omega}) = \boldsymbol{x}^{+}(\boldsymbol{\omega} \boldsymbol{1} - \boldsymbol{\Omega})^{-1} \boldsymbol{x}$$

We adopt the ADC approach directly for the (N-1)-particle part of the one-particle $_{GF}$ $G^{-}(\omega) = (x^{I})^{+} (\omega 1 - \Omega^{I})^{-1} x^{I}$ $G^{-}(\omega) = f^{+} (\omega 1 - K - C)^{-1} f$

 $C = C^{(1)} + C^{(2)} + \dots$

 $f = f^{(0)} + f^{(1)} + \dots$



nD-ADC(3) and ADC(3) direct comparison

Dyson ADC(3)

 $K_1 + \Sigma (\infty)$

Non-Dyson ADC(3)

 $K_1 + C_{11}^{(2)} + C_{11}^{(3)}$

 $C_{11}^{(3)} = C_{11}^{(A)} + C_{11}^{(B)} + C_{11}^{(C)} + C_{11}^{(D)} + \sum_{1}^{(D)} (\infty)$

is a function of the 04 integrals

 $C^{(A)}_{_{ii}}$

• To make the code simpler and more readable, the core of the integral-driven code is constituted by one routine which implements the equation (except of the loop over virtual indices) and is called as many times as needed for each integral, with the appropriate set and permutation of argument indices. •We actually use the \sum (DEM) approximation for the static self-energy, we will use the \sum (4+) to avoid completely the use of the (N+1)-particle space.





num. Lanczos Iterations: 200 num. Lanczos iterations for affinity reduction 50

num. 1h confs. 16 num. 1p confs. 89 num. 2h1p confs. 5696 num. 2p1h confs. 31684

| | Step 1 s. | Step 2 s. | Step 3 s. | Tot s. |
|---------------|-----------|-----------|-----------|--------|
| ADC(3) | 719.4 | 8168.5 | 371.8 | 9259.7 |
| ADC(3) redu | 719.8 | 4499.5 | 352.4 | 5204.3 |
| ND-ADC(3) | 2882.3 | 305.5 | 0.4 | 3188.2 |

J. Comp. Chem., 30 (5), 818 (2009) J. Comp. Chem (2011) in preparation

A CAP is introduced to absorb the electron that is emitted in the decay process. In this way the wave function of the scattered electron becomes square-integrable. The scattering problem may be described within the framework of standard quantum chemistry methods. The CAP method can be combined with virtually any electronic correlation method.



In the CAP method a an absorbing potential is added to the physical hamiltonian H, and one works with a parametrized operator:

$$\hat{H}(\eta) = \hat{H} - i \eta \hat{W}$$

W is typically a real "soft" boxlike potential in the dissociation coordinate, and η is a strength parameter.

In the framework of a finite basis set E_{res} will depend on W. One typically studies the trajectories of the complex eigenvalues $E_i(\eta)$ of $H(\eta)$ and identifies a resonance by a minimum of the "velocity":

$$v_i(\eta) = \left| \eta \frac{\partial E_i}{\partial \eta} \right|$$

In other words for each resonance there is an optimal CAP strength (η_{OPT}) that yields the best approximation to the resonance parameters for the chosen basis set and W.



E_R

- The constants c_i define the size L of the box.
- The box is defined in order to spatially confine the basis set.

$$W(r; c; n) = \sum_{i=1}^{i=3} W_i(x_i; c_i; n)$$

$$W_i(x_i; c_i; n) = \begin{cases} 0, & |r_i| \le c_i \\ (|r_i| - c_i)^n & |r_i| > c_i \end{cases}$$

$$\vdots$$

i = x, y, z



- It is computationally hard to obtain the resonance parameters. One needs to diagonalize the "big" complex symmetric CAP/ADC(3) matrix many times to search for the minimum of the velocity.
- Subspace projection technique. The result of the subspace projection is a smaller complex symmetric matrix. It is easier to diagonalize for many values of the η parameter
- This approach is simple to use with the filter diagonalization method.

AUGER SPECTROSCOPY



The population analysis provides a qualitative as well as a quantitative description of the charge distribution for each dicationic state and estimates of spectral intensities



The nuclear dynamics analysis provides the correct energy centroids and broadenings of the bands. These can be very different in different spectra

CO and CO₂ Auger spectra

J. Chem. Phys. 123, 224306 (2005)



The new observed feature is not an interatomic effect, but an effect of the nuclear dynamics. The shift between the bands in the two spectra was theoretically predicted.



O=C=O

- •A single total symmetric normal mode (symmetric stretching)
- •We used the aug-cc-pVTZ basis set
- •We performed a full diagonalization of the ADC(2) matrix
- •The number of dicationic states found to be relevant for reproducing the Auger spectra is about 2000 up to a DIE (Double Ionization Energy) of 110 eV


DIE



DIE

N₂O Auger spectra

J. Chem. Phys. 125, 054306 (2006)

N===N===-O bond order = 1.61 bond order = 2.73

•We used the aug-cc-pVTZ basis set.

•We performed a full diagonalization of the ADC(2) matrix.

•The N atoms 1s ionization energies differ by 3.9 eV.





A more precise assignment than previous attempts as well as a better understanding of the relative intensities of the different features in the unselected spectrum have been achieved.



SF₆ direct double photoionization spectra

J. Chem. Phys. 122, 144309 (2005)



We used a dzp basis set.
We used the block-Lanczos iterative diagonalizer.
The computed spectrum comprises nearly 29000 electronic states up to a binding energy of 110 eV.









CF₄ direct double photoionization spectra

J. Chem. Phys. 125, 194318 (2006)



We used aug--cc-pVDZ basis set.
We used the block-Lanczos iterative diagonalizer.







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Each iteration can be subdivided in several steps:

- 1. Serial Part
- 2. **J+K matrix**: the DKS matrix is computed.
- 3. Level Shift: The level shift is applied to the DKS matrix by adding a weighted virtual orbital projection operator. This procedure involves two matrix-matrix multiplications.
- 4. **Diagonalization**: The hermitian DKS matrix diagonalization is carried out.
- 5. **Density**: The density matrix is computed as a matrix-matrix multiplication of positive occupied eigenvectors.

JCTC Journal of Chemical Theory and Computation, 6, 384, (2010) •Parallel Computing: From Multicores and GPU's to Petascale, ed.: B. Chapman et al. p. 501-512 (IOS Press, Amsterdam, 2010)





First step: use a profile and optimize the serial code.

Second step: parallelization of the code

Step 2: IF (my rank .eq. master) THEN RECV FROM ANY_SLAVES (blockdim, block_position) IF (blockdim < 0) then FXIT FI SF **RECV FROM slave (block)** copy block into J+K matrix **FNDIF** ELSE DO block num = 1, max nom of block IF (func(my rank, block num)) ALLOCATE block **COMPUTE** block SEND (blockdim, block_position) SEND (block) **END IF ENDDO** SEND (blockdim = -1) EXIT END IF

- Communication time is more or less independent from the number of processors involved.

- The small dimension of each block, guarantee by itself a good load balancing and good overlapping of communication and computation time.

- Last but not least, the small dimension of each block guarantee a better cache reuse, respect to the serial algorithm



Next step try to use AMPI (Charm++)

Step 3, 4, 5 (using ScaLAPACK) : call DISTRIBUTE(DKSmat, master) call LEVELSHIFT(DKSmat) call DIAGONALIZE(DKSmat) call COLLECT(EIGENVEC, master) call DENSITY(EIGENVEC) call COLLECT(DENSmat, master)

| p.q | ο | 1 | 2 | З | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
|----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 0 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 |
| 1 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 |
| 2 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 |
| З | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 |
| 4 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 |
| _B 5 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 |
| 6 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 |
| 7 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 |
| 8 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 |
| 9 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 | 0,0 | 0,1 | 0,2 | 0,3 |
| 10 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 | 1,0 | 1,1 | 1,2 | 1,3 |
| 11 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 | 2,0 | 2,1 | 2,2 | 2,3 |

(a) Assignment of global block indices, (B, D), to processes, (p, q).





| # of processors | | | $Time(s) \ COLLECT$ | | |
|----------------------------|--|---|---|--|--|
| # of processors | dim. 1560 dim. 3120 | | <i>dim.</i> 6240 | dim. 12480 | |
| 4 | 0.12 | 0.36 | 1.41 | 5.90 | |
| 16 | 0.12 | 0.44 | 1.60 | 6.26 | |
| 32 | 0.10 | 0.39 | 1.56 | 6.32 | |
| 64 | 0.13 | 0.51 | 2.12 | 8.23 | |
| 128 | 0.14 | 0.52 | 2.13 | 8.62 | |
| | | | | | |
| # of processors | | | $Time(s) \ DISTRIBUTE$ | | |
| # of processors | <i>dim</i> . 1560 | dim.~3120 | Time(s) DISTRIBUTE dim. 6240 | dim. 12480 | |
| # of processors 4 | <i>dim.</i> 1560 | <i>dim</i> . 3120 | Time(s) DISTRIBUTE dim. 6240 1.29 | <i>dim.</i> 12480 5.07 | |
| # of processors 4 16 | <i>dim.</i> 1560 0.12 0.22 | <i>dim</i> . 3120 0.33 0.76 | <i>Time(s) DISTRIBUTE</i> <i>dim.</i> 6240 1.29 1.29 | <i>dim.</i> 12480 5.07 5.04 | |
| # of processors 4 16 32 | <i>dim.</i> 1560 0.12 0.22 0.27 | <i>dim</i> . 3120 0.33 0.76 0.98 | Time(s) DISTRIBUTE dim. 6240 1.29 1.29 1.38 | <i>dim.</i> 12480 5.07 5.04 5.40 | |
| # of processors 4 16 32 64 | <i>dim.</i> 1560 0.12 0.22 0.27 0.27 | <i>dim</i> . 3120 0.33 0.76 0.98 1.07 | Time(s) DISTRIBUTE dim. 6240 1.29 1.29 1.38 3.78 | dim. 12480 5.07 5.04 5.40 6.03 | |

Communication time is "independent" from the number of processors







If we consider the Amdahl's law using 128 processors we reached roughly the 60% of the maximum theoretical speedup. (AMPI and use more processors)

Amdahl's law Speedup = 1 / F



DO block_num = 1, max_nom_of_block IF ((my_rank+((num_of_processors)*my_block_num)) == block_num) my_block_num = my_block_num + 1 ALLOCATE block COMPUTE block END IF ENDDO

CALL DISTRIBUTESPARSE

Each process compute a subset of all blocks constituting the entire J+K matrix, and store the result in a local array. At the end of the procedure the matrix is naturally distributed among all the processes,

DISTRIBUTESPARSE re-distributes the matrix obeying the two-dimensional block cyclic distribution, so that it can be used by the ScaLAPACK routines.

Physical Chemistry Chemical Physics, 13 (27), 12368, (2011)

do I = 1, NOB
 2D_CBD_BLOCK(I) = transform (NDBLOCK(I))
 collect process rank in processor_ranks vector
enddo

call barrier

```
do i=0,numprocs-1
i-th process broadcast processor_ranks vector
```

if (myrank.eq.i) then for each j in processor_ranks if (j.ne.myrank) send new_block to j endif endfor else if (myrank is in processor_ranks) receive new_block endif

call barrier enddo

Parallelization of Betha

| | | Processor grid | | | | | | |
|------------------|-----------------|----------------|-----------|--------------|--------------|--------|--|--|
| Cluster | Parallel scheme | 2×2 | 4 	imes 4 | 4×8 | 8×8 | 8 × 16 | | |
| Au ₂ | MS | 2.9 | 10.2 | 14.6 | 27.5 | 27.5 | | |
| - | DP | 3.8 | 9.7 | 14.5 | 23.3 | 21.1 | | |
| Au ₄ | MS | 3.0 | 13.3 | 24.3 | 36.2 | 55.8 | | |
| | DP | 3.9 | 14.4 | 23.7 | 33.1 | 46.3 | | |
| Au ₈ | MS | 3.0 | 14.8 | 30.8 | 63.8 | 117.7 | | |
| Ū. | DP | 3.9 | 15.6 | 31.9 | 63.7 | 103.9 | | |
| Au ₁₆ | MS | 3.0 | 15.0 | 31.5 | 62.8 | 124.2 | | |
| •• | DP | 4.0 | 16.1 | 32.4 | 63.8 | 123.8 | | |

Parallelization of Bertha

- The DKS arrays are always explicitly distributed among all processes and there is no need for a single global allocation. This also mean that, in the J + K matrix construction, no process is lost to the task of coordinating the workload, which is a non-negligible gain in case only few processes are available.
- This explicit matrix distribution and the effective computation parallelism make the applicability range of the code essentially "open-ended" and, most of all, essentially portable on any parallel architecture including low-cost clusters

Parallelization of Bertha



DKS/BLYP contour plot of the electron density difference upon bond formation between Copernicium and an Au20 cluster. Red isodensity surfaces identify zones of density decrease, blue ones of density increase.

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GRID programme:

a computational procedure for determining energetically favourable binding sites on molecules for functional groups of known structure through the use of **PROBES**.

The PROBE is moved through a grid of points suporimposed on the target molecule. Its interaction energy with the target molecule is computed by an empirical energy function.



$\mathsf{E}_{\mathsf{XYZ}} = \Sigma[\mathsf{E}_{\mathsf{LJ}}] + \Sigma[\mathsf{E}_{\mathsf{HB}}] + \Sigma[\mathsf{E}_{\mathsf{Q}}] + [\mathsf{S}]$

 E_{LJ} = Lennard-Jones potential E_{HB} = hydrogen bonding interaction energy E_{Q} = electrostatic function S= entropic term





 pKa prediction for small molecules (and proteins)
VolSurf, Almond and SHOP use molecular descriptors from 3D Molecular Interaction Fields (MIFs) produced by GRID
MetaSite is a computational procedure that predicts metabolic transformations related to cytochrome-mediated reactions in phase I metabolism

> J. Chem. Inf. Model., 47 (6), 2172 (2007) J. Chem. Inf. Model., 49 (1), 68 (2009) PROTEINS: Structure, Function, and Bioinformatics, (2009)



Easiest way is one thread for each probes (excellent speedup)One thread for each XY plane of the grid

| N threads | CPU Time | Wall Time | Speedup | N threads | CPU Time | Wall Time | Speedup |
|---------------------------------------|-------------|-----------|---------|--------------|-------------|--------------|---------|
| Serial | 234.40 | 234.40 | 1 | Serial | 181.54 | 181.57 | 1 |
| 2 | 235.05 | 119.67 | 1.96 | 2 | 185.28 | 95.12 | 1.91 |
| 3 | 235.81 | 83.15 | 2.82 | 3 | 184.20 | 64.72 | 2.81 |
| 4 | 237.24 | 62.89 | 3.35 | 4 | 182.68 | 48.50 | 3.74 |
| Intel Core2 Quad CPU Q6600 2.40GHz | | | | 5 | 183.58 | 39.72 | 4.57 |
| | | | | 6 | 184.78 | 33.46 | 5.43 |
| | | | | 7 | 184.51 | 28.45 | 6.38 |
| | | | | 8 | 185.46 | 24.76 | 7.33 |

Intel Xeon E5420 2.50GHz

Pka prediction



Pka prediction



PROTEINS: Structure, Function, and Bioinformatics, (2009)



Pka prediction



Even though the topological method MoKa was noticeably faster than ACD, the accuracy of those two methods and Marvin was statistically indistinguishable, with a root-mean-squared error of about 1 pKa unit compared to experiment

J. Chem. Inf. Model., 2010, 50 (4), pp 565–571



European Journal of Medicinal Chemistry, 45(9), 4270, (2010)

Tautomer enumeration and stability



Tautomer enumeration and stability



We introduced also an initial "normalization" procedure, to be sure to produce always the same series of tautomers.

Journal of Chemical Information and Modeling, 49 (1), 68 (2009)

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Moore's law



Architecture Evolution: A Collision Course

Multi-threading

Multi-core

Many Core

CPU

^Drogrammability

CPU

- Evolving toward throughput computing
- Motivated by energy-efficient performance

GPU

- Evolving toward general-purpose computing
- Motivated by high throughput performance

Throughput Performance

Fully Programmable

Partially Programmable

Fixed Function

CPU

GPU



GPU



Coalescing binaries



Signal detection - Single GPU





MultiGPU - Multithreading



MultiGPU - MPI



Results

• The CPU implementation of the algorithm was able to compute 3 templates per seconds, the GPU implmentation, taking advantage of up to 4 GPUs, we achieved an improvement by 2 orders of magnitude being able to process about **400** templates per second.

Einstein gravitational wave Telescope conceptual design study", ET-0106A-10

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Dye-sensitized solar cells



Random Sphere Packing



Random Sphere Packing



Coordination Number



PSD calculation



To solve the problem I used pyOpt is a Pythonbased package for formulating and solving nonlinear constrained optimization problems

PSD



Random Nanoparticle packing



Nanoparticle packing properties



Coordination number intersection of nanoparticles

Pore Size Distribution



Real Time Collision Detection



The point Q on the tetrahedron ABCD closest to P.

Real Time Collision Detection



Computation time reduced by more than two orders of magnitude

PSD using **TR**



PSD using **TR** for nanoparticles





PSD using **TR** for nanparticles





PSD


Different Packing Procedure



Thanks for your attention