## Exascale simulations via the

 submatrix matrix methodR. Schade, T. Kenter, M. Lass, C. Plessl \& T. D. Kühne

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AB INITIO QUANTUM CHEMISTRY: A SOURCE OF IDEAS FOR LATTICE GAUGE THEORISTS

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Ab initio quantum chemistry is an emerging computational area that is fifty years ahead of lattice gauge theory, a principal competitor for supercomputer time, and a rich source of new ideas and new approaches to the computation of many fermion systems. An overview of the history, current prospects and future frontiers of quantum chemistry is given, with special emphasis on lessons for lattice gauge theory. Particular reference is given to the role of Gaussian basis functions (in place of grids) and analytic (as opposed to Monte Carlo) methods. The main recommendation to lattice gauge theorists is for greater emphasis on infinite momentum frame studies, using Gaussian basis functions.

## Mother of HPC Problems

Combine all Levels of the Computer Technology Stack:


## Computational Microscope



## Schrödinger Equation



## Schrödinger Equation


„The fundamental laws necessary for the mathematical treatment of large parts of physics and the whole of chemistry are thus fully known ..."

$$
\mathcal{H}(\mathbf{r}, \mathbf{R}) \Psi(\mathbf{r}, \mathbf{R})=E \Psi(\mathbf{r}, \mathbf{R})
$$

## Schrödinger Equation


,,.. the difficulty lies only in the fact that application of these laws leads to equations that are too complex to be solved."

## Schrödinger Equation


,,... hence it would be desirable to develop practical approximation schemes for the application of quantum mechanics"

## Born-Oppenheimer

Electrons


Electrons


$$
\begin{gathered}
\mathcal{H}_{e}(\boldsymbol{r} ; \boldsymbol{R}) \psi(\boldsymbol{r} ; \boldsymbol{R})=\varepsilon(\boldsymbol{R}) \psi(\boldsymbol{r} ; \boldsymbol{R}) \\
M_{I} \ddot{\boldsymbol{R}}_{I}=-\nabla_{\boldsymbol{R}_{I}}\left[\varepsilon(\boldsymbol{R})+V_{K K}(\boldsymbol{R})\right]
\end{gathered}
$$

## CP2K: Overview

- Static Calculations

Energy \& Structure Optimization
Transition Paths (String, NEB)
Properties: NMR, EPR \& XAS

T. D. Kühne et al., JCP 152, 194103 (2020)

- Sampling Techniques

MC, MD \& Path-Integral Methods RT-TDDFT/Ehrenfest Dynamics Accelerated FES: Metadynamics

- Energy \& Force Methods

All-Electron Calculations (GAPW)
Quickstep: PP Calculations (GPW)
Post-HF Methods (RPA, MP2, GW) DFT/HF Methods (HFX, CDFT)
Behler-type NN Potentials
Semiempirical QC \& TB Methods
Classical Molecular Mechanics Embedding Methods (IS, QM/MM)

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## CP2K: Recent Development

- Large Scale Computational Kernels PW-based DFT (SIRIUS)
Hybrid DFT, MP2 \& RPA
Linear Scaling Algorithms

- Approximate Molecular Dynamics $2^{\text {nd }}$ Generation Car-Parrinello MD Approximate Computing
- Massive Parallelism

Mixed MPI / OpenMP
GPU / FPGA support

- Sparse Matrix Algebra

Distributed Block CSR
Cannon's Algorithm \& SMM

- Open Source
1.5 mio. lines of code
$>6500$ regression tests


## Schrödinger Equation



$$
\begin{gathered}
\mathbf{H}[\mathbf{C}] \mathbf{C}=\varepsilon \mathbf{S C} \\
\mid \mathcal{O}\left(N^{3}\right) \\
E=\sum_{i=1}^{N_{e}} \varepsilon_{i}-V_{d c}=\operatorname{Tr}\left[\mathbf{C}^{T} \mathbf{H C}\right]-V_{d c} \\
=\left.\min _{\mathbf{P}} \operatorname{Tr}[\mathbf{P H}]\right|_{\mathbf{P S P}=\mathbf{P}}-V_{d c}
\end{gathered}
$$

D. Richters and T. D. Kühne, J. Chem. Phys. 140, 134109 (2014)

## Self-Consistent Field



## The Sign Method

$$
\mathbf{P}=\frac{1}{2}\left(\mathbf{I}-\operatorname{sign}\left(\mathbf{S}^{-1} \mathbf{H}-\mu \mathbf{I}\right)\right) \mathbf{S}^{-1}
$$

- matrix sign function and inversion can be evaluated iteratively

$$
\begin{gathered}
\operatorname{sign}(x)=\frac{x}{|x|}=\frac{x}{\sqrt{x^{2}}} \\
\operatorname{sign}(\boldsymbol{A})=\boldsymbol{A} \cdot\left(\boldsymbol{A}^{2}\right)^{-1 / 2}
\end{gathered}
$$

- linear-scaling approach $\mathcal{O}(N)$

$$
\begin{aligned}
\boldsymbol{X}_{0} & =\boldsymbol{A} \\
\boldsymbol{X}_{i+1} & =\frac{1}{2} \boldsymbol{X}_{\boldsymbol{i}} \cdot\left(3 \boldsymbol{I}-\boldsymbol{X}_{i}^{2}\right) \\
\operatorname{sign}(\boldsymbol{A}) & =\lim _{i \rightarrow \infty} \boldsymbol{X}_{i}
\end{aligned}
$$

- only multiplications of distributed sparse matrices are required
o but usually bound by inter-node communication!

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)

## The Sign Method


M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)

## The DBCSR Library

- Distributed

MPI parallelization based on Cannon, 2.5D, Carma, or Cosma algorithm On node parallelization via OpenMP

- Block Compressed Sparse Row

Block-sparse, where block corresponds to atoms

- Small matrix-matrix multiplication library on multicore CPUs \& GPUs libxsmm, libcusmm, libsmm_acc

T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)


## The DBCSR Library


http://dbcsr.cp2k.org
T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)

## The DBCSR Library

- 1. Random permutation of row and column block indices to balance load Each processor is approximately holding the same amount of data, with roughly the same amount of Flops
- 2. 2D grid decomposition over P processors Block-sparse, where block corresponds to atoms

T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)


## The DBCSR Library

- DBCSR is based on blocked structure

Non-zero elements are small dense blocks, typically $5 \times 5,13 x 13,23 \times 23, \ldots$
Take full advantage of the block structured sparse nature of the matrices
Each block corresponds to the interaction between two atoms

- Dense limit is as important as the sparse limit
- Provide good scalability for a large number of processors
 distant atom pairs
T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)


## SMM Libraries

- Optimized libraries were developed that outperform vendor BLAS for SMM

LIBXSMM for Intel-based CPU/KNL systems
LIBCUSMM for Nvidia GPUs using CUDA
LIBSMM_ACC for Nvidia/AMD GPUs using CUDA and HIP

- LIBXSMM generates executable code just-in-time (JIT) by assembling the instructions in-memory

All flavors of AVX extensions are supported
Avg. speed-up of approx. 3 for LIBXSMM over MKL-DGEMM on KNL

- LIBCUSMM employs a double-buffering technique, based on CUDA streams, to maximize occupancy of the GPU and hide data transfer latency
- LIBSMM_ACC GPU kernels are JIT compiled at runtime
- LICUSMM \& LIBSMM_ACC includes an auto-tuning framework to find the best parameters for every ( $\mathrm{m}, \mathrm{n}, \mathrm{k}$ )-kernel out of $>100 \mathrm{k}$ combinations
T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)


## SMM Libraries



Additional factor 5 speed-up, when using LIBSMM_ACC instead of LIBXSMM on CRAY XC50 node with 12 core Intel Haswell CPU and Nvidia V100 GPU
T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)

## FPGA-based Noctua@PC2



## FPGA-based Inversion

$$
\begin{aligned}
B_{k+1} & =\frac{1}{p}\left[(p-1) B_{k}-\left(\left(I-B_{k}^{p} A\right)^{q}-I\right) B_{k}^{1-p} A^{-1}\right] \\
& \stackrel{p=1}{=}\left[I-\left(I-B_{k} A\right)^{q}\right] A^{-1} .
\end{aligned}
$$

D. Richters, M. Lass, A. Walter, C. Plessl \& T. D. Kühne, Comm. Comp. Phys. 25, 564 (2019)


M. Lass, T. D. Kühne and C. Plessl, IEEE Embedded Systems Letters PP, 1 (2017)

## Approximate Computing

$$
\begin{gathered}
M_{I} \ddot{\mathbf{R}}_{I}=\underbrace{\mathbf{F}_{I}^{\mathrm{BO}}+\boldsymbol{\Xi}_{I}^{N}-\gamma_{N} M_{I} \dot{\mathbf{R}}_{I}}_{\mathbf{F}_{I}^{\mathrm{FPGA}}-\gamma_{N} M_{I} \dot{\mathbf{R}}_{I}} \\
\left\langle\boldsymbol{\Xi}_{I}^{D}(0) \boldsymbol{\Xi}_{I}^{D}(t)\right\rangle=2 \gamma_{D} M_{I} k_{B} T \delta(t) \\
\left\langle\frac{1}{2} M_{I} \dot{\boldsymbol{R}}_{I}^{2}\right\rangle=\frac{3}{2} k_{B} T
\end{gathered}
$$


T. D. Kühne, F. R. Mohamed, M. Krack \& M. Parrinello, Phys. Rev. Lett. 98, 066401 (2007) V. Rengaraj M. Lass, C. Plessl and T. D. Kühne, Computation 8, 39 (2020)

## Approximate Computing


V. Rengaraj M. Lass, C. Plessl and T. D. Kühne, Computation 8, 39 (2020)

## Approximate Computing


V. Rengaraj M. Lass, C. Plessl and T. D. Kühne, Computation 8, 39 (2020)

## Submatrix Method

Purpose: Estimate matrix function (e.g. sign or inversion) of a large sparse matrix

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)
M. Lass, R. Schade, T. D. Kühne \& C. Plessl, IEEE Proc. of SC20 1, 80 (2020)

## Submatrix Method

Step 1: Identify nonzero values in every column

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)
M. Lass, R. Schade, T. D. Kühne \& C. Plessl, IEEE Proc. of SC20 1, 80 (2020)

## Submatrix Method

Step 2: Build submatrix $\mathcal{T}_{i}(\boldsymbol{A})$ for every column $i$ with only the rows that have non-zero elements

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)
M. Lass, R. Schade, T. D. Kühne \& C. Plessl, IEEE Proc. of SC20 1, 80 (2020)

## Submatrix Method

Step 3: Apply matrix function $f$ to submatrices $\mathcal{T}_{i}(\boldsymbol{A})$

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)
M. Lass, R. Schade, T. D. Kühne \& C. Plessl, IEEE Proc. of SC20 1, 80 (2020)

## Submatrix Method

Step 4: copy resulting columns to result matrix

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)
M. Lass, R. Schade, T. D. Kühne \& C. Plessl, IEEE Proc. of SC20 1, 80 (2020)

## Submatrix Method

Properties of the Submatrix method:

- large distributed sparse matrix $\Rightarrow$ many small dense matrices
- suitable for dense linear algebra
- massively parallel
o linear-scaling approach

M. Lass, S. Mohr, H. Wiebeler, TDK \& C. Plessl, ACM Proc. of PASC 7, 1 (2018)
M. Lass, R. Schade, T. D. Kühne \& C. Plessl, IEEE Proc. of SC20 1, 80 (2020)


## Non-Orthogonal Local SM

Implementation with GPUs:

R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Non-Orthogonal Local SM


$\Rightarrow$ for intermediate sized matrices $(\geq 1000)$ about $60 \%-85 \%$ of peak can be reached
R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Pre-Exascale Simulation

- 936 GPU-nodes with each:
- CPU: 2xAMD EPYC 7402
- Memory: 512 GB DDR4-3200 RAM
- GPU: $4 \times$ NVIDIA A100, 40 GB, NVLink3
- Network: $4 \times$ Mellanox HDR200 InfiniBand ConnectX 6 (200 Gbit/s each)
- Peak TC Performance:
- FP64: 73 PFLOP/s

- FP16/FP32: 1170 PFLOP/s

| Code, Year | Method | Basis | System | \# Atoms | \# Cores | Machine | Peak <br> Performance | Efficiency |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| CPMD [22] 2005 | DFT | PW | bulk SiC | 1k | 1.2k CPU | IBM p690 | 1.087 TFlop/s | $\approx 20 \%$ |
| Qbox [23] 2006 | DFT | PW | bulk Mo | 8*1k | 128k CPU | IBM BlueGene/L | 207.3 TFlop/s | 56.5\% |
| LS3DF [24] 2009 | DFT | PW | bulk ZnTeO | 36k | 147k CPU | Cray Jaguar | 442 TFlop/s | $\approx 33 \%$ |
| CP2K [25] 2012 | LS-DFT | GPW | bulk $\mathrm{H}_{2}$ | 1 m | 47k CPU | Cray XT5 |  |  |
| ONETEP [26] 2014 | LS-DFT | NGWF | amyloid fibril trimer | 42k | 115k CPU | IBM BlueGene/Q |  |  |
| RSDFT [27] 2014 | DFT | RS-FD | Si nanowire | 107k | 664k CPU | K-Computer | 5.48 PFlop/s | 51.67\% |
| LDC-DFT [28] 2014 | SS-DFT | RMG-PW | bulk SiC | 6.3 m | 786k CPU | IBM Blue Gene/Q | 5.08 PFlop/s | 50.5\% |
| OpenAtom [29] 2016 | DFT | PW | periodic MOF | $32 * 424$ | 262k CPU | IBM BlueGene/Q |  | $\approx 52 \%$ |
| MGmol [30] 2016 | LS-DFT | FD | bulk $\mathrm{H}_{2} \mathrm{O}$ | 1.2 m | 1.6 m CPU | IBM BlueGene/Q |  | $\approx 39 \%$ |
| DFT-FE [31] 2019 | DFT | FEM | Mg cluster | 10.5k | $\begin{aligned} & 159 \mathrm{k} \mathrm{CPU} \\ + & 22.8 \mathrm{k} \mathrm{GPU} \end{aligned}$ | IBM Summit | 46 PFlop/s | 27.8\% |
| CONQUEST [32] 2020 | LS-DFT | PAO | bulk Si | 1 m | 200k CPU | K-Computer |  |  |

R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Pre-Exascale Simulation

## Strong scaling of bulk water with 102 million atoms:


R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Pre-Exascale Simulation

Strong scaling of bulk water with 102 million atoms:
performance of NOLSM for bulk water
Peak multiply performance ( $312 \mathrm{TFLOP} / \mathrm{s} / \mathrm{GPU}$ ) -
average submatrix dimension $\approx 660$


$\Rightarrow$ small matrix sizes limit achievable performance
R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Combination of Submatrices

Idea: use flexibility of submatrix method and combine submatrices with similar columns

$\Rightarrow$ fewer .but larger submatrices!
R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Combination of Submatrices




HIV-1 capsid in aqueous solution with 62 million atoms average submatrix dimension $654 \rightarrow 1202$ and reduction of floating-point operations by factor 1.65 !
R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Combination of Submatrices

Strong scaling of HIV-1 with 62.5 million atoms:
average submatrix dimension $\approx 1200$


$\Rightarrow 324$ PFlops FP16/FP32 for 384 nodes (68\% of TC Peak)
R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)

## Summary \& Outlook

- extended electronic-structure based molecular dynamics simulations to more than 100 million atoms
- 102 million atoms for bulk water
- 62 million atoms for HIV-1 capsid
- Non-orthogonal local submatrix (NOLSM) method:
- for matrix functions of large sparse matrices
- massively parallel communication-avoiding method
- GPU-accelerated for NVIDIA GPUs


HIV-1 capsid in aqueous solution with 62
million atoms

- minimal transfer between host and GPUs
- matrix construction on GPUs
- mixed-precision on NVIDIA tensor cores
- compensation schema for numerical noise
- candidate for one of the first scientific FP...16/FP32-exaflop simulations
R. Schade, T. Kenter, H. Elgabarty, M. Lass, ..., TDK \& C. Plessl, arXiv:2104.08245 (2021)


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- Alfio Lazzaro, Cray EMEA Research Lab: DBCSR
- Hans Pabst, Intel Extreme Computing: LIBXSMM
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- Stephan Mohr, BSC: Submatrix Method
- Matthias Krack, PSI: CP2K
- Jürg Hutter, UZH: CP2K


T. D. Kühne et al., J. Chem. Phys. 152, 194103 (2021)

