

Paul Gibbon Jülich Supercomputing Centre



Jülich Supercomputing Centre

Supercomputer operation for

- Centre FZJ
- Regional JARA
- Helmholtz & National NIC, GCS
- Europe PRACE, EU communities

Application support

- SimLabs
- Cross Sectional Groups
- Peer review coordination

R&D work

- Algorithms, performance analysis and tools
- Community data management service
- Novel computer architectures:
- Exascale Laboratories: EIC (IBM), ECL (Intel), NVIDIA

Education and Training

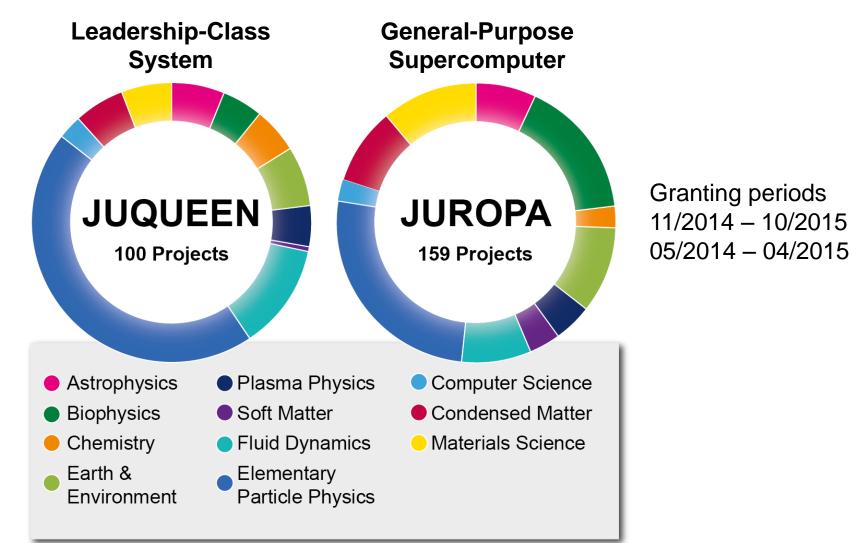




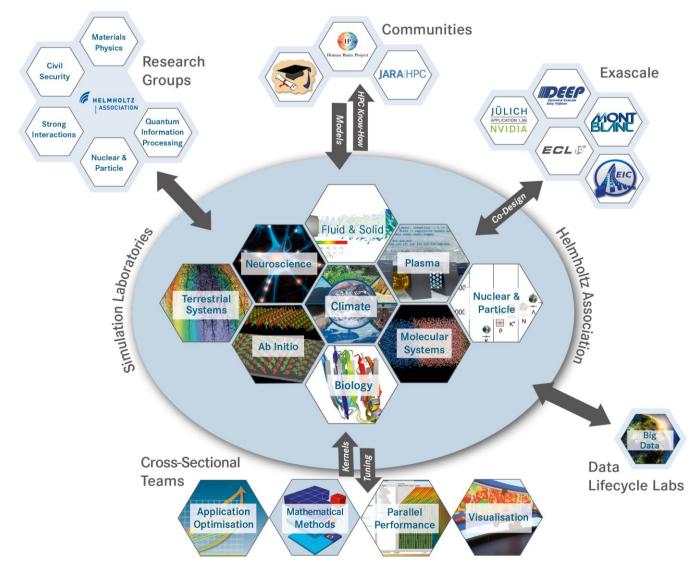
HPC Systems: Dual Architecture Strategy IBM Power 4+ JUMP, 9 TFlop/s 2004 **IBM Blue Gene/L IBM Power 6** JUBL, 45 TFlop/s JUMP, 9 TFlop/s JUROPA **IBM Blue Gene/P** 2009 200 TFlop/s **JUGENE**, 1 PFlop/s File Server **HPC-FF** 100 TFlop/s **IBM Blue Gene/Q** JUQUEEN Lustre **GPFS** 5.9 PFlop/s 2014 **JUROPA** successor ~ 2 PFlop/s + Booster **JUQUEEN** successor ~ 10 Pflop/s ~ 50 PFlop/s 2019 **General-Purpose Cluster Highly-Scalable System**

02.01.2015

Research Fields of Current National Projects



Domain-specific User Support and Research



Jülich Simulation Laboratory Concept

Staff (4-8 members)

- Senior scientist recruited from field
- 1-2 postdocs + technical staff (informatics)
- Jointly supervised PhD & MSc students

Support

- Porting & tuning (integral part of application advisory)
- Algorithm scaling; code clinics (day-visits)
- Workshops (BG/Q); schools (CECAM)

Research

- Common/generic methods
- Scalable algorithms
- 3rd party projects: FZJ, JARA, DFG, BMBF, EU, G8

The Simulation Laboratory as HPC Enabler

Advisory Board

Simulation Laboratory

Support:

- Application analysis
- Re-engineering
- Community codes
- Workshops

Research:

- Scalable algorithms
- XXL simulations
- 3rd party projects
- Hardware co-design

Exascale Labs

Cross-Sectional Teams

Community Groups

Active Simulation Labs @ JSC



Science Climate

Terrestrial Molecular

Systems

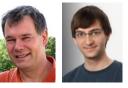
Systems





















Nuclear & Particle

Solid Eng.

Fluid &

Plasma Physics























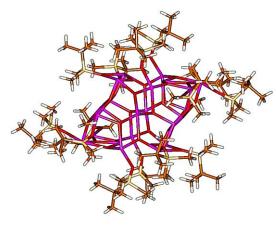






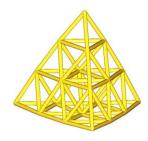
Simulation Laboratory Molecular Systems

 TURBOMOLE: Parallel two-component DFT for large molecular clusters containing heavy elements [jointly implemented into



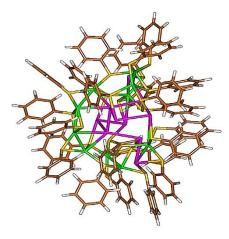
[Bi₂₂O₂₆(OSiMe₂tBu)₁₄]

370 atoms, 3876 bfn DHF-SVP-2c/BP86 **realistic** molecular transition metal clusters accessible on general purpose systems such as JUROPA



[Au₂₀]⁻

20 atoms, 1400 bfn DHF-TZVP-2c/TPSS

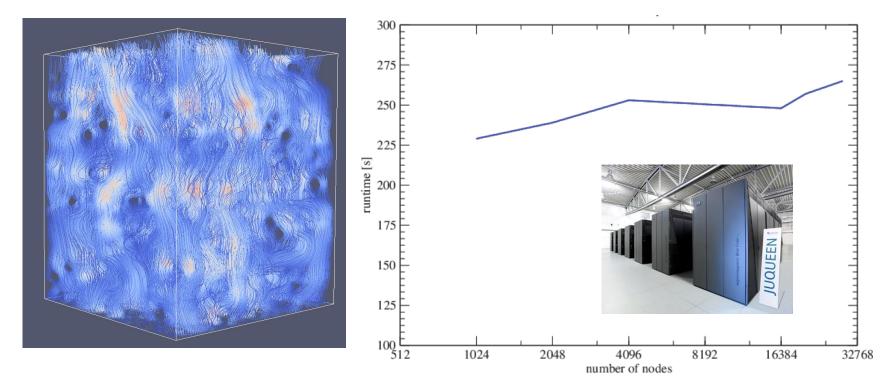


Bi₁₀Cu₁₀(SPh)₂₄]²⁻ 308 atoms,7162 bfn DHF-TZVP-2c/BP86

Simulation Laboratory Molecular Systems



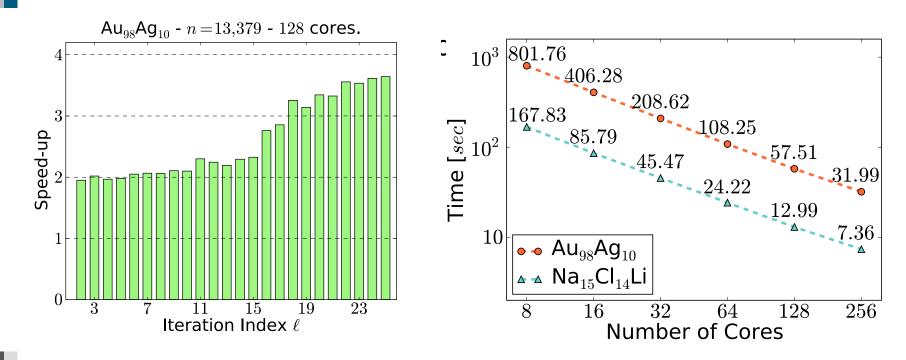
MP2C: particle-based hydrodynamics



- Flow field in a gas diffusion membrane
- With stochastic geometry

 Weak scaling on full JUQUEEN

Simulation Laboratory ab initio Methods



Speed-up when inputing the eigensolver approximate solutions vs random vectors Strong scalability on Juropa showing the potential for simulating larger crystals

SL Biology: protein folding highlight

results

•92-residue

- complex topology
- •Estimated folding time: few ms
- •ProFASi w. parallel tempering
- •32 independent simulations
- •Free energy minimum at 3.5 Å
- •~ 19.000 CPU-h/folding event

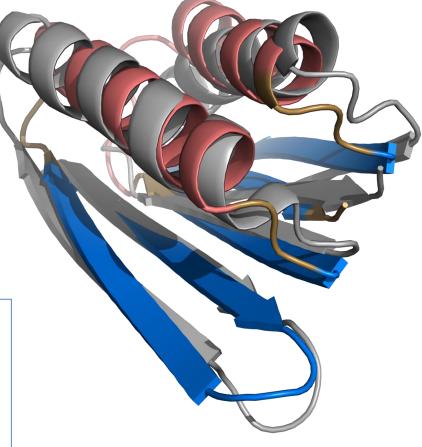
•Experimental folding time: 1 s



Folding of Top7 in unbiased all-atom Monte Carlo simulations

Sandipan Mohanty,* Jan H. Meinke, and Olav Zimmermann

Jülich Supercomputing Centre, Institute for Advanced Simulation, Forschungszentrum Jülich, D-52425 Jülich, Germany



SL Biology: whole cell simulation

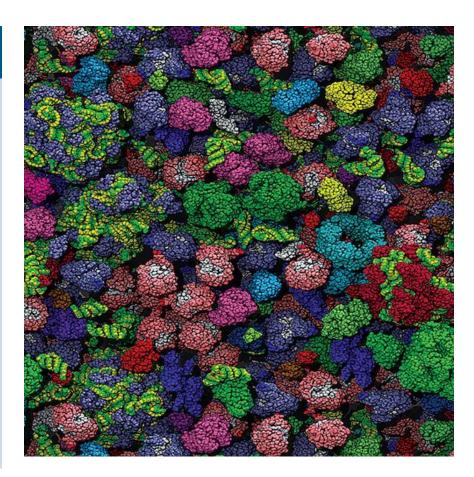
BMBF project

•PI: Eric v. Lieres (IBG-1)
•PostDoc: Slavko Kondrat
•Multiscale simulation
•Combining BD + CA +PDE

•Main focus:

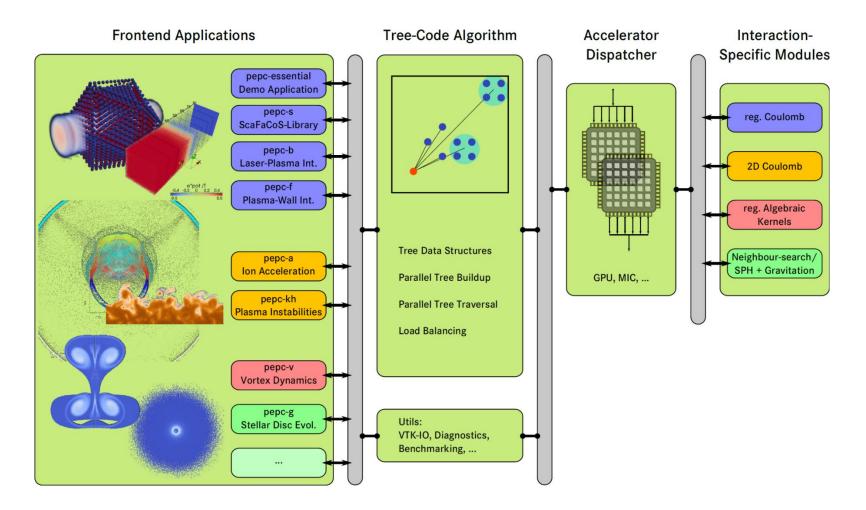
•What <u>quantitative</u> effect has the spatial inhomogeneous distribution of proteins on the metabolic network level

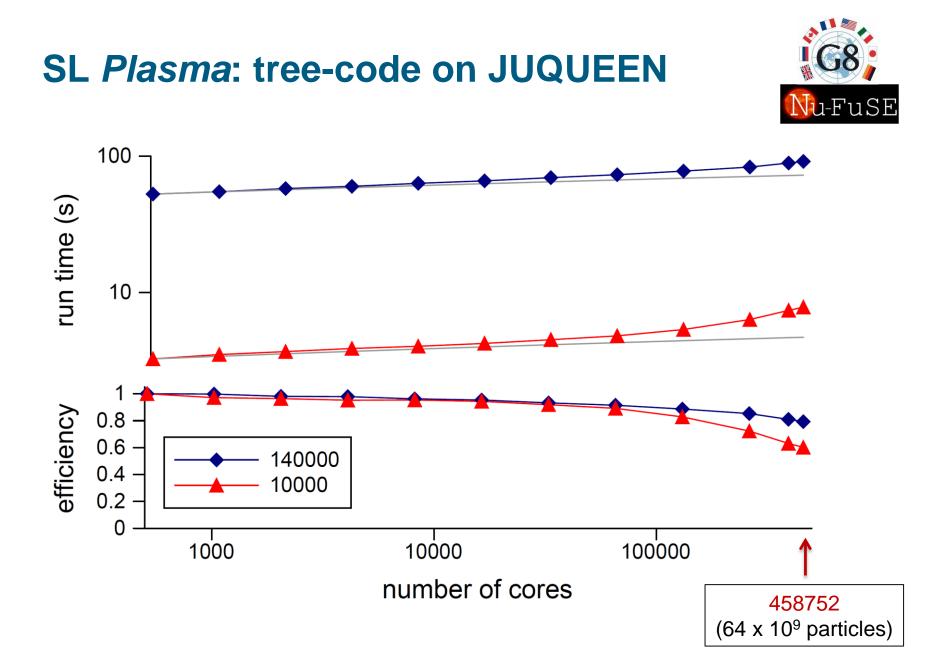
•Challenges: many!!



(graphics taken from work of A. Elcock)

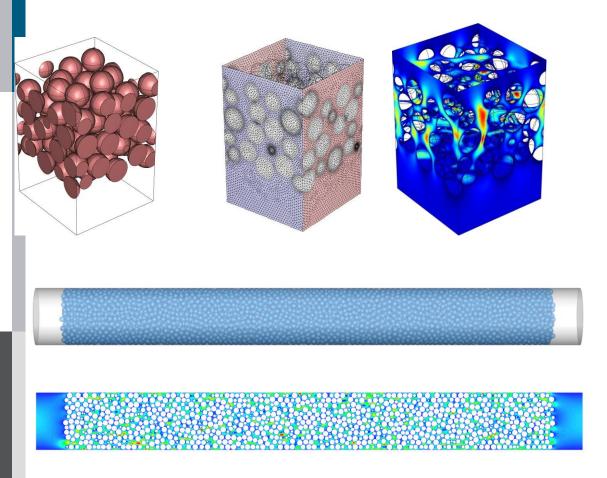
SimLab Plasma Physics Parallel tree code development (PEPC)





SL Fluids and Solid Engineering

Fluid flow and porous media mixed simulations using FEM.



2011 Simulations with commercial code COMSOL.

 Largest chromatography simulations with 750 beads take days.

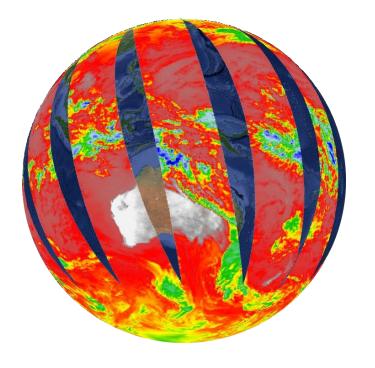
 2013 Modelling with with RWTH/JSC research code XNS.

 Simulation up with 7681 beads can be done easily in under one hour on 4096 cores of JUQUEEN.

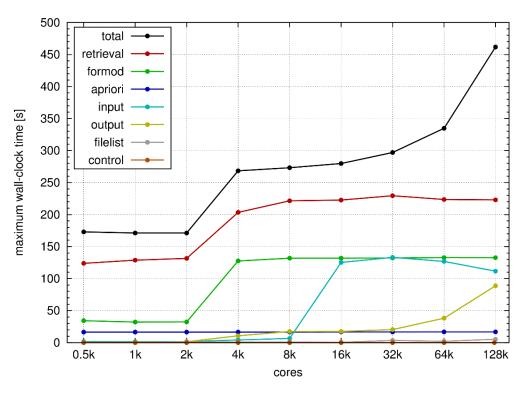
 GOAL: full-sized columns with millions of beads

Simulation Laboratory Climate Science: Highlight

JURASSIC: fast infrared radiative transfer calculations



AIRS/Aqua satellite observation
 of atmospheric composition



Weak scaling of AIRS temperature retrieval
 with JURASSIC on JUQUEEN

Simulation Lab Terrestrial Systems Klaus Görgen, Stefan Kollet

TerrSysMP:

- Fully integrated groundwatervegetation-atmosphere simulation platform; earth system models at regional scale
- Water cycle processes and variability across scales



use impacts



Scalasca performance analysis

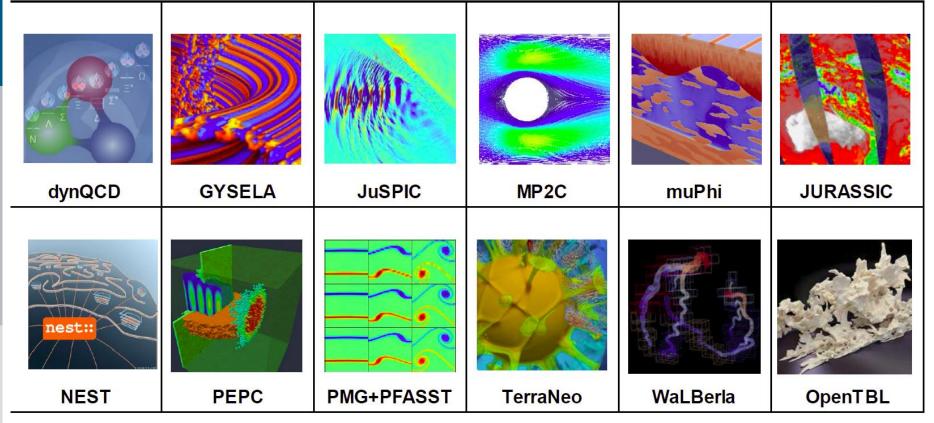
- Refactoring of OASIS-MCT coupling interface to remove scaling bottleneck
- Scaling now to 32k cores:
 64x increased problem size!



High-Q Club: Exascale-Ready Applications on JUQUEEN







12+ codes scaling across 458,752 JUQUEEN cores

WWW: http://www.fz-juelich.de/ias/jsc/EN/Expertise/High-Q-Club/_node.html 02.01.2015