

Optimizing Molecular Dynamics Simulations with Dynamic Auto-Tuning

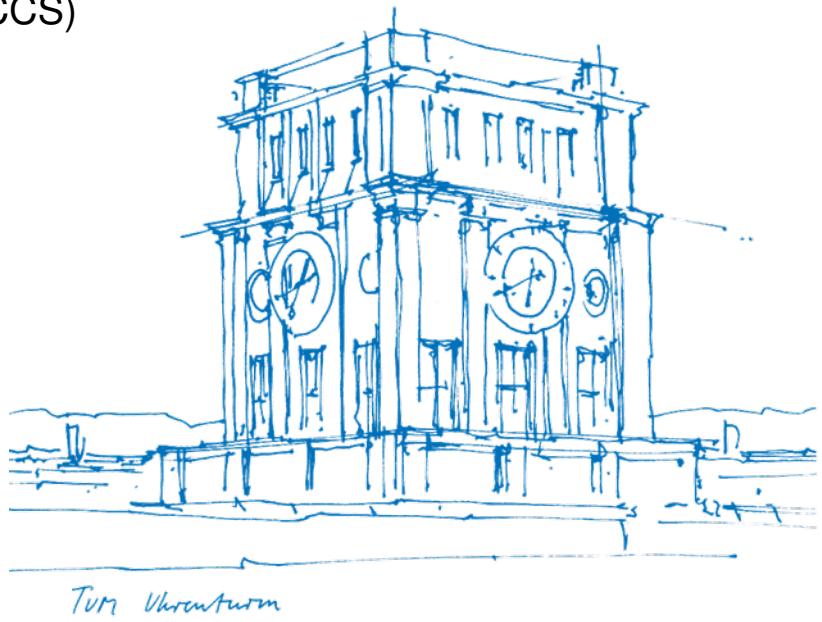
Fabio Gratl, Steffen Seckler, Hans-Joachim Bungartz, Philipp Neumann

Technical University of Munich

Department of Informatics

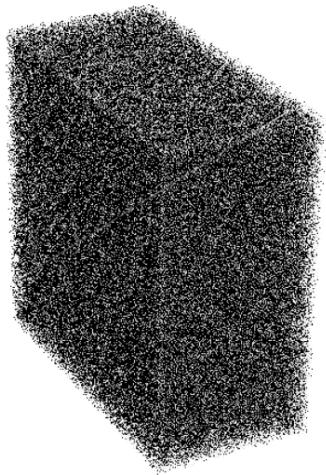
Chair of Scientific Computing in Computer Science (SCCS)

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Bundesministerium
für Bildung
und Forschung

Motivation



Molecular Dynamics

Molecular Dynamics - Short Range

- Here: small rigid molecules
- Simulation of movement of particles
- Computation of pairwise forces
- Newton's Laws of Motion
- N -Body problem $\Rightarrow O(N^2)$
- Force cut-off $\Rightarrow O(N)$

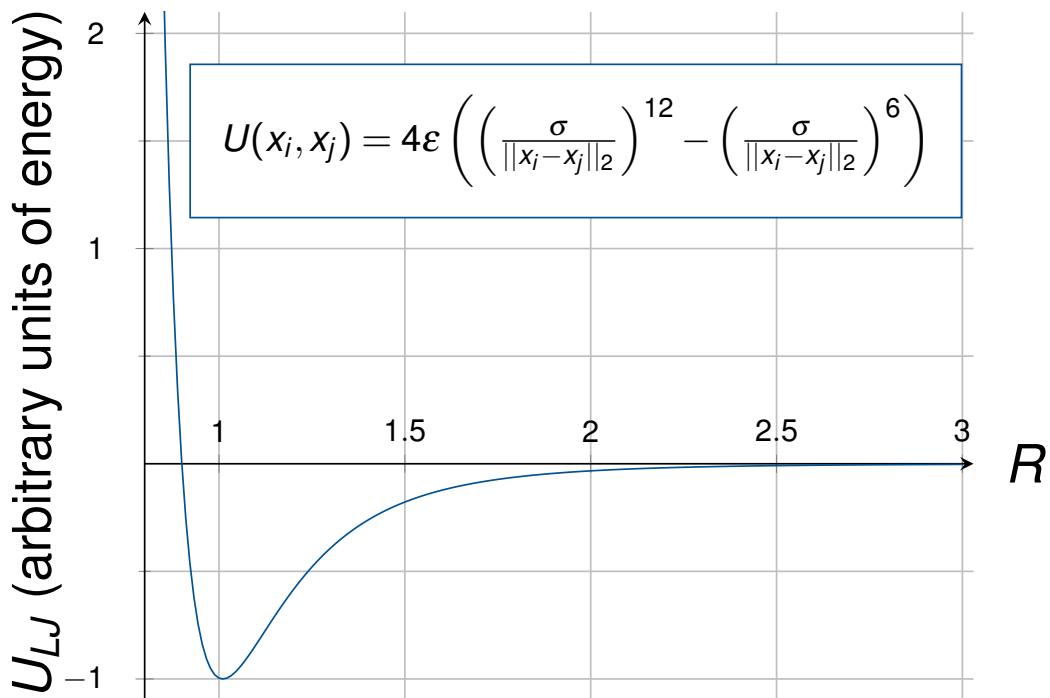
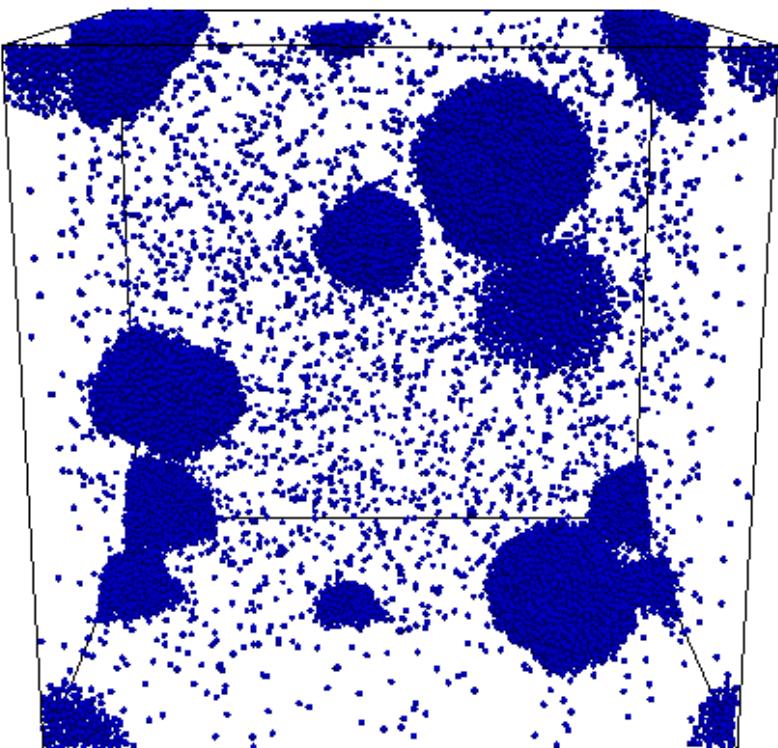


Figure: Lennard Jones Potential for $\epsilon = 1$ and $\sigma = 0.9$

Challanges

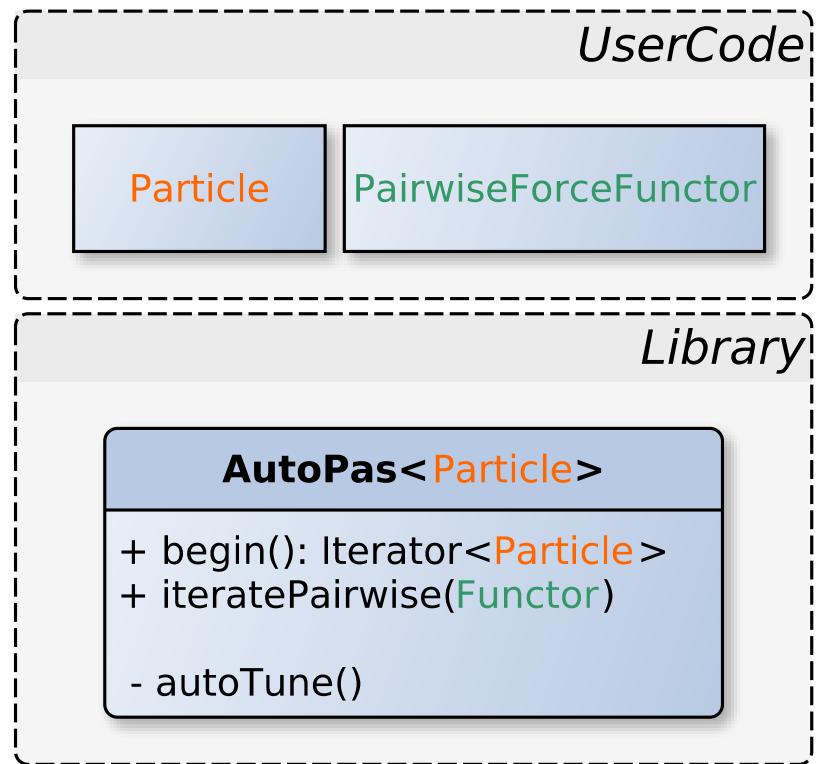
- Total number of particles
- Particle density
- (In-)Homogeneity
- Systems changing over time
- Many possible algorithms
- Overall goal:
Minimize time to solution!



AutoPas

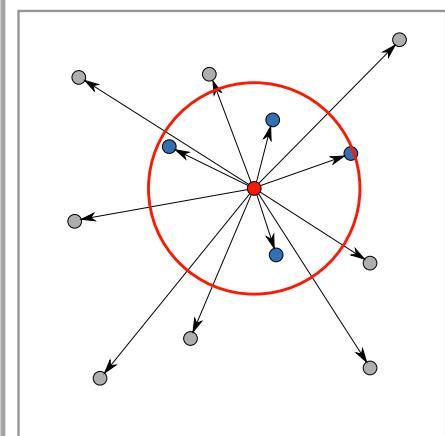
AutoPas: Overview

- Node-Level C++ library
 - Black Box container
 - User defines:
 - Properties of particles
 - Force for pairwise interaction
 - AutoPas provides:
 - Containers, Traversals, Data Layouts, ...
 - Dynamic Tuning at run-time
- ⇒ General base for N-Body simulations

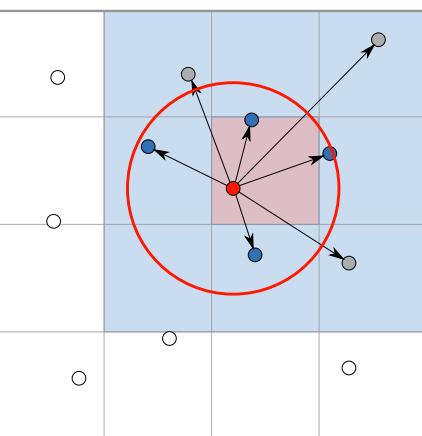


<https://github.com/AutoPas/AutoPas>

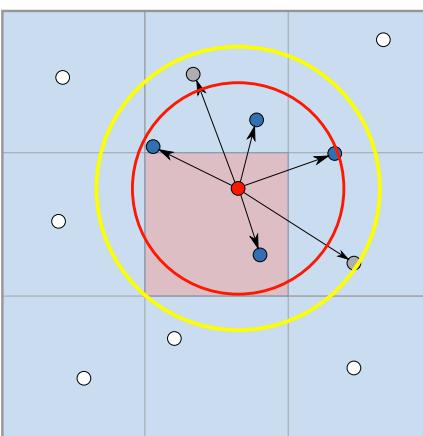
AutoPas: (Some) Implemented Options



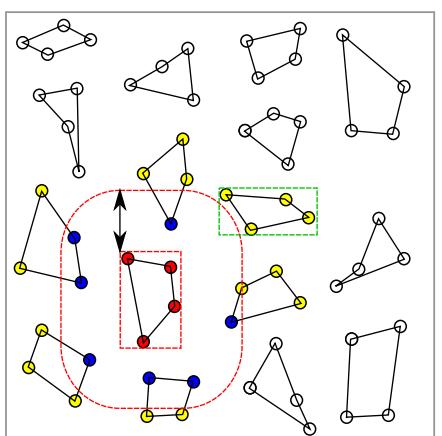
Direct Sum



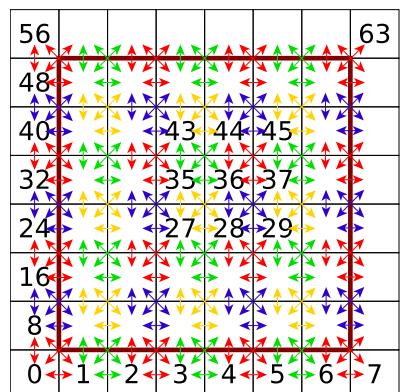
Linked Cells



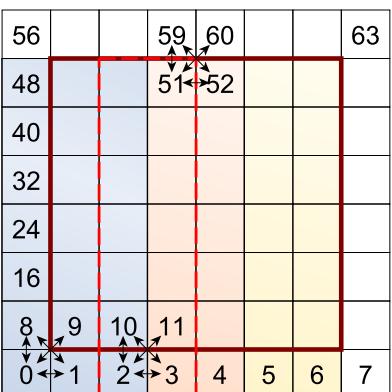
Verlet Lists



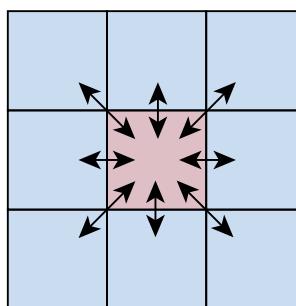
Verlet Cluster Lists



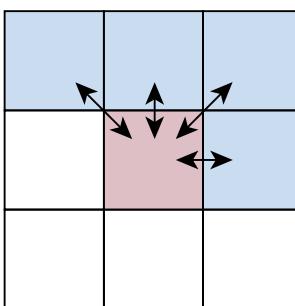
Coloring



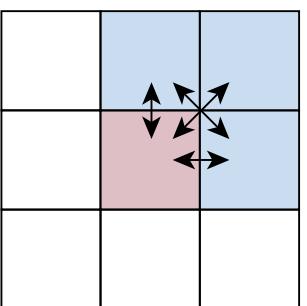
Slicing



C01



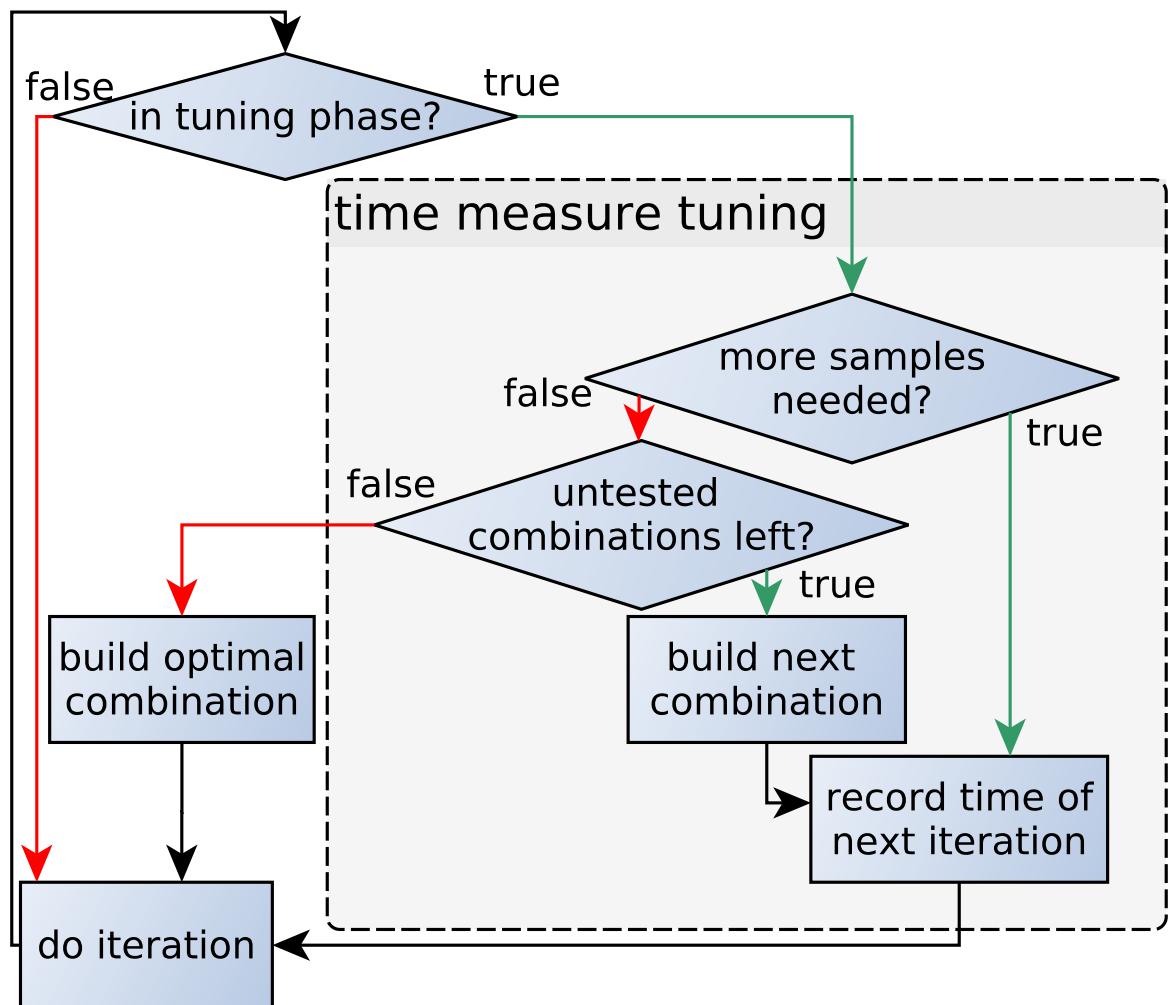
C18



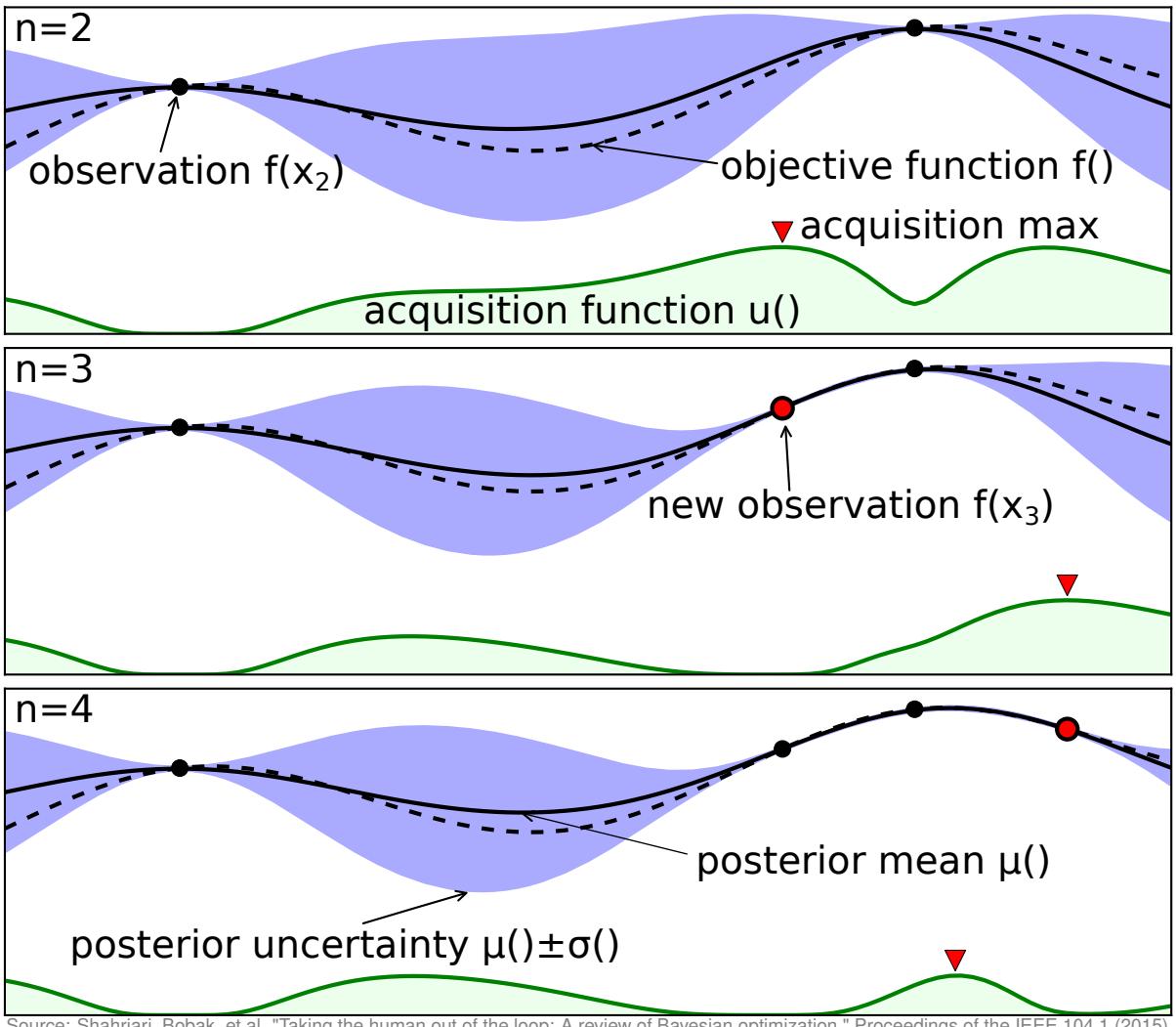
C08

AutoPas: Auto-Tuning

- Common interfaces for containers, traversals, etc
⇒ Strategy pattern
⇒ "Verlet-like" approach
- Repeated periodically
- User can restrict search space



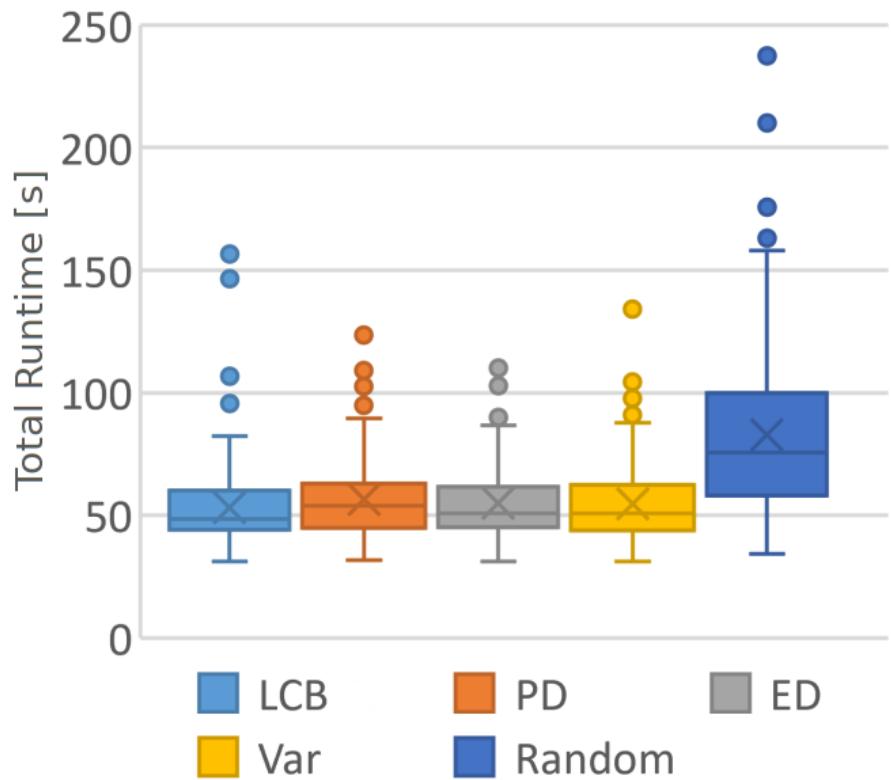
Auto-Tuning Strategies WiP - Bayesian Inference



Source: Shahriari, Bobak, et al. "Taking the human out of the loop: A review of Bayesian optimization." Proceedings of the IEEE 104.1 (2015)

Auto-Tuning Strategies WiP - Bayesian Inference

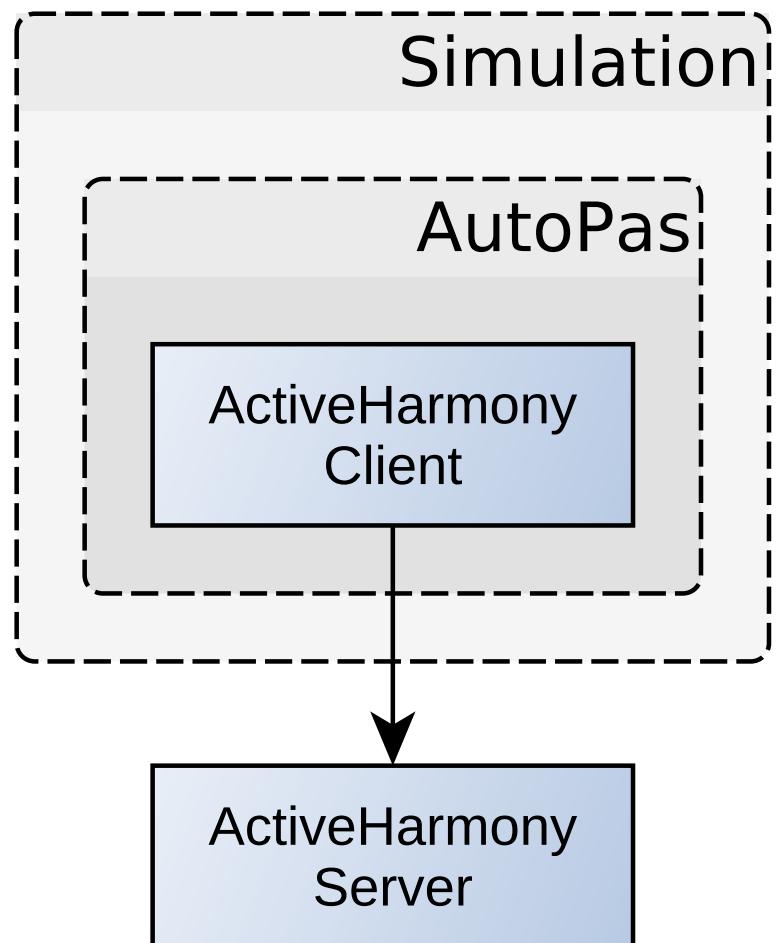
- 10 evidences sufficient instead of > 70
 \Rightarrow Less iterations spent in tuning.
 \Rightarrow Less testing of inefficient configurations.
- Here: No major differences in acquisition functions.



Scenario: 150k Particles densely Gaussian distributed; 50 iterations; 200 runs per column

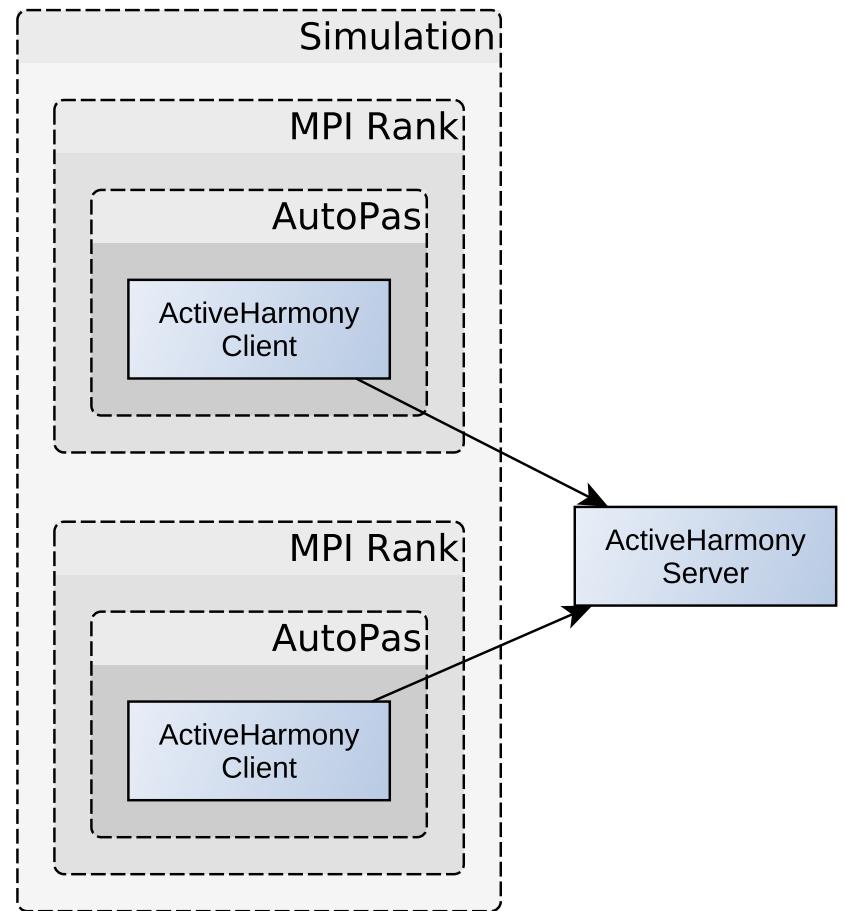
Auto-Tuning Strategies WiP - Active Harmony

- Open Source Auto-Tuning Framework
<https://www.dyninst.org/harmony>
- Client-Server system
- Internally: Nelder Mead Simplex



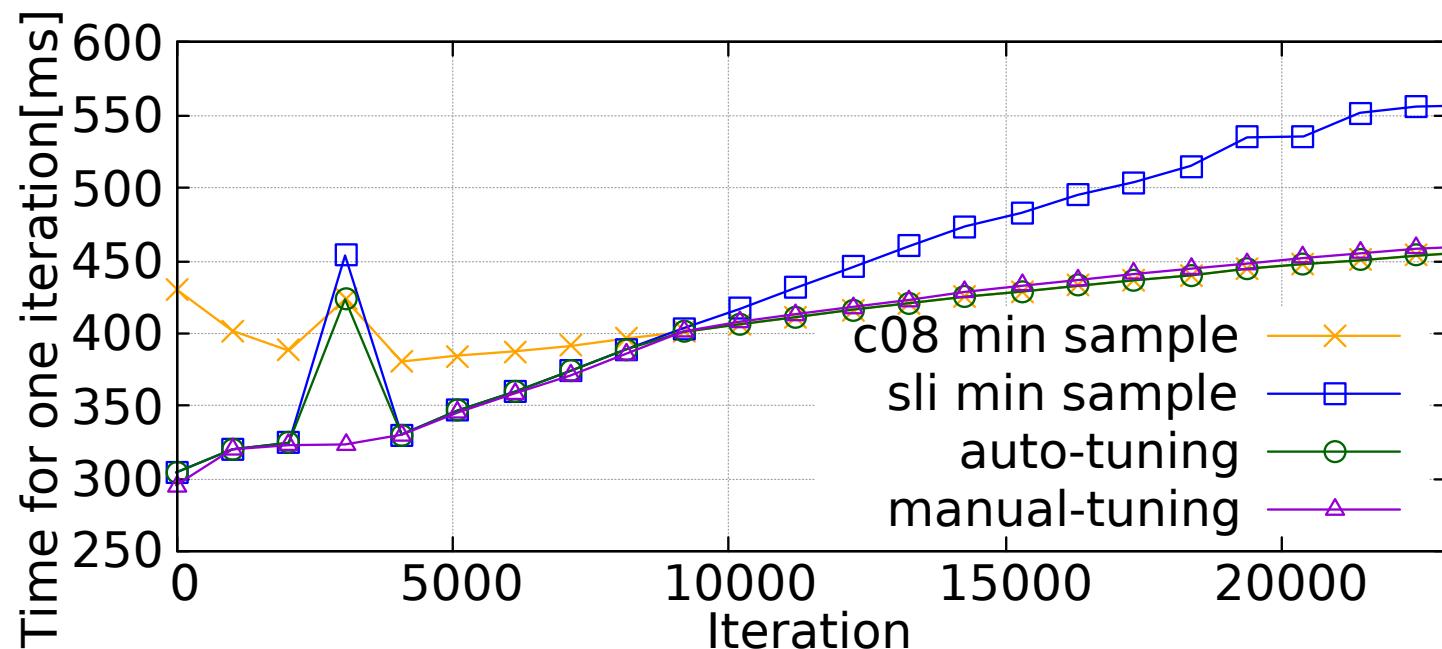
Auto-Tuning Strategies in Future - Distributed Search

- Spread Tuning over MPI Ranks
- Collect all tuning information in one server
- Greatly reduces number of tuning steps



Auto-Tuning Strategies in Future - Performance Extrapolation

- Start with full search
- Extrapolate performance from previous evidences
- Decide if testing is worthwhile
- Easier Outlier detection



Actual Applications and Results

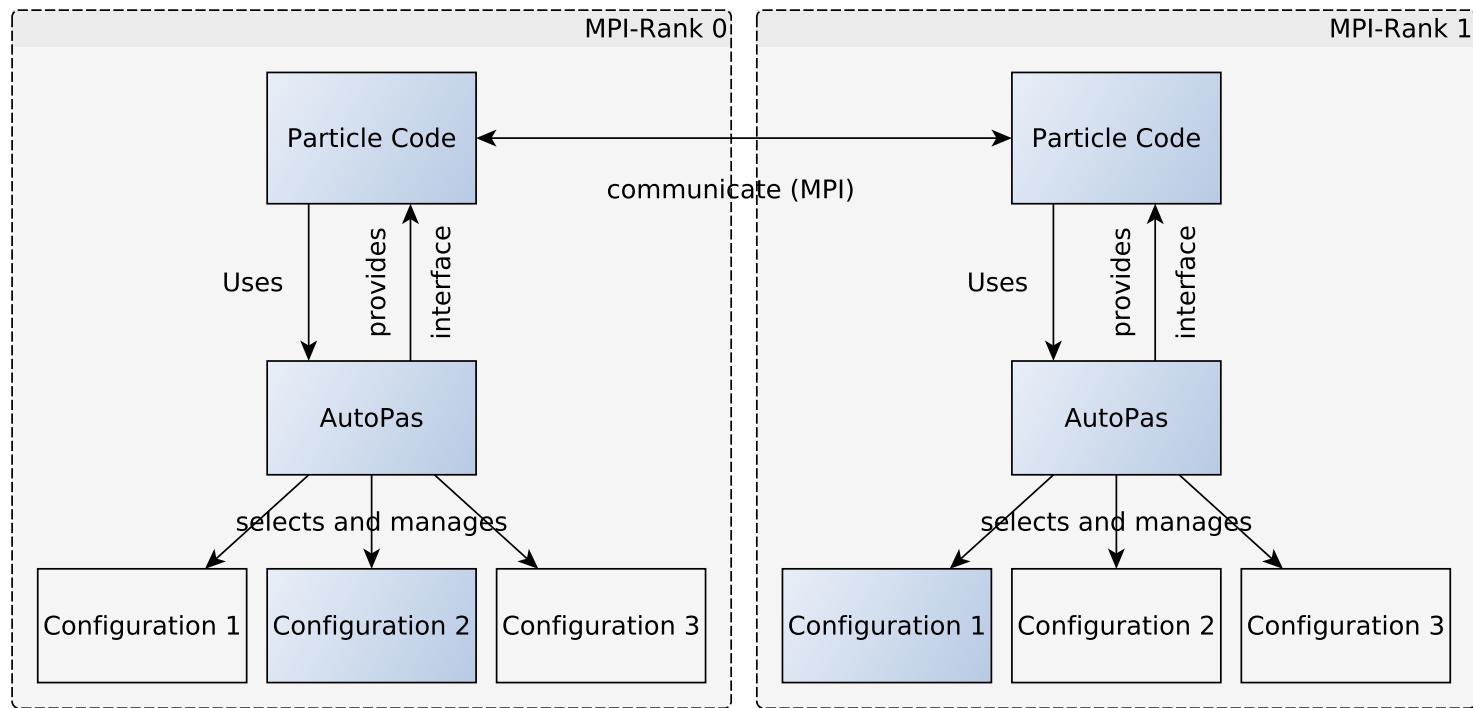
Integrating AutoPas into ls1 mardyn

- ls1 mardyn:
 - Large number of small rigid molecules.
 - Linked Cells Based.
 - MPI + OpenMP hybrid parallelization.
 - Actively used in chemical engineering.
- Example Lennard-Jones functor from AutoPas
- New particle class
 - Inherits from AutoPas and ls1 mardyn particle interface.
 - Acts as coupler
- New particle container class
 - Only wrapper around AutoPas main interface.

ls1
Mardyn

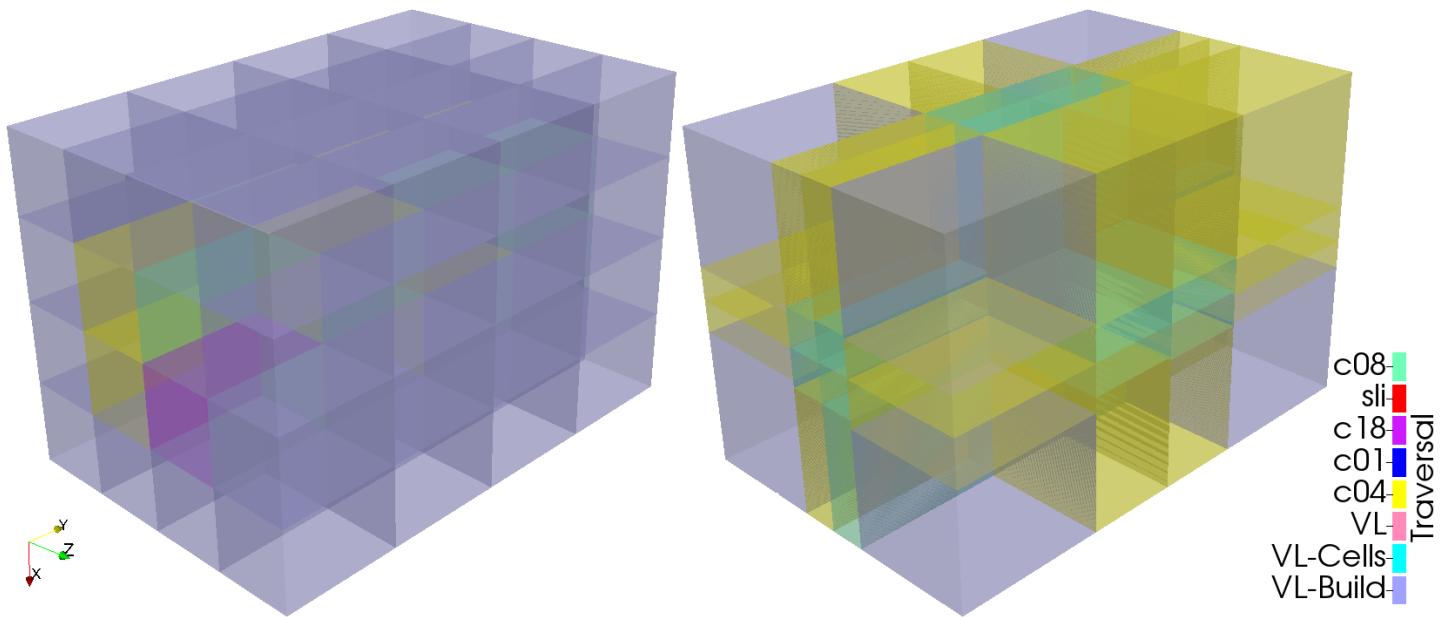


Integrating AutoPas into ls1 mardyn

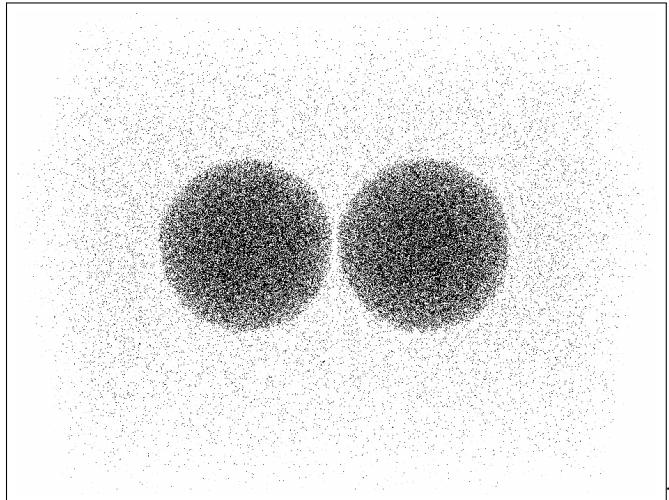


- One AutoPas instance per Rank.
- Independent tuning!
- Interfaces independent of algorithms.
- AutoPas acts as black-box container.

Experiment: Droplet Coalescence



- 64 Ranks; 3M particles
- Auto-Tuning + Diffusive Loadbalancing
- Speed-up about 50% vs vanilla ls1



Conclusions

- AutoPas is a black box N -Body container.
- Dynamic tuning enables optimal performance for changing scenarios.
- Independent tuning over MPI parallel simulation.
- Achievable for users without expert knowledge.

... and future work

- New Auto-Tuning strategies.
- Tuning for more parameters and algorithms.

<https://github.com/AutoPas>