





# Introduction to ESPResSo



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#### All-Atom Models

- Model all atoms and their interactions with semi-quantitative parameters
- Only small systems and short times can be simulated
- Coarse-Grained Models
  - Only model "important" degrees of freedom
- Allows for much larger time and length scales
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# Why yet another Simulation Package?

- Coarse-grained Bead-spring models:
   Combine several atoms into a single bead
- Often combined with other methods
  - Special interactions (DPD, Gay-Berne ellipsoids, ...)
  - Special integrators (MCPD, Hybrid MC/MD, ...)
  - Combined with lattice models (Lattice-Boltzmann, MEMD, ...)
  - Uncommon simulation protocols (Simulated annealing, Parallel tempering, ...)
  - Special constraints (Walls, Pores, ...)
- Standard MD simulation packages (GROMACS, NAMD, AMBER, ...) are not flexible enough to deal with these models

## Package must be flexible!

- In research, new methods are developed
- Building new methods into highly optimized code (GROMACS, NAMD, AMBER, ...) is very hard
- Package must be extensible!







- ES provides the methods for coarse-grained simulations
- However, an understanding of the methods is required to be able to use ESPResSo
- ES can not check whether what you do makes sense!

# **Golden Rules**

- 1. ESPResSo can *not* be used as a black box
- 2. ESPResSo does not do the physics for you



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### **Methods**

- Integrators and ensembles: Velocity-Verlet algorithm (NVE), Langevin thermostat (NVT), Barostat by Dünweg (NPT), Generalized Hybrid Monte-Carlo, Quarternion integrator for non-spherical particles or point-like dipoles, ...
- Nonbonded interactions: Lennard-Jones, Gay-Berne, Buckingham,, …
- Bonded interactions: harmonic, FENE, tabulated, bond-angle interaction, dihedral interaction, ...
- Long-range interactions: for electrostatics: P<sup>3</sup>M, MMM1D, MMM2D, Ewald, ELC and MEMD; for point-like dipoles: dipolar P<sup>3</sup>M, ScaFaCoS (FMM, ...), ...
- Hydrodynamic interactions: DPD, Lattice-Boltzmann fluid (on GPGPU) coupled to particle simulation
- Constraints: Particles can be fixed in any directions; walls, pores, spheres...
- Analysis: energy components, pressure tensor, forces, distribution functions, structure factors, polymer-specific analysis functions (radius of gyration, ...), output to VMD
- ...and it is continuously growing...



- Free, open-source
- Source code hosted at GNU Savannah (not a GNU core project, though)
- GNU General Public License (GPLv3)
  - Code may be freely downloaded, modified and redistributed
  - Provided that the GPL is kept
- Portable
  - Can be easily compiled and run on all POSIX platforms (think: Unix) known to us
  - Windows?
- Distribution packages exist for
  - Gentoo Linux (Christoph Junghans)
  - Fedora Linux (Thomas Spura; in progress)
  - ... anybody interested in packaging for other distributions?



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https://savannah.nongnu.org /projects/espressomd/



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#### **Distribution**

- 163 Citations of the 2006 article (Web of Knowledge)
- Used by ~20 scientific working groups



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#### Code

- From Ohloh (https://www.ohloh.net/p/ESPResSo\_MD)
- 4,946 commits from 59 Contributors
- ~ 123,650 lines of code
- Estimate: ~31 person years, ~1.7M\$ cost

#### Languages



#### Lines of Code



In a Nutshell, ESPResSo Soft Matter Simulation Software...

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- ...has had 4,946 commits made by 59 contributors representing 123,650 lines of code
- ... is mostly written in C with a well-commented source code

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- ...has a well established, mature codebase maintained by a large development team with stable year-over-year commits
- ...took an estimated 31 years of effort (COCOMO model) starting with its first commit in November, 2001 ending with its most recent commit 2 days ago



\*Using the Basic COCOMO Model

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# Web resources

#### Home page http://espressomd.org

- Hosted at ICP
- Central resource for users
- Downloads
- Documentation  $\rightarrow$  next slide
- Community and Support
  - (Link to) Bug tracker
  - (Link to) Mailing lists
  - (Link to) Wiki
- Developer's Zone (in the wiki)
  - Developer's docs
  - (Link to) Savannah project
  - (Link to) Source code repository

 Savannah Project Page https://savannah.nongnu.org/projects/espressomd

- Hosted at GNU Savannah servers
- Download area
  - Releases and NEWS
- Mailing list espresso-users@nongnu.org
  - Only mailings from members are accepted
- Bug tracker
  - Report bugs in releases!
- Mostly intended for Developers
  - Mailing list espresso-devel@nongnu.org
  - News
  - Source code repository
  - Task manager
  - Patch manager

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### **User Documentation**

- User's Guide
  - PDF document
  - In release package
    - Off-line
    - Matches the release
  - On web site (from build server)
    - Up-to-date
    - Contains ToDo-Boxes
  - Outline
    - Introduction
    - First steps: Quick start
    - Rest: Reference manual
- FAQ (on home page)
  - Not very complete
  - Please contribute!
- Mailing list archive
- Bug tracker





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### **Getting Help**

- RTFM!
  - FAQ
  - User's Guide
  - Mailing list archives
- Use Mailing List
  - Include version, OS, features
  - Also send replies to the list
    - If you send huge files, better provide a link
    - In a long, detailed discussion you can just send a summary at the end
  - Please remember: the developers are not paid for replying!
  - Please do not write to developers personally
    - All mailings are archived so others can benefit
    - Mailing list reaches everybody



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#### Requirements

- C-Compiler (GNU CC is best tested)
- Bourne shell, GNU make
- Tcl
  - Including headers / devel package!
- Optional
  - FFTW
    - Including headers
    - Required for P3M
  - MPI
    - e.g. OpenMPI, MPICH
    - Including headers
    - Required for parallel execution
    - Useful to know how to use it
  - CUDA
    - For LB-GPU code
    - More in the future?



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# Compiling

- Necessary evil
  - Few binary packages exist
  - For optimal performance, recompilation is necessary
- Typically 3 steps
  - Configure code configure
    - Use - help to get options
    - Use CPPFLAGS and LDFLAGS when libraries are installed non-standard
    - Logfile config.log contains additional information
  - Compile code make
    - Use j np to compile in parallel
  - Run testsuite make check
    - Use processors="1 2" to specify the numbers of tasks

- Installation is usually not required
- Separate source and build dir
  - The Source dir is where the source code resides
  - The Build dir is where all files created by the compilation are created
  - No file in the Source dir is modified
  - Call configure from the build dir cd \$builddir; \$srcdir/configure

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#### **Activating and Deactivating Features**

- ESPResSo supports various different features
- Not all features are compiled in
- To check, call code\_info
- Create file myconfig.h in build or source dir to change the default set of features
- Use minimal set of features for optimal performance
- The term "features" is probably not well chosen
  - The code has a lot of features that do not have a compiler switch
  - Goal: remove all features

#### Example myconfig.h

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### Architecture

- Simulation core
  - Written in ANSI C
  - MPI parallelized
  - Optimized
- Control layer
  - Simulation core is controlled via the scripting language Tcl
  - High-level Tcl commands to control the simulation and analyze the system
  - A simulation is defined by an "ESPResSo script"
  - Tcl script is not executed in parallel!



Example ESPResSo script



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### Writing an ESPResSo Script

- Example files: lj.tcl and stretched\_polymer.tcl
  - lj.tcl: Lennard-Jones fluid
  - stretched\_polymer.tcl:
     Stretched polymer
- Outline
  - Set up the system
  - Set up the particles
  - Set up the interactions
  - Running the simulation
    - Warmup integration
    - Main integration
  - Analysis
- Sections correspond roughly to chapters in UG
- Detailed command syntax can be found in UG



#### Snapshot of the LJ system



Schema of the stretched polymer

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## **Setting Up the System: Global Variables**

- Set global variables with <u>setmd</u> varname value
- e.g. Box size, Periodicity, Time step, Skin size, Cell size, …
- Many are set to sensible defaults
- Get global variable with <u>setmd</u> varname
- Many commands can be used without argument to get information

```
# define the system size
setmd box_l $box_size $box_size $box_size
# set up the integrator time step
setmd time_step 0.01
# the skin has no effect on the result, only on the speed
setmd skin 0.4
# uncomment the following to output the box size
#puts [setmd box_l]
```



# Setting Up the System: Thermostat

- Command <u>thermostat</u>
- Misnomer: used to set ensemble (e.g. Barostat)
- Turn on Langevin thermostat
   <u>thermostat</u> <u>langevin</u> temperature gamma
- Turn off thermostat <u>thermostat off</u>
- Other "thermostats"
  - npt\_isotropic (NPT)
  - Generalized Hybrid Monte-Carlo (GHMC; NPT and more)
  - DPD (see Friday)

# set up the thermostat
set langevin\_gamma 1.0
thermostat langevin \$temperature \$langevin\_gamma



## Setting Up the System: More

- Nemd: "Non-equilibrium MD": special method for creating a shear flow
- <u>cellsystem</u>: Changing the cell system
  - Turn on Domain decomposition (default)
  - Turn off Verlet lists
  - Turn off Cell lists (<u>nsquare</u>)
  - Use "layered" system (only for MMM2D)
- adress: Turn on ADResS
- <u>cuda</u>: Set up CUDA device
- <u>collision\_detection</u>: Turn on collision detection
   → Recent developments
- <u>reactions</u>: Turn on reactions → Recent developments



### **Setting Up Particles**

- Create a single particle: <u>part</u> pid arguments
  - pid specifies a numeric id
  - Holes in *pid* order cost memory
- Possible arguments: position (required in first call), velocity, charge, mass, type
- Create bonds to other particles (bond)
- Fix particle in one or more directions (<u>fix</u>)
- Apply external force to particle (<u>ext\_force</u>)
- Set individual temperature
- Make it virtual → Recent developments
- Delete a particle (<u>delete</u>)
- Get particle properties part print arguments

```
# generate $n_part particles at random positions
for {set i 0} { $i < $n_part } {incr i} {
    set x [expr $box_size*[t_random]]
    set y [expr $box_size*[t_random]]
    set z [expr $box_size*[t_random]]
    part $i pos $x $y $z type 0
}</pre>
```





#### Tcl commands to create many particles at once

- Polymers polymer
- Counterions
   counterions
- Salt salt
- Diamond polymer networks diamond
- Icosaeder icosaeder
- Copy existing particles

copy\_particles

- Create extended objects <u>constraint</u>
  - Walls, Spheres, Cylinders, Pores, Rods, Rhomboid, Planes
  - External magnetic field

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### **Oriented Particles**

- Feature ROTATION
- Particles have an orientation
- Useful for
  - GB-ellipsoids (coarse-grained liquid crystals)
  - Directional Lennard-Jones
  - Point-like dipoles
     (→ dipolar P3M, Thursday)
- Quarternion integrator
- Roughly 30% slower!
- Currently, all particles have the rotational degrees of freedom
- Switchable rotation is under review



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# **Setting Up Interactions**

- Non-bonded Short-range Interactions
  - Work between particle *types*
  - Lennard-Jones, Morse, Buckingham, Smooth-step (DPD), ...
  - Tabulated
- Bonded interactions
  - Work between two (or more) specific particles (can be set in part)
  - Have a bondid
  - Bond-length 2-body interaction: Harmonic, FENE, ...
  - Bond-angle 3-body interaction: Harmonic, Cosine, ...
  - Dihedral 4-body interaction
  - 2-body interactions can be made rigid
    - Not well-tested

- Long-range Interactions
  - Electrostatics
  - Magnetostatics (point-like dipoles)
  - Hydrodynamic interactions
  - Interview → next days
- No force fields built in!



set lj epsilon 1.0 set lj sigma 1.0 set lj cutoff 2.5 inter 0 0 lennard-jones  $\setminus$ \$lj\_epsilon \$lj\_sigma \ \$lj cutoff puts "Interactions:\n[inter]"

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#### **Exclusions**

- Often, neighboring particles in a chain should not interact via nonbonded interactions
- Two possibilities
  - Bonded subtracted LJ potential lj\_subst
  - Exclusions (Feature EXCLUSIONS)
    - Explicitly exclude interactions between particles
    - Automatically exclude some interactions

part exclude
part auto\_exclusions



### **Running the simulation**

- Main integrator: Velocity Verlet
- Do a number of integration steps <u>integrate</u> steps
- Use integrate 0 to update the forces or positions of virtual sites
- Warmup integration
  - Cap the maximal force <u>inter</u> <u>ljforcecap</u> F\_max
  - Prevents overlapping particles and very high forces
  - Do steps until the large forces disappear
- Main integration
  - Switching between Tcl and C has an overhead
  - Do as many steps in a single integrate command
- Advanced commands for integration
  - Parallel tempering
  - Metadynamics

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#### **Analysis**

#### Analysis can be done on Tcl level!

- Use part print to get particle positions, velocities, etc.
- Allows for anything you can think of
  - ... but maybe slow
    - slow numerics in Tcl
    - not parallel

#### Parallel Analysis in C analyze

- Many different observables
  - Energies, pressures, stress tensor...
  - Minimal distances, RDF, structure factor, …
  - Polymer observables: end-to-end distance, radius of gyration, ...
- Analyzing several configurations
  - Store configuration analyze append
  - Retreive stored configurations
     analyze configs
  - Some analysis commands can handle stored configs (e.g. analyze <rdf>)

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# File I/O and Visualization

- No general ESPResSo-format
  - What should be stored in the file?
    - Particle positions, box size
    - Interactions, Tcl variables?
- No real checkpointing
  - It is not clear what belongs to the state of the simulation
    - e.g. RNG state, number of tasks, ...
- Blockfile format
  - Allows to write specified blocks of information blockfile \$f write particles
  - Can read in these blocks blockfile \$f read auto
- Jump into the main loop needs to be done manually

Visualize best with VMD

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- Off-line
  - Recommended: Create VTF files
  - writevsf to output the structure into the VTF file
  - writevcf to output a configuration into the VTF file
  - Can also create PSF and PDB
- On-line
  - VMD has a protocol for on-line visualization
  - In general, off-line is more useful

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# That's all. Thanks for your attention!

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