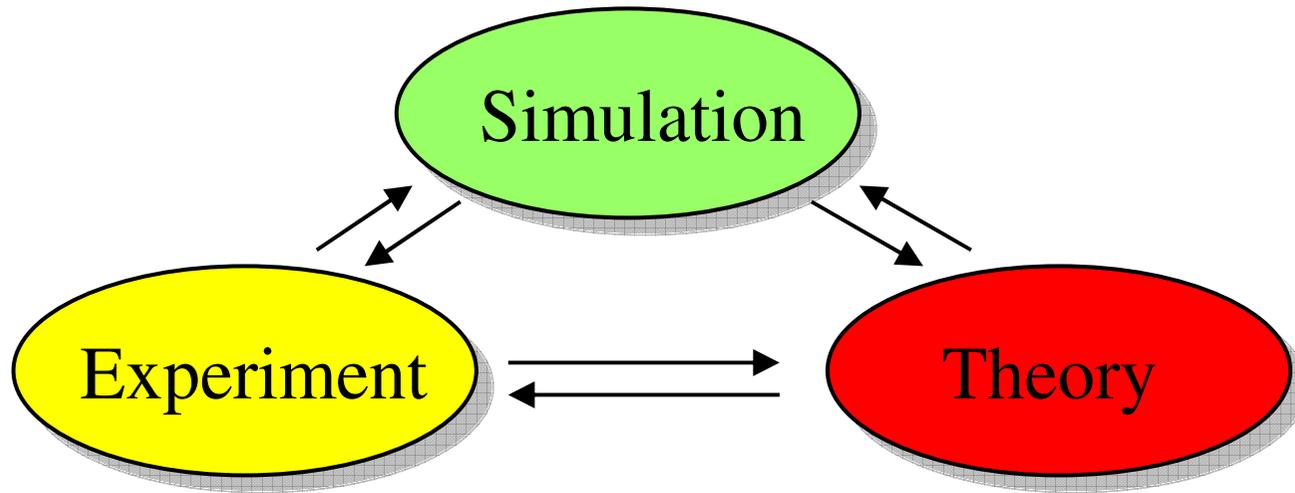


# Computer Simulations in Statistical Physics

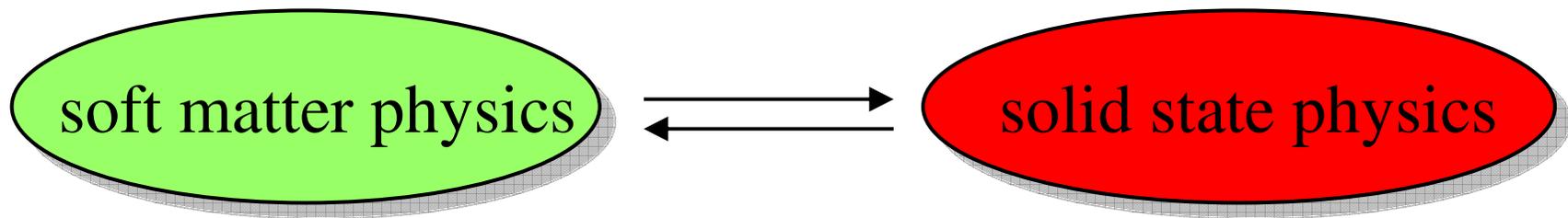


## *What do we learn?*

- Interesting physics (modelling ...)
- How to work with computers (programming, Linux, networks)



# Computer Simulations in Statistical Physics

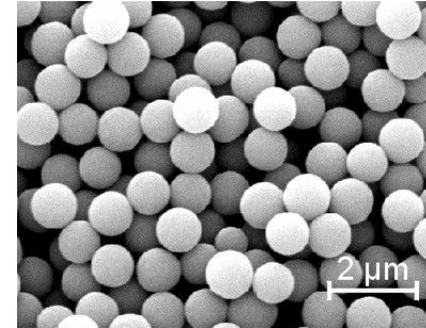


Dr. Peter Virnau

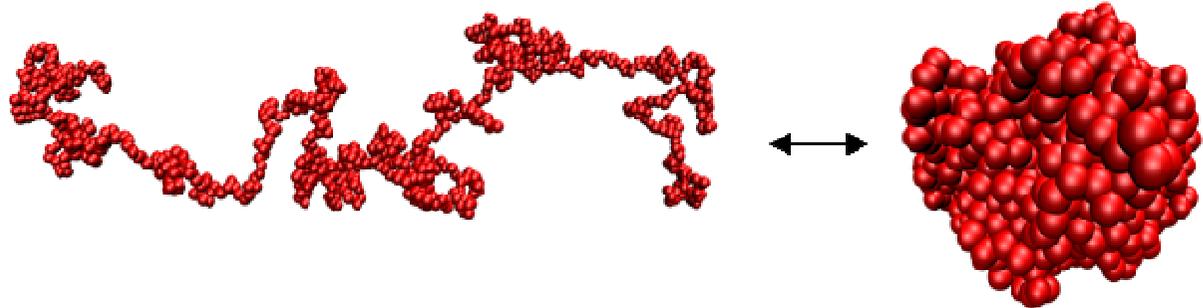
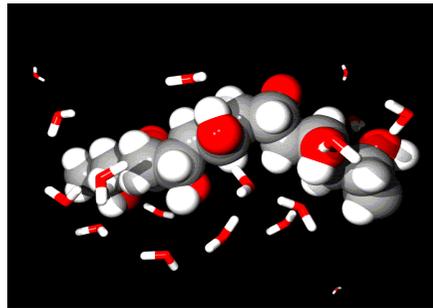
Prof. Nils Blümer

# Typical soft matter systems?

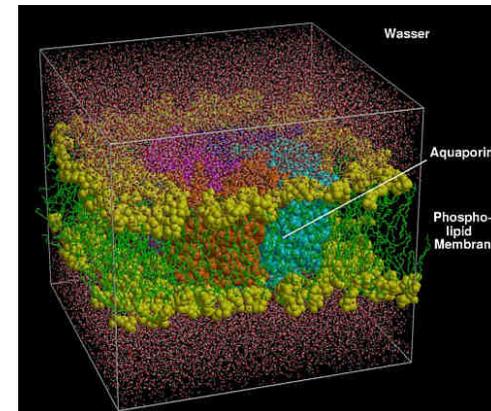
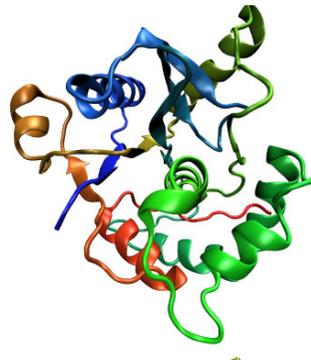
Polymers, Proteins, DNA, Lipids, Colloids, ...



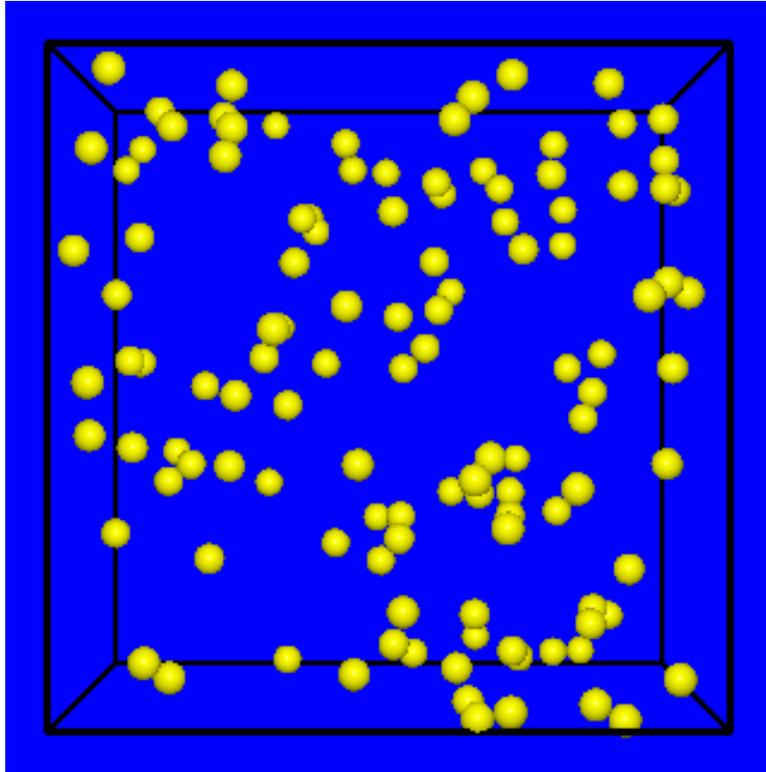
## Oligomers / Polymers



## Biopolymers: Proteins, DNA, Membranes



# Classical molecular simulation - How does it work?



Starting point:

e.g. cubic simulation box filled with particles

Goal: Determine equilibrium properties (e.g. typical distance between particles) or dynamical properties of the system

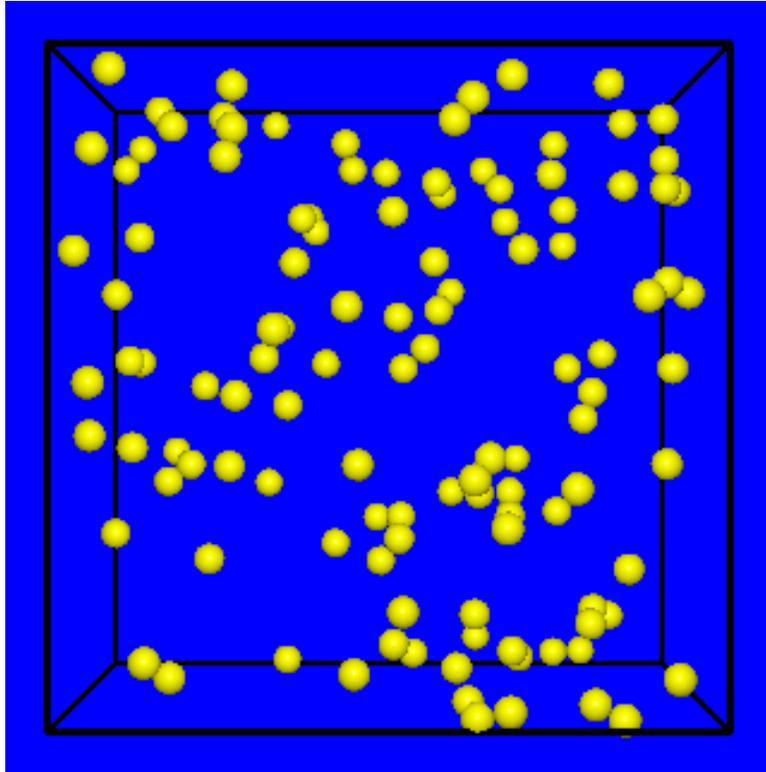
How?: Generate many statistically independent configurations and "measure" quantities

**Molecular Dynamics / Monte-Carlo**

**Determine equilibrium properties** by averaging over all configurations

**Analyze evolution of systems with time (dynamics)**

## Statistical ensembles:



### Example:

#### **Canonical (N, V, T) ensemble**

i.e., particle number, volume and temperature are fixed

→ pressure fluctuates

#### **(N, P, T)-ensemble**

i.e. particle number, pressure and temperature are fixed

→ volume of the simulation box fluctuates

#### **Grandcanonical ( $\mu, V, T$ ) ensemble**

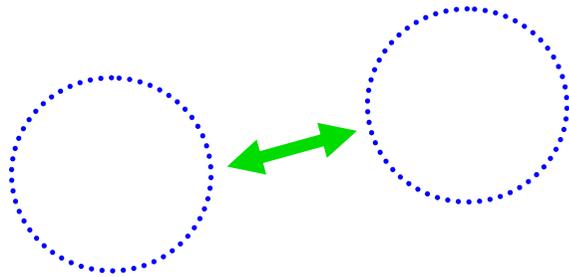
i.e., chemical potential, volume, and temperature are fixed

→ Particle number in the box fluctuates (insert/delete particles)

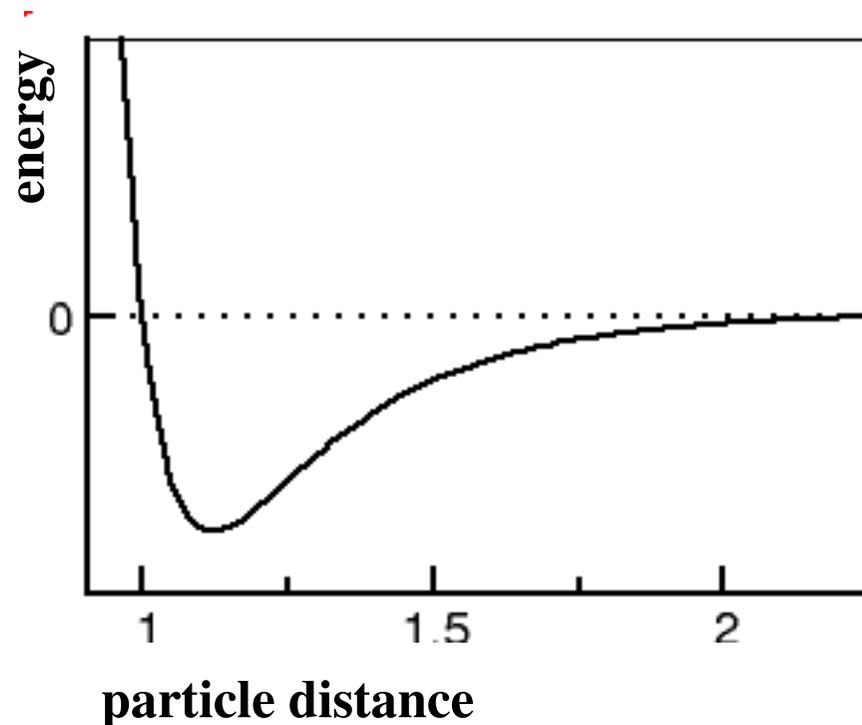
# How do we describe molecules in (classical) simulations?

“via force-fields” (expression for the energetic interactions between two particles)

Example: The Lennard-Jones potential (noble gases)

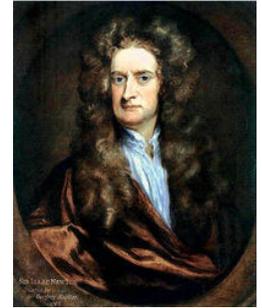


$$U_{LJ} = \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 + \frac{127}{16384} \right]$$



# Simulation techniques: Molecular Dynamics

Idea: "Solve Newton's equation of motion"



$$\vec{F} = m\vec{a} = -\nabla U$$

"Recipe":

Starting configuration, "force field" (potential)

In each time step:

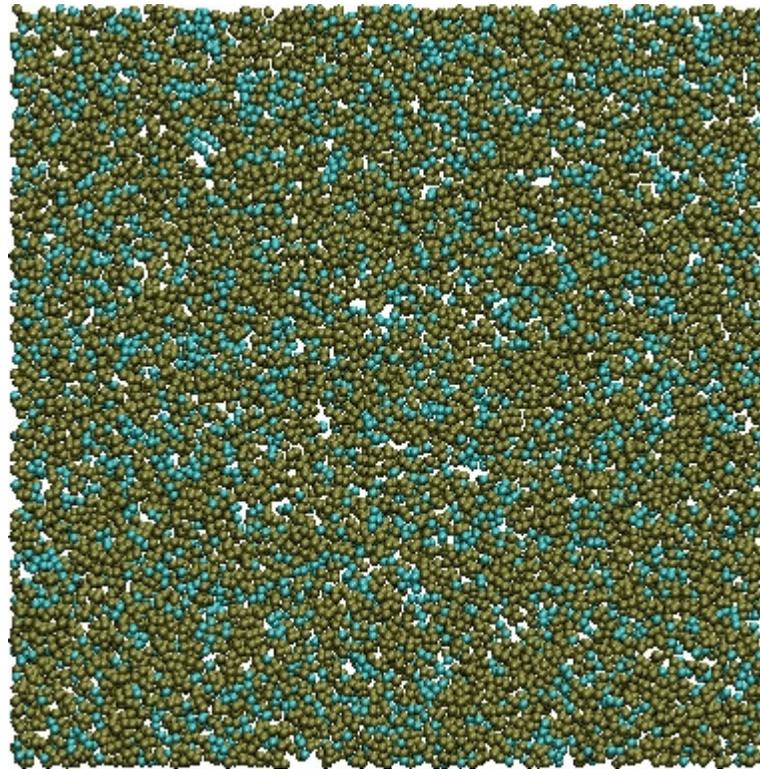
|: Determine forces between all particles

→ move particles :|

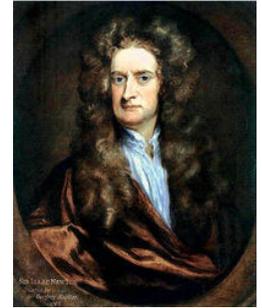
# Simulation techniques: Molecular Dynamics

Idea: "Solve Newton's equation of motion"

Example: Demixing of polymer solution



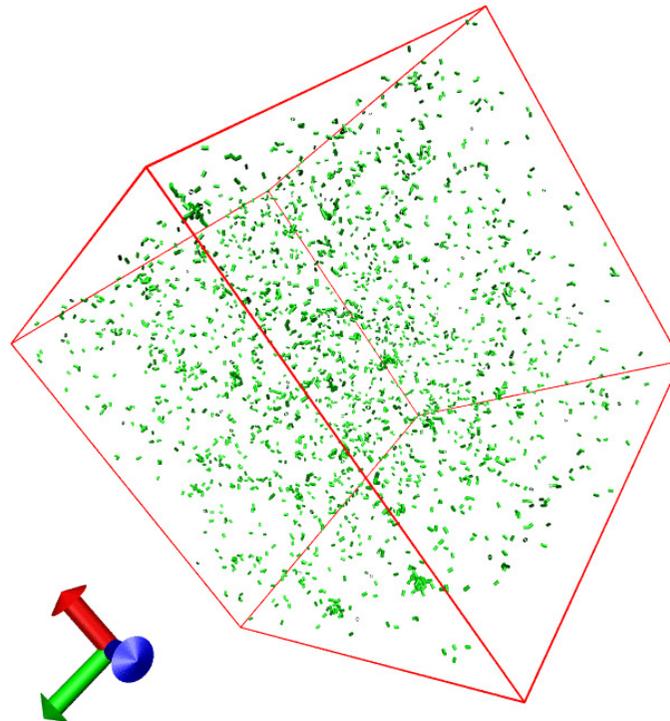
Dr. Leonid Yelash



# Simulation techniques: Molecular Dynamics

Idea: "Solve Newton's equation of motion"

Example: Nucleation on NVIDIA GPU (with HOOMD)



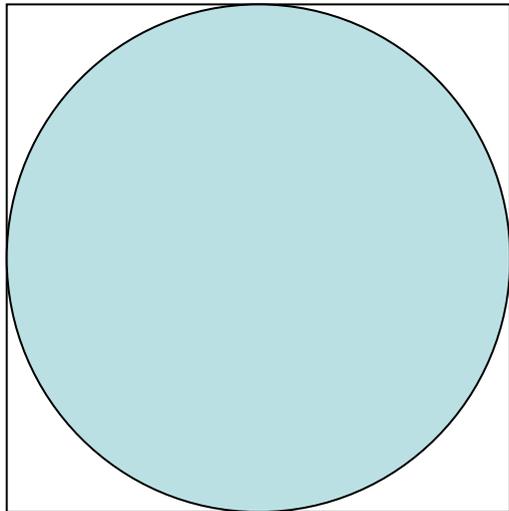
Daniel Reith

## Simulation technique: Monte Carlo

Idea: "Solve problems by drawing random numbers"



Example: Determine Pi:



$$\pi = \frac{4A_{circle}}{A_{square}}$$

Implementierung:

<http://www.eveandersson.com/pi/monte-carlo-circle>

# Simulation technique: Monte Carlo

Idea: "Solve problems by drawing random numbers"



## Recipe: Metropolis algorithm

Starting configuration, "force field" (potential)

|: Modify existing configuration (e.g. move a particle)

Determine the energy difference between two particles

Energy lower? → accept new configuration

Energy higher? → accept with probability  
 $\exp(-1/kT \Delta E)$

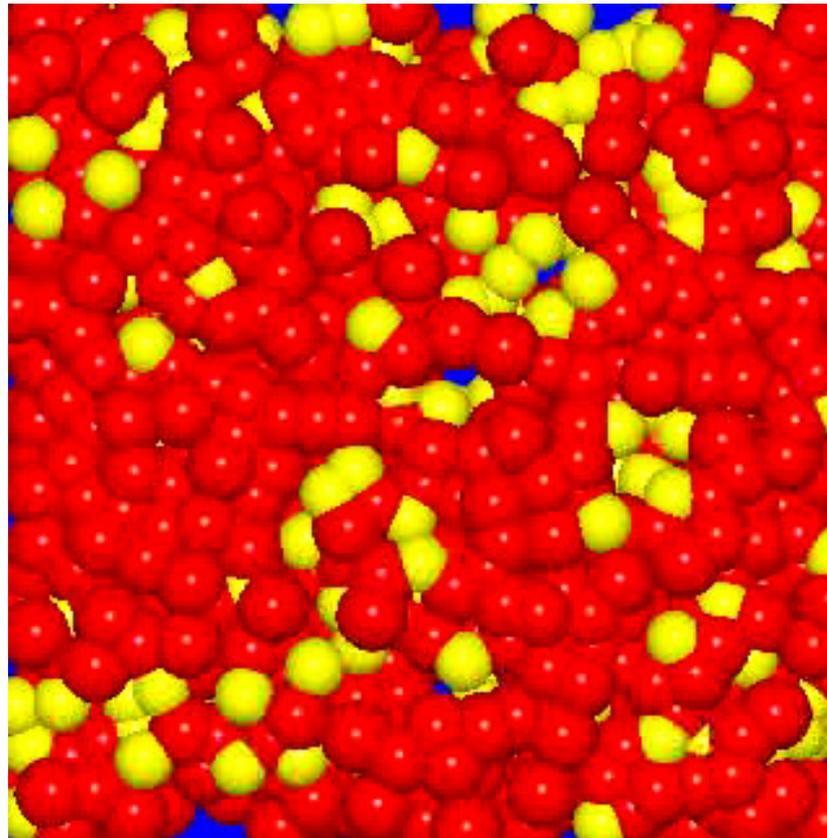
:|

# Simulation technique: Monte Carlo

Idea: "Solve problems by drawing random numbers"



Example: Nucleation



# Time and length scales in simulation

