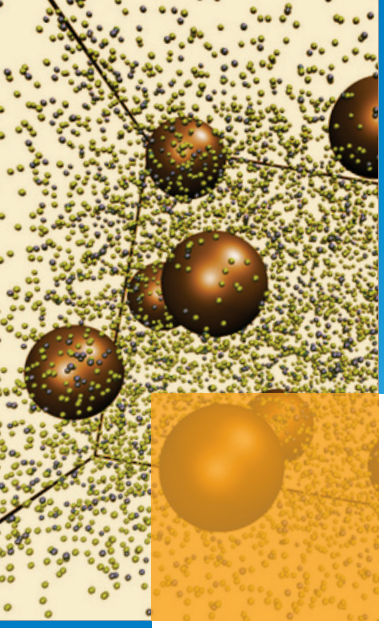

SFB 716

University of Stuttgart
Germany

Colloquium of the SFB 716

November 17, 2016 | 4 pm

University of Stuttgart
Campus Vaihingen
Allmandring 3
Room 1.079

The Collaborative Research Center (SFB) 716 invites colleagues and interested person to the upcoming colloquium. In this lecture series renowned researchers and members of our subprojects talk about their research findings regarding dynamic simulation of systems with large particle numbers.

www.sfb716.uni-stuttgart.de

TALK

Prof. Dr. Dario Anselmetti

Bielefeld University, Exp. Biophysics & Appl. Nanoscience, Bielefeld Institute for NanoScience (BINAS)

Single Molecule Biophysics: From Catch Bonds, Microfluidics and Nanopores

Over the last two decades our ability to measure and manipulate single biomolecules has dramatically increased. A bunch of single molecule methods like atomic force microscopy (AFM), optical tweezers (OT) and magnetic tweezers (MT) have been developed that allowed investigation and quantification of structural and functional aspects of molecular individuals under near physiological conditions.

In my lecture, I will summarize some of our results in the field of single-molecule biophysics and comment on effects like molecular catch bonds, absolute negative mobility, dielectrophoretic trapping in microfluidic environments and nanopore translocation.

TALK

Florian Weik

Institute for Computational Physics (ICP), Subproject C.5

Particle Coupling for Continuum Electrokinetics

All-atom MD simulations of macromolecules in electrolyte solutions are prohibitively expensive, due to the large number of solvent particles and the large length and time scales introduced by the macromolecules. We will introduce a model, in which only the macromolecule is represented by particles and the solvent is modeled on a continuum level. This approach allows us to simulate relevant processes such as DNA translocation on experimentally relevant length and time scales.

Obtaining the proper statistics for the internal degrees of freedom for the macromolecules in such a simulation proves challenging. We will detail our progress on a thermodynamically consistent coupling for this scheme.