

A Molecular Model for Platelets at Multiple Scales and Simulations on Supercomputers

ACM Student Research Competition (SRC) Poster



Li Zhang¹, Yuefan Deng^{1,2} (Advisor)

¹Department of Applied Mathematics & Statistics, Stony Brook University, Stony Brook, NY 11794, USA

²National Supercomputer Center in Jinan, Shandong Computer Science Center, Jinan, Shandong 250101, PRC



Introduction

A molecular model at multiscale for human platelets is designed and implemented on large-scale supercomputers. The essence of this research involves development of a platelet model and studies of the model numerically. The molecular model for human blood platelets characterizes the principal physiological functions of several key components of a single platelet. As such, the model will require simulations at spatial scales as small as a typical molecule and as big as a complete cell, spanning several orders of magnitude in space and time. To simulate the dynamics accurately and efficiently, multiscale must also be considered. All in all, a more realistic model will require massive computations. This research will be enabled by the rising power of supercomputing in solving the most crushingly difficult problems in many fields including biomedical engineering. Numerical experiments with our model require considerations of large number of particles and the physiological phenomena at multiscale and thus demand development of the-state-of-the-art parallel algorithms, the main thrust of this work.

Supercomputing Methodologies

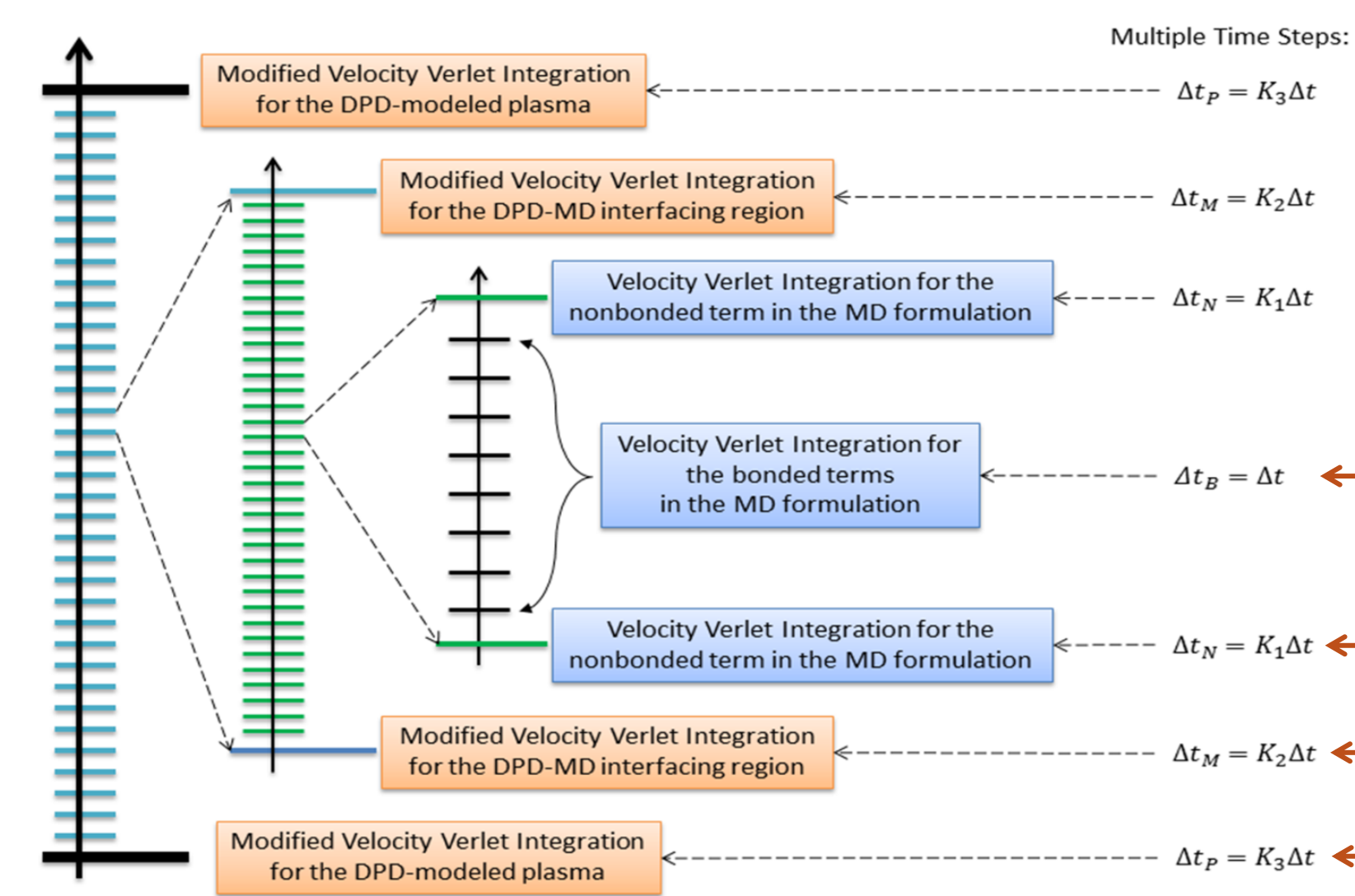
Packages

LAMMPS, NAMD, VMD, HEMD*

*HEMD: in house algorithms package, which is built in and developed by our own group for multiscale simulations.

Algorithms

Temporal I Interfacing Algorithm – Multiscale Multiple Time Stepping



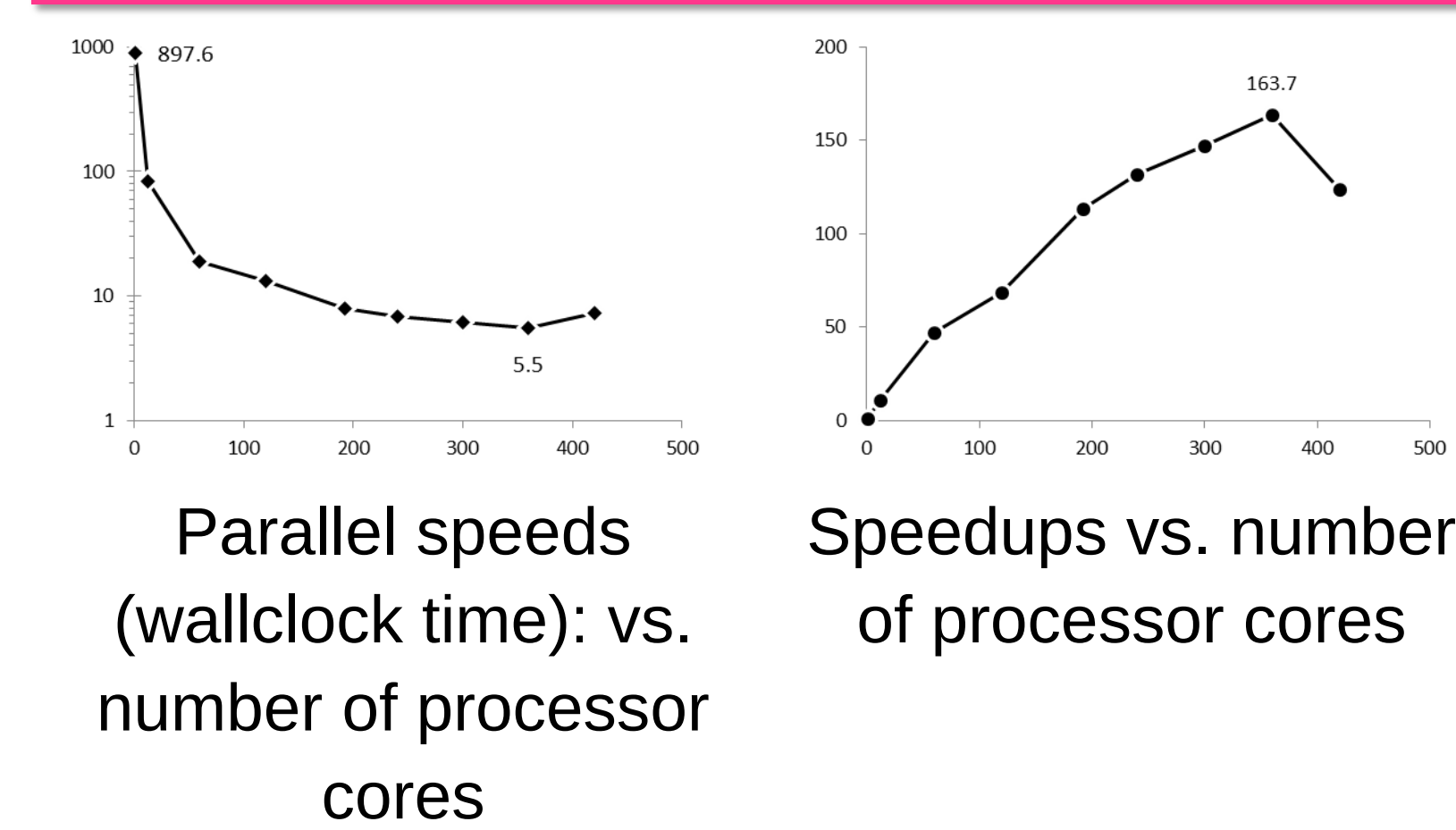
Platforms

Seawulf Cluster, Galaxy (Stony Brook University)

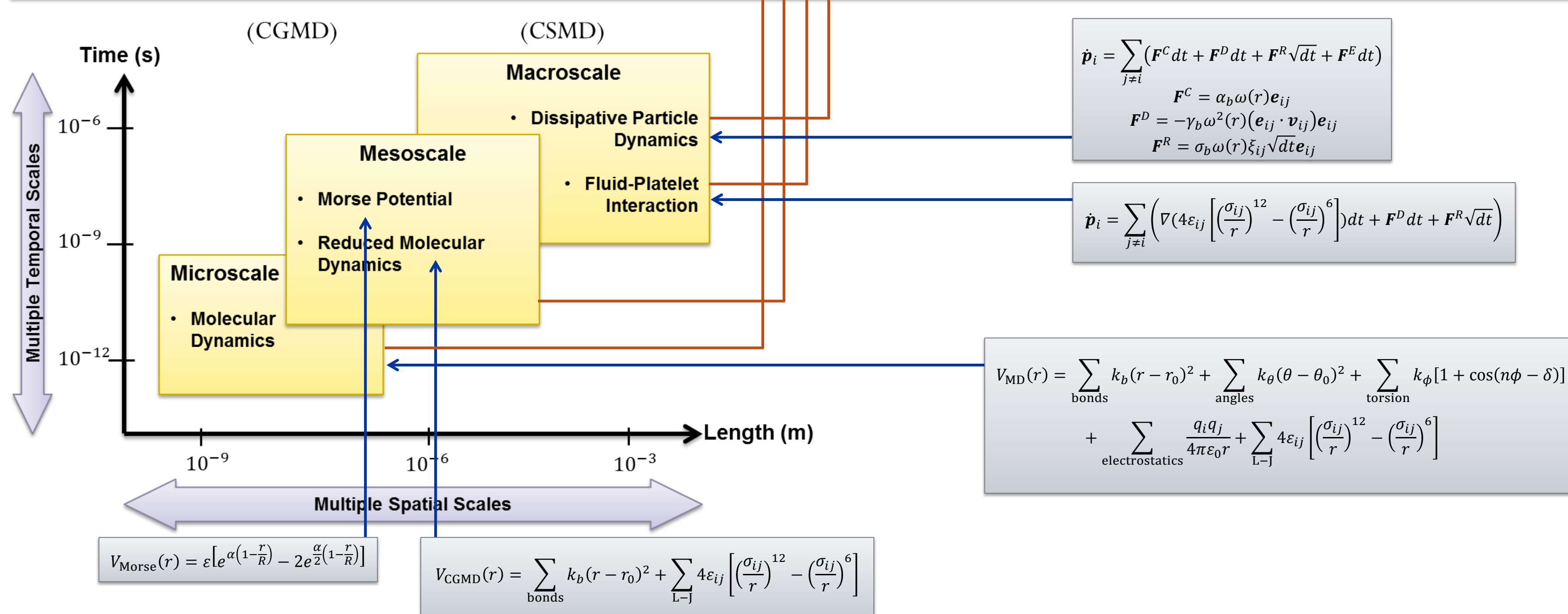
Sunway Blue Light System (National Supercomputing Center in Jinan, China)

Stampede (Texas Advanced Computing Center)

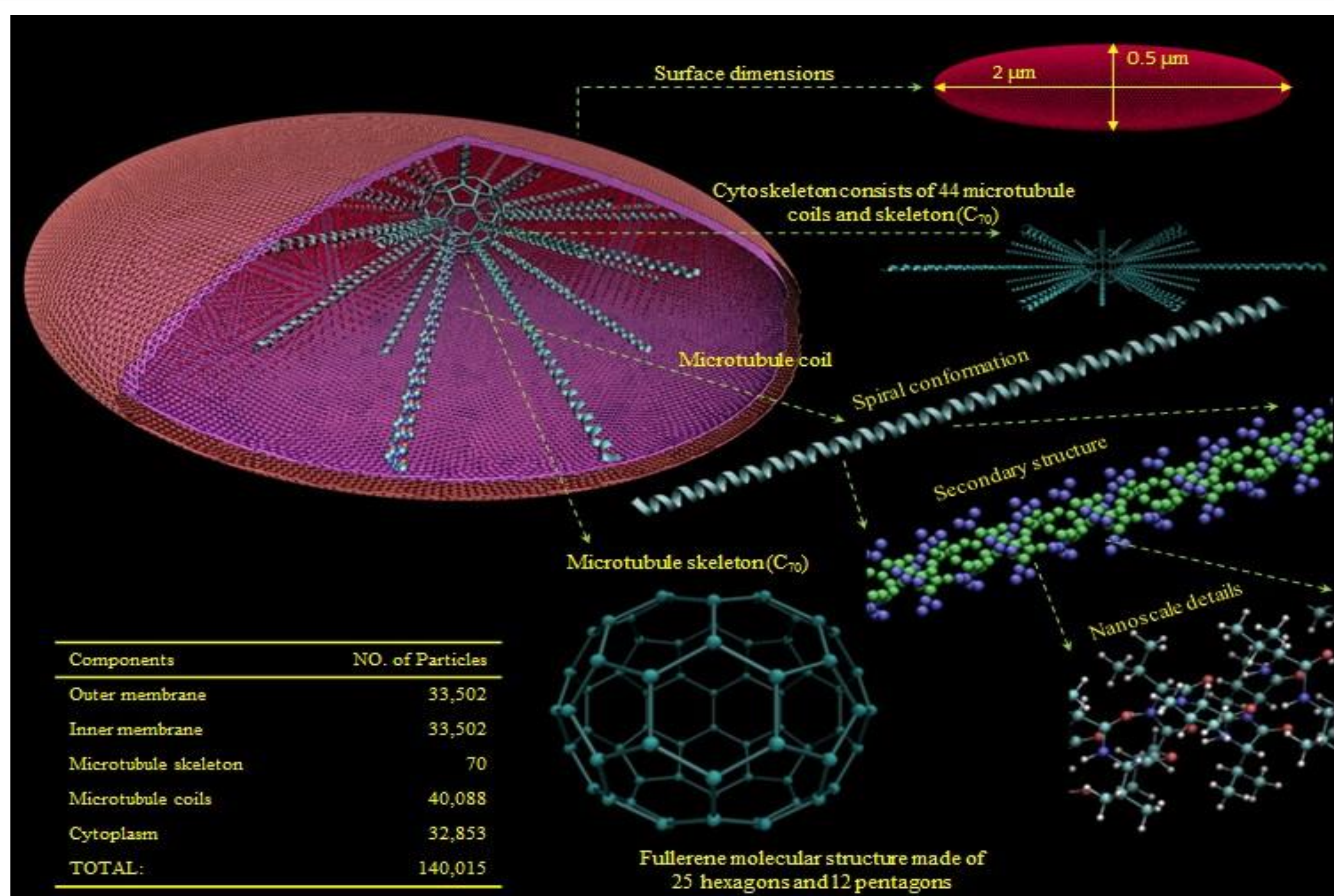
Performances



Multiscale Modeling



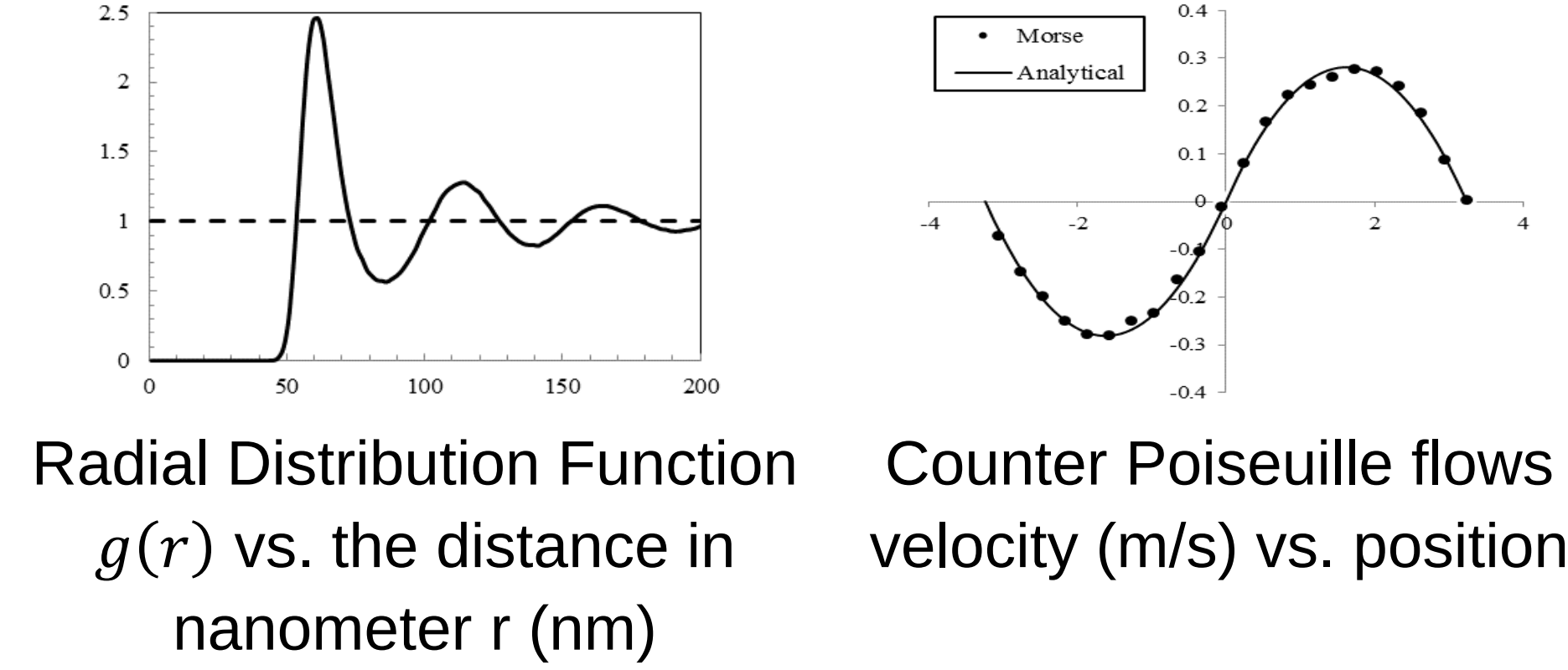
Structures and Constituents



Simulation Results

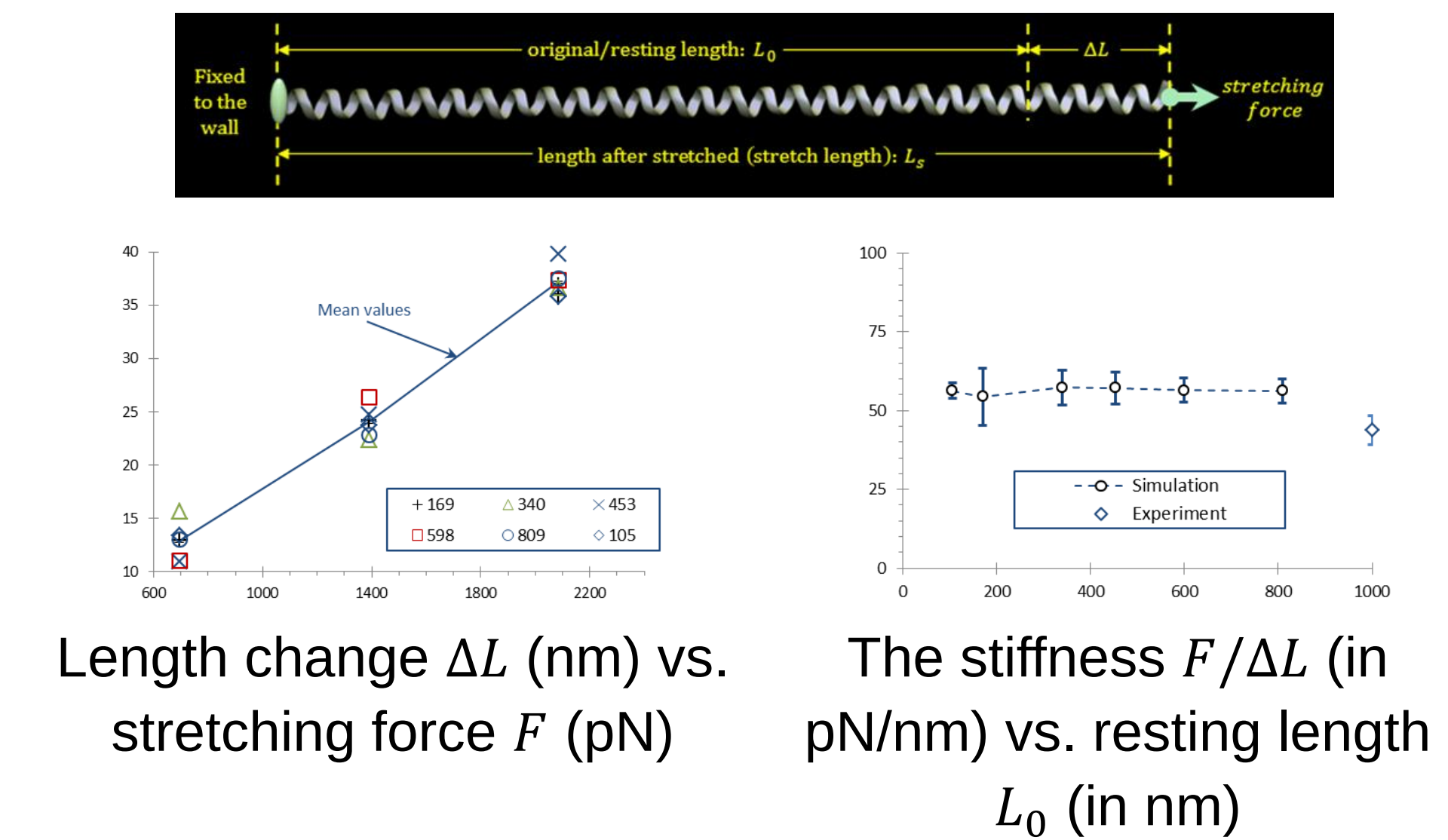
Cytoplasm

Biorheology of cytoplasm



Filaments

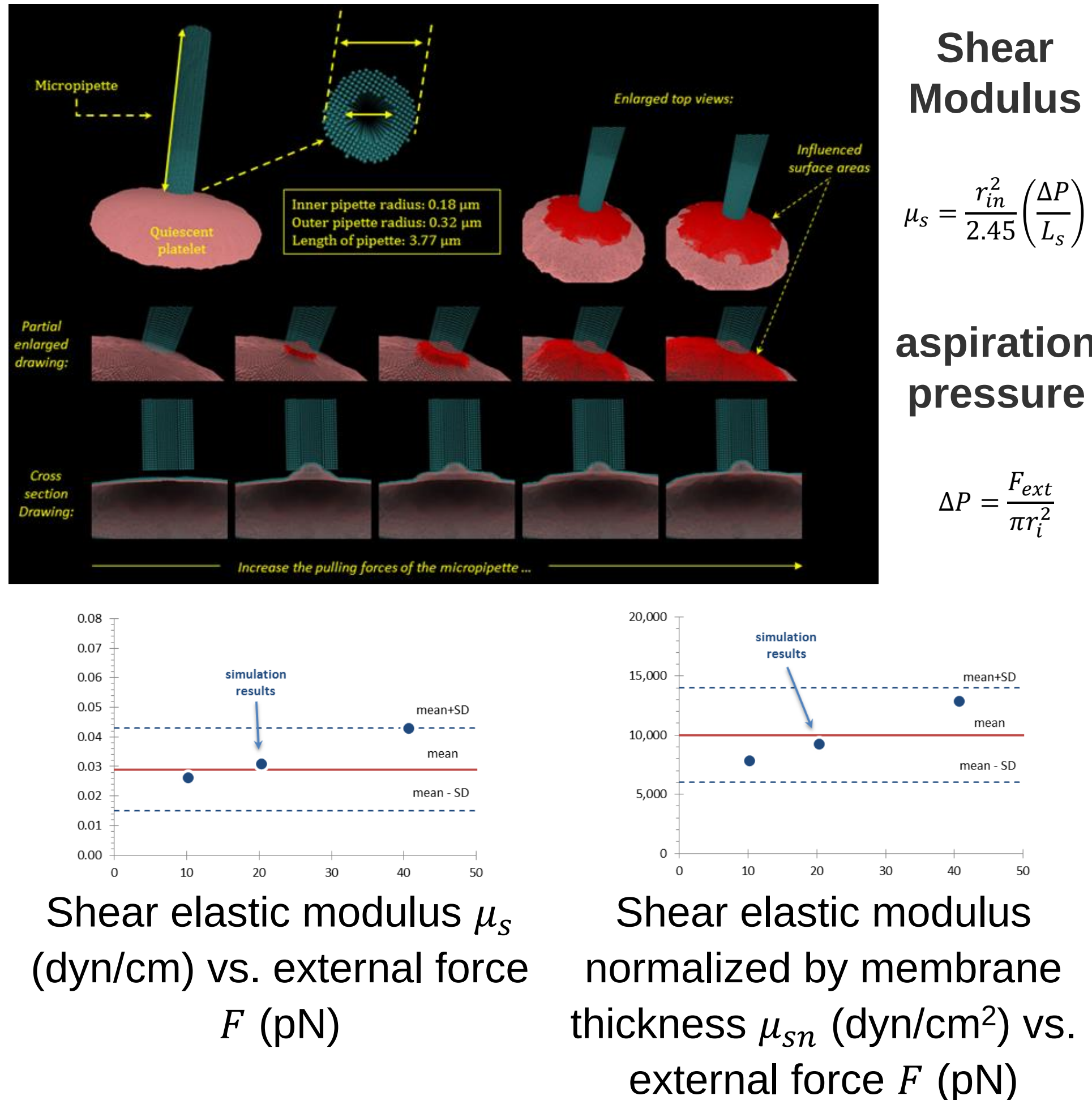
Stiffness of filaments



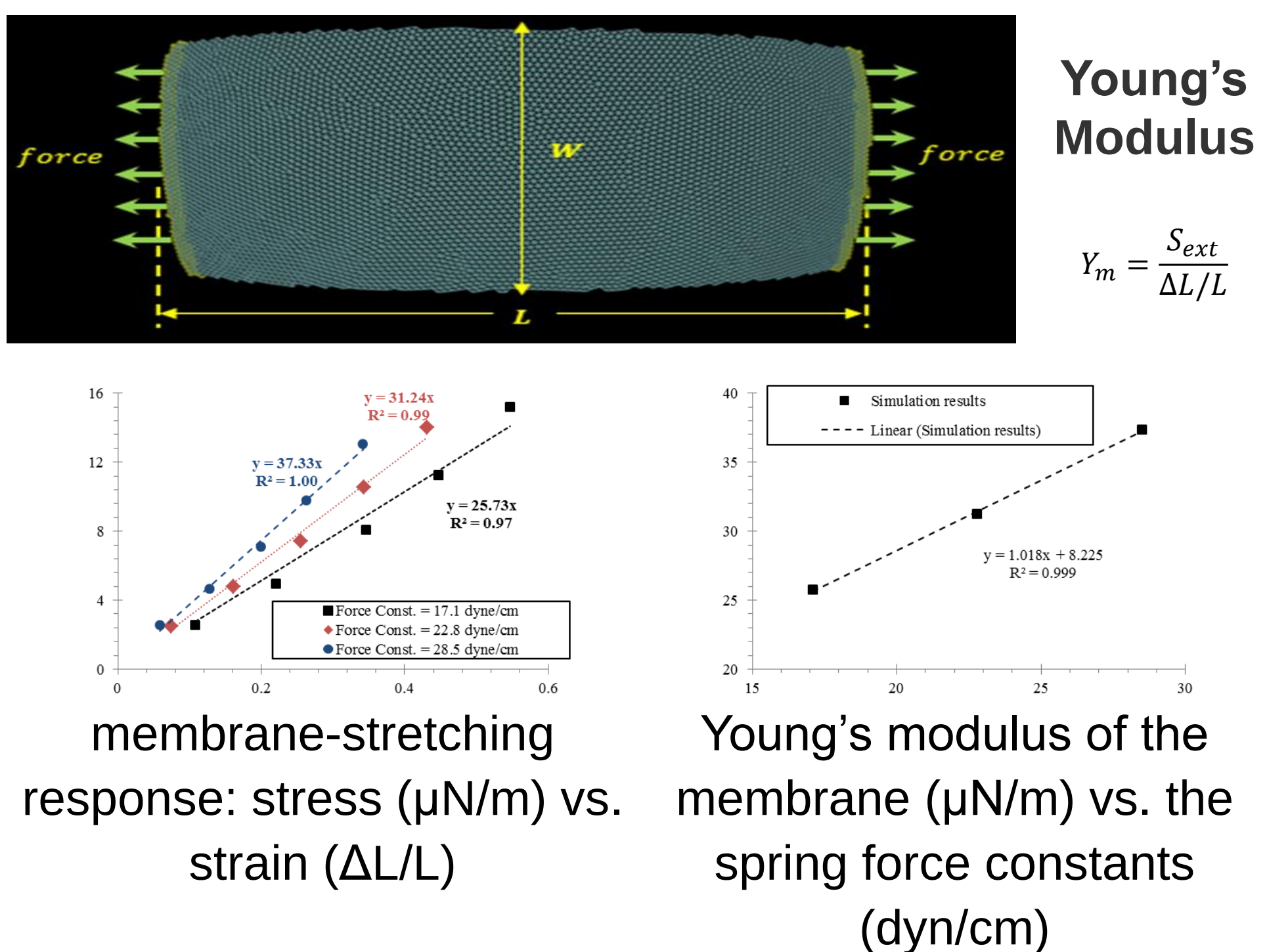
Membrane

Elasticity of membrane

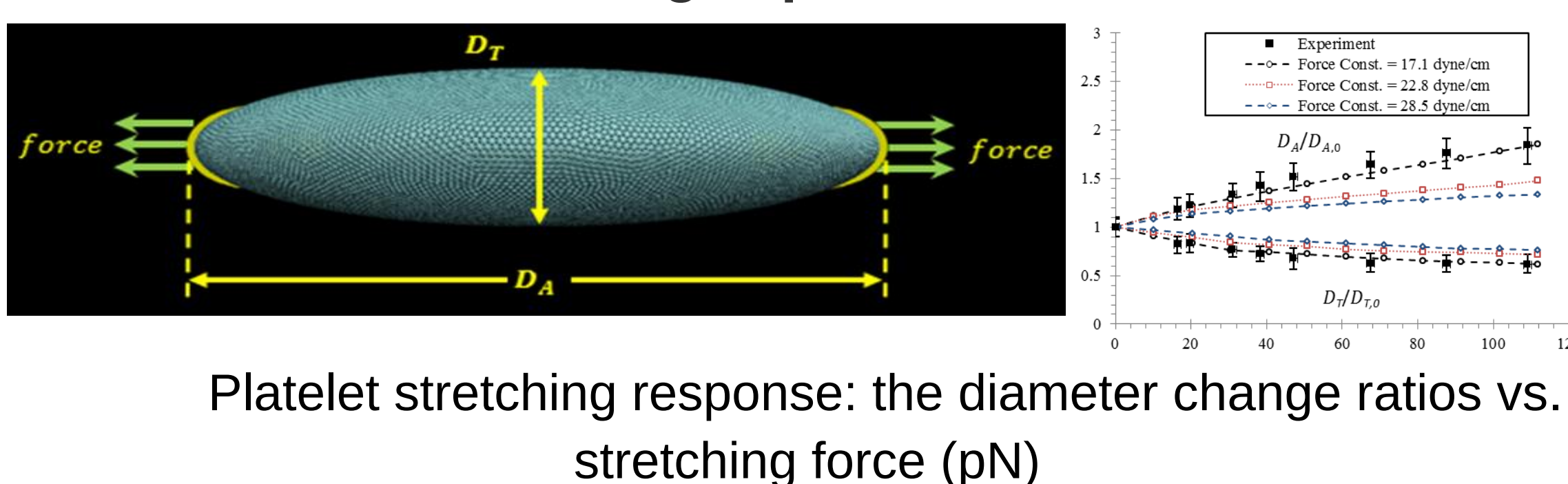
• micropipette aspiration experiment



• 2D area-stretching experiment

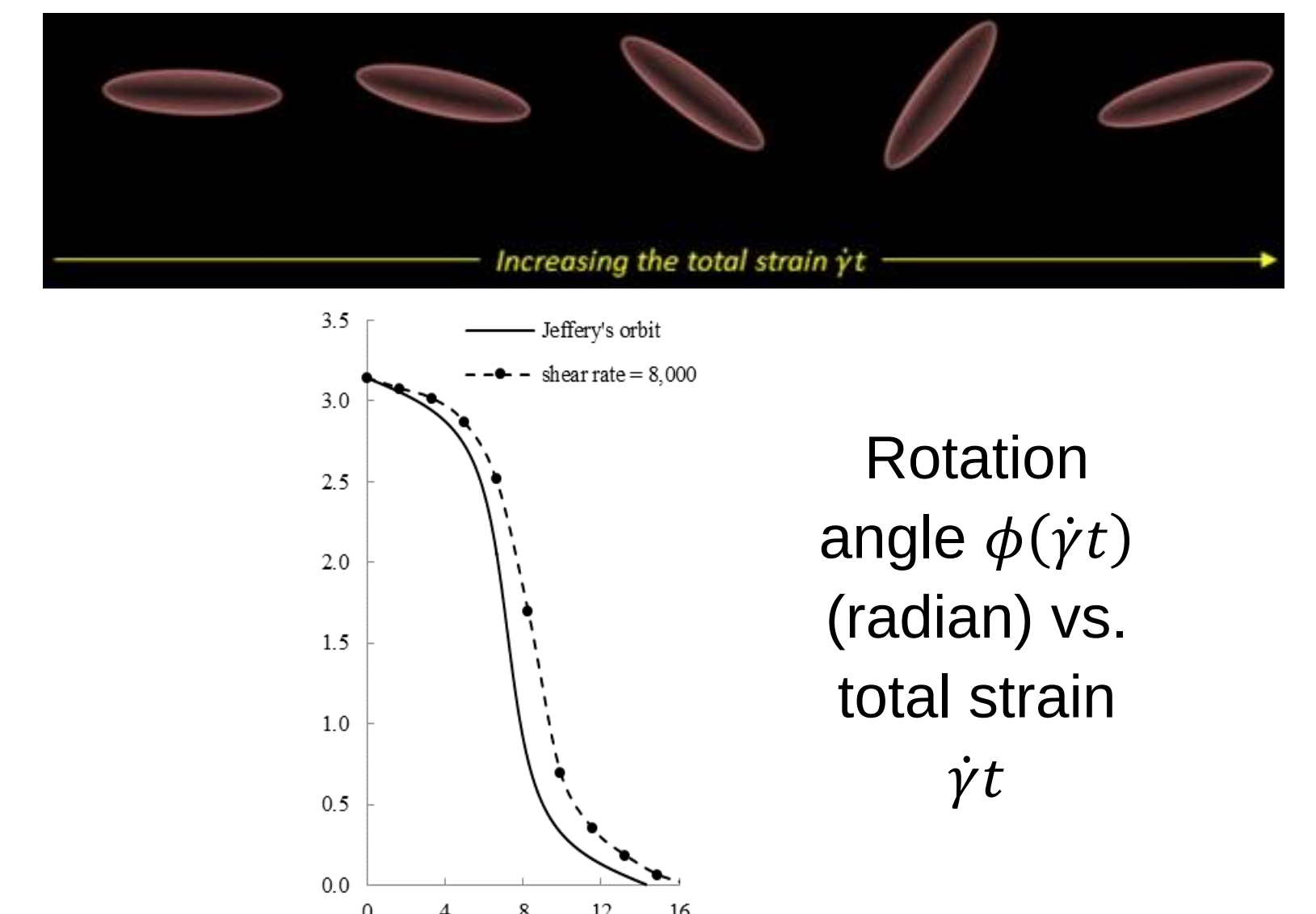


• 3D volume-stretching experiment

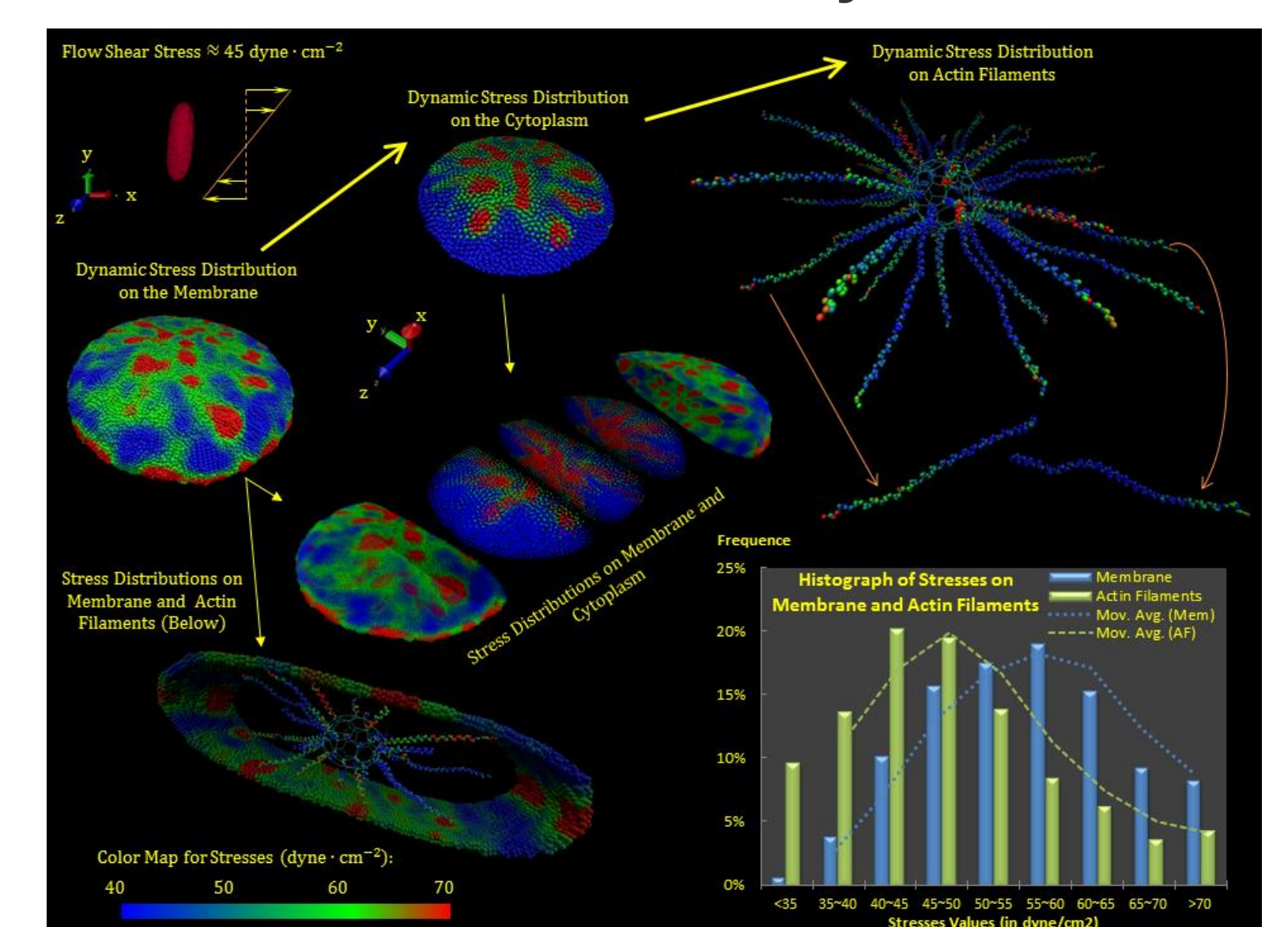


Biophysics

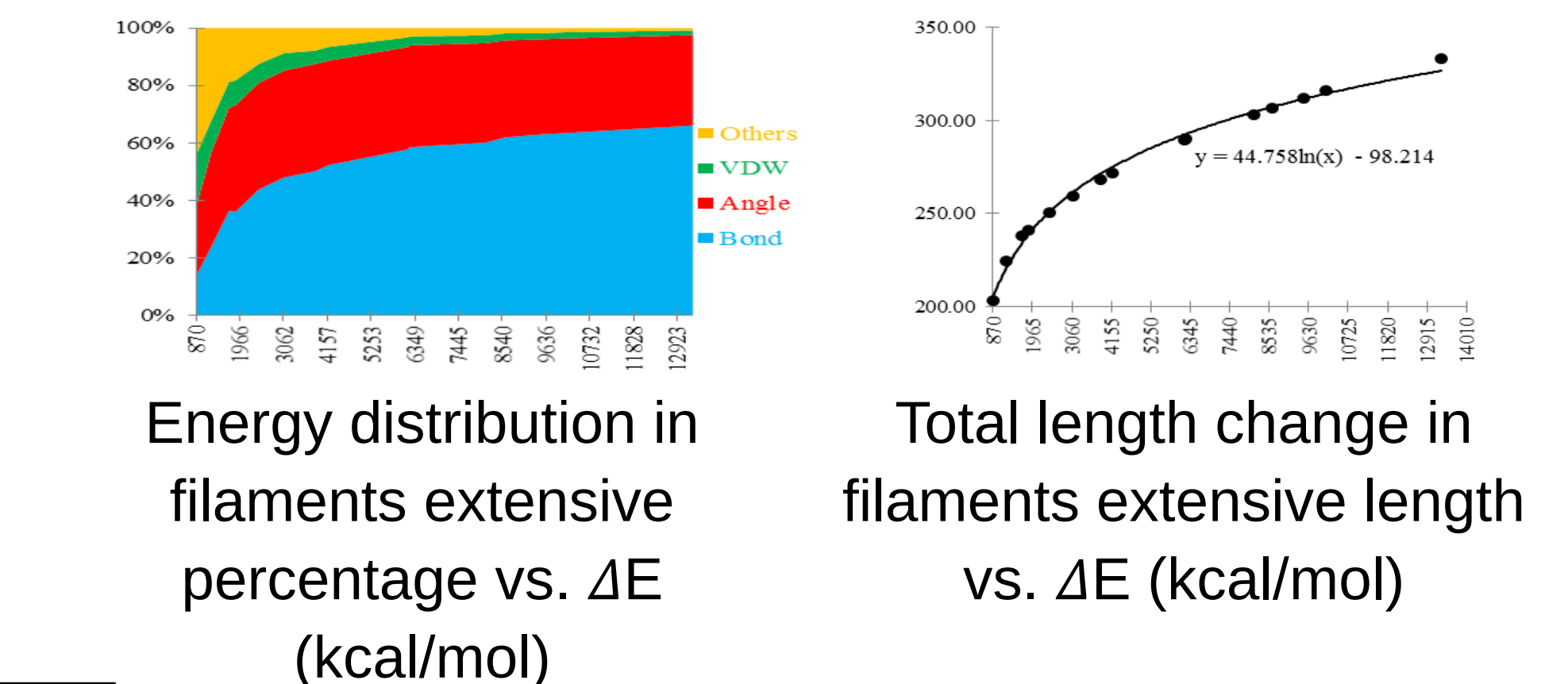
• Flipping dynamics under shear flows



• Mechanotransduction analysis



• Activation potentials



CONTACTS:

Li Zhang

– li.zhang.2@stonybrook.edu

Yuefan Deng (Advisor)

– yuefan.deng@stonybrook.edu

