1.021, 3.021, 10.333, 22.00 Introduction to Modeling and Simulation Spring 2018

Problem set #3 (posted March. 6, 2018)

Instructor: Markus Buehler (mbuehler@MIT.EDU)
TA: Francisco Martin-Martinez (fmartinm@mit.edu)
Due: March 19, 2018

Note: You are encouraged to work as a team and submit only one problem set per team. Please indicate all members that participated in the Pset. Force field parameter files have been posted on Stellar. Each simulation is ~1 hour. Please make sure to run the simulations early.

Important: Specify all resources you use for your solution (lecture note, book, and web).

The following set of exercises is designed to train you in setting up simulations of materials deformation and failure. In this assignment, problems will be carried out via the nanoHUB tool. For each exercise, show us how you came to your answer and result. We highly encourage you to make drawings where appropriate. **Note to carefully select the parameters before submitting your job to nanoHUB; the default parameters may not have been adapted to the case you are studying.**

---

1. Supersonic fracture of brittle crystal

The maximum speed of cracks in brittle materials is related to the wave speeds in a material. Some years ago, it was discovered that due to nonlinear elastic effects (hyperelasticity), cracks can exceed the limit given by the wave speeds and propagate at supersonic speeds. In contrast, for other conditions, the limiting speed of cracks is reduced and the maximum crack speed is limited to speeds below the wave speeds, leading to subsonic crack speeds. The goal of this exercise is to explore this behavior in a small model crystal under mode I loading. In the next few steps we will introduce you to this problem by first considering a reference system that resembles a linear elastic fracture model, followed by an analysis of tow nonlinear, hyperelastic systems that lead to either supersonic or subsonic fracture. This exercise illustrates the approach of model potential building and explains how develop interatomic potentials to represent nonlinear behavior for application in brittle fracture.

To solve this problem, use the **crackprop** module in nanoHUB. This module implements a simulation geometry as shown in Figure 1.1, featuring a 2D triangular lattice with pair interaction potentials between atoms. Atomic bonds can only break along a prescribed weak interfacial layer, at a breaking distance r_{break}. Bonds in the rest of the system can never break. This module enables you to tune the shape of the interatomic potential (and thus interatomic forces) by using a biharmonic potential (See lecture notes, as well as Figure 1.2).

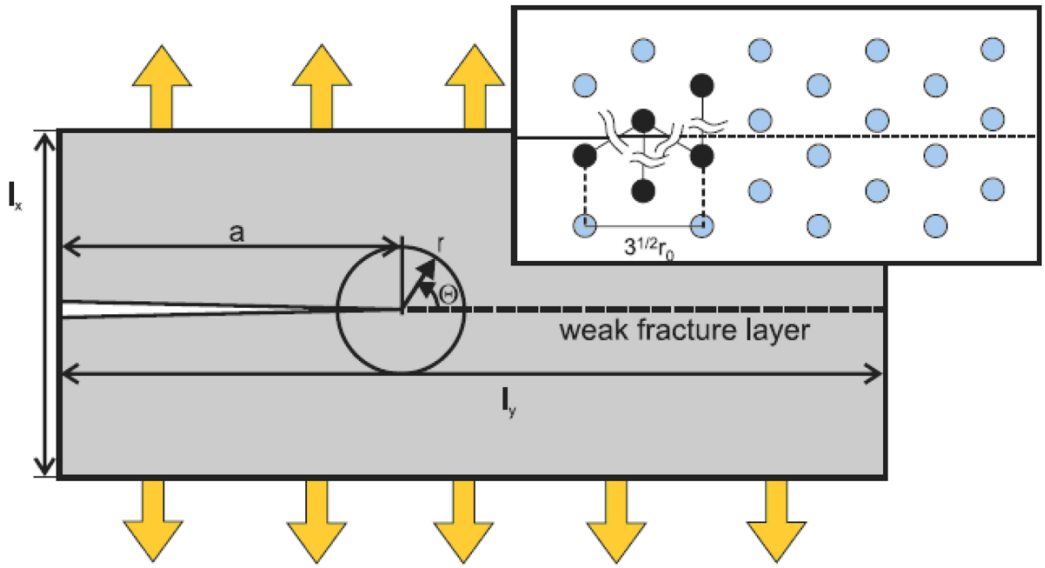

Figure 1.1: Geometry of MD simulations. The **crackprop** module implements this geometry, using a triangular 2D atomic lattice with pair potential interactions. Bonds can only break along a weak fracture layer. The atomic equilibrium distance is $r_0 = 1.12246$, and the density is $\rho = 0.9165$.

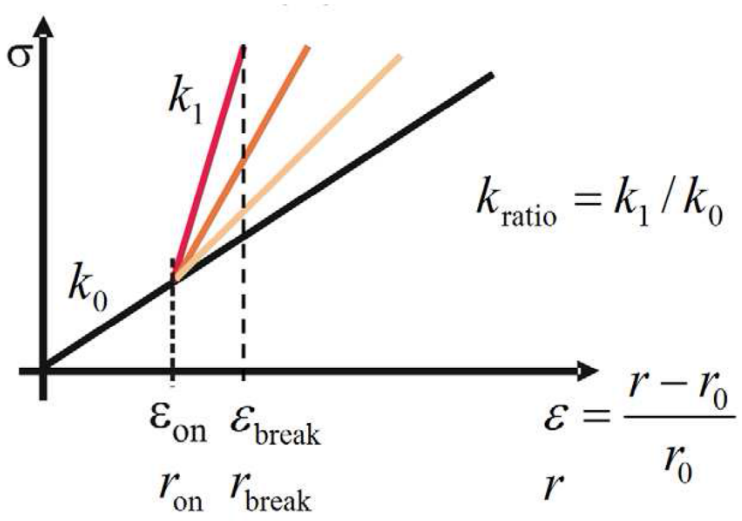

Figure 1.2: Biharmonic potential, leading to bilinear stress-strain/force-distance relationship. Bonds across the weak layer break at a critical distance, and bonds in the rest of the crystal never break. If $k_{ratio} < 1$, hyperelastic softening will be obtained; if $k_{ratio} > 1$, hyperelastic stiffening occurs (show in the graph above).

(a) For $k_0 = 28.57$, calculate all three wave velocities and Young's modulus.

(b) For a fracture distance $r_{break} = 1.15$, determine the fracture surface energy.

(c) Using the **crackprop** module, set up a system that features harmonic interactions (parameter for k_0 and r_{break}, see above). Carry out a fracture simulation at strain at a strain rate 0.0005 in mode I, simulation for 30,0000 MD steps, stopping the loading at 6,000 steps, for a harmonic system ($k_{ratio} = 1.00$). Use a system size of $x = 400$ by $y = 100$ unit cells, with an initial crack length of 30% of the slab size in the x direction. (c.1) Include the sketch of the interatomic forces, marking the specific potential parameters chosen. (c.2) Plot the crack tip position over time, as well as the crack tip velocity over time. (c.3) Determine the maximum crack speed and discuss whether this is a steady state speed. (c.4) Is the observed speed larger than the Rayleigh-wave speed? Calculate the ratio of maximum crack speed observed in the simulation and the Rayleigh-wave speed.

(d) Introduce a strong hyperelastic stiffening effect, by choosing $r_{on} = 1.13$, and $k_{ratio} = 3.00$ (this ratio parameter is the ratio of the second spring constant and the first spring constant in the biharmonic potential). (d.1) Include a sketch of the interatomic forces, marking the specific potential parameters chosen. (d.2) Plot the crack tip position over time, as well as the crack tip velocity over time. Determine the maximum crack speed and discuss whether this is a steady state speed from studying the crack speed history. (d.3) Is the observed speed larger than the Rayleigh-wave speed? Calculate the ratio of maximum crack speed and the Rayleigh-wave speed. (d.4) Repeat the calculation for $k_{ratio} = 2.50$.

(e) Change the parameter k_{ratio} to 0.666 while keeping $r_{on} = 1.13$. Plot the maximum crack speed as a function of k_{ratio} (for all values you studied above). (e.1) Include a sketch of the interatomic forces, marking the specific potential parameters chosen. (e.2) Plot the crack tip position over time, as well as the crack tip velocity over time. Determine the maximum crack speed and discuss whether this is a steady state speed from studying the

crack speed history. (e.3) Is the observed speed larger than the Rayleigh-wave speed? Calculate the ratio of maximum crack speed and the Rayleigh-wave speed. (d.4) Repeat the calculation for $k_{ratio} = 0.75$.

(f) Plot the maximum crack speed as a function of the parameter k_{ratio}, for the five cases considered. Discuss your observation and a possible physical mechanism to explain this behavior, using a schematic.

Note: all numbers in crackprop module are expressed in units of a reference lengh l^*, reference mass m^*, and reference energy E^*. There is no need to convert to real (physical) units for the analysis.

2. Deformation and unfolding of protein structures of the cell's cytoskeleton

The goal of this exercise is to use MD for analyzing and understanding the behaviour of small alpha-helical protein domains by performing a tensile test using the CHARMM force field implemented in the code NAMD. We use the Steered Molecular Dynamics (SMD) technique to apply a tensile load to the ends of the molecule. This computational approach is implemented in the stretchmol module in nanoHUB.

Together with beta-sheets (BSs), alpha-helical (AH) protein structures are the most abundant structural motifs found in proteins. Beta-sheets and AHs are particularly common because they result from hydrogen bonding between the N–H and C=O groups in the polypeptide backbone. An alpha helix is generated when a single polypeptide chain twists around on itself stabilized by hydrogen bonds (H-bond) made between every fourth residue, linking the O of peptide i to the N of peptide i + 4 in the residue chain. Consequently, at each convolution, approximately 3-4 H-bonds are found in parallel arrangement that stabilize the helical configuration.

Here we investigate a single alpha-helical segment of the 2B part of the vimentin intermediate filament (IF) dimer. A schematic of the vimentin dimer structure, along with its organization in the cellular structure, is shown below (Figures 2.1 and 2.2). The entire rod-like structure is 310 residues long and consists of four coiled-coil alpha helices (1A, 1B, 2A, 2B) divided by linkers (L1, L12, L2).

IFs, in addition to microtubules (MTs) and microfilaments (MFs) are one of the three major components of the cytoskeleton in eukaryotic cells. The cytoskeleton plays a critical role in determining the shape and the mechanical properties of the cell, and is vital for numerous additional functions such as cell motility and protein synthesis. A great diversity of mechanical properties enables the vimentin IFs to satisfy their specific mechanical role in cells, such as to guarantee their structural integrity or their shape. It has been hypothesized that IFs are critical to provide strength to the cell under large deformation, and to absorb large amounts of energy upon a certain load by unfolding. This represents a means to reinforce the cell in extreme deformations so that cells can withstand dramatic loads and deformations, leading to the term "safety belt of cells".

Please take a look also at the paper posted on Stellar which may help in the analysis of your results:

[1] Z. Qin, et al., "Hierarchical structure controls nanomechanical properties of vimentin intermediate filaments", PLoS ONE, Vol. 4(10), paper # e7294, 2009 (online: http://dx.plos.org/10.1371/journal.pone.0007294).

Note: The simulation input files for this problem are posted on Stellar. See: **pset2_vimentin.zip**. (Units used in this simulation, *time:* fs, *length:* Å, *energy:* kcal/mol, *force:* kcal/mol/Å). However, the force in the force-displacement output is in the unit of pN. Detailed instructions about how to use the **stretchmol** module in nanoHUB (https://nanohub.org/tools/stretchmol) are found in recitation notes on Stellar.

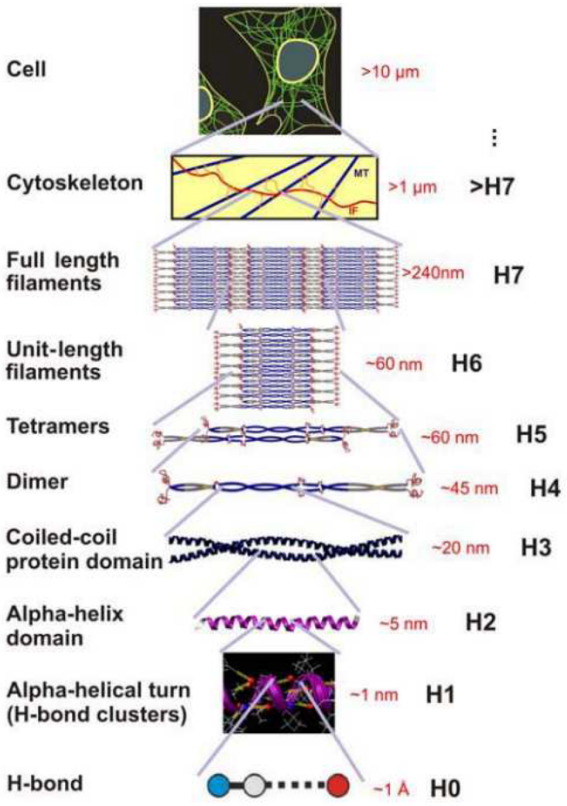

Figure 2.1: Overall structural organization of the cellular cytoskeleton, illustrating the vimentin intermediate filament (IF) network (adapted from reference [1])

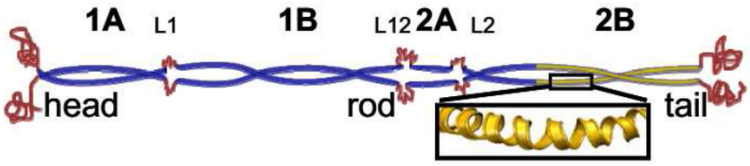

Figure 2.2: Molecular structure of the vimentin dimer (structural level H4 in Figure 1.1); the structure shown is the one you will simulate in this assignment, a piece of the alpha helical domain.

(a) Create different visualizations of the protein molecule using VMD, (i) show all atoms (with water), (ii) show all atoms plus an overlayed "New Cartoon" representation of the protein (with "Structure" color coding), and (iii) only a "New Cartoon" representation of the protein (with "Structure" color coding). Compare with the dimer geometry and indicate its position.

(b) Perform a protein stretching simulation of the vimentin 2A segment (all input files provided on the website, see link above), using the SMD method. Use the following parameters:

DCD Frequency = 150

Velocity = 0.002
Number of Steps = 150000 Number of Averaging Bins = 300

What stretching velocity does this correspond to (in m/sec)? What is the total simulated time (in seconds)?

Note: A run of 100,000 steps takes approximately 6-8 hours. Also, make sure that you pull in the axial direction of the molecule (measure first using VMD and then input the direction of pulling into the simulation tool.)

(c) Plot force versus extension of the molecule.

(d) Plot stress versus strain.
Hint: Use Excel or Matlab to process your data and convert displacements to strains and forces to stresses (stress is defined as force per cross-sectional area). You should discuss the challenges of defining the stress for this molecular geometry. You may measure the geometry of the molecule using VMD ("Mouse◊Query" function for "Bonds").

(e) Analyze the molecular mechanisms associated with the overall extension of the molecule. Which of the chemical bonds break first, and why? Add snapshots of the molecular structure to your report and discuss, clearly label each plot with appropriate time point. Choose visualizations that allow you to gain insight into the mechanisms of deformation. Try different choices in NAMD.

(f) Explain the different regimes of deformation you see in the force-extension plot based on the atomistic mechanisms you can identify in VMD.

(g) Estimate Young's modulus of the vimentin 2A segment and compare with values reported from other studies, e.g. from reference [1] given above.

(h) The focus now is on the analysis of the angular point (the point when the first Hbonds break, which is associated with a sudden change of the slope in the force-extension plot) and its dependence on loading rate. Table 1.1 (see "Supplementary data") below shows a summary of simulation results, providing the force at the angular point for varying pulling speeds. Plot the force at the angular point as a function of the log of the pulling speed. Discuss the observations and explain the observed behavior.

(i) Carry out a Bell analysis to determine the energy barriers and the distances to the energy barriers. Compare with published results and discuss possible mechanisms of deformation. Explain how these results relate to the simulation results you observed earlier. Indicate the data point for the angular point in the graph generated in part (h).

Supplementary data:

Pulling speed (m/sec)	Force at angular point (in pN)
100	1607
75	1420
50	1328
40	1325
20	1151
10	960
5	642.1
2.5	521.7
1.0	488.8
0.75	365.1
0.5	321.8
0.3	480.7
0.2	355.6
0.1	319.9
0.075	297.3
0.05	419
0.026	315.8
0.01	161.6
0.001	153.1
0.0001	86.42

Table 1.1: Summary of MD simulation results, providing the force at the angular point for varying pulling speeds.