1.1 The force field describes the geometry and the interaction energy. Which variables
does it depend on?
[Only one answer is correct.]
A) The coordinates and velocities of the atoms.
B) The coordinates of the atoms.
C) The forces instantaneously applied on individual atoms.
D) The coordinates of the electrons surrounding the atoms.

1.2 Which one of the following sentences concerning a classical force field is NOT
correct?
A) It is used to represent the potential energy of a (macro)molecule usually in the con-
densed phase (e.g., protein in water).
B) The set of parameters on which it is based is derived from experiments and high-level
quantum mechanical calculations.
C) It represents the interactions which arise between atoms in biological macromolecules.
D) It describes the response of the electrons to an external electric field.

1.3 The nonbonded energy terms...
[True or False? More than one of the following sentences could be true.]
A) ... consist only of the Coulombic interactions between partial charges.
B) ... are usually approximated with pairwise interactions.
C) ... are usually calculated within a distance threshold.
D) ... mimic only intermolecular interactions between different molecules.
1.4 The van der Waals energy between a pair of atoms...
[True or False? More than one of the following sentences could be true.]

A) ... consists of a repulsive term at long distances and of an attractive term at short distances.

B) ... has several minima.

C) ... approaches zero at long distances.

D) ... depends on the value of two parameters: the optimal distance and the energy at the optimal distance

1.5 Consider a single C-C bond and a double C=C bond. Which bond is more difficult to break, i.e. needs more energy to be broken? Which bond is shorter? How are these property translated in the force field? (Hint.: which term of the force field describes covalently bonded atoms?)

1.6 Consider a carbon atom that is bound to an oxygen atom by a double bond (C=O) and a carbon atom that is bound to an hydrogen atom (C-H). In which of the two previous cases is the bond more polarized? In which of the two cases the carbon feels a depletion of electrons? How is this reflected in the partial charges of the carbon in the two different cases?

1.7 Imagine that by mistake you run a simulation of a protein in vacuo, i.e., without solvating it. Which of the following artifacts do you expect to observe? [More than one of the following sentences could be correct.]

A) The Coulombic interactions are negligible.

B) The charged side chains form clusters of salt bridges.

C) The binding sites of substrates or ligands shrink.

D) The overall shape of the protein tends to become spherical.

1.8 Which one of the following sentences concerning implicit solvent models is NOT correct?

A) They allow to determine the structure of the water molecules around a protein.

B) They are used in order to improve the computational speed.

C) They reproduce the effect of solvation as a mean field effect.

D) They do not reproduce the directionality of the hydrogen bonds of biomolecules with the solvent.

1.9 Periodic boundary conditions ...
[True or False? More than one of the following sentences could be true.]

A) ... are used to prevent water molecules to evaporate.

B) ... consist in replicating the simulation system in space.

C) ... are used to keep the number of molecules in the simulation box constant.

D) ... are used only for constant volume simulations.
1.10 Molecular Dynamics simulations...
[True or False? More than one of the following sentences could be true.]

A) ... can be based on the Newton equations or motion.
B) ... reproduce the actual motion of the atoms.
C) ... can be performed only at constant temperature.
D) ... require a description of the electronic orbitals.

Go to the page [http://www.biochem-caflisch.uzh.ch/movies/](http://www.biochem-caflisch.uzh.ch/movies/)

1.11 Watch the movie "Folding and unfolding of the three-stranded $\beta$-sheet peptide beta3s".

This MD simulation was performed at the melting temperature (i.e., under conditions in which the folded and denatured state are populated at about 50% each) with a simple implicit solvent model based on the solvent accessible surface. You can observe formation of transient nonnative secondary structure elements (cylinders that represent alpha helices).

Which one of the following sentences concerning this simulation is correct?
[Only one answer is correct.]

A) The force field adopted must be wrong because the formation of transient nonnative secondary structure elements is not expected.
B) The peptide reaches the folded state which is rather stable.
C) The simulation does not provide a good description of folding because it starts from the folded state.
D) The simulation can not be descriptive of the folding process because folding is governed mainly by the motion of the electrons.

1.12 Watch the movie "Simulation of Fibril Formation".

This MD simulation was performed with a very simplified (phenomenological, coarse-grained) model of a short peptide.

The coarse-grained model was used because
[True or False? More than one of the following sentences could be true.]

A) ... it allows to reduce the computational time and therefore to better sample the aggregation process.
B) ... an accurate force field for a short peptide is not available.
C) ... it allows to describe with atomic resolution the structure of the fibril.
D) ... its use reduces significantly the number of simulated atoms.