Εικόνα που περιέχει κείμενο

Περιγραφή που δημιουργήθηκε αυτόματα

JOINT INSTITUTE FOR NUCLEAR RESEARCH

Frank Laboratory of Neutron Physics

**MD-SIMULATION RESEARCH (FROM ATOMIC FRAGMENTS TO MOLECULAR COMPOUND)**

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# Introduction

*History*

The original idea of Molecular Dynamics simulations emerged in theoretical physics in 1950s and was later introduced to chemical and material science and biological molecular simulations. In 1960s, Lennard-Jones potentials were introduced for lipid simulations, but the computational power of the time limited the system’s size and time scale. In 1970s the first MD simulation study of the dynamics of a protein bovine pancreatic trypsin inhibitor was reported and ever since more and more research has been carried out, turning MD simulations into a powerful tool in studying macromolecules and their interactions.

*Fundamentals*

Molecular Dynamics simulation is the computer-based N-Body simulation of systems containing atoms and molecules. The system components are left to interact together for a certain period while monitoring the system’s physical properties (either macroscopic e.g. volume, pressure, temperature etc., or microscopic e.g. velocities, positions etc.) The output comes in the form of ensemble of frames. All frames share the same macroscopic state but may differ in the microscopic states. Each frame represents the system at a specific point of time/microscopic state. [1]

Why use Molecular Dynamics Simulation

MD simulation is essentially an experiment inside a computer. It is used when real life experiments are too expensive, too time consuming or impossible.

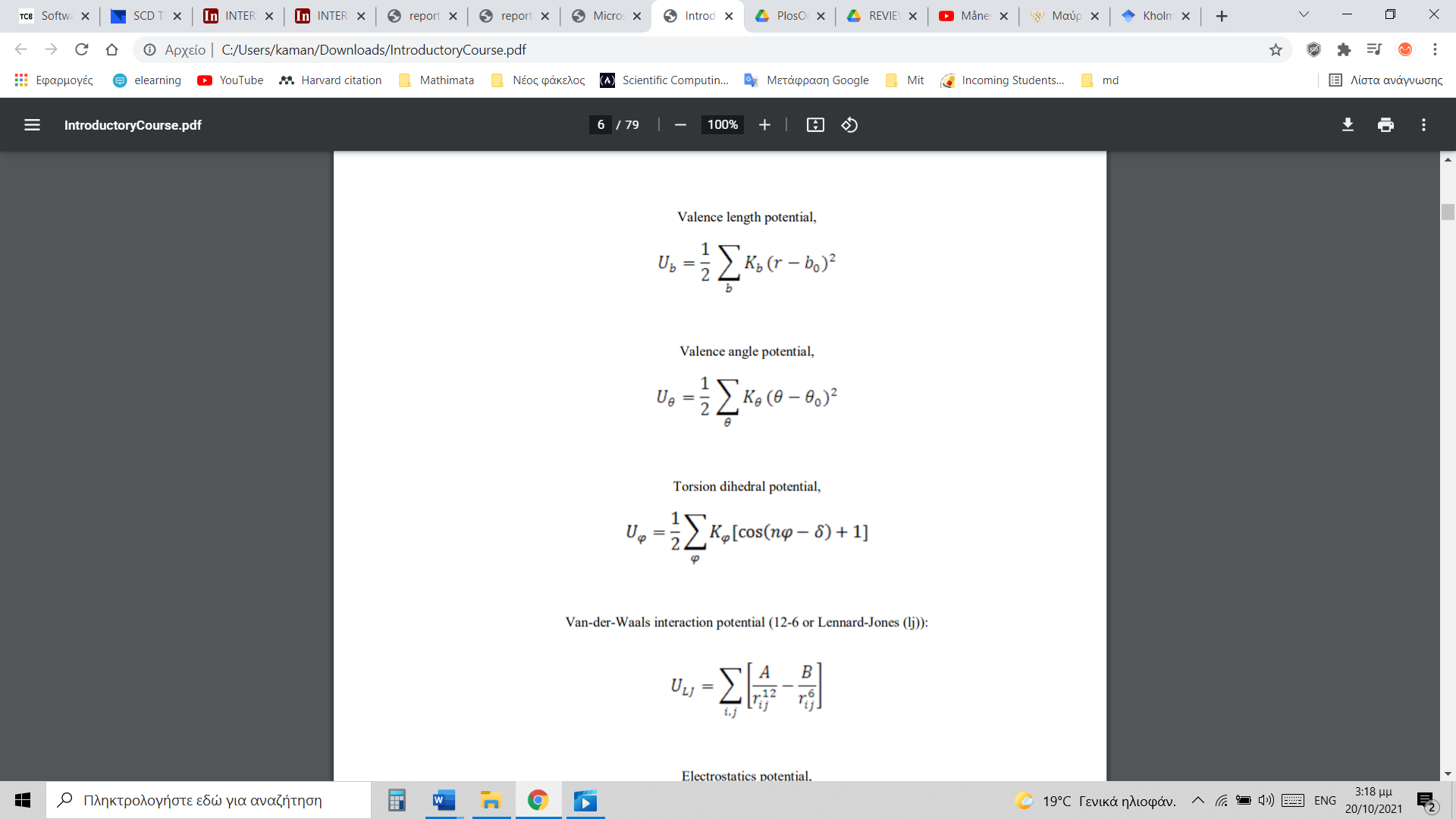
# Basic equations, potentials, and simulation techniques

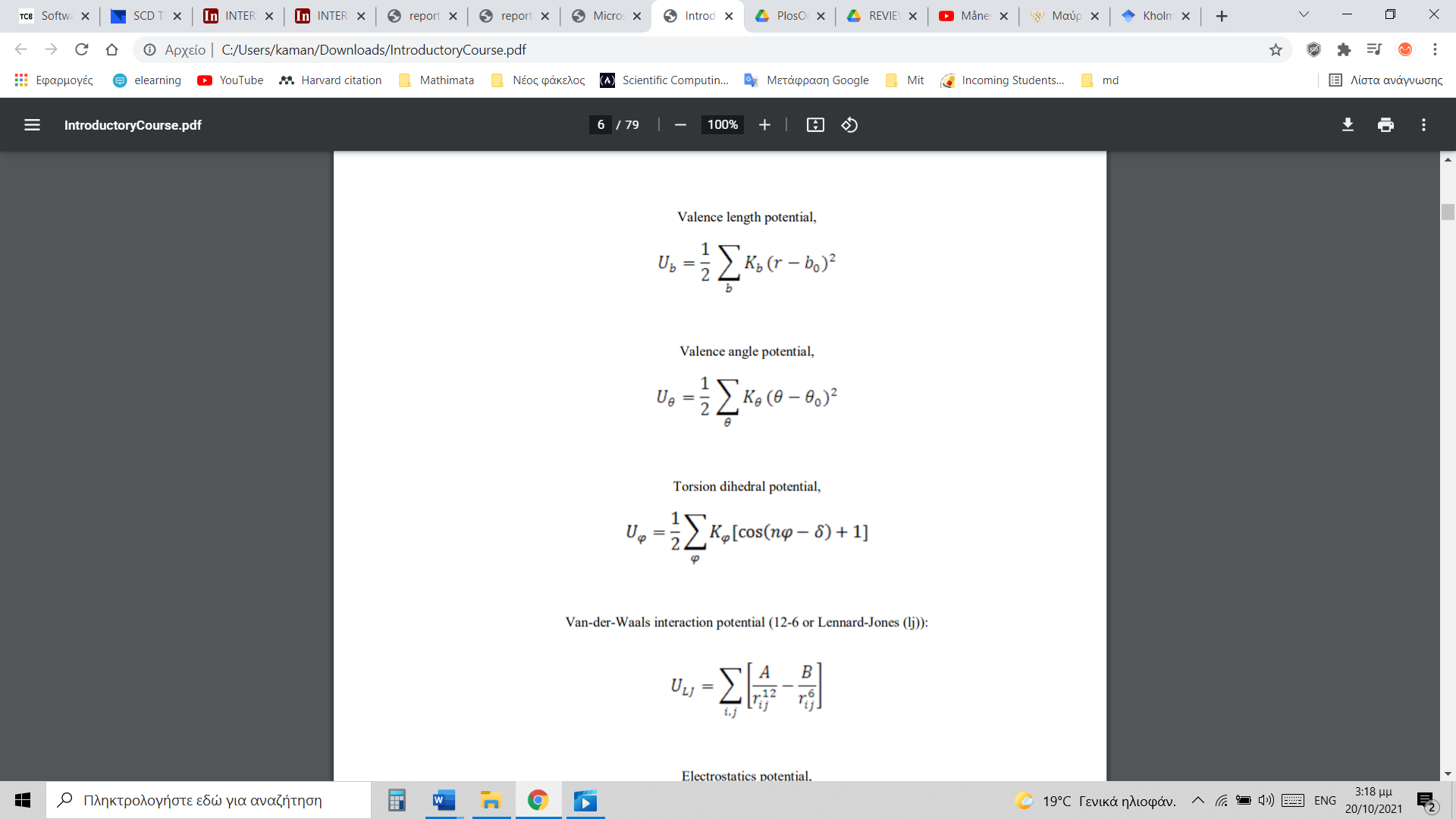
Classic Molecular Dynamics is based on Newton’s second law:

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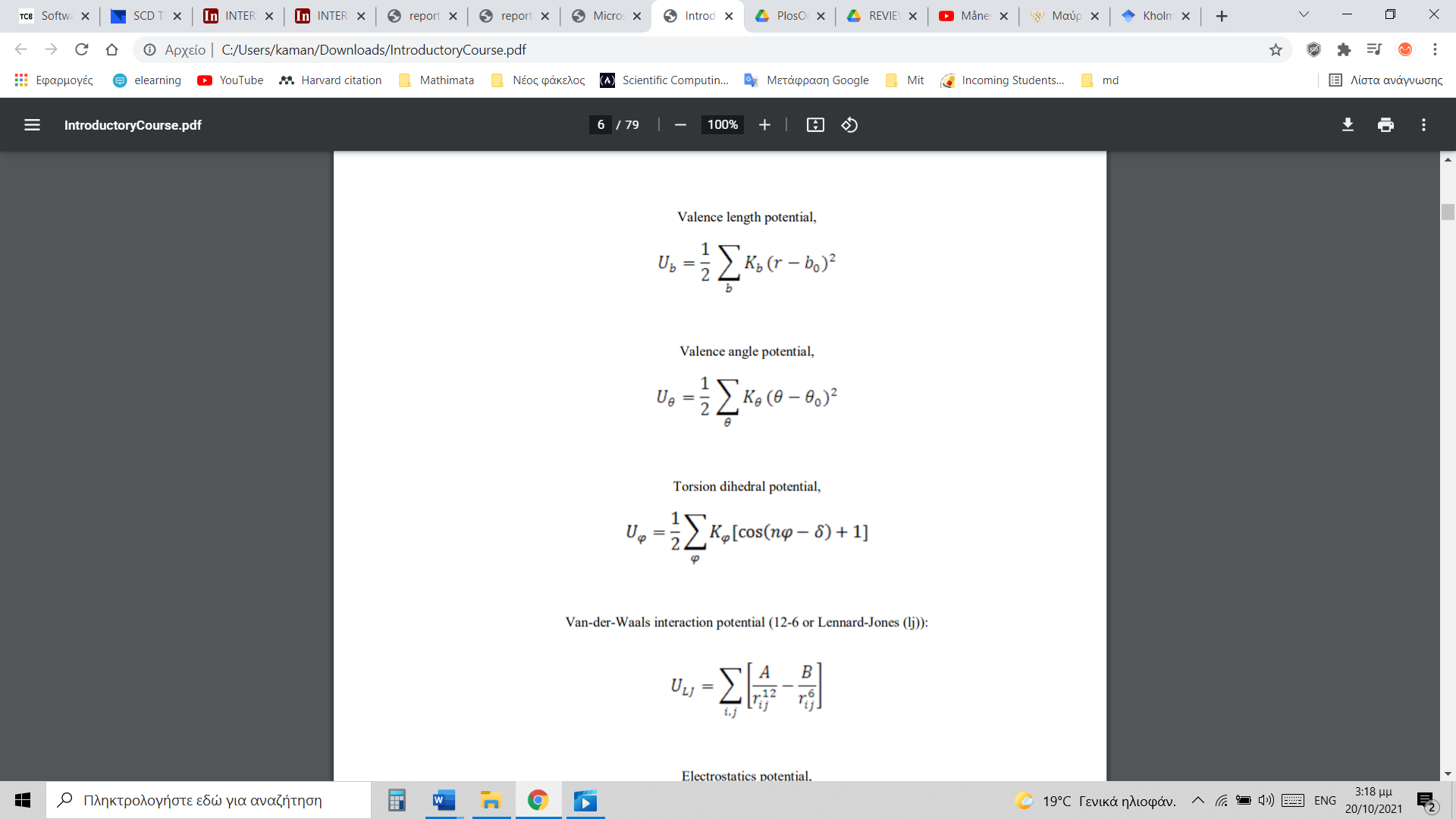
Περιγραφή που δημιουργήθηκε αυτόματαThe total potential energy can be calculated by adding the individual potential energies of the molecule caused by:

* Bond stretching (between two atoms)
* Angle bending (between three atoms)
* Fixed torsion (between four atoms)
* Van der Waals interactions
* Electrostatic interactions
* Hydrogen bonding

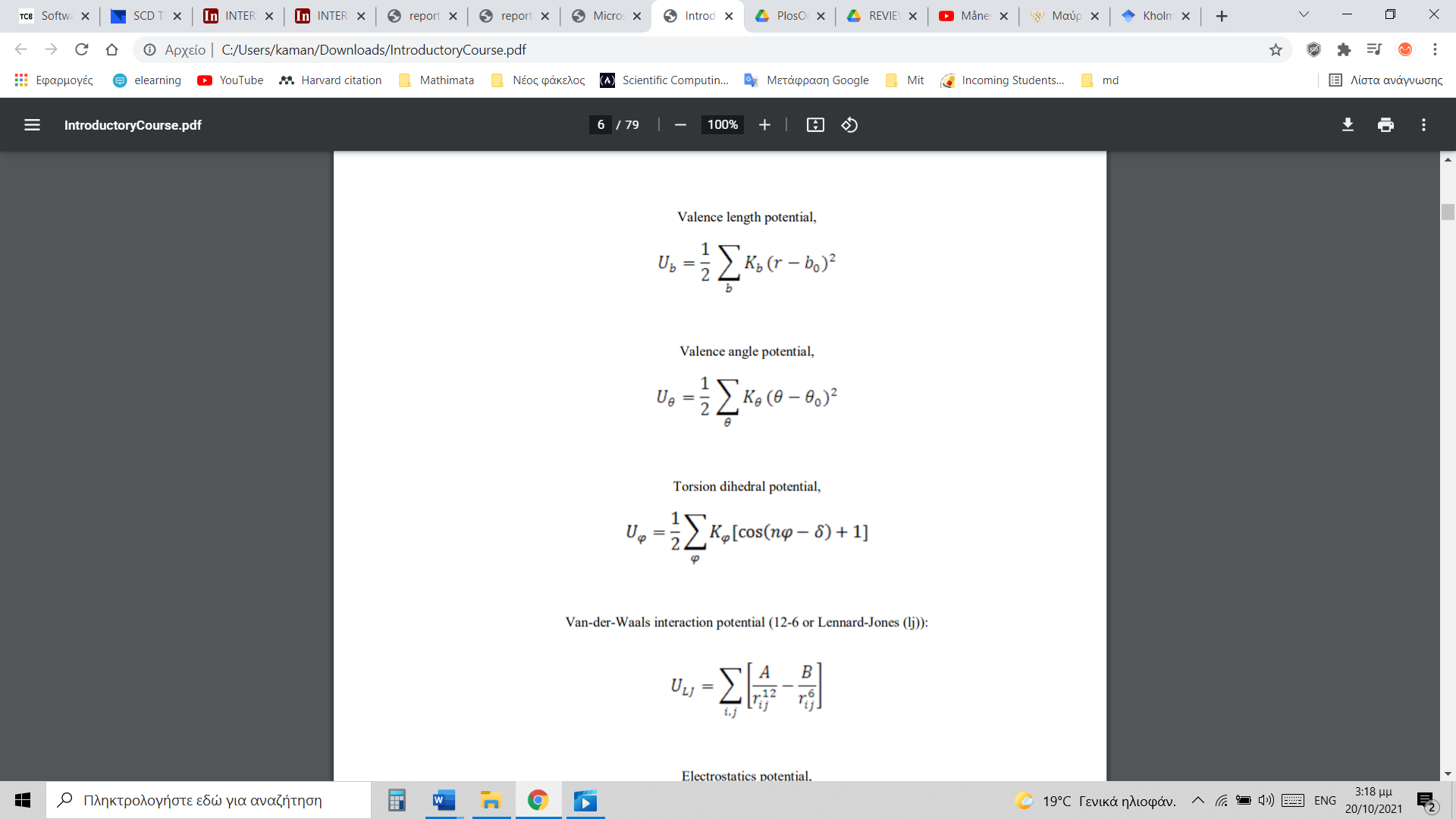
Valence Length potential:



Valence Angle Potential:



Torsion Dihedral Potential:



Van der Waals Interaction Potential:

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Electrostatics Potential:

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Hydrogen Bonding Potential:

After giving force field potentials, the next step is velocity generation:

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this can be achieved by either Maxwell velocity distribution or random number generators.

# MD Simulations of Leonard-Jones Systems

Lennard-Jones potential is the most widely used potential and is commonly expressed by the following equation:

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σ and ε are parameters that differ from atom to atom.

*Radial Distribution Function*

To monitor the systems equilibrium states in MD simulation, the Radial Distribution Function (RDF) is commonly used:



N: total number of atoms

ρ: atomic density

rij : radius vector between two centers i & j

RDF describes how density varies as a function of distance from a reference particle.

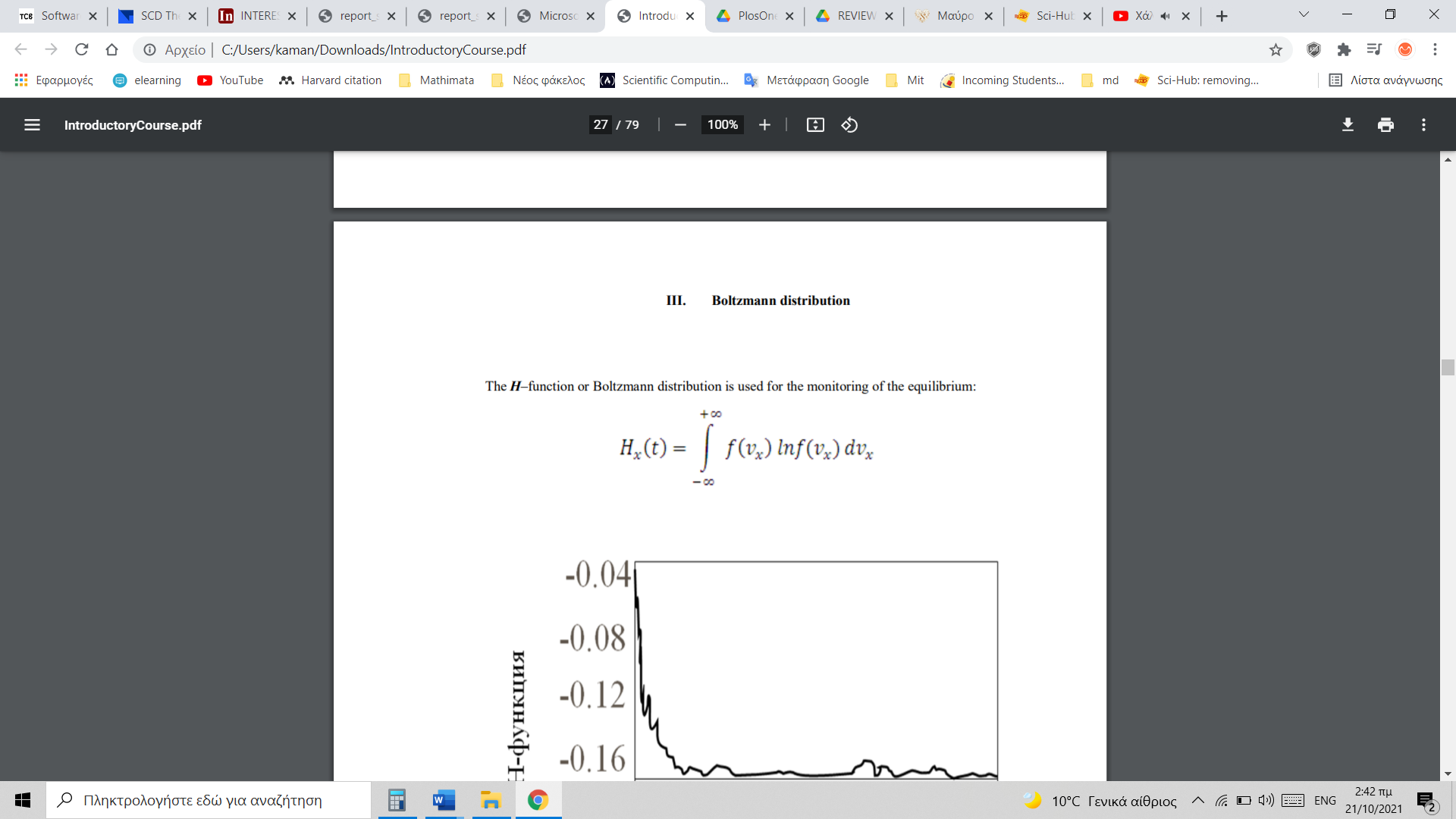
*Order Parameter*

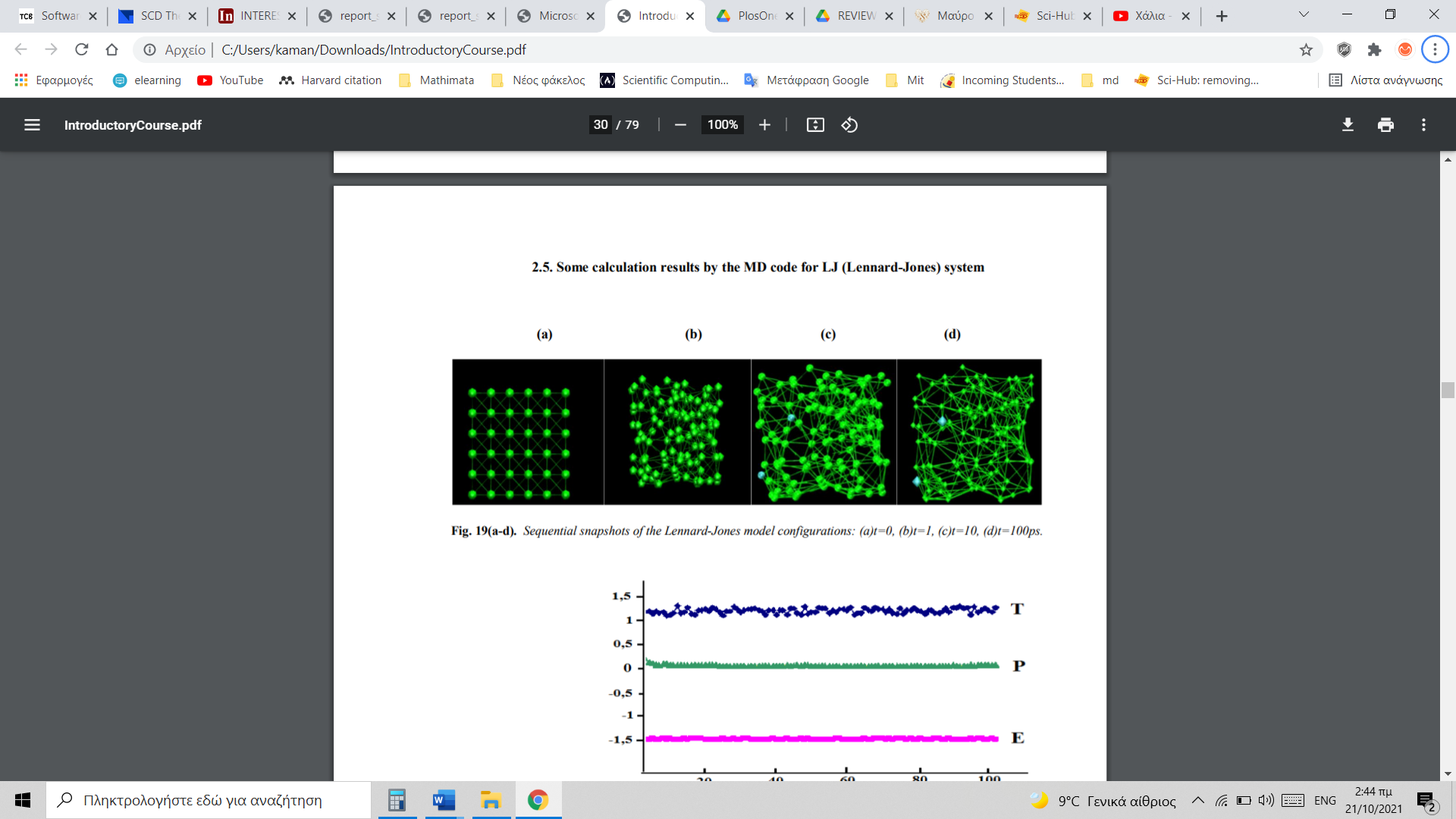
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Περιγραφή που δημιουργήθηκε αυτόματαFunction-parameter γ is used for distinguishing of the equilibrium states:

*Boltzmann Distribution*

Used for the monitoring of the equilibrium



*Lennard-Jones system MD simulation results- Example*

(a): t=0 , (b): t=1, (c): t=10, (d): t=100 ps

# MD Simulation Packages

There are many MD simulation packages. Amongst them are: DL\_POLY, AMBER, CHARMM, NAMD, etc.

In the DL\_POLY code there are three input and three output files.

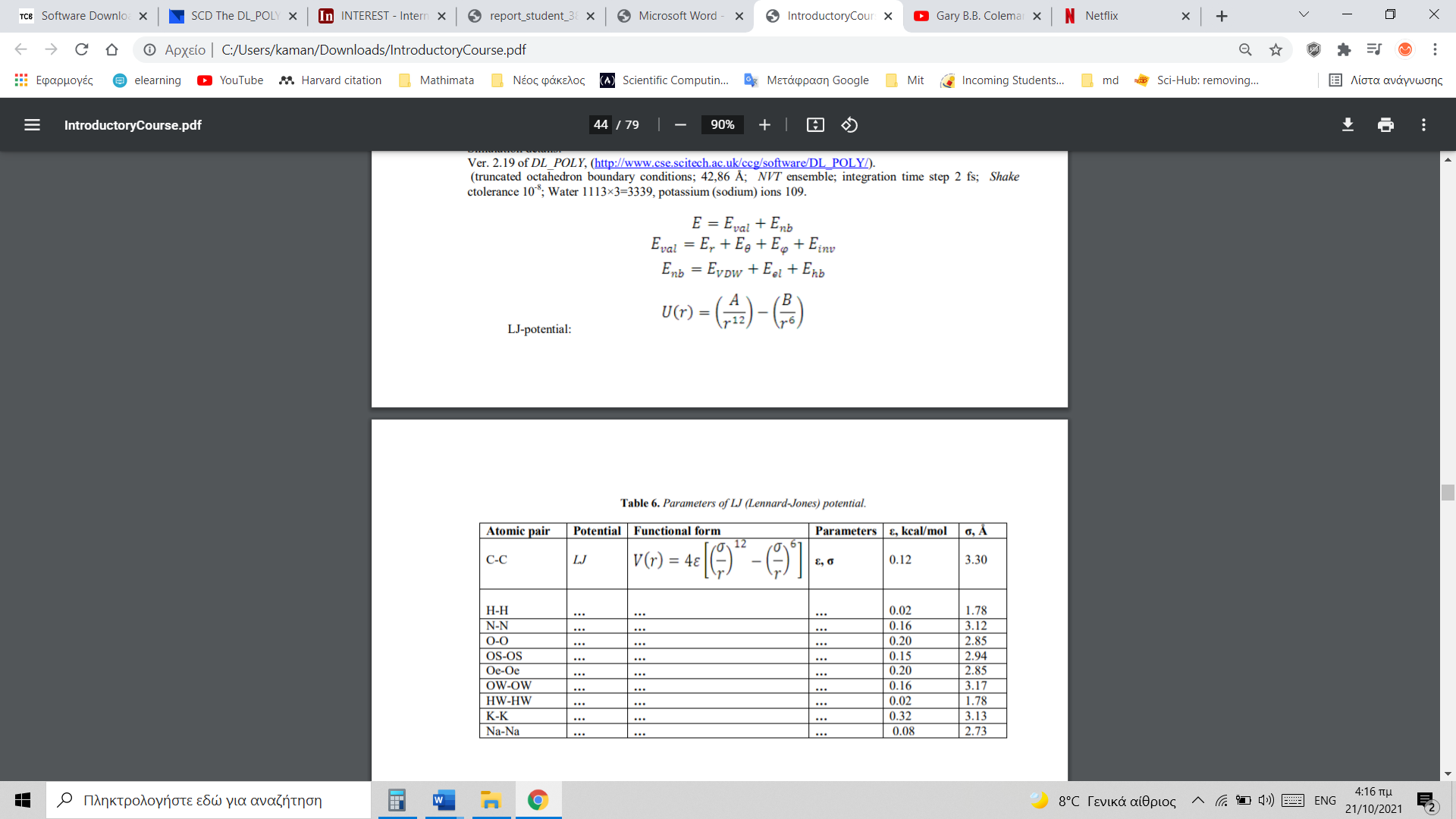
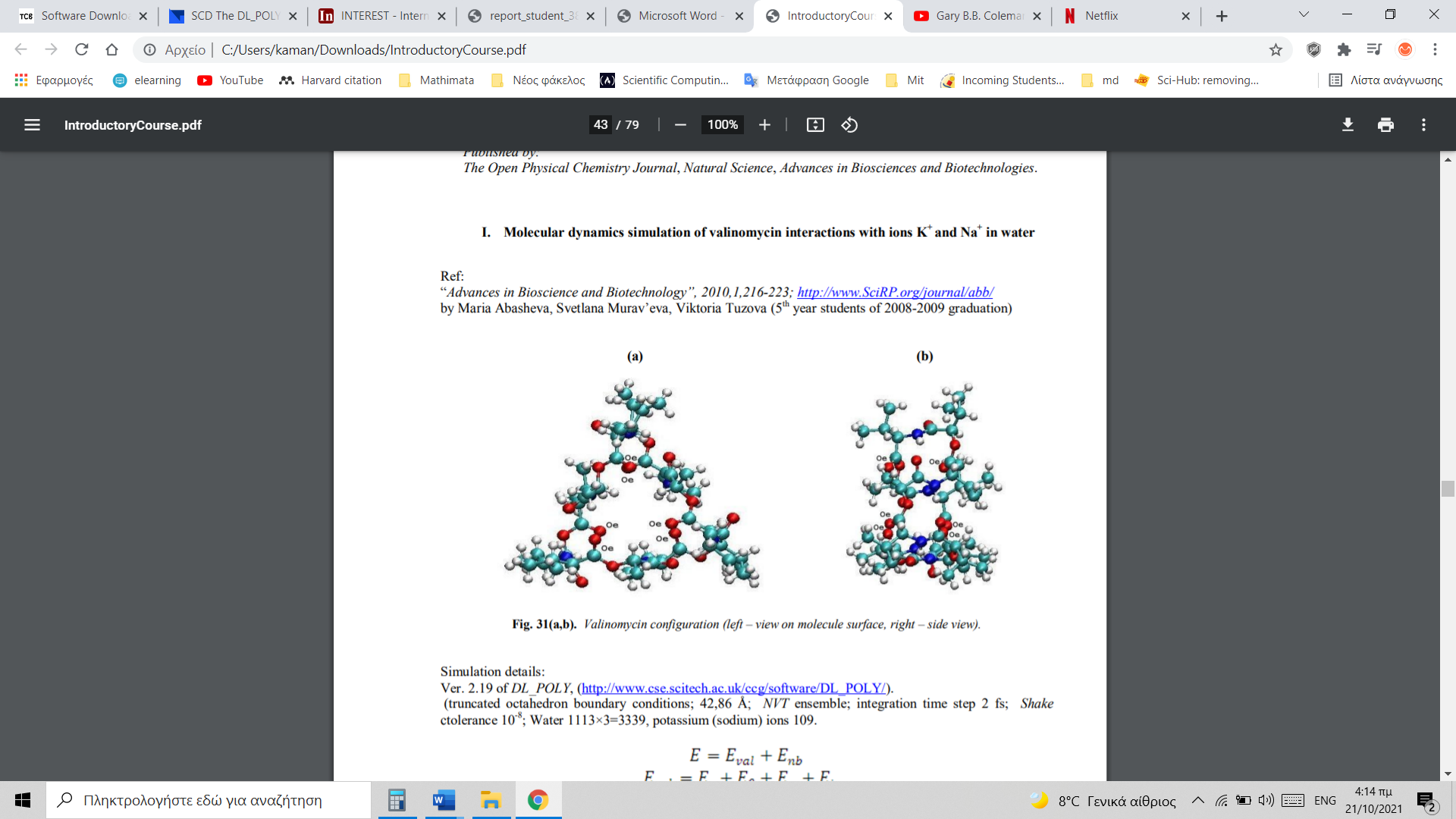
Input files: CONFIG, CONTROL, FIELD

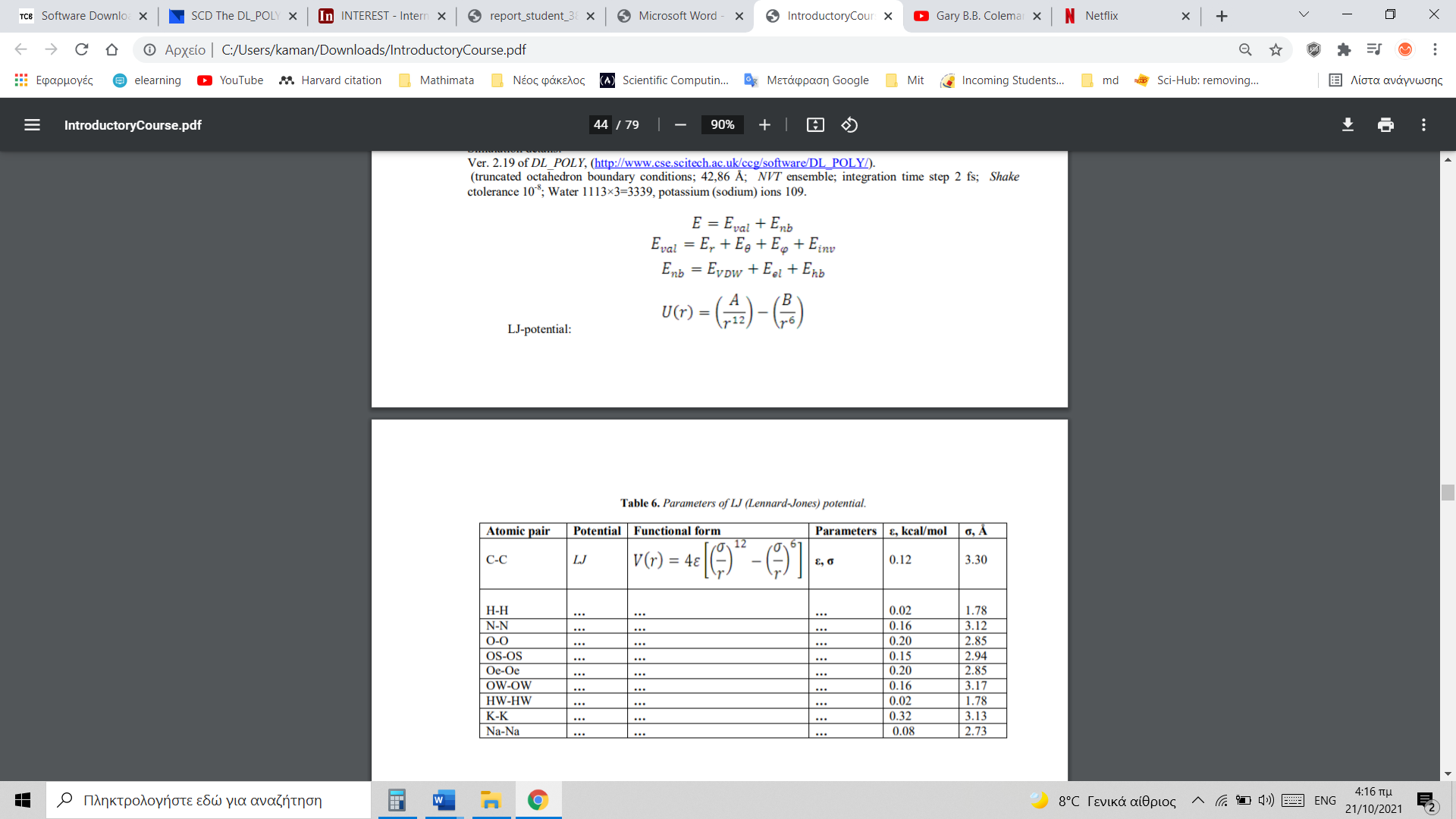
* CONFIG: Contains x-, y- and z- coordinates of all atoms, sets initial values of velocities (Vx, Vy, Vz) and inter-atomic forces (Fx, Fy, Fz), as well as boundary conditions.
* CONTROL: Contains data on: Temperature, Pressure, Step of Integration, Thermodynamic Parameters etc.
* FIELD: Contains information about atoms and molecules (structure, mass, charge, interaction potentials).

Output files: OUTPUT, REVCON, HISTORY

# MD Simulation Example

Molecular dynamics simulation of valinomycin interactions with ions K + and Na+ in water

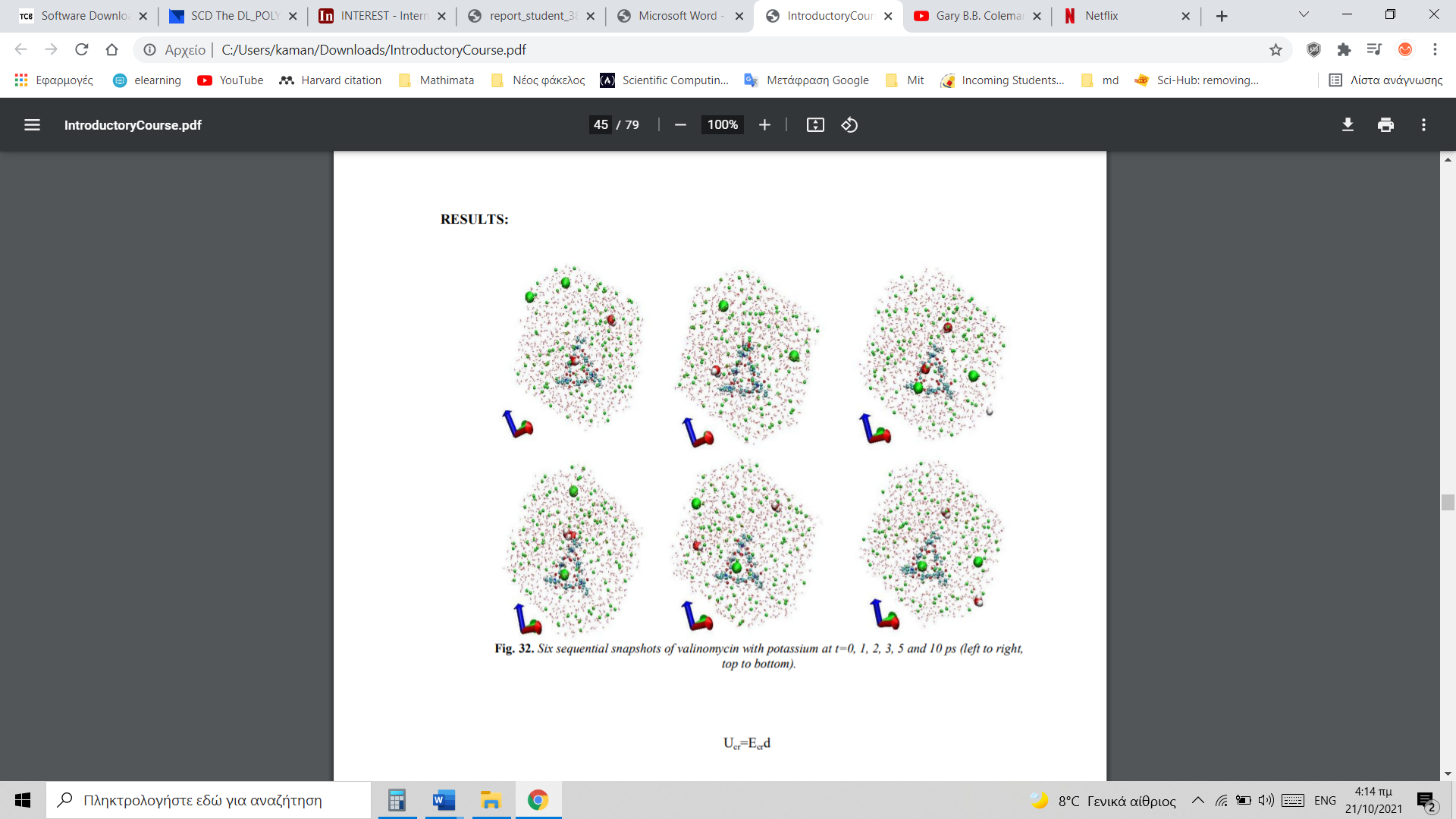




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Results:



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Περιγραφή που δημιουργήθηκε αυτόματαat t= 0, 1, 2, 3, 5, 10 ps

Εικόνα που περιέχει πίνακας

Περιγραφή που δημιουργήθηκε αυτόματα

[2]

# Future Goals

After I graduate, I would like to do a Master’s in Biomedical Engineering with a specialty in neuroscience. One of the main challenges for neuroscientists Alzheimer’s Disease (AD). A key player in AD is Amyloid-β, a short peptide that forms soluble oligomers, filaments and fibrils and finally plaques in patients’ brains. Design of anti-aggregation drugs requires knowledge of Amyloid-β’s molecular structure, which is difficult to obtain using experimental methods due to the abundance of its aggregation states. [3] Therefore, Molecular Dynamics Simulation is a powerful tool to be used instead.

# References

[1] Zheng, L., Alhossary, A. A., Kwoh, C.-K., & Mu, Y. (2018). Molecular Dynamics and Simulation. Reference Module in Life Sciences. doi:10.1016/b978-0-12-809633-8.20284-7

[2] Kh. Kholmurodov MD-Simulation in Chemical Research: From Atomic Fragments to Molecular Compound // Dubna, Russia, 2011.

[3] Söldner, C. A., Sticht, H., & Horn, A. H. C. (2021). Molecular Simulations and Alzheimer׳s Disease. Systems Medicine, 54–70. doi:10.1016/b978-0-12-801238-3.11541-7