



Designing Materials with modeFRONTIER

An application of modeFRONTIER to the optimization of physical and chemical properties of polymers

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What Polymers are

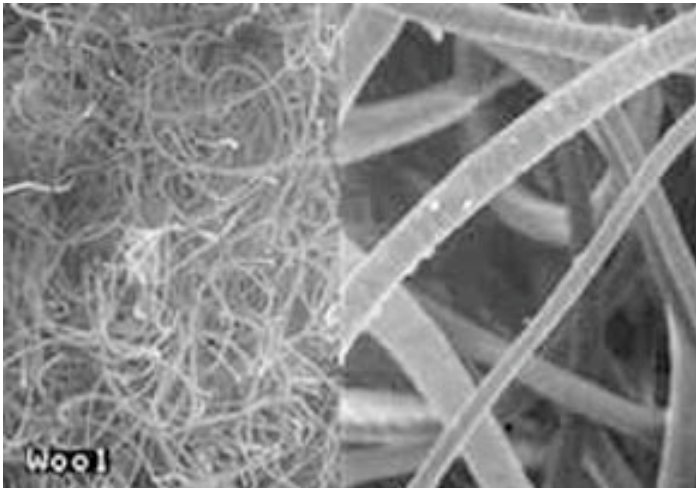
- Polymers are macro-molecules composed by hundreds or possibly thousands subunits called monomers. The polymer presents a regular repetition of its monomer in such a way to build regular structures, especially long chains organized in sheets, elices,...
- There are two very general and broad classes of polymers: biopolymers (e.g. proteins) and synthetic industrial polymers (e.g. plastics, resins,...)
- They have very different chemical composition and physical-chemical properties



How Polymers look



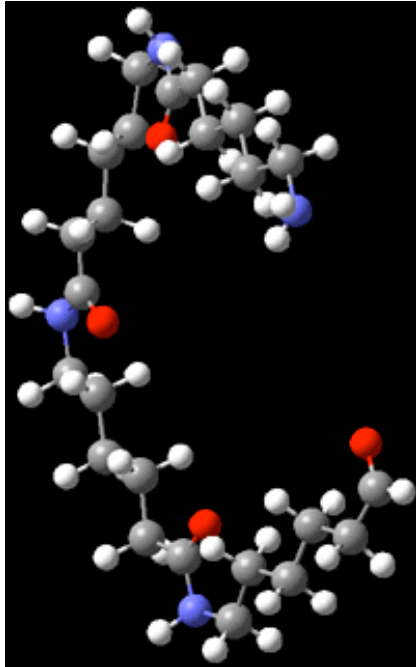
Polyethylene fibers by Optical Microscopy



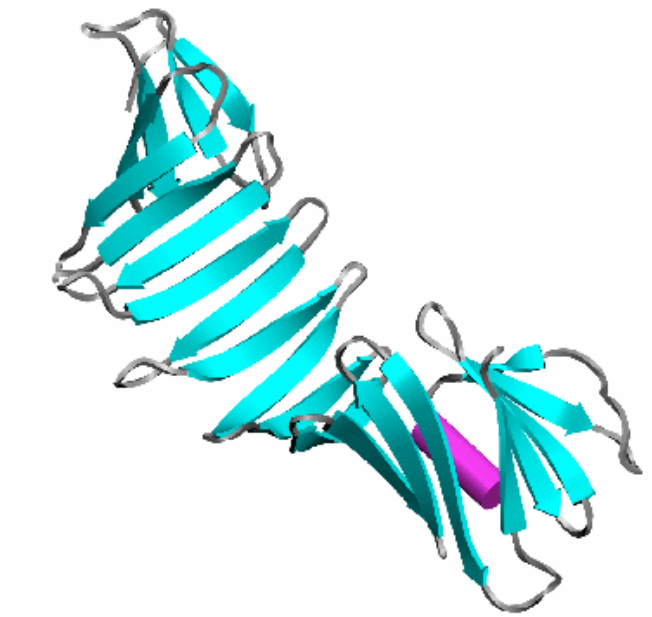
Wool fibers by Scanning Electron Microscopy



Structural Models for Polymers



Ball and Stick Model

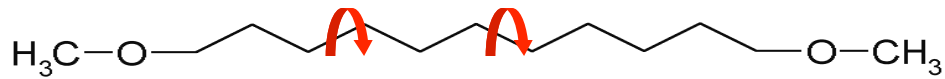
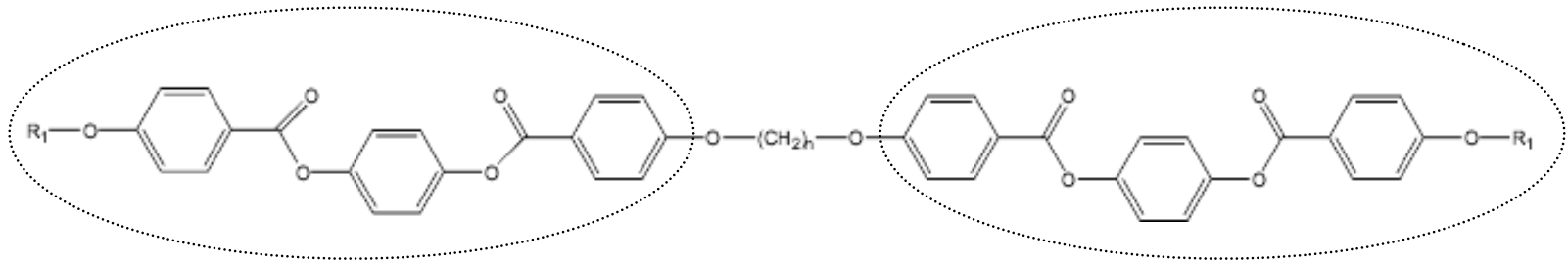


Ribbons Model

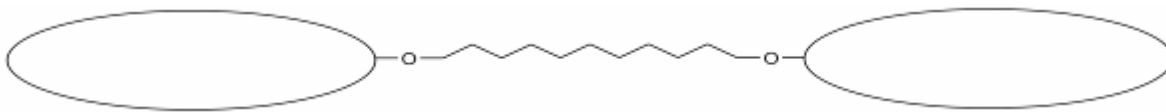
Models can be built at different resolutions so capturing several aspects of structural properties



An example: a Liquid Crystal



Rotations around C-C bonds are the main kind of internal motion for this molecule



Terminal groups are conformationally rigid: an ellipsoidal rigid rotor can model it



The Dynamic Picture

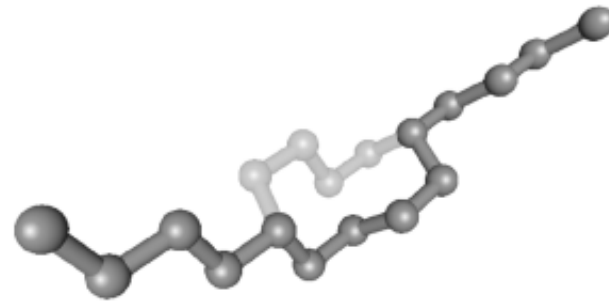
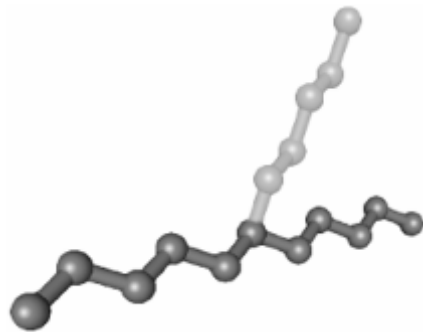
A stochastic model based on Langevin equation permits the calculation of kinetic constants for conformational transitions and the relative displacement of single particles

Cranklike conformational transitions in polyethylene, G.J Moro, B. Nigro, D. Di Stefano, A. Rassa
Journal of Chemical Physics, 2004 Sep 1;121(9):4364-76



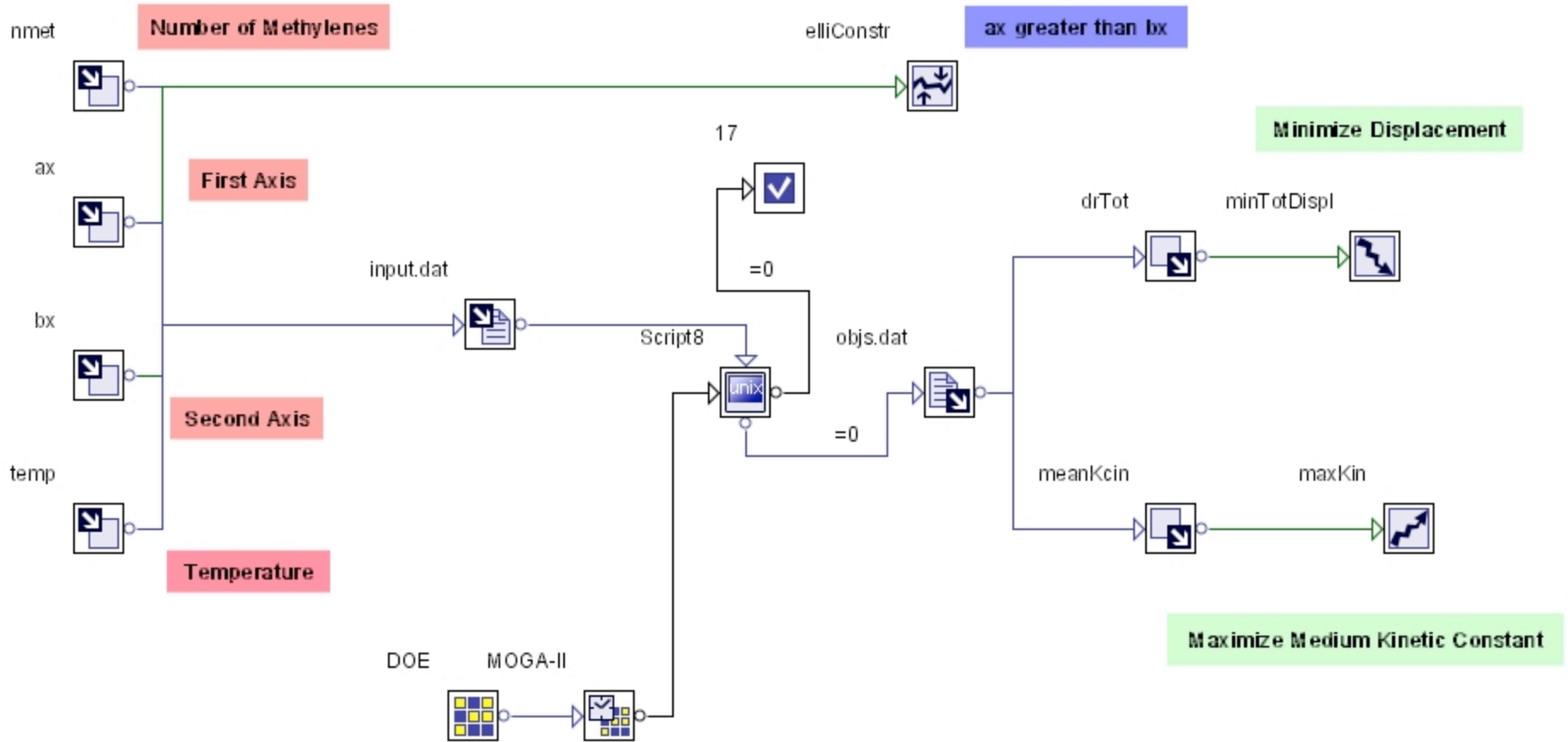
Optimization of Dynamic Properties

- An interesting property of this kind of molecules is their ability to regularly orient themselves with respect to an electrical field and to preserve this orientation into a somewhat large temperature interval
- Optimizing such a property, from a point of view of the stochastic model, implies to minimize the total displacement of the molecule and to maximize the mean value of the kinetic constants, so preserving the possibility to equilibrate with the environment





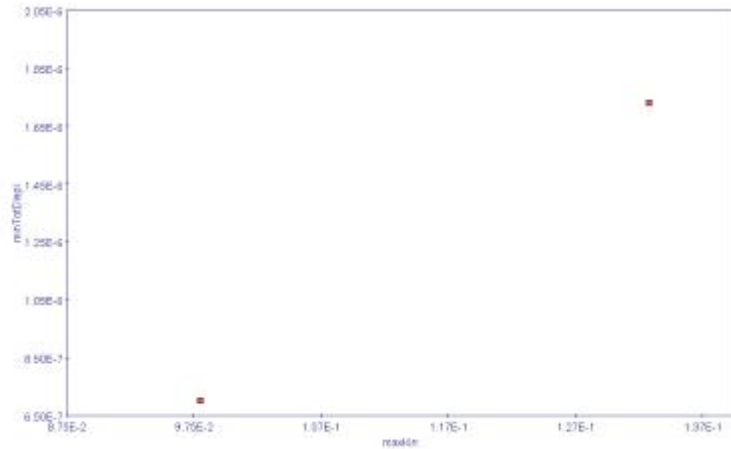
modeFRONTIER WorkFlow



Sobol DOE with 10 designs. MOGA-II with 150 generations.



Best Solutions

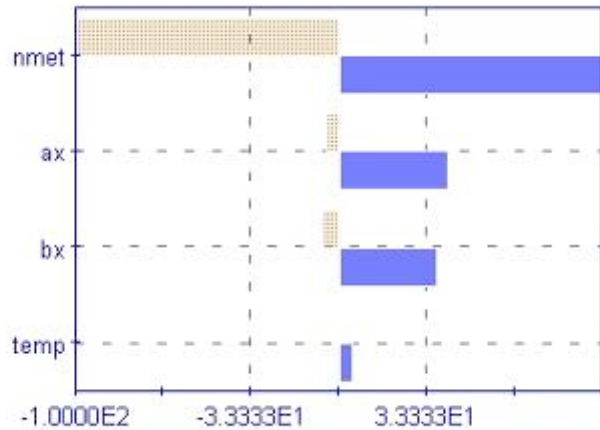


The best solutions tend to push the temperature on its upper limit and the ellipsoid on its minimum dimensions. The length of the spacer can be 14 or 22 methylene groups.

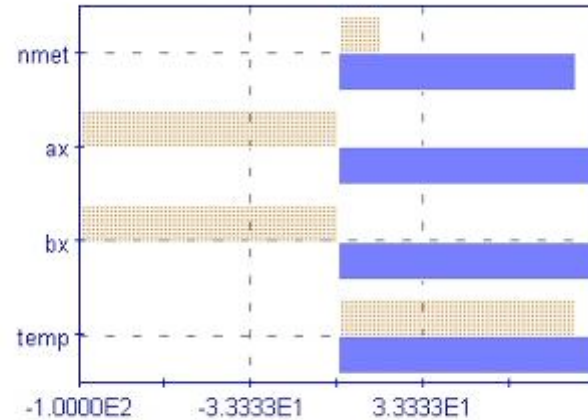
Best Designs											
ID	M	C	nmet	ax	bx	temp	drTot	meanKcin	minTotDispl	maxKin	elliConstr
181	<input type="checkbox"/>		14	1.0000E1	1.5290E0	3.1000E2	1.7310E-6	1.3318E-1	1.7310E-6	1.3318E-1	8.4710E0
382	<input type="checkbox"/>		22	1.0000E1	1.5290E0	3.1000E2	7.0464E-7	9.7920E-2	7.0464E-7	9.7920E-2	8.4710E0



Considerations on the Results



t-student on mean displacement



t-student on mean kinetic constant

The number of methylene groups has an inverse strong correlation with the mean displacement. Temperature is strongly correlated with the mean kinetic constant, while ellipsoid dimensions have an inverse strong correlation with it.

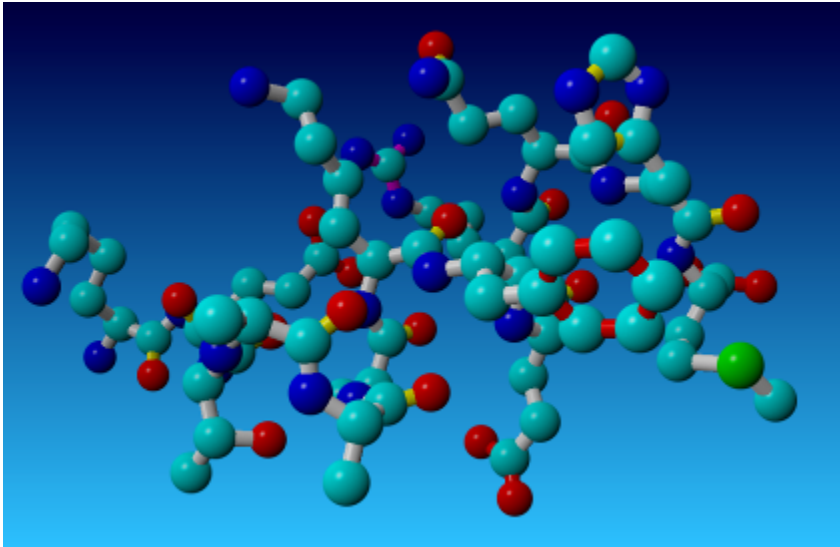


Conclusions and Future Developments

- If the results for the influence of temperature and ellipsoid dimensions on design objectives could be expected based on Boltzman kinetic theory, a precise indication for the length of the spacer is of great importance
- Future developments will involve the application of the model to the problem of protein – ligand docking, where modeFRONTIER performs a search for the favourable conformations. The so far presented stochastic algorithm will furnish a scoring methodology for the different candidate solutions

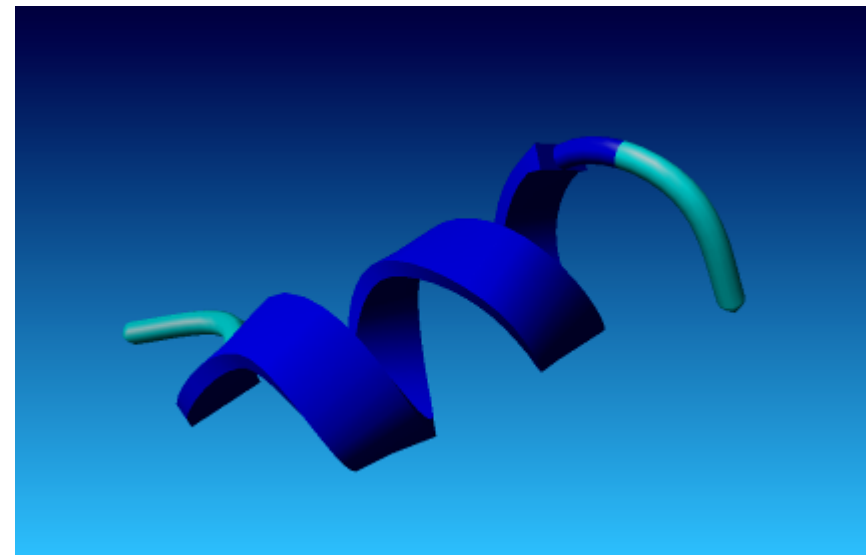


Work in Progress...



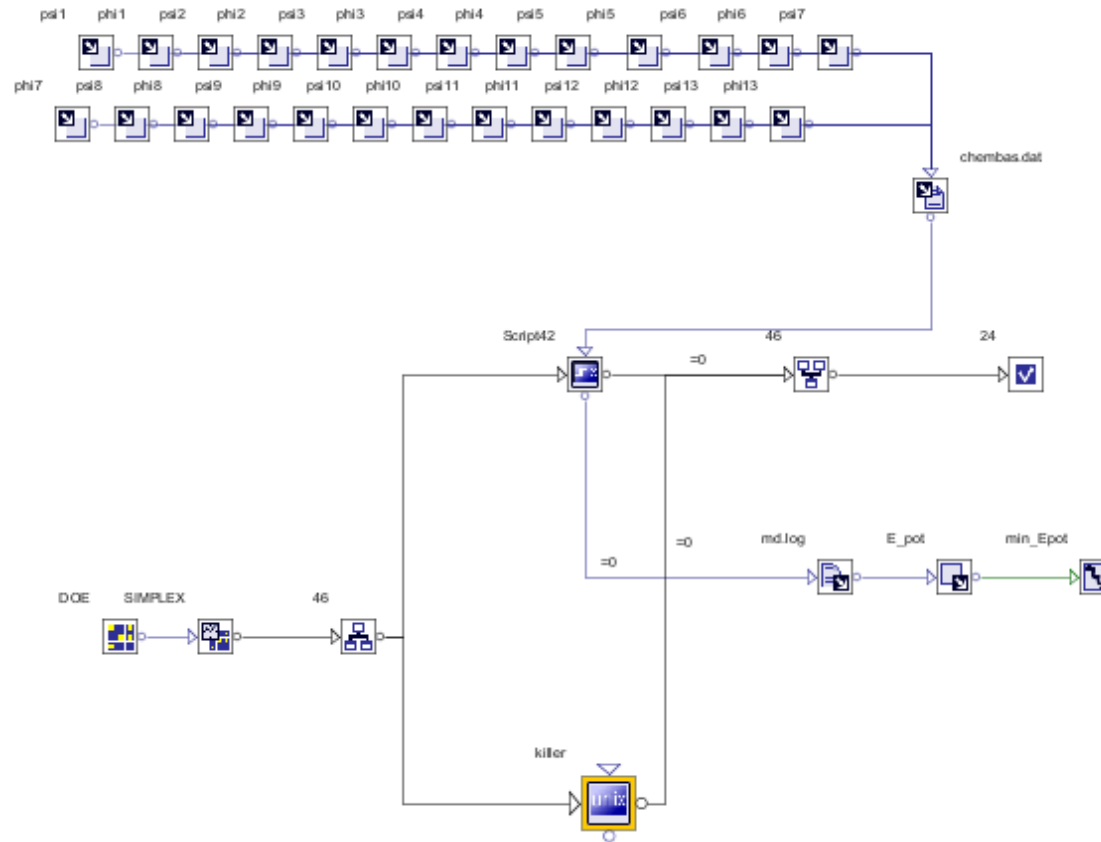
The aim of the optimization is the minimization of the potential energy of the system formed by a small peptide in water. The design variables are the φ, ψ angles of the peptide.

Interfacing **modeFRONTIER** with **Gromacs** molecular dynamics package for the analysis of biological interesting molecules





modeFRONTIER – Gromacs Interface



Treating molecules of biological interest requires a careful choice for the design variables, so avoiding an uncontrolled increase of problem complexity