Research Internship Opening

- **Title** : Modelling of non-equilibrium molecular flexibility at atomic scale
- **MSc thesis advisor** : Sergei Grudinin, sergei.grudinin@inria.fr, Phone: +33 4 38 78 16 91
- **Laboratory** (+working place) : Nano-D, Inria Grenoble,

Minatec Campus 17 rue des Martyrs, 38054 Grenoble France, https://team.inria.fr/nano-d/

- **If PhD position is possible** : yes

Duration: 4-8 months

Internship presentation :

Macromolecules such as proteins are flexible, and this flexibility plays an important role in their function. In most of the cases, the flexibility of a protein can be described with only a few collective degrees of freedom. Theses can be computed with normal mode analysis (NMA), which is computationally inexpensive technique, but assumes the molecules to ***be at the equilibrium*** [1-2]. NMA solves exactly a linear approximation of Newton's equation of motion. The approximate differential equation is then solved by diagonalizing the Hessian matrix of the potential function. The eigenvectors of the Hessian matrix are called the normal modes. The normal modes corresponding to the lowest eigenvalues, or frequencies, can be used to represent collective motions of a molecule.

Internship objectives:

The goal of this internship is to extend the near-equilibrium NMA technique to ***non-equilibrium*** cases. This will imply (i) the formulation of the problem from first principles; (ii) solving large-scale sparse systems of linear equations using efficient optimisation methods (including eigensolvers); (iii) validating and benchmarking the results; (iv) creating a QT-based GUI inside SAMSON [3] for interactive validation of the produced motions. The current interface is shown below.

Requirements :

We are looking for candidates from a computer science / applied math background with strong knowledge of applied maths and physics and an interest in biophysics. Knowledge of C++, Python, parallel programming (e.g. multi-threading), and QT will be an asset.

References:

[1] A. Hoffmann & S. Grudinin. NOLB : Non-linear rigid block normal mode analysis method. Journal of Chemical Theory and Computation, 2017, 13 (5), pp.2123-2134.

[2] https://team.inria.fr/nano-d/software/nolb-normal-modes/.

[3] https://www.samson-connect.net/