BioAFMviewer: Towards automation in analysis and interpretation of AFM data of biomolecules

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Simulating the Atomic Force Microscopy (AFM) scanning of biomolecules, our BioAFMviewer software [1] aims at supporting the interpretation of experimental data by inferring the 3D atomistic conformation of molecules. However, the current method is limited to equilibrium PDB/Alpha-fold structures.

In this communication, we are going to report on our collaboration with the Tama's lab at Nagoya University for the implementation of their newly developed method (Normal Mode Flexible Fitting AFM [2]), allowing to infer the 3D atomistic conformation of molecules beyond the equilibrium state, into the BioAFMviewer taking advantage of the speed of its algorithms to highly fasten the method [3].

Additionally, we are going to present our progress in the automation of AFM image analysis of biomolecules: molecule detection, domain detection, tracking, automatic measurements, etc.

References

[1] R. Amyot and H. Flechsig, PLoS computational biology 16(11), e1008444 (2020)

[2] X. Wu, O. Miyashita and F. Tama, The Journal of Physical Chemistry B, 128(39), 9363-9372 (2024).

[3] R. Amyot, et al. bioRxiv (2025)