MARIE SKŁODOWSKA-CURIE POSTDOCTORAL FELLOWSHIPS 2021

EXPRESSION OF INTEREST FOR HOSTING MARIE CURIE FELLOWS

HOST INSTITUTION

NOVA University Lisbon | ITQB NOVA - Instituto de Tecnologia Química e Biológica António Xavier

RESEARCH GROUP AND URL

Multiscale Modeling Lab
https://www.itqb.unl.pt/labs/multiscale-modeling/

SUPERVISOR (NAME AND E-MAIL)

Manuel N. Melo
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SHORT CV OF THE SUPERVISOR

Manuel is the head of the Multiscale Modeling lab within the MOSTMICRO unit of ITQB NOVA.

Work at the Multiscale Modeling lab is centered on elucidating the molecular-level details of lipid–lipid, lipid–protein, and protein–protein interactions, using coarse-grained, atomistic, and hybrid molecular dynamic simulations. Recent collaborations also focus on modeling bacterial-specific structures. The spirit of the lab is to connect biophysics to microbiology, bridging these two sometimes far-apart fields. The lab actively develops simulation models — as contributing developers to the Martini framework — and analysis software — with emphasis on large-scale parallelization of analysis.

Manuel carried out postdoctoral work at the Marrink lab, at the University of Groningen, where he became involved in the development and application of the Martini coarse-grain model. This followed a Ph.D. at the University of Lisbon studying the molecular-level interactions of antimicrobial peptides with cellular membranes, using spectroscopic techniques coupled to mathematical modeling.

5 SELECTED PUBLICATIONS

1. F. M. Sousa, L. M. P. Lima, C. Arnarez, M. M. Pereira, and M. N. Melo Coarse-Grained Parameterization of Nucleotide Cofactors and Metabolites: Protonation Constants, Partition Coefficients, and Model Topologies, Journal of Chemical Information and Modeling, 2021, 61(1): 335–346

2. J. Su, S.J. Marrink, MN Melo, Localization Preference of Antimicrobial Peptides on Liquid-Disordered Membrane Domains; Frontiers in Cell and Developmental Biology 2020, 8: 350

3. S. Dadsena, S. Bockelmann, J. G. Mina, D. G. Hassan, S. Korneev, G. Razzera, H. Jahn, P. Niekamp, D. Müller, M. Schneider, F. G. Tafesse, S. J. Marrink, M. N. Melo, and J. C. M. Holthuis, Ceramides bind VDAC2 to trigger mitochondrial apoptosis; Nature Communications 2019, 8: 1832

4. H. I. Ingólfsson, M. N. Melo, F. J. van Eerden, C. Arnarez, C. A. Lopez, T. A. Wassenaar, X. Periole, A. H. De Vries, D. P. Tieleman and S. J. Marrink, Lipid organization of the plasma membrane; Journal of the American Chemical Society 2014, 136(41):14554-59

5. M. N. Melo, H. I. Ingólfsson, S. J. Marrink, Parameters for Martini sterols and hopanoids based on a virtual-site description; The Journal of Chemical Physics 2015, 143(24):243152

6. M. N. Melo, R. Ferre and M. A. R. B. Castanho, Antimicrobial peptides: linking partition, activity and high membrane-bound concentrations; Nature Reviews Microbiology, 2009, 7:245-50

PROJECT TITLE AND SHORT DESCRIPTION

Meso-Scale, Large-Complexity Simulations of Antimicrobial Peptide Action

The antimicrobial peptide (AMP) class often acts by porating or otherwise disrupting bacterial membranes[6]. Although many advances have been made in their characterization, precise mechanisms and determinant factors remain elusive. Molecular dynamics simulations can provide important insight into the molecular-level processes by which AMPs perform their action. Notably, coarse-grain methods can reach the micro to millisecond timescales needed for the observation of these events.

In this project the recently-released Martini 3 Coarse-Grain model will be used to simulate different AMPs in a membrane setting and infer mechanisms and promoting/inhibiting conditions. It will innovate relative to other approaches by i) employing realistically complex membrane compositions ii) developing and adapting simulation methods to force pore formation and measure energies therefrom, and iii) employing hybrid CG—all-atom approaches.

This project can be further expanded by taking advantage of the lab's collaborative network in experimental biophysics to validate results, namely with UV/Vis/NMR spectroscopies, and with confocal/single-molecule fluorescence microscopy.

SCIENTIFIC AREA WHERE THE PROJECT FITS BEST*

Chemistry (CHE)