

Introduction: The emerging technologies related to AI and Quantum Computing are shifting the nano-bio-info paradigm, reconsidering the presently assumed bioenergetic processes of the living cells. Thus, a key process as ATPase can be considered through a model governed by quantum field theory (QFT) describing the how the activities in living cells are carried out through the protein conformational dynamics. As long as proteins are seeking for quantum coherence, and the donor-acceptor length fluctuations are generating phonon tunneling effect (PCET) the collective effect matches the network-like behavior at cell level and the signaling mechanism that occurs as a collective effect.

Computational Methods: Bose-Einstein condensation equations were used in Molecular Dynamics (MD) modeling research meant to describe the quantum superposition and quantum entanglement of proton/phonon pumping mechanism. The MD model exported in MATLAB® was thereafter exported in COMSOL Multiphysics® through LiveLink™ for MATLAB®.

Results: A cell membrane model was designed in COMSOL Multiphysics® ; its functional properties were described through CFD, Semiconductor, Heat Transfer and Structural Mechanics modules.

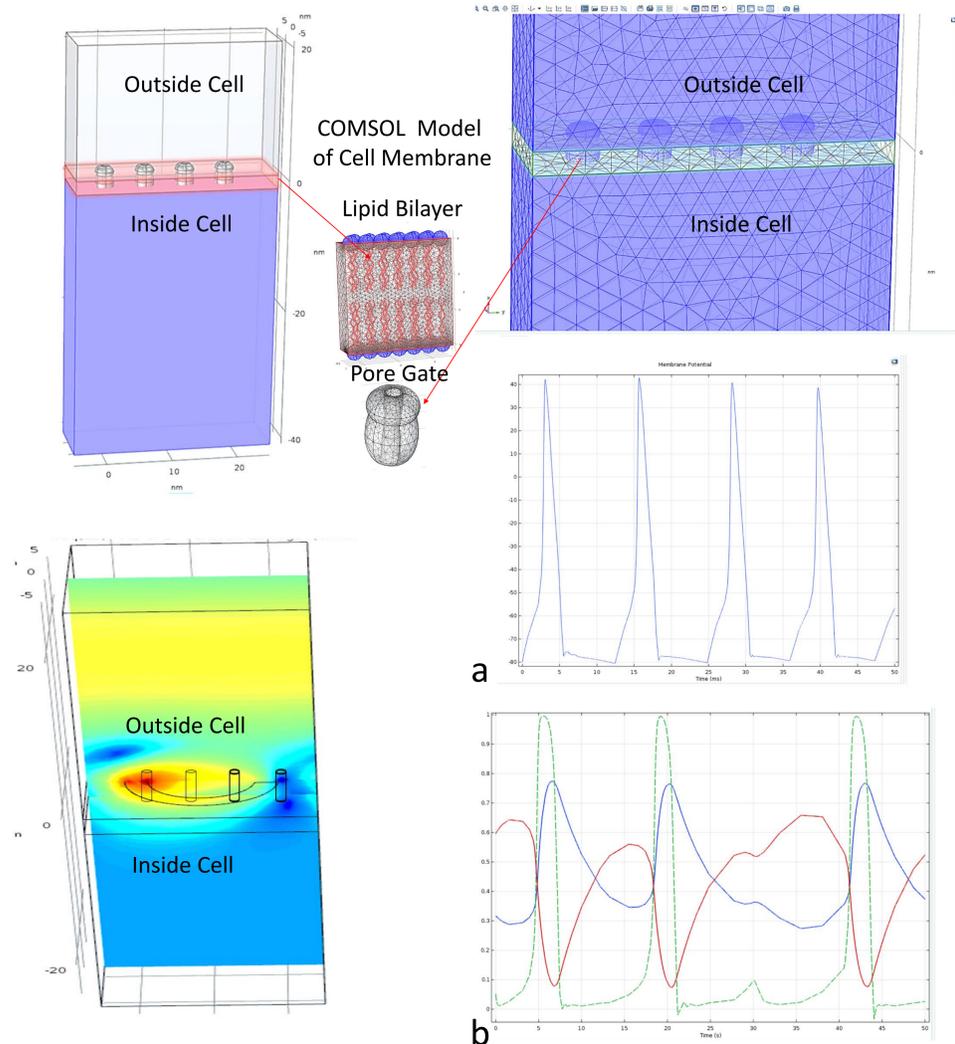


Figure 4.
COMSOL® Model
of Cell Membrane

Figure 5.
a. Cell Membrane potential
(Hodgkin-Huxley)
b. Electron Tunneling Effect

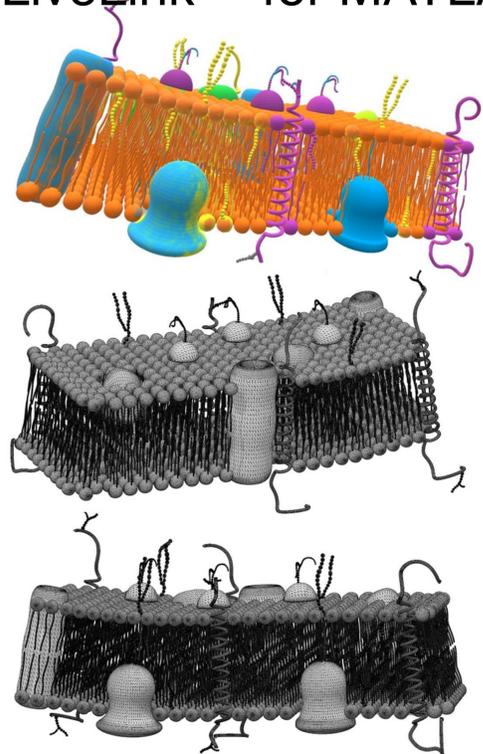


Figure 1. Cell Membrane

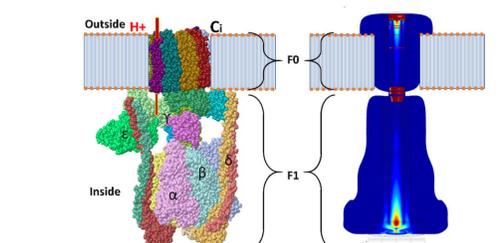


Figure 2. MD and COMSOL
functional description of ATP

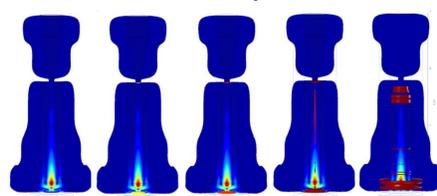


Figure 3. Functional stages on
ATP Synthase
(COMSOL Multiphysics®)-
Dynamic model

Conclusions: The envisaged cell membrane model has to describe ion channel gating pores, voltage-gated pores and the ATPase mechanism to create reliable nano-bio-info interfaces of the integrated modular-design concept for next generation of proactive biosensors.

References:

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