JCAD Reims 2023

Using high-performance computing to simulate plant membrane models and decipher lipid behavior

Camille Depenveiller[1,2], Benjamin Bouvier[1], Jean-Marc Crowet[3], Manuel Dauchez[3], Catherine Sarazin[1]

[1] UMR CNRS UPJV 7025 GEC (Génie Enzymatique et Cellulaire) – Université de Picardie Jules Verne

[2] UMR CNRS UB 5200 LBM (Laboratoire de Biogenèse Membranaire) – Université de Bordeaux

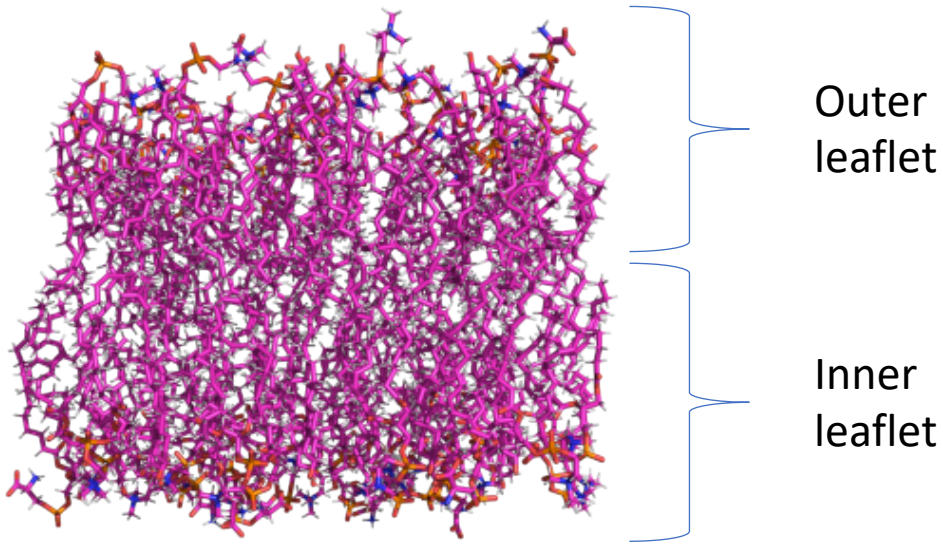
[3] UMR CNRS URCA 7369 MEDyC (Matrice Extracellulaire et Dynamique Cellulaire) – Université de Reims Champagne-Ardenne

October 3rd, 2023

Biological context

Studying plant membranes with numerical simulations

- Membranes are a lipid bilayer in which proteins are embedded
- Membranes constitute a barrier between cell and extracellular medium, site of numerous interactions
- Membrane fluidity: molecules and messages pass through thanks to membrane movements
- Studies and data from experiments such as biophysics
- Simulations for animal membranes, but poorly studied for plants



Molecular dynamics

Classical molecular dynamics in a few words

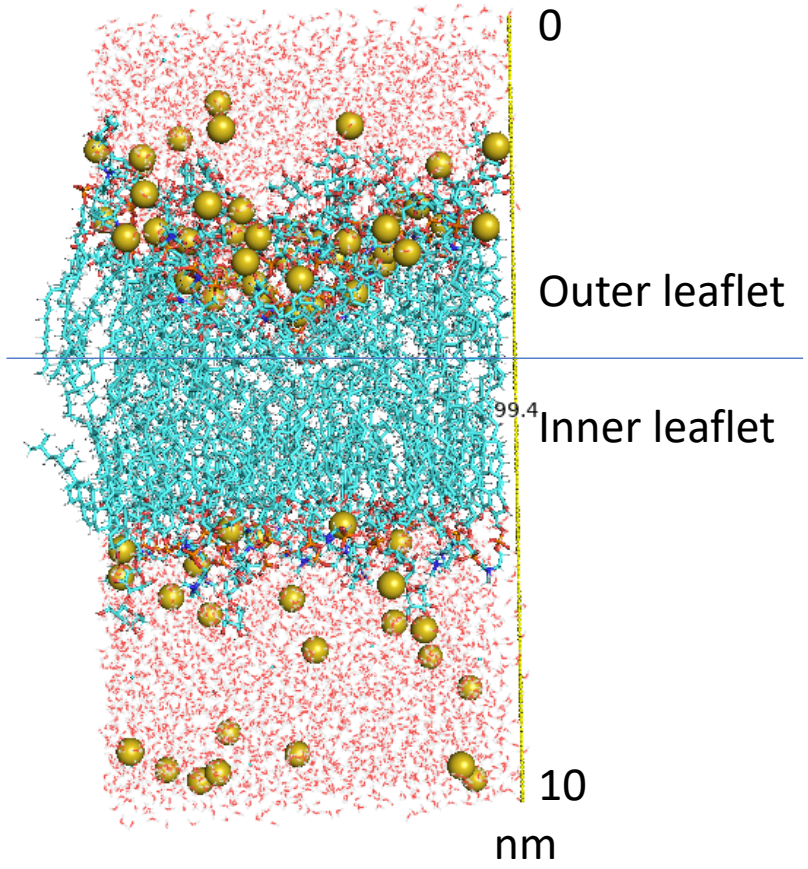
- Simulation method aiming at studying the evolution of a system
- Atom movements → forces → potential
- Potential energy equation: $E_{pot} = \underbrace{\sum_{bonds} + \sum_{angles} + \sum_{torsions}}_{\text{Bonded energy terms (chemical connectivity)}} + \underbrace{\sum_{elec} + \sum_{vdW}}_{\text{Non-bonded energy terms (interactions between atom pairs)}}$
- Molecular dynamics trajectories generate thousands of conformations, each composed of thousands of atoms

Molecular dynamics simulations

Preliminary simulation

Simulation parameters

- Membrane composition (representative of plants): 100 lipids of 3 different types (GIPC, POPC, cholesterol)
- 12,899 atoms of lipids, 29,639 with water molecules
- Simulation time: 200 ns



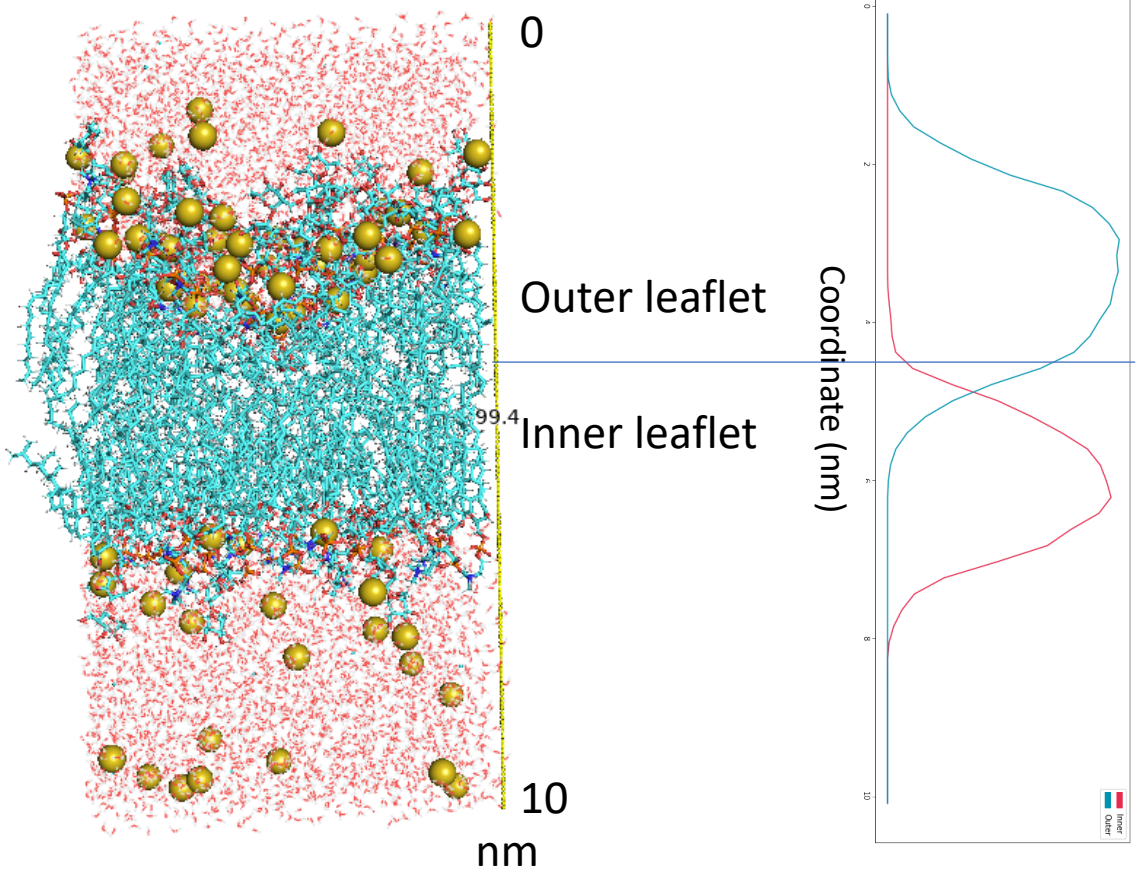
Infrastructure and technical aspects

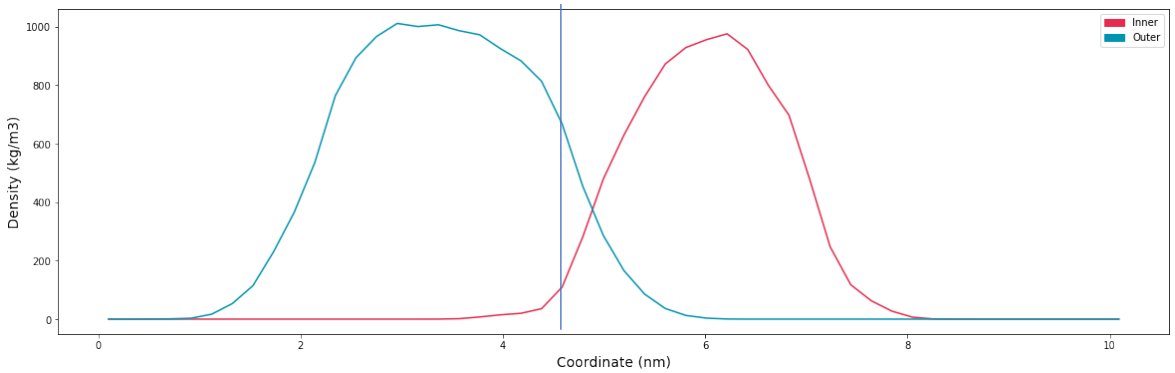
- ROMEO supercomputer: nodes with CPU Intel Skylake and GPU NVIDIA P100
- 1 node, 28 cores and 2 GPU
- Runtime: 22h

Compute interactions, energies…

Molecular dynamics simulations

Preliminary simulation

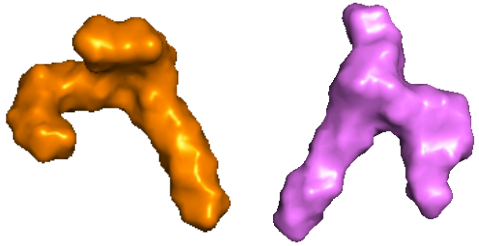




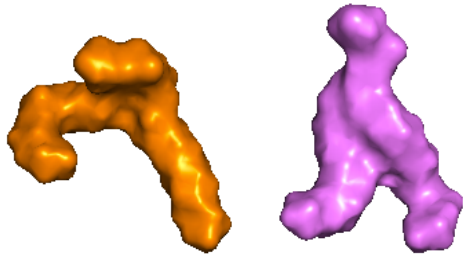
Lipids of outer leaflet are moving towards the inner leaflet

Molecular dynamics simulations

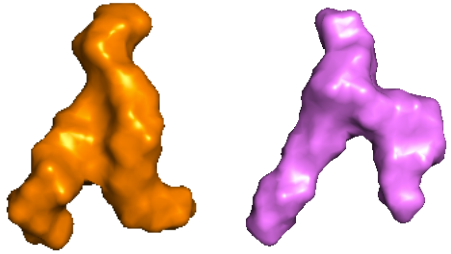
GIPC-PS simulations: 4 systems



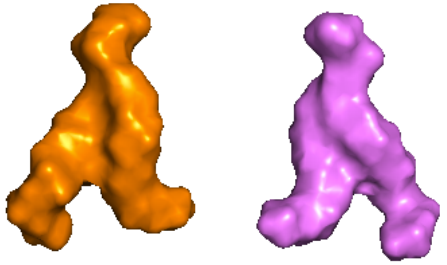
GIPC long – PS long



GIPC long – PS short



GIPC short – PS long



GIPC short – PS short

Evaluate chain length and interdigitation

Molecular dynamics simulations

GIPC-PS simulations: parameters

Simulation parameters

- Membrane composition: 100 lipids of 7 different types
- 13,316 atoms of lipids, 39,235 with water molecules
- Simulation time: 500 ns

Infrastructure and technical aspects

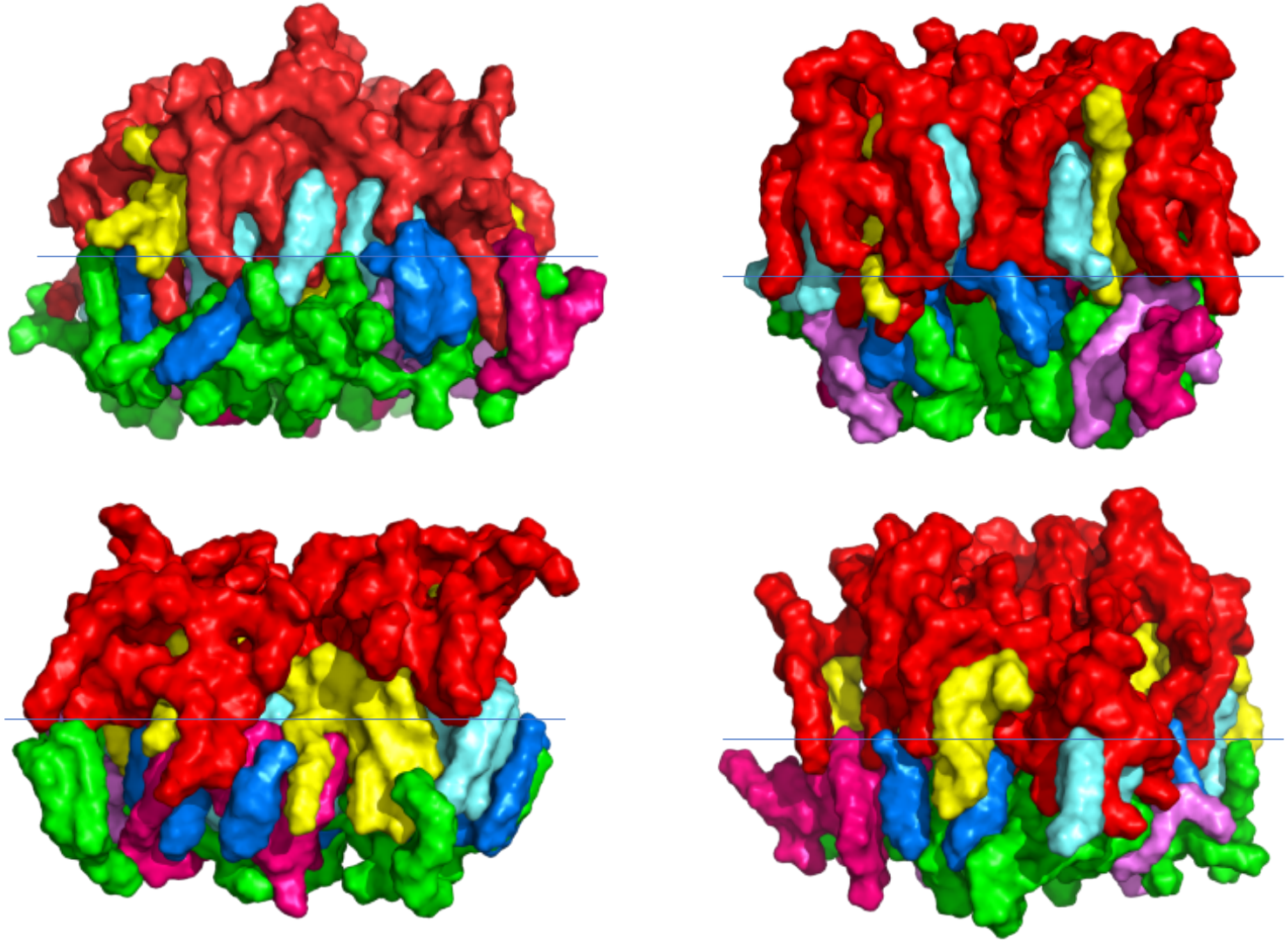
- ROMEO supercomputer: nodes with CPU Intel Skylake and GPU NVIDIA P100
- 1 node, 28 cores and 2 GPU
- Runtime: 5 days

Compute interactions, energies…

Molecular dynamics simulations

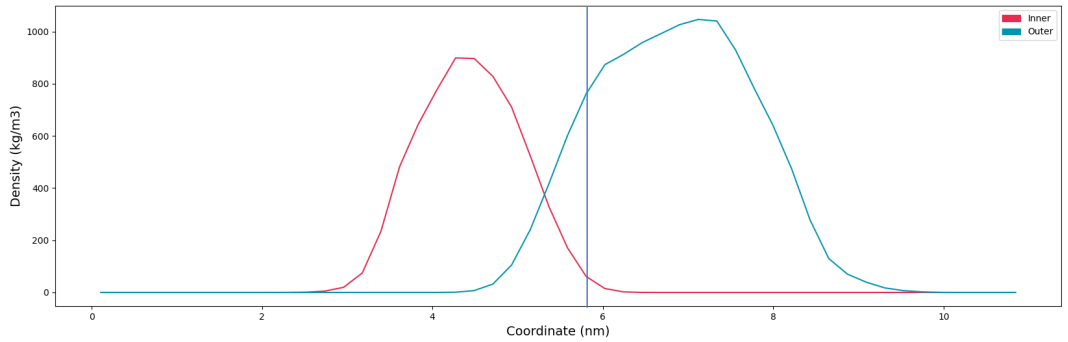
GIPC-PS simulations

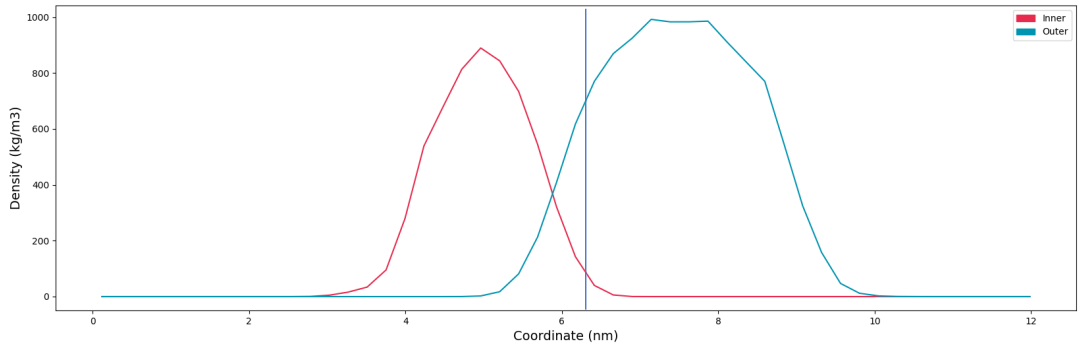
Interdigitation exists in all systems
Visually it can be easily observed

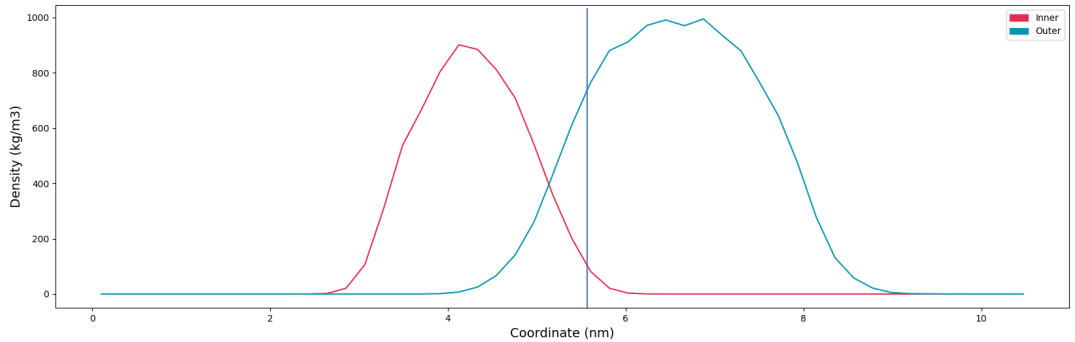


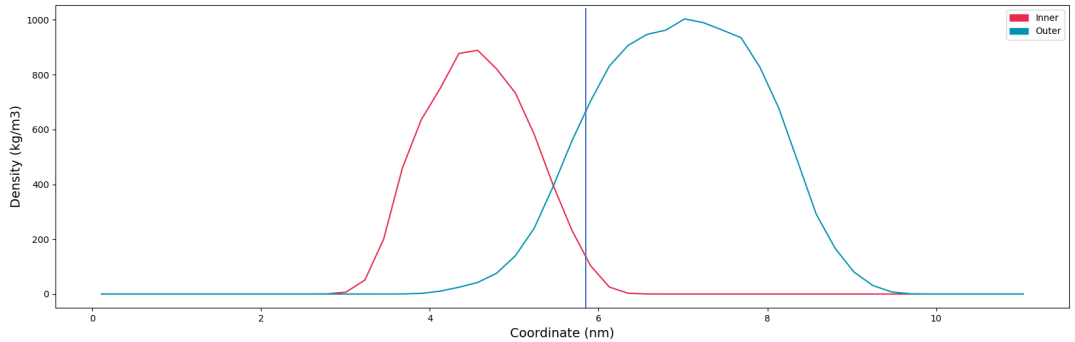
Molecular dynamics simulations

GIPC-PS simulations









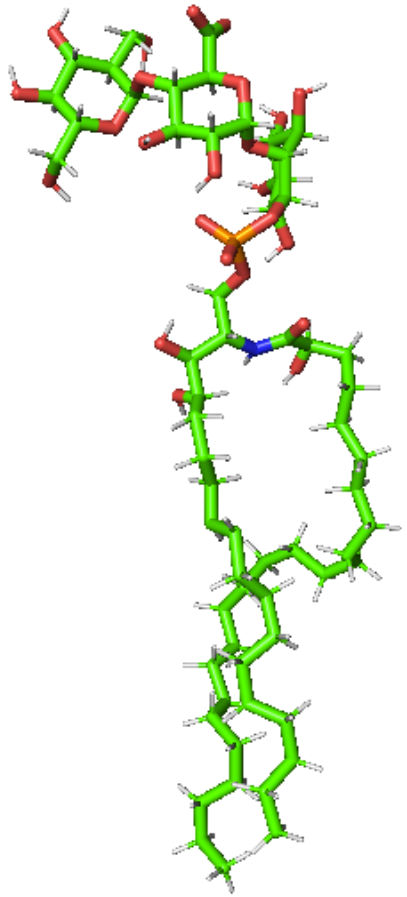
Interdigitation is confirmed in the crossing of density curves

Role of interdigitation in membrane function of transmitting messages between outside and inside

Coarse-grained simulations

Towards coarse-grained simulations

- Molecules are represented with beads, one bead corresponding generally to 4-5 atoms
- Different bead types available to reflect properties of the corresponding atoms
- Allows to reduce computing time by decreasing the number of elements in a system
- Allows to reach simulations at larger scales, on bigger systems and for longer simulation times



From all-atom to coarse-grained model

Conclusion and perspectives

Take-home messages

- Molecular dynamics simulations can help decipher plant membrane properties
- Use of computing resources with CPU and GPU allows to reach reasonable computing times together with good performance
- Molecular dynamics simulations allowed us to highlight interdigitation phenomenon in plant membrane: this communication between outer and inner leaflet shows that messages are able to pass through the membrane
- Coarse-grained simulations are an interesting method and are totally adapted to our work

Future work

- Deepen interdigitation analyses
- Simulate larger membrane systems (more representative of real plant membranes) thanks to coarse-grained simulations and the use of high-performance computing

Acknowledgments

cnrs
UNIVERSITÉ de Picardie Jules Verne
HPC Center ROMEO Centre de Calcul Régional
UNIVERSITÉ DE REIMS CHAMPAGNE-ARDENNE
université de BORDEAUX
anr agence nationale de la recherche
INRAE

Thank you for your attention!