High-throughput screening of drug-membrane thermodynamics

We introduce an importance sampling of chemical space via high-throughput MD simulations of the coarse-grained (CG) Martini model [1], in order to investigate the physical and chemical properties of small molecules inserted in a phospholipid bilayer. This approach allows us to identify linear relationships between key features of the potential of mean force and the water/oil partitioning of a compound [3]. We show that the results are representative of the transmembrane behavior of ~500,000 small molecules due the many-to-one mapping introduced by coarse-graining. We compare the coarse-grained predictions with atomistic simulations results by introducing a multiscale sampling technique which leverages CG configurations in order to enhance the sampling of the atomistic system [4].



<u>R. Menichetti</u>^{*,a}, K. H. Kanekal^{*}, K. Kremer^{*} and T. Bereau^{*}

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WHY MARTINI?



LINEAR RELATIONS [3]



Linear relations between interfacial free-energy barriers along the potential of mean force and water/oil partitioning. Inexpensive prediction for more than 500,000 compounds.

BACK TO ATOMISTIC

Efficient phase-space sampling by leveraging coarse-grained simulations [4]

- 1) Select a set of **uncorrelated** snapshot from the CG trajectory.
- 2) Backmap each CG configuration onto atomistic.
- 3) Run a set of **short** atomistic simulations.
- 4) Average over the set.



COARSE-GRAINING CHEMICAL SPACE

Automated parametrization of the Martini force-field [1][2] for coarse-graining ~500,000 small molecules.



Many compounds map onto one CG representation. - Discrete number of Martini [1] bead types coarsens variety of chemical groups.

**Max Planck Institute for Polymer Research, Mainz, Germany* a) E-mail address: <u>menichetti@mpip-mainz.mpg.de</u>

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