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ALPHA-HELICAL AND BETA-SHEET MEMBRANE-MEMBRANE PROTEIN DIMERS: CENTRALIZING INFORMATION

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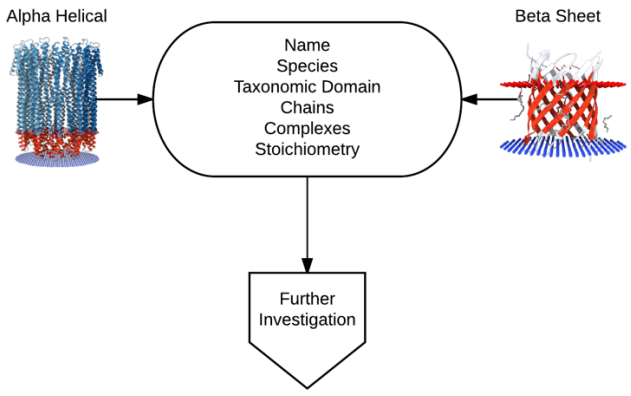
Graphical Abstract



Abstract.

Bioinformatics allows to automatically characterize a large number of proteins from numerous different databases[1], thus, uncovering new possible interactions between biomolecules in a huge set of individuals in a conscious and cost-efficient way[2]. Membrane proteins are indisputably important for the assurance of major processes in the cell, occupying approximately 25% of the whole cell genome[3]. In this work, some of the major features displayed at Protein Data Bank[4] (original species, chains and ligands, oligomer state, multimeric states, stoichiometry, among others) of membrane proteins listed in the Membrane Proteins with Known 3D Structure[5] database were registered together using manual and automated methods - some of these methods include the usage of python specific tools (like Selenium[6] and BioPython[7]). We aimed to construct a membrane-membrane dimers database that will serve as input for data-mining algorithms to unveiling new functional and evolutionary knowledge.

References

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