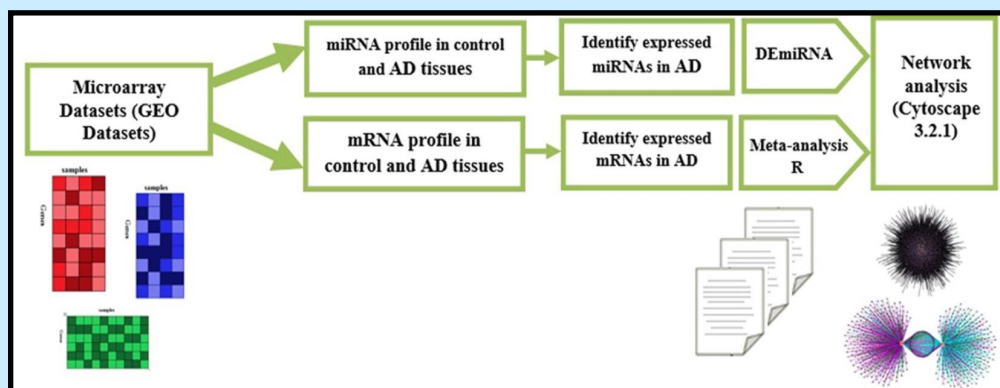


Analysis of microRNA and Gene Expression Profiles in Alzheimer's Disease: A Meta-Analysis Approach

The molecular mechanisms underlying Alzheimer's disease (AD) is necessary for the diagnosis and treatment of this neurodegenerative disorder. It is therefore important to detect the most important genes and miRNAs, which are associated with molecular events, and studying their interactions for recognition of AD mechanisms. Here researchers focus on the genes and miRNAs expression profile, which they have detected the miRNA target genes involved in AD. These are the most quintessential to find the most important miRNA, to target genes and their important pathways. A total of 179 differentially expressed miRNAs (DEmiRs) and 1404 differentially expressed genes (DEGs) were obtained from a comprehensive meta-analysis.

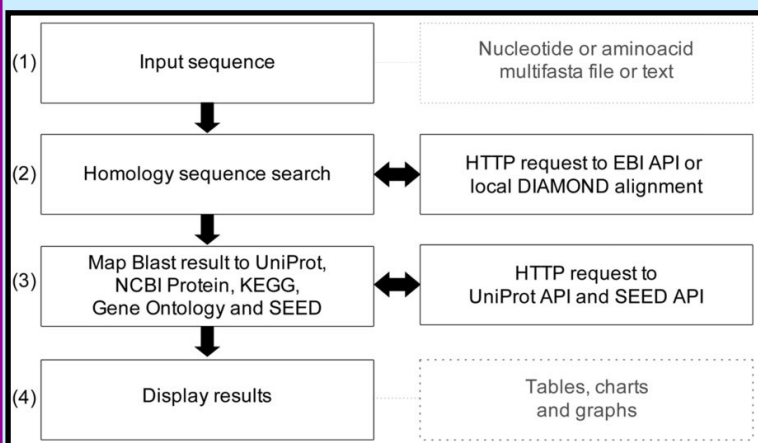


Also, regions specific genes with their molecular function in AD have been demonstrated. Then they focused on miRNAs which regulated most genes in AD, alongside we analyzed their pathways. The miRNA-30a-5p and miRNA-335 elicited a major function in AD after analyzing the regulatory network, they showed they were the most regulatory miRNAs in the AD. In conclusion, the most important genes, miRNAs, miRNA-mRNA interactions and their related pathways in AD using Bioinformatics methods. Accordingly, their defined genes and miRNAs could be used for future molecular studies in the context of AD.

Source :Shirin Moradifard *et al.* J Scientific Reports(2018)

GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data.

Downstream analysis of genomic and transcriptomic sequence data is often executed by functional annotation that can be performed by various bioinformatics tools and biological databases. However, a full fast integrated tool is not available for such analysis. Besides, the current available software is not able to produce analytic lists of annotations and graphs to help users in evaluating the output results. Therefore, researchers present the Gene Ontology Functional Enrichment Annotation Tool (GO FEAT), a free web platform for functional annotation and enrichment of genomic and transcriptomic data based on sequence homology search. The analysis can be customized and visualized as per users' needs and specifications. GO FEAT is freely available at <http://computationalbiology.ufpa.br/gofeat/> and its source code is hosted at <https://github.com/fabriciopa/gofeat>.



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Source: Fabricio Almeida Araujo *et al.* J Sc. Reports,(2018)

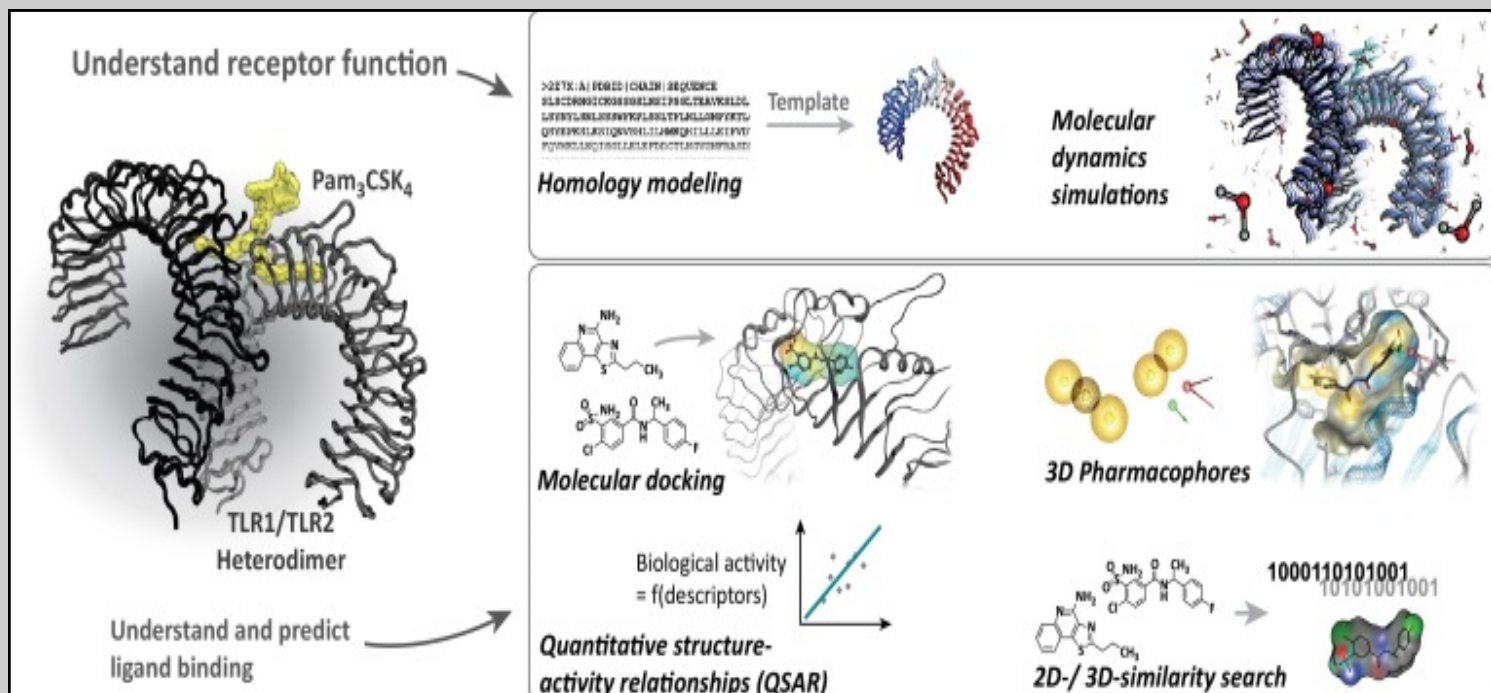
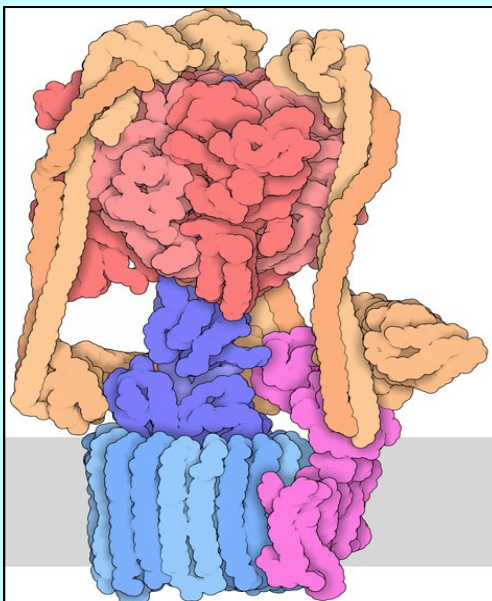


Fig: Overview on Aims and Methods in Computer-Aided Drug Design

An overview on the key methods used to understand protein function (top) and to elucidate and predict ligand binding (bottom) in computer-aided drug design is given. Molecular dynamics simulations and homology modeling are often utilized to unravel structure and function of the receptors. Molecular docking, QSAR, similarity searches and 3D pharmacophores are used to identify novel receptor ligands and understand their binding modes.

Vacuolar ATPase

The vacuolar ATPase (V-ATPase) is an ATP-powered proton pump composed of two rotary motors, as shown here from PDB entry 5vox. The portion at the top (shown in pink) is an ATP-driven motor that turns an axle (shown in dark blue). This then turns a second motor (light blue and magenta) that pumps protons across the membrane. The remaining protein chains (shown in orange) hold the whole complex together and make sure that the rotation of one motor is used to power the rotation of the other. V-ATPase is regulated by breaking the complex in half when it is not needed.



The ATP-powered motor separates from the proton pumping motor, stopping the process. Then, when they are needed again, they are re-connected and pumping restarts. V-ATPases are made by eukaryotic cells and are used to control acidity. V-ATPases are complex molecular machines with many moving parts, so they have proven difficult to study. Currently, the most complete structures have been obtained by cryoelectron microscopy.

V/A-ATPases (PDB entry 5gar) have a variety of functions, as proton pumps or ATP generators. As an additional twist, some of these rotary pumps use sodium ions instead of protons.

Source : <http://pdb101.rcsb.org/motm/219>



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Intelligent data integration system

Taylor *et al.*

Data objects stored in a data store include data attribute(s) and associated value(s) for the attributes. Data analysis tools (DATs) stored in a data store are associated with reference data attribute(s). The data objects are identified by one or more DATs based on each reference data attribute(s) of a corresponding DAT matching one of the data attribute(s) of the corresponding data object(s) and independent of the value for the data attribute(s). The DATs generate an additional data object as a function of the identified data object, and the additional data object is stored in the data store.

Kindly send us your feedback to

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