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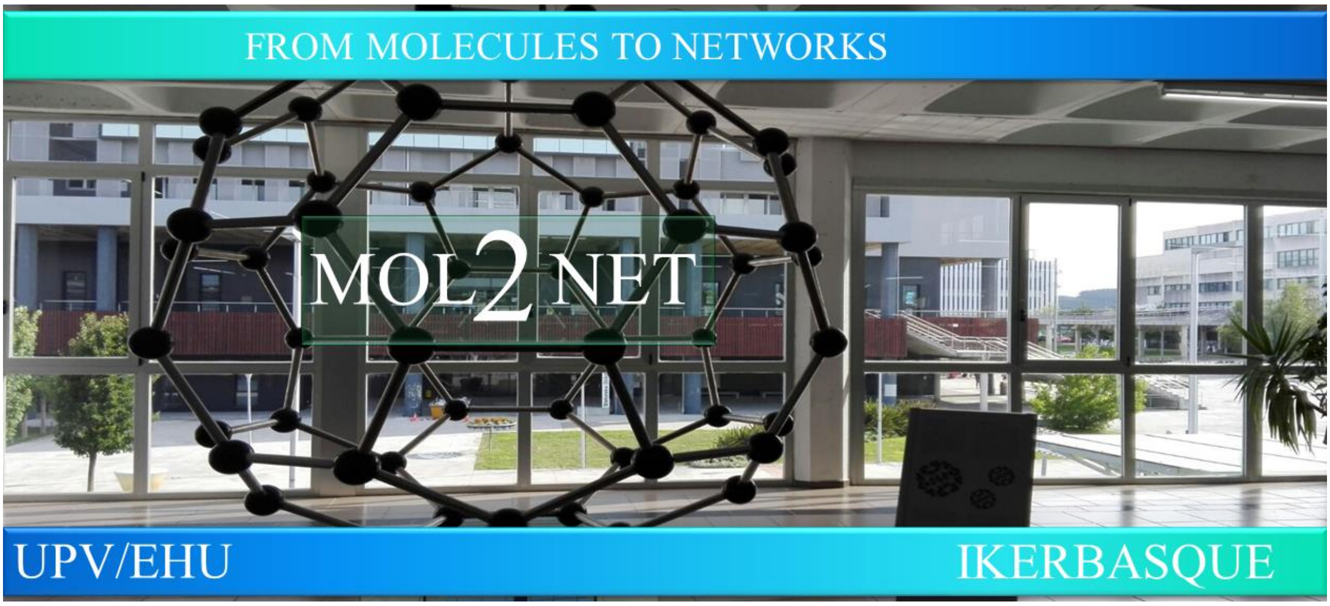

Computational Methods Applied to Alzheimer’s Disease

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Abstract.

Alzheimer's disease (AD), the most common type of dementia in older people, causes neurological problems associated with memory and thinking. Different computational analysis could act as useful tools in gaining more information about the development of the disease or potential target drugs. That is why different computational methods will be reviewed.

Alzheimer's disease (AD), the most common type of dementia in older people, causes neurological problems associated with memory and thinking. The scientists are dedicated to studying the detection of Alzheimer's disease onset to find a cure, or at the very least, medication that can slow the progression of the disease. Identifying AD involves a deliberate diagnostic process owing to its innate traits of irreversibility with subtle and gradual progression. These characteristics make AD biomarker identification from structural brain imaging scans quite challenging. In this context, different computational analysis could act as useful tools. That is why different computational methods will be reviewed in the next sections.

To start with, Iroshan Aberathne, Don Kulasiri and Sandhya Samarasinghe [1] determined whether longitudinal analysis and machine learning would be useful on the detection of AD onset using MRI and PET neuroimaging. They explored the efficiency of longitudinal data analysis, artificial intelligence, and machine learning approaches based on magnetic resonance imaging and positron emission tomography neuroimaging modalities for progression estimation and the detection of Alzheimer's disease onset. They concluded that developing automated methods to improve the aforementioned research areas would enable specialists to determine the progression of the disease and find the link between the biomarkers and more accurate detection of Alzheimer's disease onset.

Moreover, Qazi Mohammad Sajid Jamal *et al.* [2] used Docking Simulations for the identification of natural compounds of the apple as inhibitors against cholinesterase for the treatment of AD. Acetylcholinesterase (AChE) and butyrylcholinesterase (BuChE) are one of the key enzymes involved in AD pathways. Due to this, there is a lot of interest in finding new AChE and BuChE inhibitors. In this context, computational tools and biological databases were used to investigate enzymes and natural compounds. Molecular docking techniques were used to analyze the interactions of natural compounds of the apple with enzymes involved in the central nervous system (CNS), acetylcholinesterase, and butyrylcholinesterase, followed by binding affinity calculations using the AutoDock tool. The molecular docking results revealed that CID: 107905 exhibited the best interactions with AChE, with a binding affinity of -12.2 kcal/mol, and CID: 163103561 showed the highest binding affinity with BuChE, i.e., -11.2 kcal/mol. Moreover, the results of the Molecular Dynamics Simulation (MDS) analysis indicated interaction stability. This study showed that CID: 12000657 could be used as an AChE inhibitor and CID: 135398658 as a BuChE inhibitor to treat Alzheimer's disease and other neurological disorders.

Last but not least, Ahmad Wisnu Mulyadi *et al.* [3] estimated explainable AD likelihood map via clinically-guided prototype learning. They proposed a novel deep-learning approach through eXplainable AD Likelihood Map Estimation (XADLiME) for AD progression modeling over 3D sMRIs. Specifically, they established a set of topologically-aware prototypes onto the clusters of latent clinical features, uncovering an AD spectrum manifold. Considering this pseudo map as an enriched reference, they employed an estimating network to approximate the AD likelihood map over a 3D sMRI scan. Additionally, they promote the explainability of such a likelihood map by revealing a comprehensible overview from clinical and morphological perspectives. During the inference, this estimated likelihood map served as a substitute for unseen sMRI scans for effectively conducting the downstream task while providing thorough explainable states.

In conclusion, the significance of computational methods in the healthcare field is steadily growing. Numerous studies have demonstrated the value of techniques like machine learning, docking simulations, and prototype learning in obtaining valuable insights about diseases and potential treatments. The potential of these methods to aid scientists in making critical decisions is apparent, which may lead to increased adoption of these tools in the near future. As the field of healthcare continues to evolve, computational methods are expected to play an even more pivotal role in advancing our understanding and treatment of diseases.

References

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