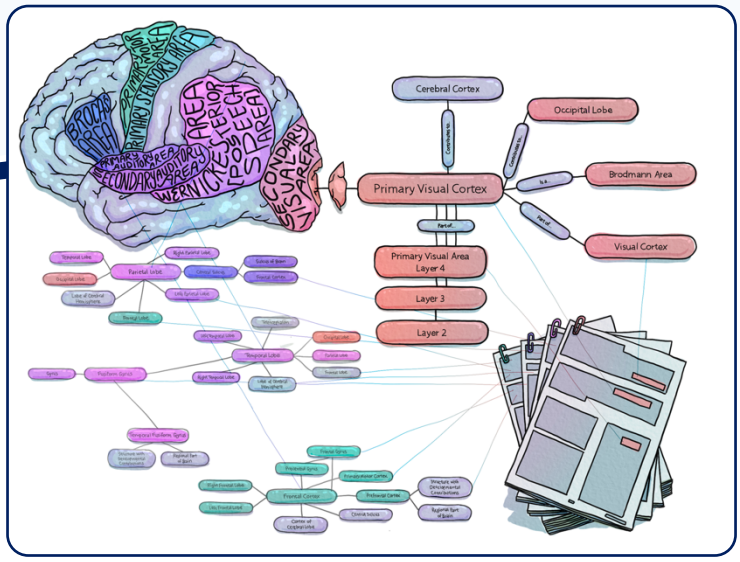
VirtualBrainCloud

Personalized Recommendations for Neurodegenerative Disease



Public deliverable report

D5.4: Demonstrator and publication: A semantically enhanced multi-viewer that embeds a newly developed TVB 3D viewer that allows for integration of personalized 3D coordinates with knowledge about pathways and mechanisms “in situ”

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1. Introduction

The objective of The VirtualBrainCloud (TVB-Cloud) project is to develop and validate the VirtualBrainCloud, a dedicated cloud-based environment that leverages the potential of big data and high-performance computing (HPC) for personalized prevention and treatment of neurodegenerative diseases (NDD). TVB-Cloud is embedded in The European Open Science Cloud Initiative. It combines already existing technologies and contributes to the development of new Information and communication technology (ICT) services while ensuring the appropriate data safety and protection.

To facilitate the integration of various multimodal knowledge and data sources into one consistent framework, we developed a software tool "The Virtual Brain Knowledge Base Adapter - TVBase" that maps semantic information from the automated literature-mining derived knowledge base SCAIView[1] to a parcellated 3D template brain. This quantitative analysis of semantic metadata (semantic meta-analysis) is further enriched by raw data from receptor autoradiography and transcriptomics, as well as with results from coordinate-based meta-analyses.

- TVBase bridges literature mining and brain simulation
- Biological knowledge about the brain is projected on to a 3D template brain in the form of semantic association maps
- The maps created show high validity compared to established tools for automated meta-analysis
- TVBase proposes framework for integrating multi-modal data and metadata from brain research

2. Results

For this framework, we developed a novel methodological workflow that maps and integrates information from ontologies, and neuroscientific databases onto existing human brain atlas parcellations in standard coordinate spaces. A common reference space based on the minimal processing pipelines of the Human Connectome Project (HCP) was used (Glasser et al., 2013) to foster comparability and interoperability. Our methodology enables the complete anatomical mapping of any biomedical concept.

2.1 Demonstrator

A demonstration video illustrating the functionality of the new tool TVBase has been published on our website and in our YouTube channel

https://virtualbraincloud-2020.eu/tvb-cloud-videos.html

https://www.youtube.com/watch?v=QzEyD-9HOw8

[1] https://academia.scaiview.com/

2.2 Publication

The general concept of the new tool that provides a means to integrate biological knowledge and data in brain network models has been published in Stefanovski et al., 2021 (Figure 1). A methods paper describing the innovative technology is in preparation.

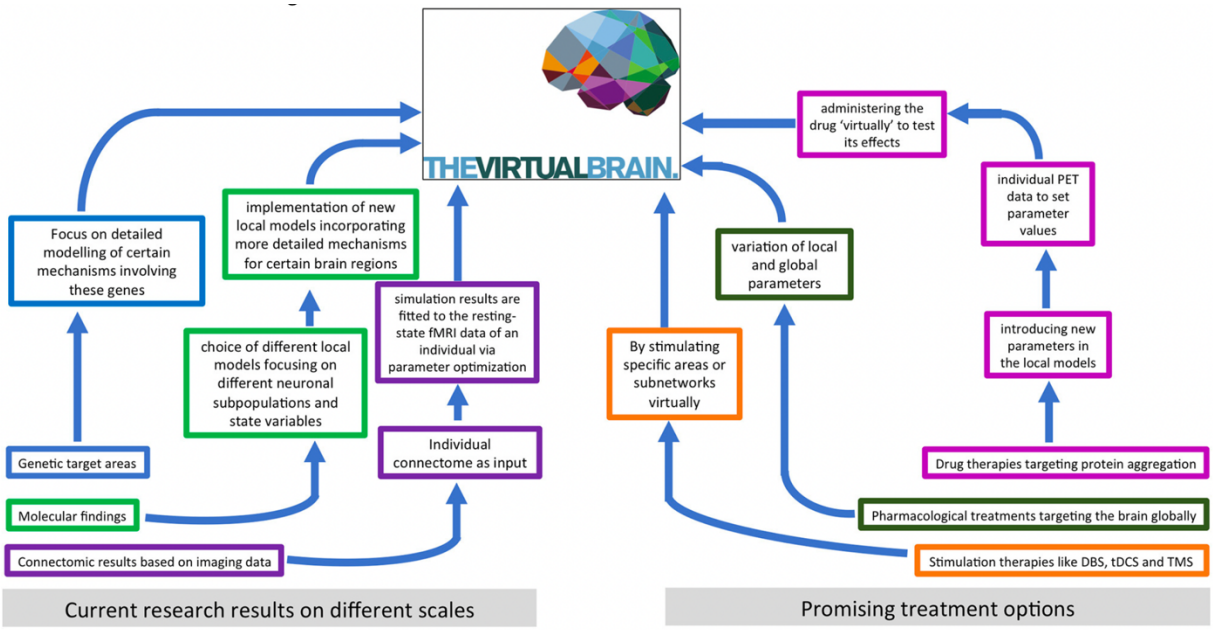

Figure 1: How to integrate different advances from Alzheimer's Disease research into The Virtual Brian computational modeling framework? Computational modeling provides a powerful tool to link empirical findings from different scales and disciplines to new insights for improved diagnostics and treatments. PET, positron emission tomography; DBS, deep brain stimulation; tDCS, transcranial direct current stimulation; TMS, transcranial magnetic stimulation. (Stefanovski et al. 2021)

Our recent publications demonstrate the potential of complex multiscale simulation for innovative breakthroughs in diagnostics, prediction, classification, in silico intervention planning and mechanism discovery in Alzheimer's disease (Meier et al., 2021; Schirner et al. 2021; Stefanovski et al. 2019; Triebkorn et al., 2021).

3. Conclusions

Using complex computational multi-scale models for brain simulations in future research may lead to improved diagnostics in the early stages of dementia, to a more precise prognostic prediction and differential diagnosis which are the fundamentals of rational medical treatment of AD patients. The here developed TVBase tool helps to enrich computational models of the brain with existing biological knowledge from various and data sources.

4. References

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