

Materials List for

DeepOmicsAE: Representing Signaling Modules in Alzheimer's Disease with Deep Learning Analysis of Proteomics, Metabolomics, and Clinical Data

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jove.com/video/65910

Materials

Name	Company	Catalog Number	Comments
Computer	Apple	Mac Studio	Apple M1 Ultra with 20-core CPU, 48-core GPU, 32-core Neural Engine; 64 GB unified memory
Conda v23.3.1	Anaconda, Inc.	N/A	package management system and environment manager
conda environment DeepOmicsAE	N/A	DeepOmicsAE_env.yml	contains packages necessary to run the workflow
github repository DeepOmicsAE	Microsoft	https://github.com/elepan84/DeepOmicsAE/	provides scripts, Jupyter notebooks, and the conda environment file
Jupyter notebook v6.5.4	Project Jupyter	N/A	a platform for interactive data science and scientific computing
DT01-metabolomics data	N/A	ROSMAP_Metabolon_HD4_Brain 514_assay_data.csv	This data was used to generate the Results reported in the article. Specifically, DT01-DT04 were merged by matching them based on the individualID. The column final consensus diagnosis (cogdx) was filtered to keep only patients classified as healthy or AD. Clinical features were filtered to keep the following: age at death, sex and education. Finally, age reported as 90+ was set to 91, then the age column was transformed to float64. The data is available at https://adknowledgeportal.synapse.org
DT02-TMT proteomics data	N/A	C2.median_polish_corrected_log2 (abundanceRatioCenteredOn MedianOfBatchMediansPer Protein)-8817x400.csv	
DT03-clinical data	N/A	ROSMAP_clinical.csv	
DT04-biospecimen metadata	N/A	ROSMAP_biospecimen_metadata.csv	

Python 3.11.3	Python Software Foundation	N/A	programming language
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