Kaleidoscope: An app for exploratory data analysis of psychiatric disorders

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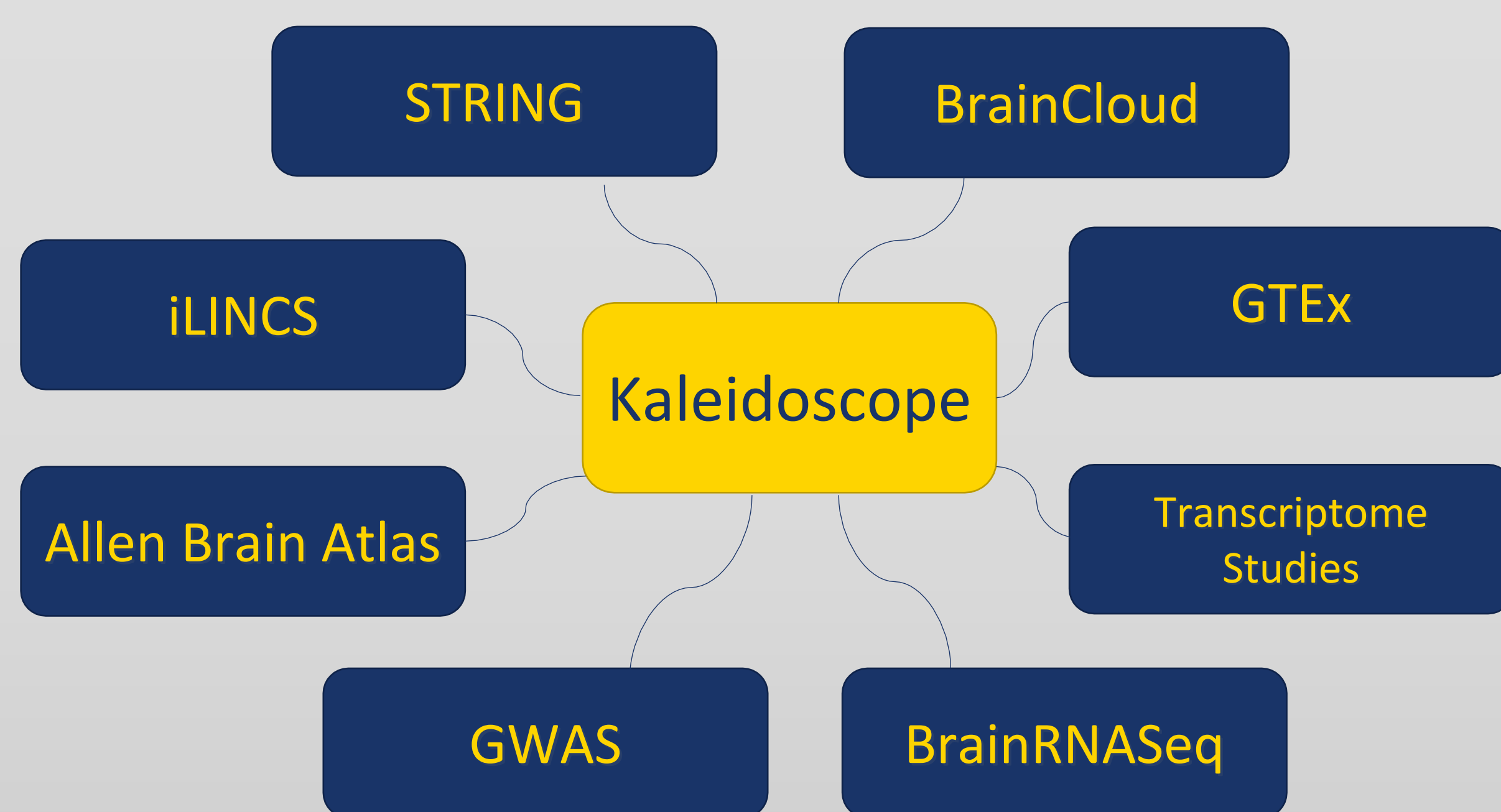
Abstract/Introduction

An ever-increasing number of bioinformatic tools are being developed to process, analyze and view a wide range of biological datasets. However, with that growing number of biological databases and bioinformatic tools, it becomes difficult to discover and learn how to use these tools, especially for those who are not well versed in the bioinformatics field. We observed that a large number of biological databases and bioinformatics tools that are relevant to psychiatric disorders are relatively untapped. We developed a platform that aims to mitigate this issue.

Kaleidoscope is an interactive R Shiny web application that provides a platform for an easy access to biological databases and bioinformatics tools via a user-friendly interface that could be explored by researchers to test hypothesis in silico. Fully utilizing these robust bioinformatics tools and rich biological databases, interesting information can be obtained that could be very valuable to the field of biological psychiatry. The observations obtained from this platform could supplement existing hypotheses, spawn new ones and possibly direct future studies
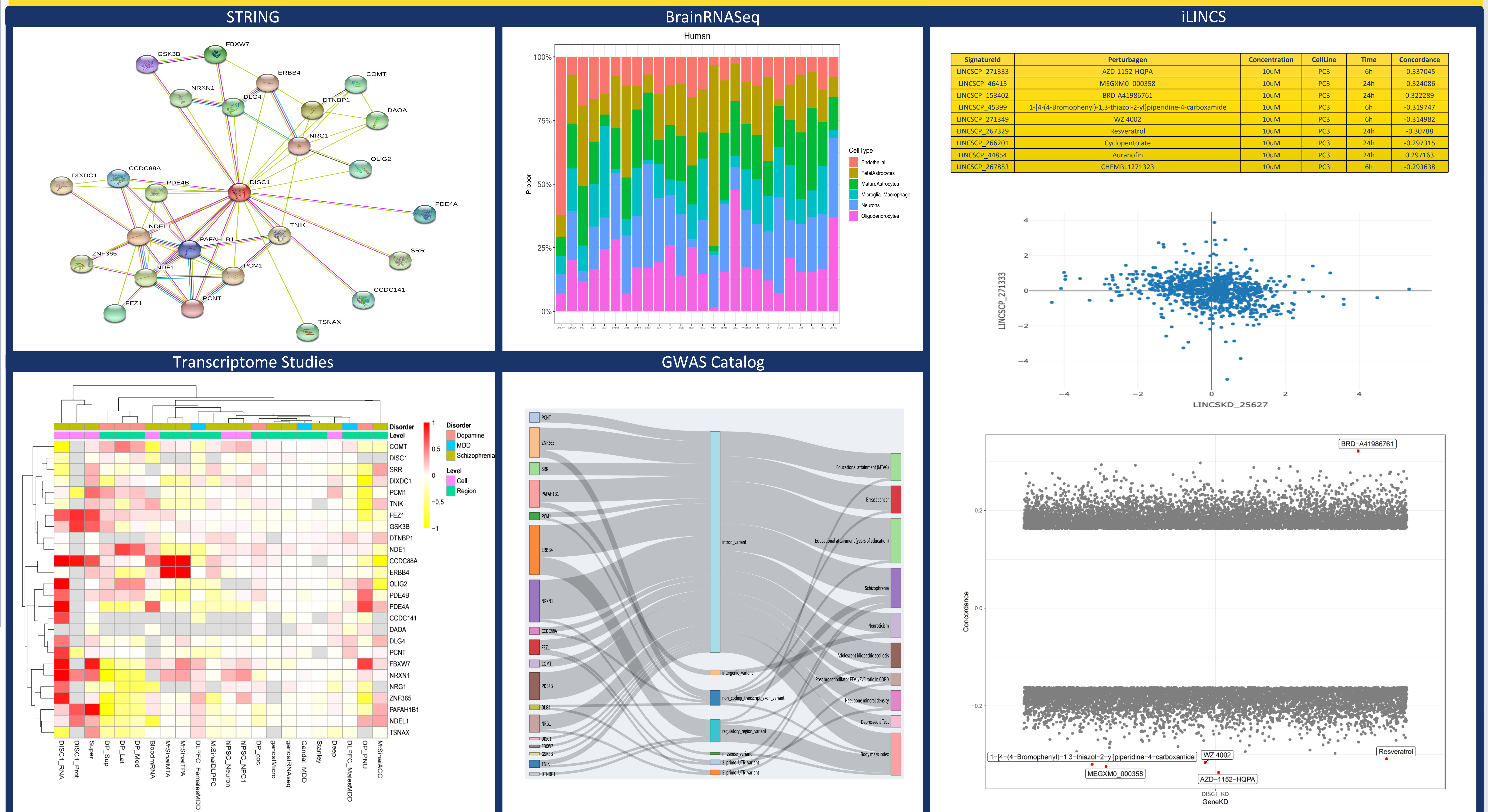
Methods

STRING — BrainCloud

iLINCS — Kaleidoscope — GTEx

Allen Brain Atlas — Transcriptome Studies

GWAS — BrainRNASeq

- The application utilizes many of these tools APIs (Application Programming Interface) to access their databases and extract and present their data in tidy tabular format and meaningful visualizations.

- The app takes advantage of published transcriptome studies and aggregate and harmonize their results to observe patterns of differential gene expressions across multiple datasets.

Results: Using DISC1 as a Demonstration Example

Disrupted in schizophrenia 1 (DISC1) has emerged as a strong candidate gene underlying the risk for major mental disorders. We performed an in-silico analysis starting with this single gene using Kaleidoscope.

STRING

BrainRNASeq

Human

CellType: Endothelial, FetalAstrocytes, MatureAstrocytes, Microglia_Macrophage, Neurons, Oligodendrocytes

iLINCS

SignatureId	Perturbagen	Concentration	CellLine	Time	Concordance
LINCSCP_271333	AZD-1152-HQPA	10uM	PC3	6h	-0.337045
LINCSCP_46415	MEGXM0_000358	10uM	PC3	24h	-0.324086
LINCSCP_153402	BRD-A41986761	10uM	PC3	24h	-0.322289
LINCSCP_45399	1-[4-(4-Bromophenyl)-1,3-thiazol-2-yl]piperidine-4-carboxamide	10uM	PC3	6h	-0.319747
LINCSCP_271349	WZ 4002	10uM	PC3	6h	-0.314982
LINCSCP_267329	Resveratrol	10uM	PC3	24h	-0.30788
LINCSCP_266201	Cyclopentolate	10uM	PC3	24h	-0.297315
LINCSCP_44854	Auranofin	10uM	PC3	24h	-0.297163
LINCSCP_267853	CHEMBL1271323	10uM	PC3	6h	-0.293638

Transcriptome Studies

GWAS Catalog

Discussion

- Seeing patterns of differential gene expressions across multiple datasets could be a strong indication that a gene or a panel of genes is involved in the disease process.

- This panel of genes can be then further investigated for pathway analysis or in silico drug discovery through iLINCS.

- Integrating multiple databases and tools and exploring them through a single and cohesive bioinformatics platform helps the users to explore their questions in a broader view. The idea of providing light and fast process of exploring databases is vital to the concept of data exploration which is the core aim of this application.

- The platform can be utilized in many forms and offers great scalability with the option of uploading user defined datasets for comparison alongside the pre-defined datasets to better suit the user's research interests.

- This tool will facilitate the introduction of bioinformatics approaches to neuroscientists, promoting educated use of bioinformatics pipelines in this field, while also providing the features of customizing it for other areas of study. The app is publicly available via a web page and can be accessed from any web browser.

References

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https://kalganem.shinyapps.io/BrainDatabases/