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## Pathway Analysis: Integrating Public Omics Datasets with ReactomeGSA



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Pathway analysis has become a cornerstone in deciphering 'omics datasets, providing a comprehensive view of biological processes affected by genetic and molecular changes. Unlike traditional single-gene analyses, quantitative pathway methods offer higher statistical power, simplifying the interpretation by linking observed alterations to defined biological pathways. Reactome Knowledgebase stands out as a premier resource, offering manually curated pathways enriched with detailed annotations, facilitating intuitive exploration of molecular transformations and biological processes.

[ReactomeGSA](#), a robust analysis platform, takes pathway analysis a step further by enabling the comparison of multiple 'omics datasets simultaneously. Recent validations confirm ReactomeGSA as a top performer in multi-omics pathway analysis, owing to its ease of use and stability. To streamline data access, ReactomeGSA integrates with leading repositories like Expression Atlas and GREIN, providing researchers with a vast array of public datasets. While Expression Atlas offers curated microarray, transcriptomics, and proteomics datasets, GREIN focuses on re-processing transcriptomics data from GEO and SRA, boasting over 25,000 datasets.

To bridge the gap between public datasets and analysis tools, ReactomeGSA introduces grein loader, a Python package facilitating direct dataset retrieval from GREIN. This open-source tool simplifies data integration into existing workflows, enhancing compatibility with Python-based bioinformatics pipelines. Additionally, ReactomeGSA extends support for GREIN through a custom cache, enabling seamless dataset loading by simply entering the GEO identifier.

The incorporation of a keyword-based search function further enhances data accessibility, allowing users to swiftly identify relevant datasets from Expression Atlas and GREIN. Leveraging the Whoosh library for fast keyword-based searches, ReactomeGSA ensures an average response time of 0.064 seconds per request. This feature, integrated into the ReactomeGSA R/Bioconductor package, facilitates efficient dataset retrieval and analysis within R-based workflows, marking a significant advancement in integrating GREIN datasets into R/Bioconductor environments.

In tandem with data integration enhancements, ReactomeGSA undergoes a user-centric redesign, featuring an intuitive web interface built on Angular and Angular Material. The addition of an interactive tutorial within the interface streamlines user onboarding, guiding users through each step of the analysis process. Furthermore, a novel table component simplifies metadata entry, supporting direct copy-paste functionality and facilitating data upload and download.

As a testament to ReactomeGSA's commitment to user empowerment, the new web frontend enables users to download both metadata and expression values of public datasets, promoting data reuse and collaboration. These updates aim to democratise pathway analysis, empowering researchers with enhanced tools for comprehensive exploration of 'omics datasets.

In conclusion, ReactomeGSA's latest advancements represent a significant leap forward in pathway analysis, facilitating seamless integration of public 'omics datasets and empowering researchers with intuitive tools for in-depth exploration and interpretation of biological processes.

Source: [Bioinformatics journal](#)

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