**API:** GSEApy and Enrichr API

**Description:** GSEApy is a suite of tools implemented in Python/Rust to conduct gene set enrichment analysis (GSEA). A subset of gene set enrichment analysis is overrepresentation analysis, which computes the significance of overlap between an input gene set and a set of related genes or enrichment terms called gene set libraries. These gene set libraries have enrichment terms that are typically biologically meaningful to give interpretability and significance to a list of genes. GSEApy is a wrapper and an API for Enrichr, a website conducting overrepresentation analysis for many well-known gene set libraries such as the Gene Ontology (GO), Kegg, Reactome, and HDSigDB. Other tools implemented in GSEApy generate publication-worthy figures from results derived from the Enrichr API. It is important to note that an internet connection is required to run the Enrichr API.

**Tutorial:**

<https://colab.research.google.com/drive/1YLipihIH9RxP6ATSQwcFvPeWD6qBV_Vj?usp=sharing>

**Use cases:**

* Identify important biological processes underlying a set of differentially expressed genes derived from statistical testing of transcriptomic data (e.g. scRNA-seq or bulk RNA-seq) between two conditions (e.g. control vs. experimental) or between clusters (scRNA-seq specific).
* Generate figures such as dot plots and bar charts, visualizing the top enrichment terms for a gene set library.