

SigBio-Shiny

A standalone interactive application for detecting biological significance on a Gene-Set.

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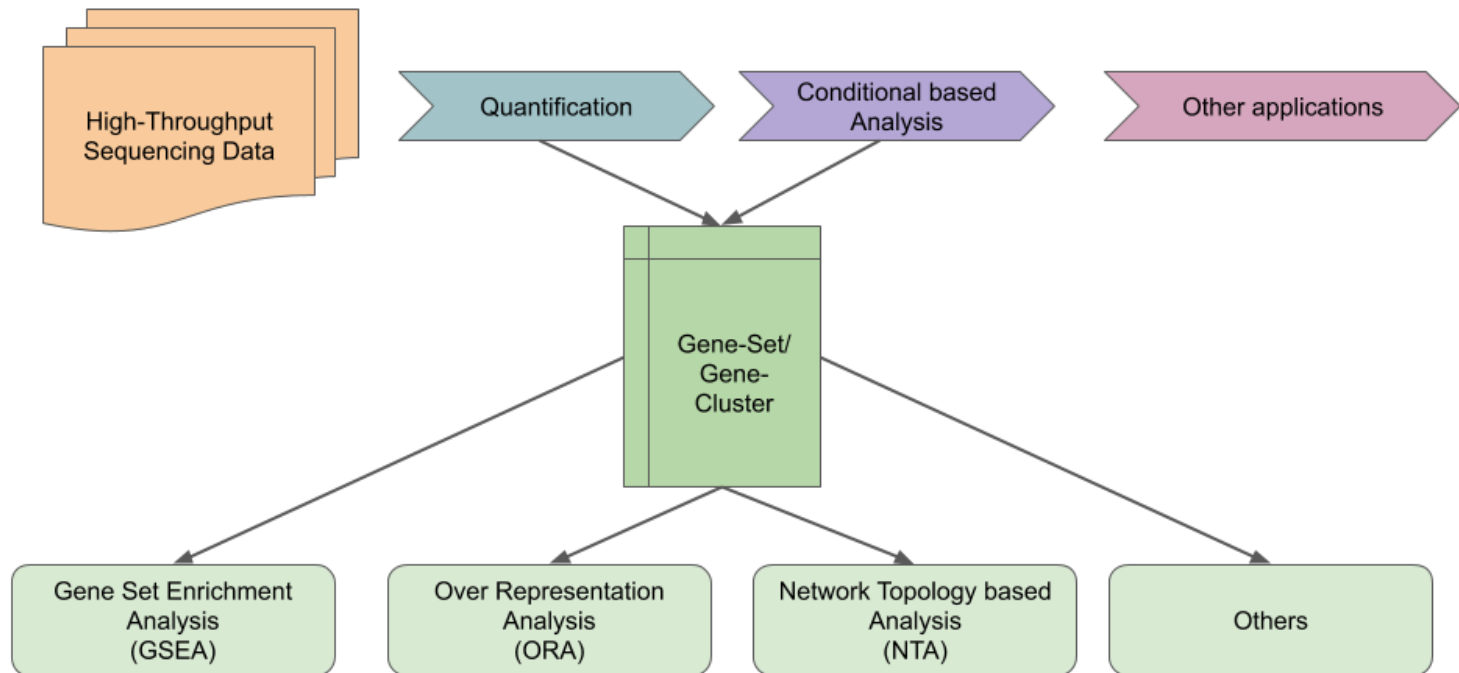
Bangalore, India

2020/07/01 (Updated: 2020-07-05)

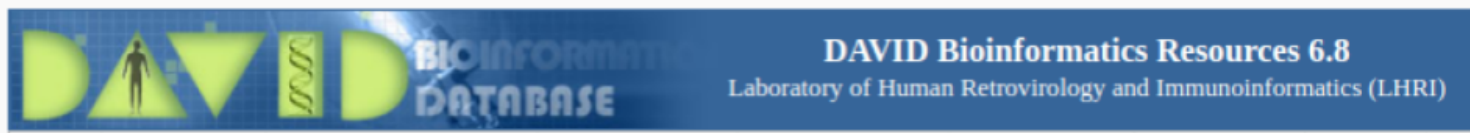
Outlines

- What is detecting Biological Significance on a Gene-Set means?
- Some of available resources
- Ideal scenarios for a gene-set based analysis
- SigBio-Shiny Overview
- Features
- Screenshots
- Usage
- Modular Design for contributors

Biological Significance on a Gene-Set



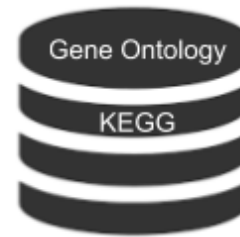
Some of available resources



Ideal scenarios for a gene-set based analysis

- An organism database
 - From Up-to-date resources
 - Support for model and non-model organisms/species
- Reproducibility
 - Keeping track of Database version
 - Statistical iterations log
- Accessibility
 - Programmatic access alongside GUI
 - Result interpretability with plots

While most available resources support some of above criteria but not all.



SigBio-Shiny Overview

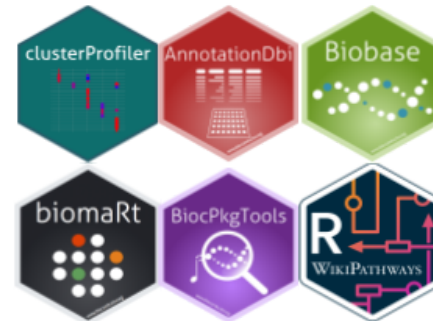
SigBio-Shiny provides a standalone R-Shiny based GUI application for doing such geneset based analysis. Build on top of already available open-source infrastructure, Such as -



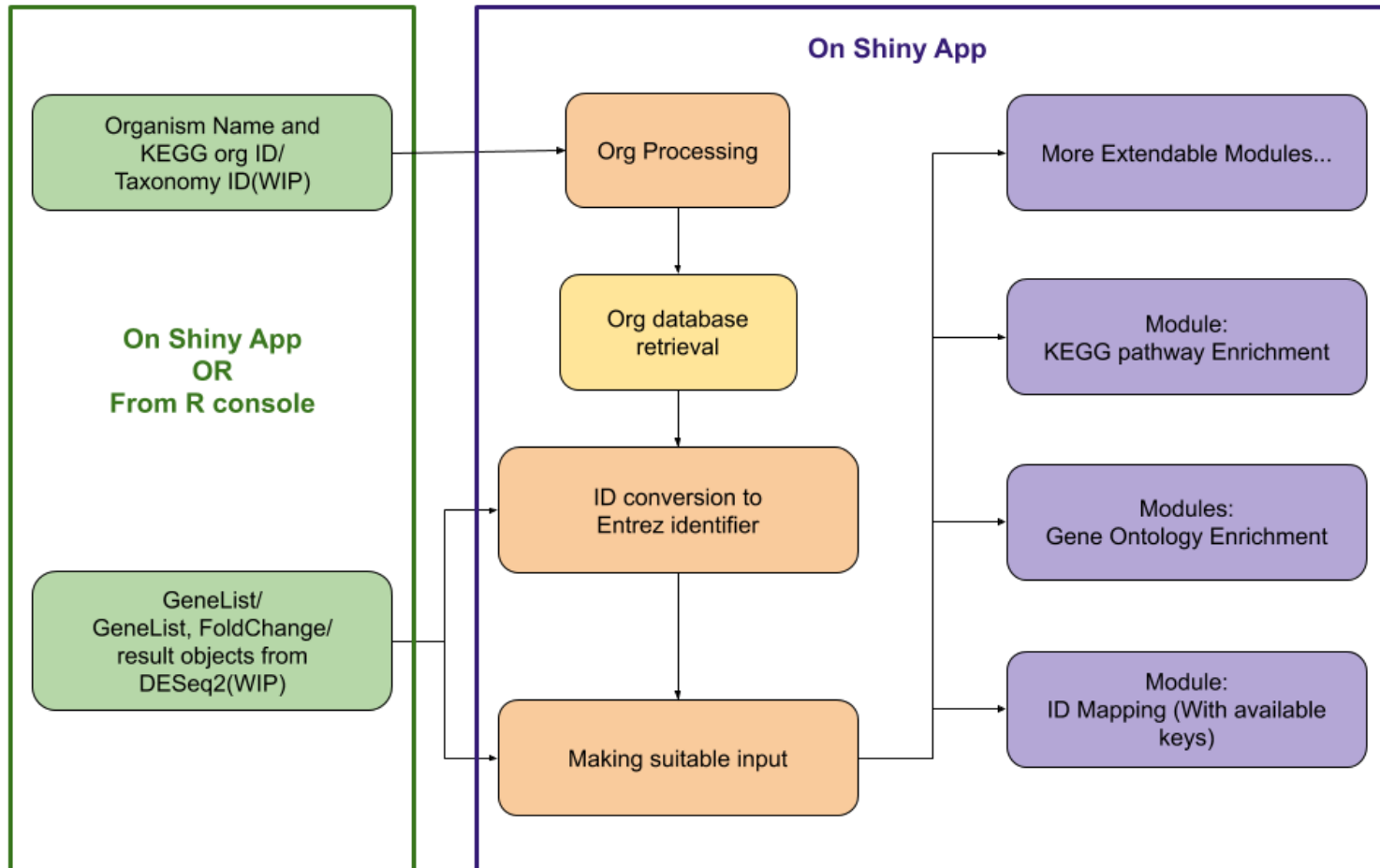
Bioconductor AnnotationHub Web Resource



Bioconductor Packages



SigBio-Shiny Structure



SigBio-Shiny Features

- Run time downloading of selected organism database with keeping a log for reproducibility. (with AnnotationHub)
- Gene ID mapping from different database. (with AnnotationDbi)
- Gene Ontology Enrichment (with clusterProfiler)
- KEGG pathway Enrichment (with clusterProfiler)
- Visualization of genes in KEGG pathway (with pathview)
- Different enrichment plots (with enrichplot)

Work in progress

- Directly launch with R objects from certain packages like DESeq2
- Complete reproducible R-script in the end of an analysis.

SigBio-Shiny Demo



SigBio-Shiny New UI

Sig-Bio v0.3.0

Input

Mapped Ids

Gene Ontology

KEGG

session-info

Help

About

Gene Input

[Gene] or [Gene,Foldchnage] list:

ENSG00000196611,0.7
ENSG00000093009,1.2
ENSG00000109255,-0.3
ENSG00000134690,0.2
ENSG00000065328,1.7
ENSG00000117399,-0.5

Input gene-id Type:

ENSEMBL

Organism Input

Organism:

Homo sapiens

KEGG Organism Short Name:

hsa

Get your KEGG Organism short name from here - https://www.genome.jp/kegg/catalog/org_list.html

Significant Values Input

pvalue-CutOff

1

qvalue-CutOff

1

After submit it may take 1-2 minutes. Check Progress bar in right side cornor.

>> Submit

Press F11 to exit full screen

SigBio-Shiny Usage

- Download as R-package and launch into browser directly from R console

```
remotes::install_github("sk-sahu/sig-bio-shiny") # Install the pack.  
SigBio::runApp() # Load the shiny application in browser  
SigBio::runApp(res) # work in progress
```

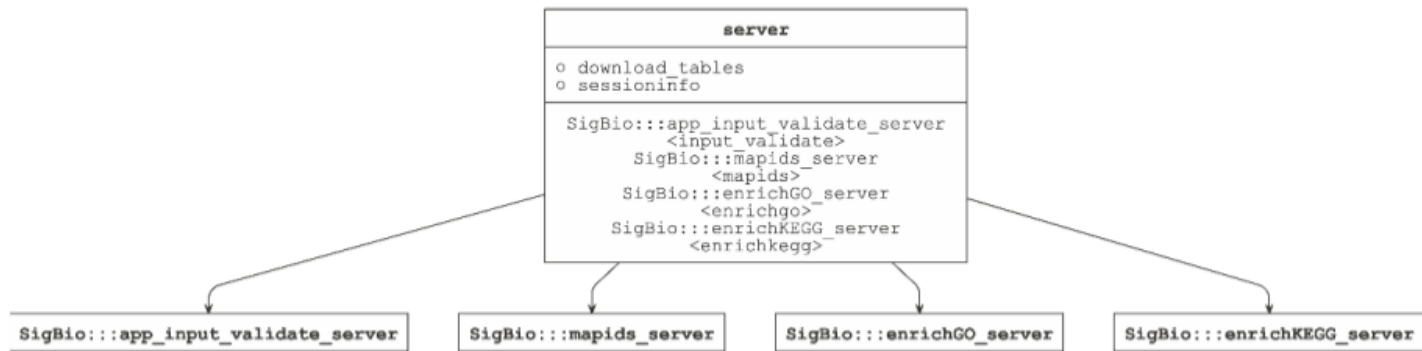
- Download as a single R-script for Shiny-Server deploy

```
wget https://raw.githubusercontent.com/sk-sahu/sig-bio-shiny/master
```

- Also can be run from a readily available docker container.

```
docker pull sudosk/sig-bio-shiny:latest  
docker run --user shiny --rm -p 80:3838 sudosk/sig-bio-shiny:latest
```

SigBio-Shiny Modular Design



Build on a modular approach such that adding a new package/functionality is easy for a contributors.

Thank you

Project Github - <https://github.com/sk-sahu/sig-bio-shiny/>

Feedback

- [Project's GitHub Issue section](#)
- [Project's Gitter chat room](#)
- Or directly reach me on twitter [@sangram_ksahu](#)