

# SigBio-Shiny

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

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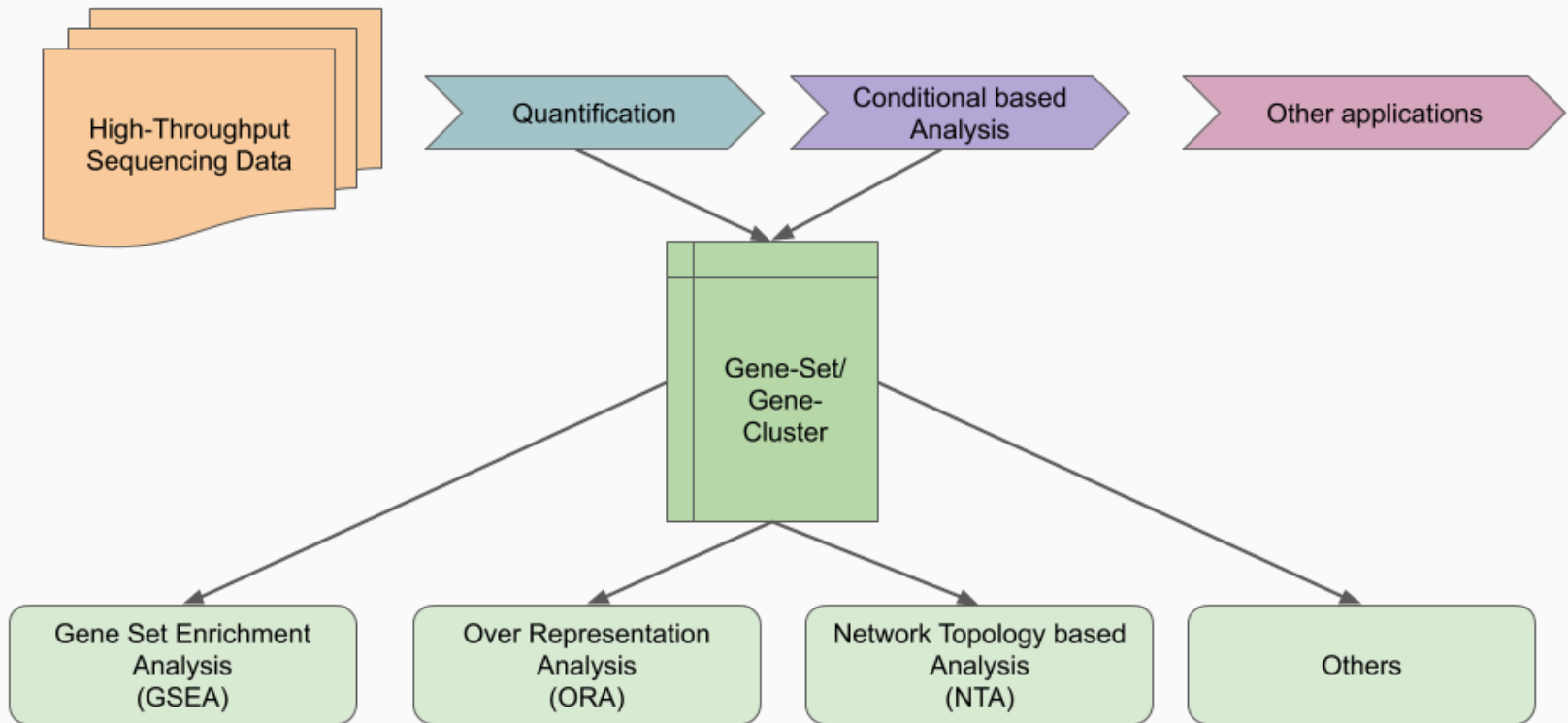
Bangalore, India

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# 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 developers

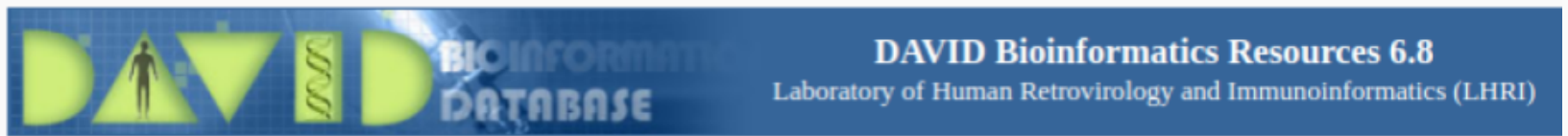
# Biological Significance on a Gene-Set



# Some of available resources

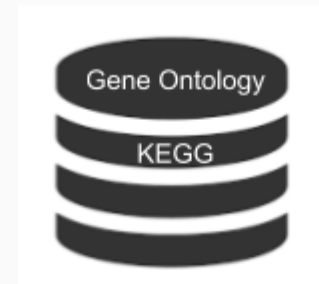


g:Profiler



# Ideal scenarios for a gene-set based

- 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 -



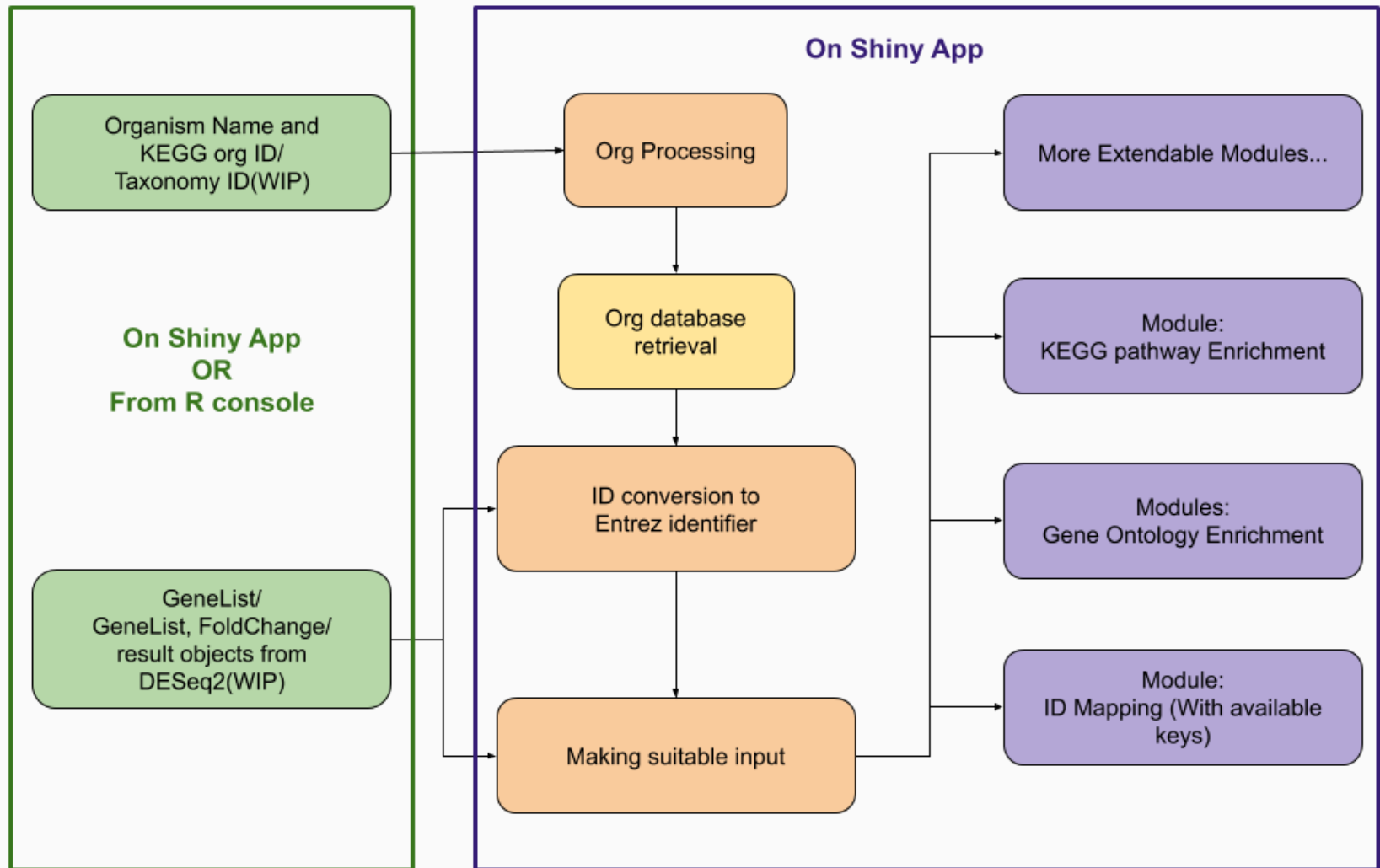
## Bioconductor AnnotationHub Web Resource



## 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

Organism Input

Significant Values Input

Press **F11** to exit full screen

**[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:**

Homo sapiens

**KEGG Organism Short Name:**

hsa

Get your KEGG Organism short name from here - [https://www.genome.jp/kegg/catalog/org\\_list.html](https://www.genome.jp/kegg/catalog/org_list.html)

**pvalue-CutOff**

1

**qvalue-CutOff**

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

» Submit

# 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 package
SigBio::runApp() # Load the shiny application in browser
SigBio::runApp(res) # work in progress
```

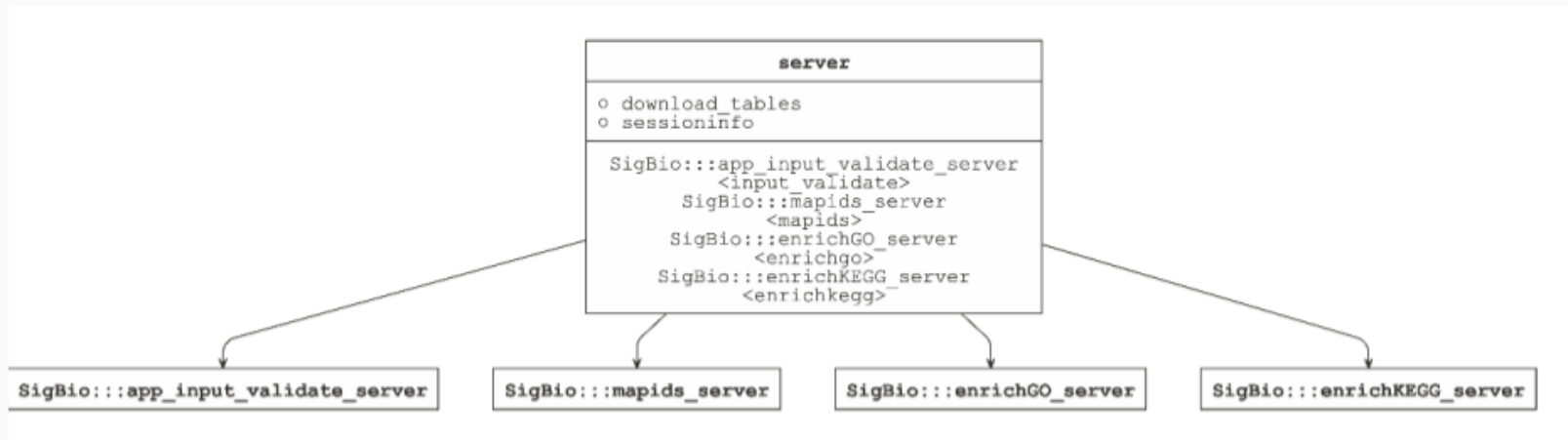
- Download as a **single R-script** for Shiny-Server deploy

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

- 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](#)

This Side URL: <https://sksahu.net/sigbio-shiny-slide>