

HMG2D-ANALYZER USER GUIDE

Version 0.1

Build-2

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1 Introduction

1.1 Scope and Purpose

HMG2D-analyzer is a java based biological tool intended to find common links between two pathologically significant databases, and further use the derived results to predict correlation between two elements that may otherwise be unrelated.

This user guide outlines the procedure which needs to be followed to use this tool efficiently and extract desired results. No prior programming knowledge is required to use this tool. And hmg2d-analyzer works offline as a standalone desktop application.

1.2 Process Overview

The user has to select any one option from the four analyte types (miRNA/Gene/Drug/Disease) on opening the main analyzer window, after which the user can select one/more elements from the list on the left for its analysis. Next, the element frequencies are shown in textual format while the element list is given in a tree table.

The users are also allowed to download the result in the form of a JSON file. This can later be loaded into the app to view again.

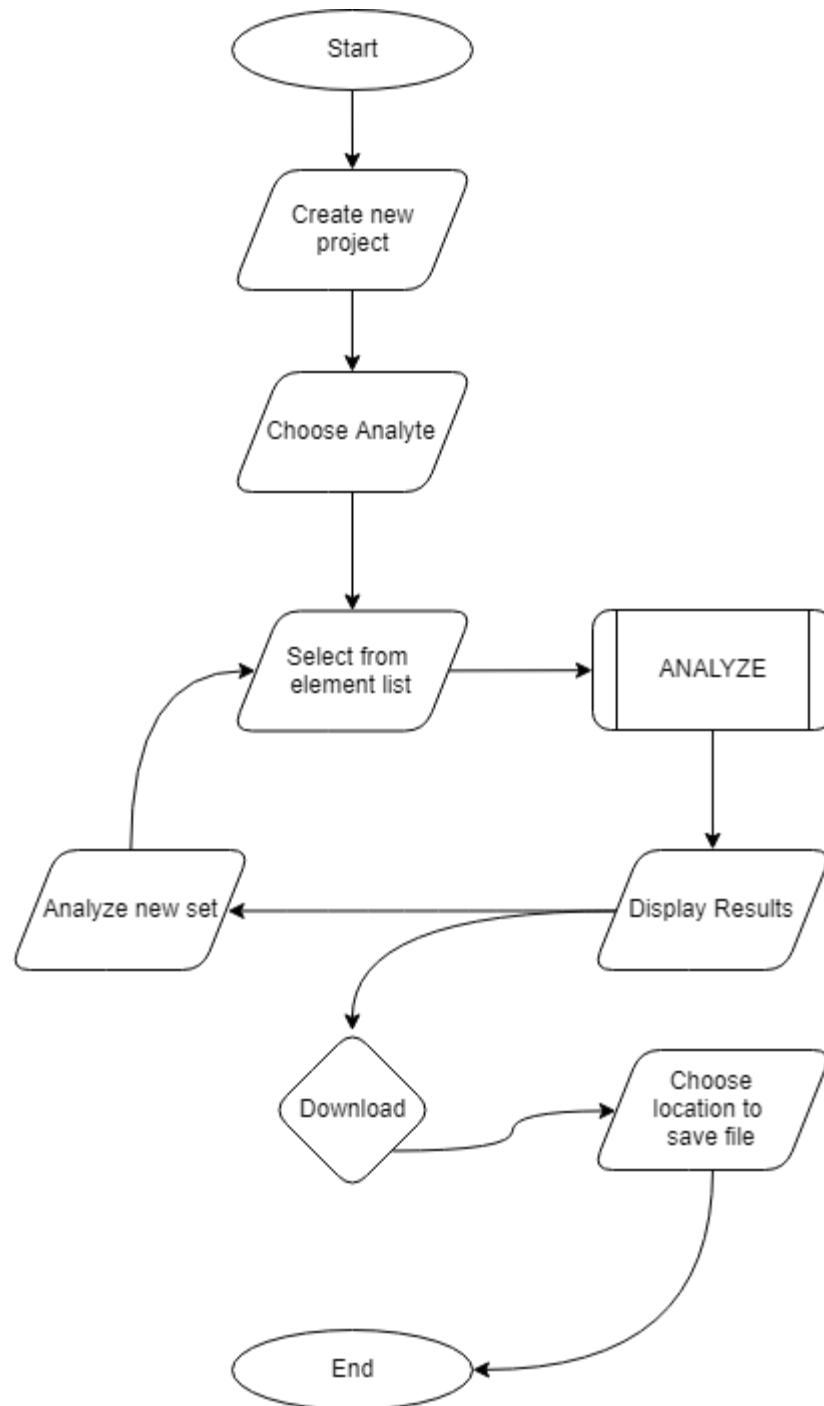
The JSON file obtained can also be fed to a third party app(eg: Cytoscape) to obtain a graphical visualization of the connections.

General sequence to be followed:

1. Create new project
2. Choose analyte (*miRNA/Gene/Drug/Disease*)
3. Select from the list of elements of the chosen analyte
4. Perform analysis
5. View and download results

1.3 Requirements

1. JDK/JRE 8 or higher
2. Windows 7 or higher
3. 2GB RAM or higher
4. Internet connection to download the tool



2 HMG2D Workflow

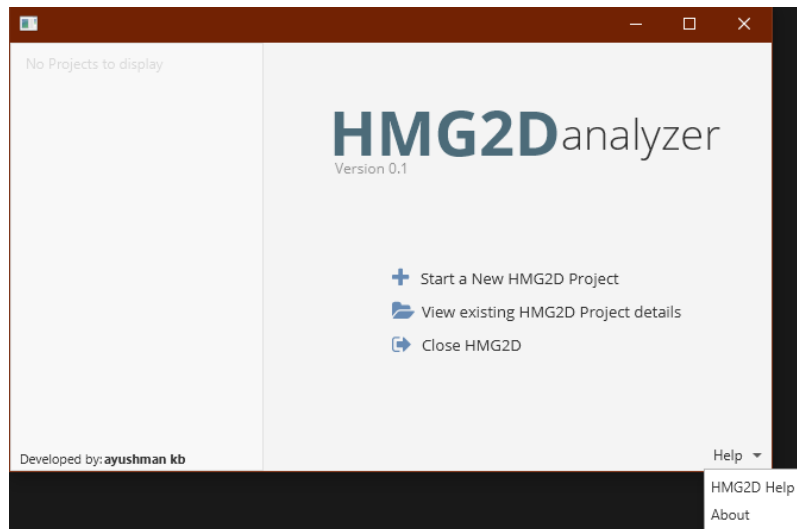
Only major requirement to run this tool is availability of JDK 8 or higher.

2.1 Using HMG2D-analyzer

On screen instructions are self-explanatory

2.1.1 Welcome Screen

1. Run the hmg2d-analyzer



2. Clicking on 'HMG2D Help' opens up this file



3. Clicking on the 'About' opens the window shown below
4. Click on 'View existing HMG2D Project details' to view summary details from existing .hmg2d files
5. Click on 'Start a New HMG2D project' to open analyzer window

NOTE: The app might not run/respond if it fails to find JDK 8 or higher installed on the system previously.

2.1.2 Performing analysis and downloading result files:

1. Choose analyte type:
 - a) Select either miRNA / Gene / Drug / Disease radio button for appropriate element list
 - b) After selecting analyte type the corresponding elements are loaded onto the list on the left
 - c) Select the desired element from the list (Multiselect option available)
 - d) Use the search bar to filter/find desired element
 - e) Click on 'Next' to perform analysis

Prediction mode:
Switch between any one prediction mode

☐ miRNA ☐ Gene ☒ Drug ☐ Disease

Search

taxol
vinblastine
cetuximab
irinotecan
doxorubicin
interferon-gamma-1b
paclitaxel
tamoxifen
sorafenib
cocaine
curcumin
docetaxel
navitoclax
cisplatin
butyrate
heparin
Count: 64

Count: 0

NEXT >

Analyte types

Transfer element to right list for analysis

Prediction mode:
Switch between any one prediction mode

☐ miRNA ☐ Gene ☒ Drug ☐ Disease

Search

taxol
vinblastine
cetuximab
irinotecan
interferon-gamma-1b
paclitaxel
tamoxifen
sorafenib
cocaine
curcumin
docetaxel
navitoclax
cisplatin
butyrate
heparin
alitretnoin
Count: 63

doxorubicin
Count: 1

NEXT >

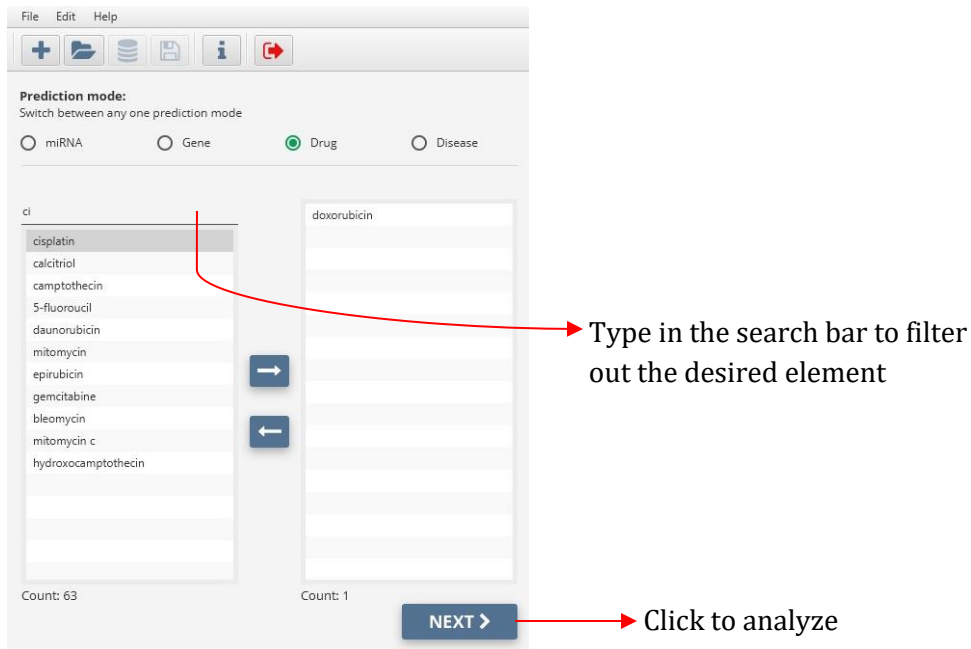
ANALYSIS RESULTS

Analyte Type	Analyte
Analyte Count:	0
Sub-Analyte 1	0
Common Sub-Analyte 1	0
Sub-Analyte 2	0
Common Sub-Analyte 2	0
Sub-Analyte 3	0
Common Sub-Analyte 3	0

Result

No content in table

DOWNLOAD

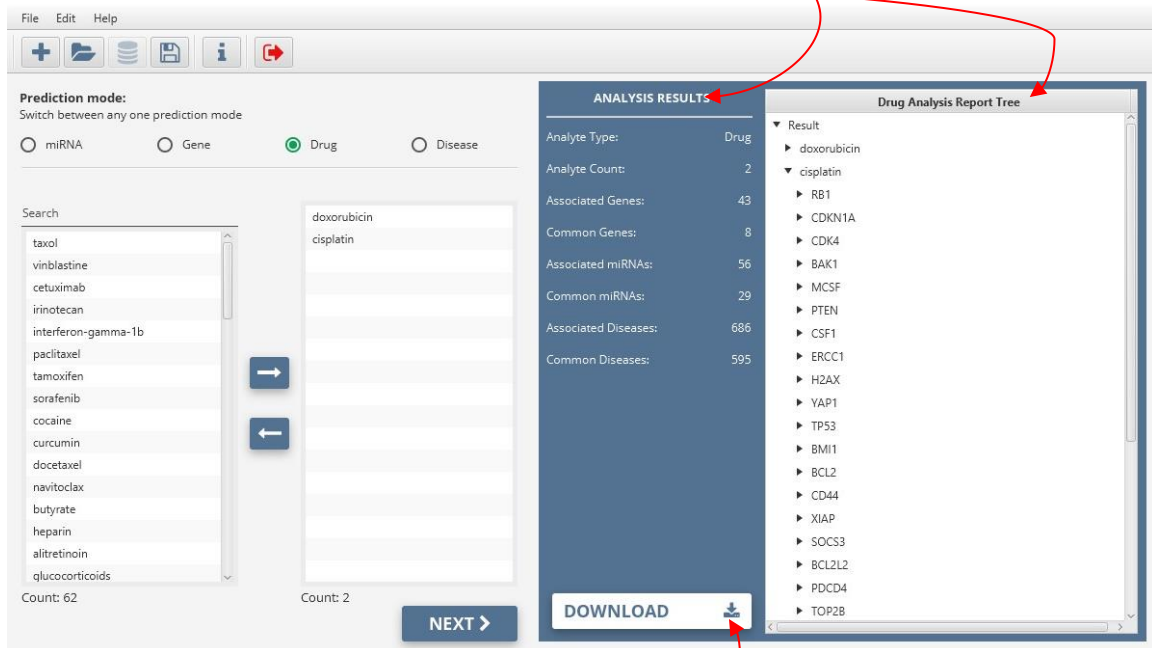


2. Results are displayed on the right column

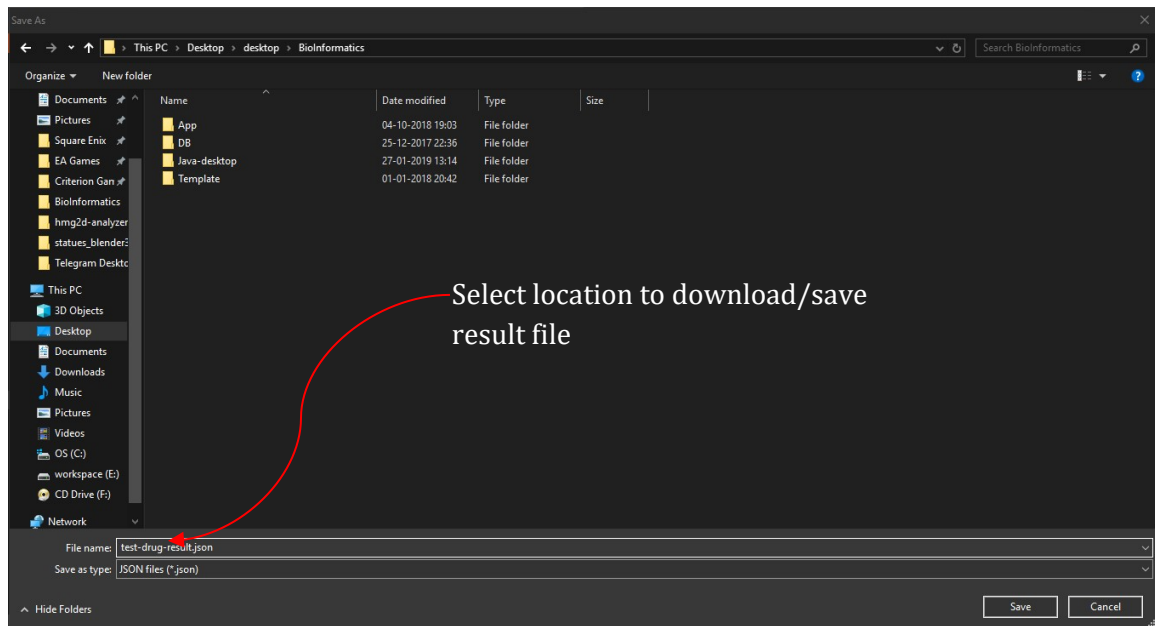
- Results:

a) Associated element counts and frequencies

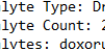
b) Element list(Tree table)



3. Click on 'Download' to export result file



```
File Edit Format View Help
{"nodes":[{"id":"doxorubicin","group":3},{id":"CASP3","group":2},{id":"hsa-let-7a","group":1},{id":"Adenocarcinoma, Lung","group":4},{id":"Allergic Asthma","group":4},{id":"Alzheimer Disease","group":4},{id":"Amyotrophic Lateral Sclerosis","group":4},{id":"Asthma","group":4},{id":"Atopic Dermatitis","group":4},{id":"Autoimmune Diseases [unspecific]","group":4},{id":"Brain Neoplasms","group":4},{id":"Breast Neoplasms","group":4},{id":"Carcinoma, Breast","group":4},{id":"Carcinoma, Breast, Triple Negative","group":4},{id":"Carcinoma, Cervical","group":4},{id":"Carcinoma, Colon","group":4},{id":"Carcinoma, Gallbladder","group":4},{id":"Carcinoma, Gastric","group":4},{id":"Carcinoma, Hepatocellular","group":4},{id":"Carcinoma, Hepatocellular, HBV-Related","group":4},{id":"Carcinoma, Lung, Non-Small-Cell","group":4},{id":"Carcinoma, Nasopharyngeal","group":4},{id":"Carcinoma, Ovarian","group":4},{id":"Carcinoma, Pancreatic","group":4},{id":"Carcinoma, Renal Cell","group":4},{id":"Carcinoma, Renal Cell, Clear-Cell","group":4},{id":"Carcinoma, Thyroid","group":4},{id":"Carcinoma, Thyroid, Papillary","group":4},{id":"Carcinoma, Urothelial, Upper Tract","group":4},{id":"Cardiomyopathy","group":4},{id":"Cardiomyopathy, Dilated","group":4},{id":"Cardiovascular Diseases [unspecific]","group":4},{id":"Cervical Neoplasms","group":4},{id":"Cholesteatoma","group":4},{id":"Chronic Kidney Disease","group":4},{id":"Chronic Obstructive Pulmonary Disease","group":4},{id":"Colon Neoplasms","group":4},{id":"Colorectal Carcinoma","group":4},{id":"Cutaneous Melanoma","group":4},{id":"Diabetes Mellitus","group":4},{id":"Diabetes Mellitus, Gestational","group":4},{id":"Diabetes Mellitus, Type 2","group":4},{id":"Diabetic
```



File Edit Format View Help

Analyte Type: Drug

Analyte Count: 2

Analytes: doxorubicin, cisplatin,

Associated Genes: 43

CASP3

FOXP1

MET

PIM1

CCNG1

CDK4

ABCC5

BMI1

4. Result is stored in two formats
 - a. Json file – to open it in the app later
 - b. hmg2d file – has analyte and frequency information for the corresponding .json file

2.2 Reading the results

Indicator	Definition
Analyte Type	miRNA / Gene / Drug / Disease
Analyte Count	Number of the above elements selected from the list
Associated sub-analyte	3 rows; each for other three analytes for each selected analyte eg: associated gene, drug and disease for main analyte as miRNA
Common sub-analyte	Common sub-analytes for the selected elements of the type of the main analyte

Table 1-1: Result reading table