

Code-free bioinformatics pipeline for building biological databases used to construct cardiovascular-SNPDB: an online database for SNPs associated with cardiovascular metabolites

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#### Abstract

Biological databases are of great importance for managing biological research data. Building databases has been a code-based process that requires integrative coding skills of different languages. Herein, we present a code-free pipeline that helps biologists to build their databases with no need for coding skills providing searchable downloadable and editable databases using Google Apps. We provided an example for an online tool including a database of SNPs associated with cardiovascular Metabolites, allowing basic features like browsing, downloading, filtering and printing. We also described a stepwise pipeline for building such an interactive database. Cardiovascular-SNPDB was made available at: https://sites.google.com/view/cvdsnpdb/browse/.

#### Introduction

Databases are crucial for management of bioinformatics research and tools. Databases manage various biological data types including DNA sequences, Protein Structures and gene expression profiles. Databases usually contain either experimental data, predicted data or both with variety of categories including but not limited to molecules, organisms, molecular pathways or diseases. Databases allow users to browse and download content in different formats. Building bioinformatics databases requires significant programming computer scientists usually use programming languages including PhP, Perl, Python or other languages in a connection with database management system like MySQL and NoSQL. Considering The huge flood of data we are witnessing now in the field of bioinformatics and it is unlimited branches,

we need easier and more flexible ways of sharing these data in such way of providing public access to improve communication between researchers and allow better management of datasets. So it would be of great beneficence if we could have a code-free stepwise pipeline that allows biologists of non-programming background to build their online databases and make it accessible to the public without a single line of code.

### Pipeline and Discussions

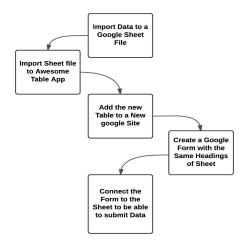


Fig-1 scheme for database building pipeline steps

## • Data input into Google Sheet

Submitting biological dataset to Google sheets enable authors to easily manage their data on the cloud, so the first step we have used in our pipeline is to import our data we have obtained out from this genetic study<sup>[1]</sup> into google sheets<sup>[2]</sup> as shown in figure-2.

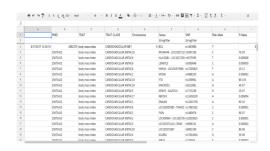


Fig-2 Google Sheet containing obtained data

# • Linking Google Sheet into Awesome Table App

Awesome Table App<sup>[3]</sup> helps to convert data sheets into searchable applications, so herein we have linked our Google sheet file into Awesome Table App to able to add suitable filters and other options including download and print options into our database App. Figure-2 shows that we have added string filters into both genes and SNPs columns so that users could be able to search these columns' text data easier. Automatically PMID chromosome columns have been embedded with number range filter. Created Table have been also supplemented with download in \*.csv format and print options to supply users with more content accessibility.

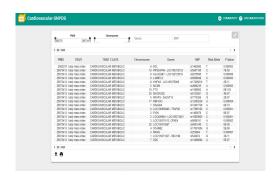


Fig-3 Awesome Table App Managing the Sheet file



## Building New Google Site Embedded with the Created App

New Google sites<sup>[4]</sup> is helpful for easy building of elegant websites that could be supplemented with Google Documents like docs, spreadsheets and forms.

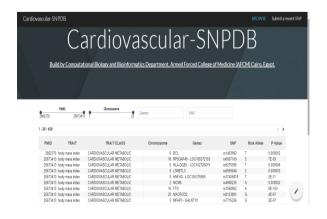


Fig-4 Browse page of the database website created by New Google SItes

then we have supplemented the new website with the public link of the created Awesome Table in a page Named "Browse" so that users could get access to the new database at this link

https://sites.google.com/view/cvdsnpdb/.

## Creating a Google Form for submittable database web Tool

bioinformatics databases often include data submission in order to keep sustainability of disease related databases to be updates to more recent studies that in this case could discover novel SNPs associated with cardiovascular metabolites. Google form<sup>[5]</sup> was connected to our Google Sheet that is considered the standard database of the web tool, so that new data submitted in a form containing question boxes that are corresponding to heads of the spreadsheet columns. In this case, each single form answer will be converted to an extra row that will be added to the Database Sheet and should be automatically updated To Awesome Table created App and subsequently to the website of the new database tool. Submission form could be accessed at this link <a href="https://sites.google.com/view/cvdsnpdb/submit-a-recent-snp/">https://sites.google.com/view/cvdsnpdb/submit-a-recent-snp/</a>.



Fig-5 Submission Page on the database website

### Conclusions

Bioinformatics is a leading future science that has been transforming biological sciences big data into an easy manageable database driven tools for both biologists and informaticians.

This code-free pipeline helps to reduce the coding process that may be an obstacle for biologists who need to make their data more accessible to the scientific community. Integrating Google Apps also helps biologists



to manage their created databases on the cloud. This pipeline could be further developed in the future to be more user-friendly and integrate new feature for the best interest of biologists. Our new database could be easily accessed at <a href="https://sites.google.com/view/cvdsnpdb/browse/">https://sites.google.com/view/cvdsnpdb/browse/</a>

### **References:**

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