

Serendipities gene Manual

1 Overview

This application named Serendipities gene is based on Android platform, which helps researchers to check the special gene combination and achieve visualization of the compare between variant gene combination and normal gene combination from tremendous gene pool database. It is convenient for researchers to check the compare results in the mobile device.

2 Install App

Considering the data security issue, this android application was released as apk document by the developer. On the one hand, this apk document was sent by email to the researchers who have permission to access the gene database. On the other hand, this apk document was uploaded on the Azure cloud services and the researchers can download from the cloud server. Then users will see the shortcut icon on the device screen.



3 environment requirement

platform	Android
cloud platform	azure cloud platform
min SDK	API 20: Android 4.4W (KitKat Wear)
compile SDK	API 26: Android 8.0 (O)
build tool	26.0.1
java compatibility	1_8
target SDK	API 26: Android 8.0 (O)
dependence	com.microsoft.azure

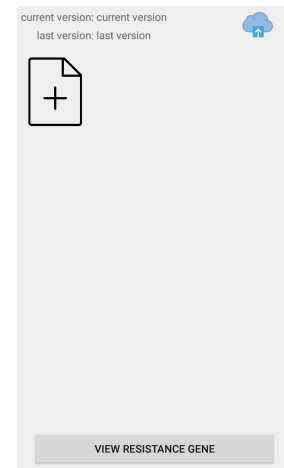
4 Introductions to Function Run the App

at the first time, you will see this main page. In the main page, there are three main functions in the view.

At the top of the page, the text view shows the version of the application. The first line is current version and the second line is the last version.

In the middle area of the page shows the fas documents and achieves the function which adds fas document from cloud server or local folder. It also can show the existing fas document in the mobile device.

In addition, there is a button at the bottom of the page. If you click this button, it will redirect to another page.

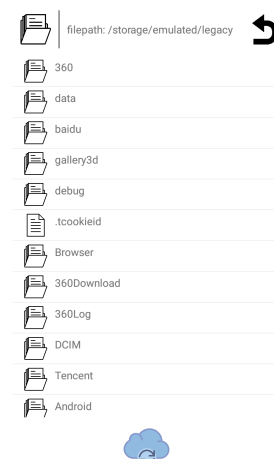


In this page, users can enter the information of binding protein, position and original gene. Then click the “upload” button, this information was updated to the local database. This page also can show the all the database information on the mobile device.



Return to the main page. After clicking the icon button, the application will redirect to the file management page. In the file list, users can load the fas document for the local device. If users click the icon button located the bottom of the page, the application will connect to the cloud server.

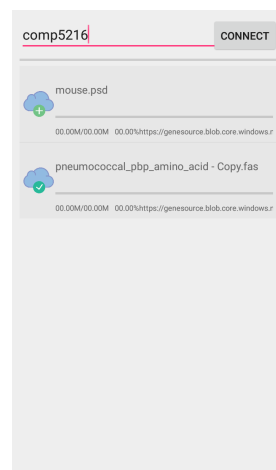
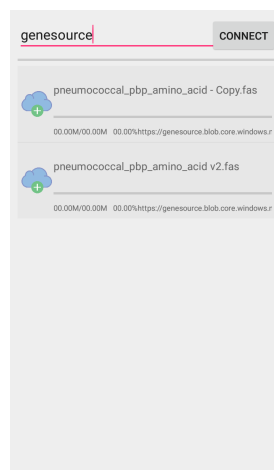
In the cloud server page, users were required enter the group ID. The cloud server divide different group for researchers depend on different ID.



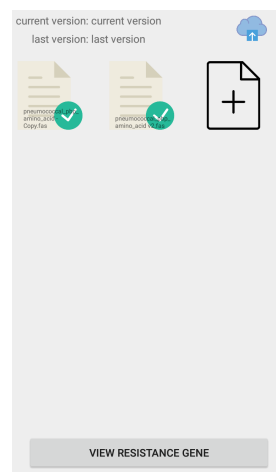
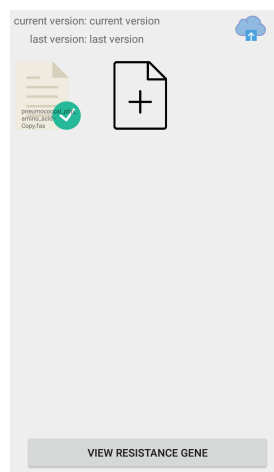
For instance, if the user enters the ID of “comp5216” and click connect button, the entire fas document in this group from the cloud server will be displayed on this page.

Moreover, this page also can compare the local fas documents and cloud server fas documents. If the cloud fas document not existing in the local database, the icon shows the plus icon.

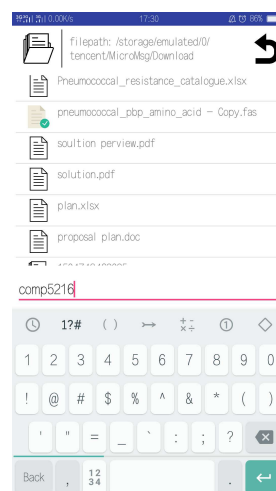
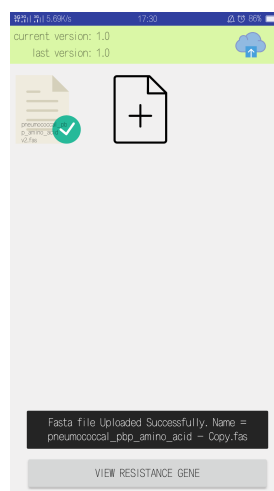
If fas document from the cloud server existing in the local database, the opposite of icon shows the check icon in the file list. If users enter the ID of “gene source”, they will gain the different fas document in the cloud server.



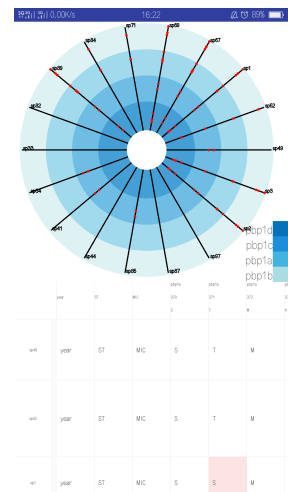
If users click the cloud document file icon, the application will download the fas document to the local file list and display on the main page like below screenshots.



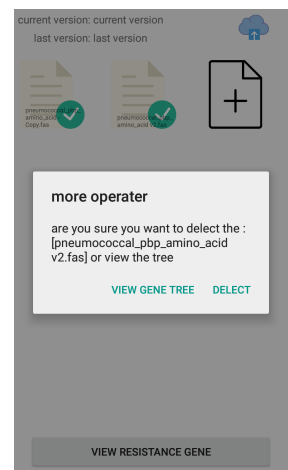
if user have new finding or new result of the trail user can upload the file to Azure for private using or public to group, user are required to input a group id to use as password. user should input the password first then click the file which user want to upload. once user finish the process of upload the system will show a result to user like the picture



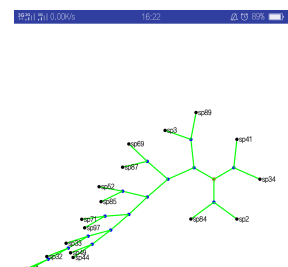
If users short click the icon of selection fas document, the program will generate a ring graphic such as the below screenshot. This graphic shows the difference between variant gene combination and normal gene combination.



If users long click the icon of selection fas document, the program will require dialogue which involved tow option. One is “view gene tree”, the other is “delete”.



If users choose “view gene tree” option, the application will generate a tree graphic to show the connection between variant gene combination and normal gene combination. The gene tree graphic was shown in the below screenshot. This graphic shows the difference between variant gene combination and normal gene combination.



If users choose “delete” option, the application will delete the selected fas document from the main page. Furthermore, this delete operation is just deleting the history on the main page; it is not deleting fas documents in the mobile device.

In the last step, if the user clicks the Back button on the main page, it will require dialogue in order to confirm whether users to exit the application.

