

# H3AbioNet Data Integration - SysBiol WG

## PostGWAS web application testing protocol

- Please find below the link to the web application.

<https://spgwas.waslitbre.org>

- The Liftover, Annotation, and Deleteriousness pipelines have been integrated and can be tested on the web application. Please find the data to test it with.
  - small.txt - it is a small data test in genomic build version hg 19 to test the Annotation and Deleteriousness tools.
  - celiac\_filtered.txt - This data includes SNPs significantly associated with Celiac disease downloaded from GWAS Catalog. The SNPs in this file are in genomic assembly hg38. Convert it to Genomic assembly hg19 with Liftover and use the resulting output in the other tools.

The test data can be found and downloaded on the “tutorials” page via the following link:

<https://spgwas.waslitbre.org/tutorials>

### Instructions on how to register on the application

- Visit the home page site: <https://www.spgwas.waslitbre.org/>

(Side note: In case you have viewed this site before, you might be viewing an old version of the site because of the way browsers cache sites. Please you might need to press SHIFT + ENTER while in focus of the browser address bar to fetch a fresh version from the server)
- Click on the “Sign UP” button on the top right corner.
- Enter your details and submit
- An email will be sent to the registered email address, please first verify the email before continuing as you won't be able to run any analysis without verifying your email. If you don't see the email, also check your spam box.
- After email verification, please Login.

## Running an analysis

- Please note that all analyses are executed with databases in genomic build hg19/GRCh37. Ensure your files are in the build version before continuing. You can also use the Liftover tool to convert your files.
- To run a tool, either click on the “Tools” navigation button on the header pane, or the yellow 'Run tool' button on the banner, or the 'click to start' link on the “Execute Individual tools” section.
- Select the tool you would like to execute (Liftover, Annotation, Deleteriousness for now).
- On the selected tool dashboard, click on the new analysis button on the tab panel.
- Upload the files you want to use for the analysis (important! - please ensure your filename doesn't have illegal characters like spaces, braces, etc!).
- Fill in the job name.
- In the next section, fill in the correct column number for the uploaded file. The column names in the uploaded file should be the column numbers filled in the text boxes (This is very important because if incorrect numbers are selected, the analysis will be incorrect) The column numbers should start from one.
- Enter or select other appropriate parameters.
- Submit a job by clicking on 'Execute Analysis'

## Viewing the results

### Liftover

- After clicking on the Execute Analysis button, you will be navigated to a result list. That page will automatically reload until the job is complete.
- Use the download buttons to obtain your result files.
- Please note: The Liftover service can only run 1 concurrent job. This might not be noticed as Liftover completes its job in a matter of seconds.

### Annotation

- After clicking on the Execute Analysis button, you will be navigated to a result list. Click on the 'view' button to go to the results page.
- You will see the status of the job, and some tables with information about your jobs. (This page will also automatically reload if the job is not done, if it is a long job, an email will be sent when it is done)
- When the job is completed, scroll down to view the results. Use the download buttons to obtain the results of your analysis.
- Please note: The annotation service can only run 2 concurrent jobs per time due to limited cpu resources, these can cause other people's jobs to be queued for long if someone is running an analysis on a big file.

### Gene Deleteriousness

- After clicking on the Execute Analysis button, you will be navigated to a result list. Click on the 'view' button to go to the results page.
- You will see the status of the job, and some tables with information about your jobs. (This page will also automatically reload if the job is not done, if it is a long job, an email will be sent when it is done)

- When the job is completed, scroll down to view the results. Use the download buttons to obtain the results of your analysis.
- Please note: the deleteriousnes service can only run 1 concurrent job per time due to limited CPU resources, these can cause other people's jobs to be queued for long if someone is running an analysis on a big file.

### **Errors, Issues, Complaints**

- If the job fails, you will see some error information from the tool about what happened. Please send a snapshot to the emails below on the errors. (Apologies, you might get a long text of errors information for now. We do this because the application is still in the development and testing stage and full error information will be useful in debugging the application. This will be changed to a shorter message later).
- If you come across any other errors, bugs, or you have some complaints, please kindly document them, (text and snapshots) and email them to the emails below. Also, there is room for improvement in the application, please kindly send your comments to the email below.

Email: [jerry.emmanuelace@stu.cu.edu.ng](mailto:jerry.emmanuelace@stu.cu.edu.ng), [yagoub.adam@covenantuniversity.edu.ng](mailto:yagoub.adam@covenantuniversity.edu.ng)

**We will appreciate your detailed testing of the application up to October 31, 2021.**

Thank you.