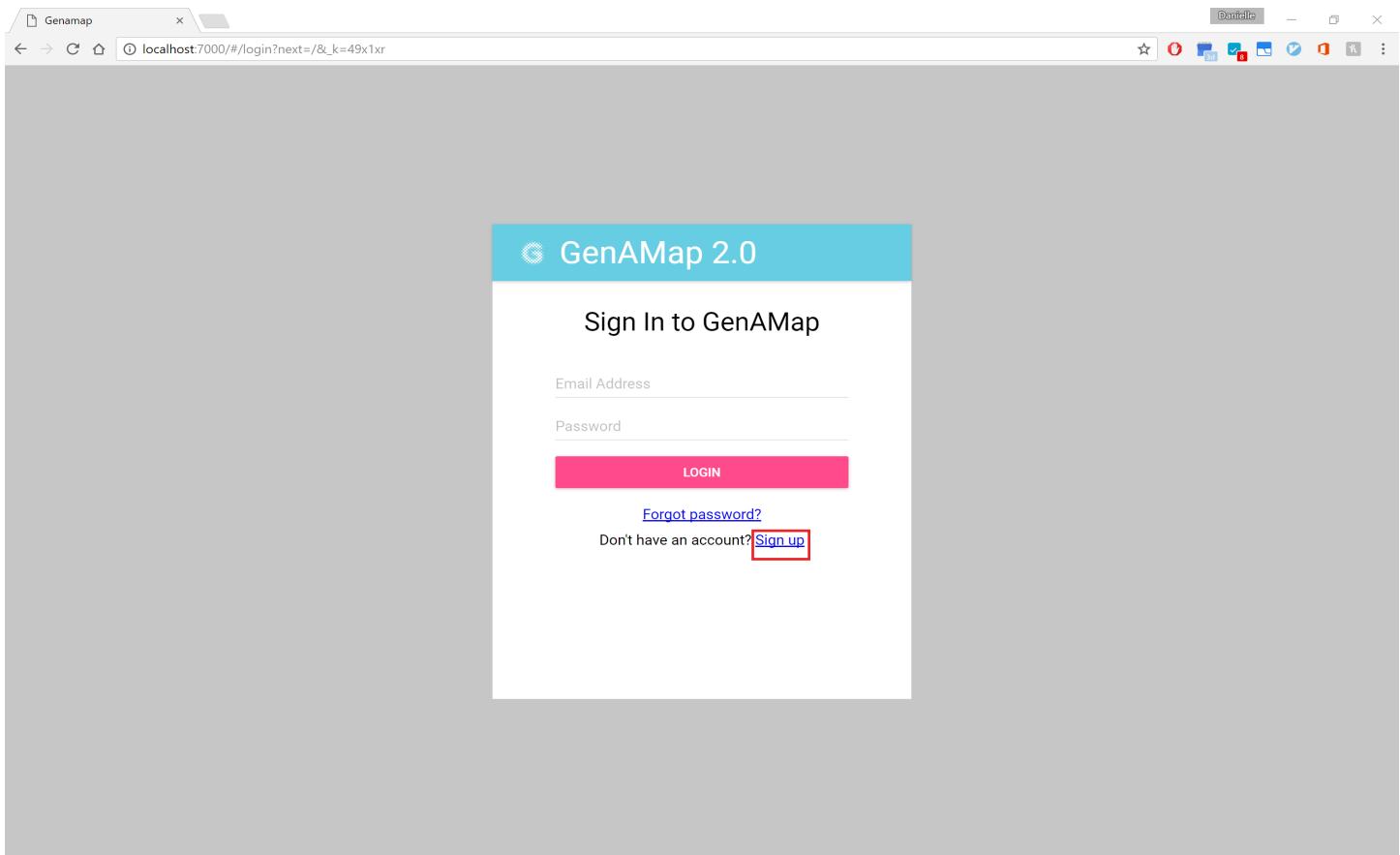


How to use GenAMap v2.0

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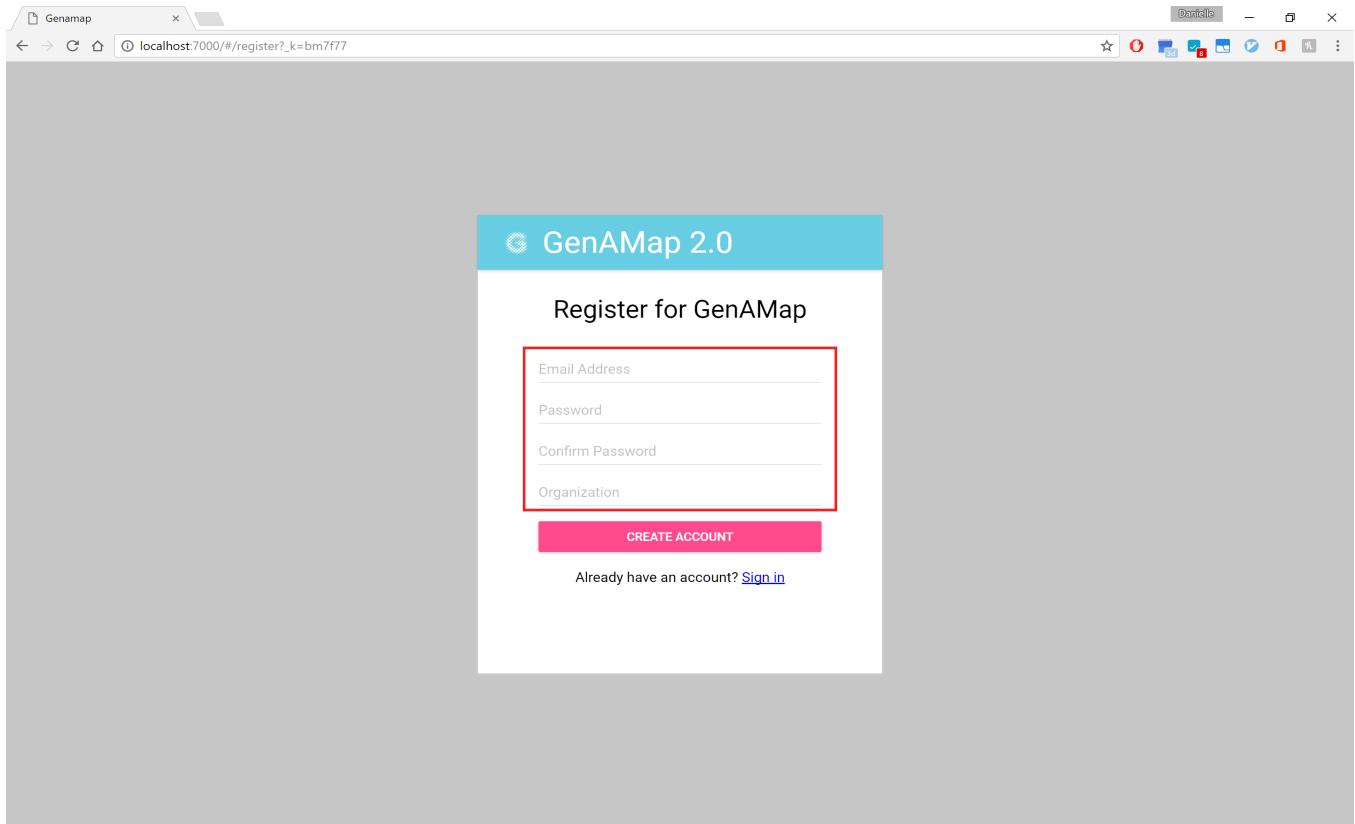
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1) Sign up for an account



Click “Sign Up” in the initial login screen for GenAMap (if you don’t have an account already)

1) Sign up for an account (cont.)



Type in your email address, password, and associated organization (if any)

2) Confirm e-mail

GenAMap Sign-up Confirmation    

 GenAMap <genamap.v2.0@gmail.com>
to me  9:38 PM (10 hours ago)   

 **GenAMap v2.0**

Welcome!

Thanks for joining GenAMap! We're excited to have you in our community!

Please confirm your e-mail address by clicking below:

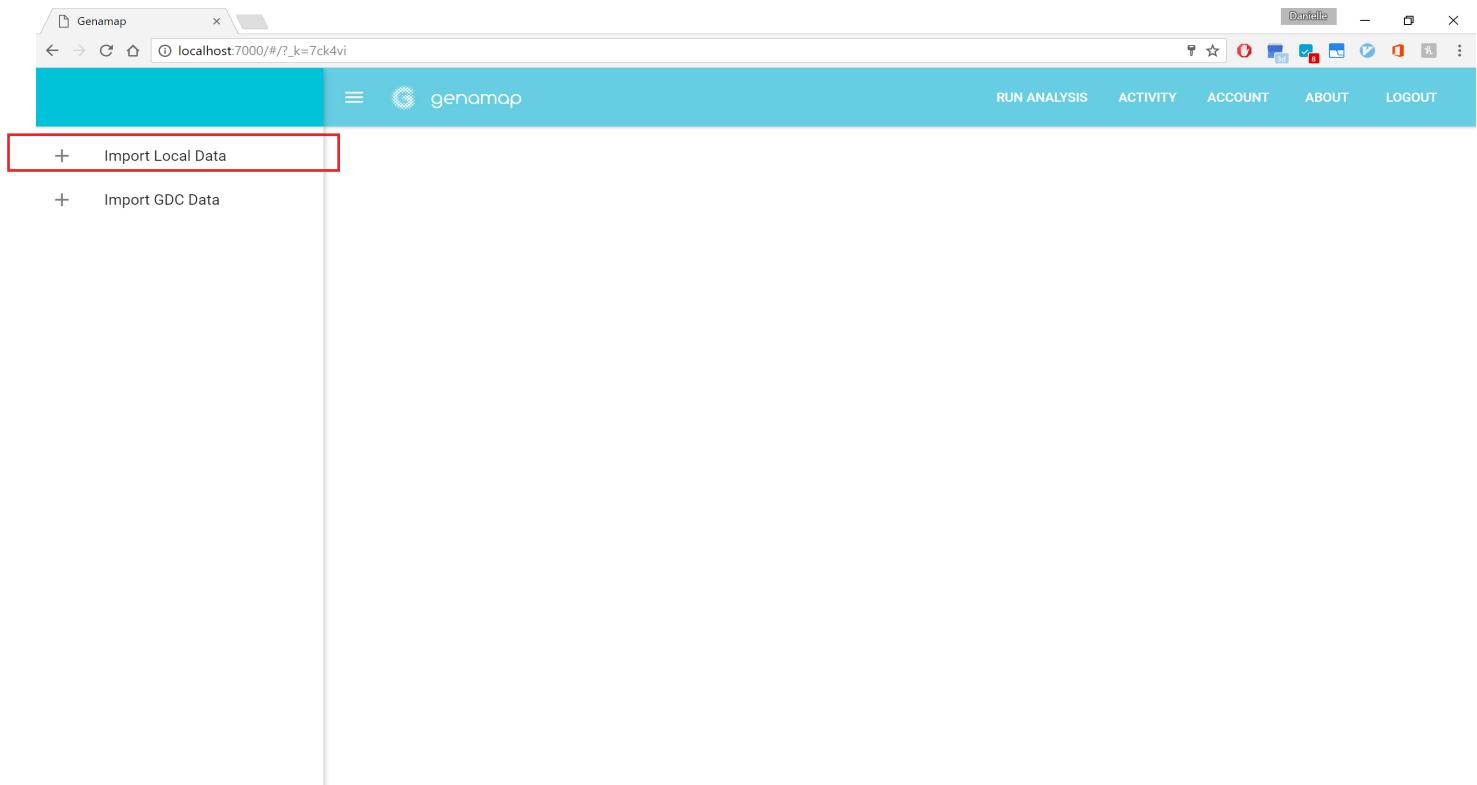
Confirm E-mail

Or copy this verification code into the confirmation field:
43be4151-4971-8686-85c8-50f218caf911

Log onto the e-mail you signed up with and confirm your account with the e-mail from “genamap.v2.0@gmail.com”

You can either click “Confirm E-mail” or you can copy and paste the bolded verification code directly into the Genamap text box that was prompted right after you registered.

3) Importing local data

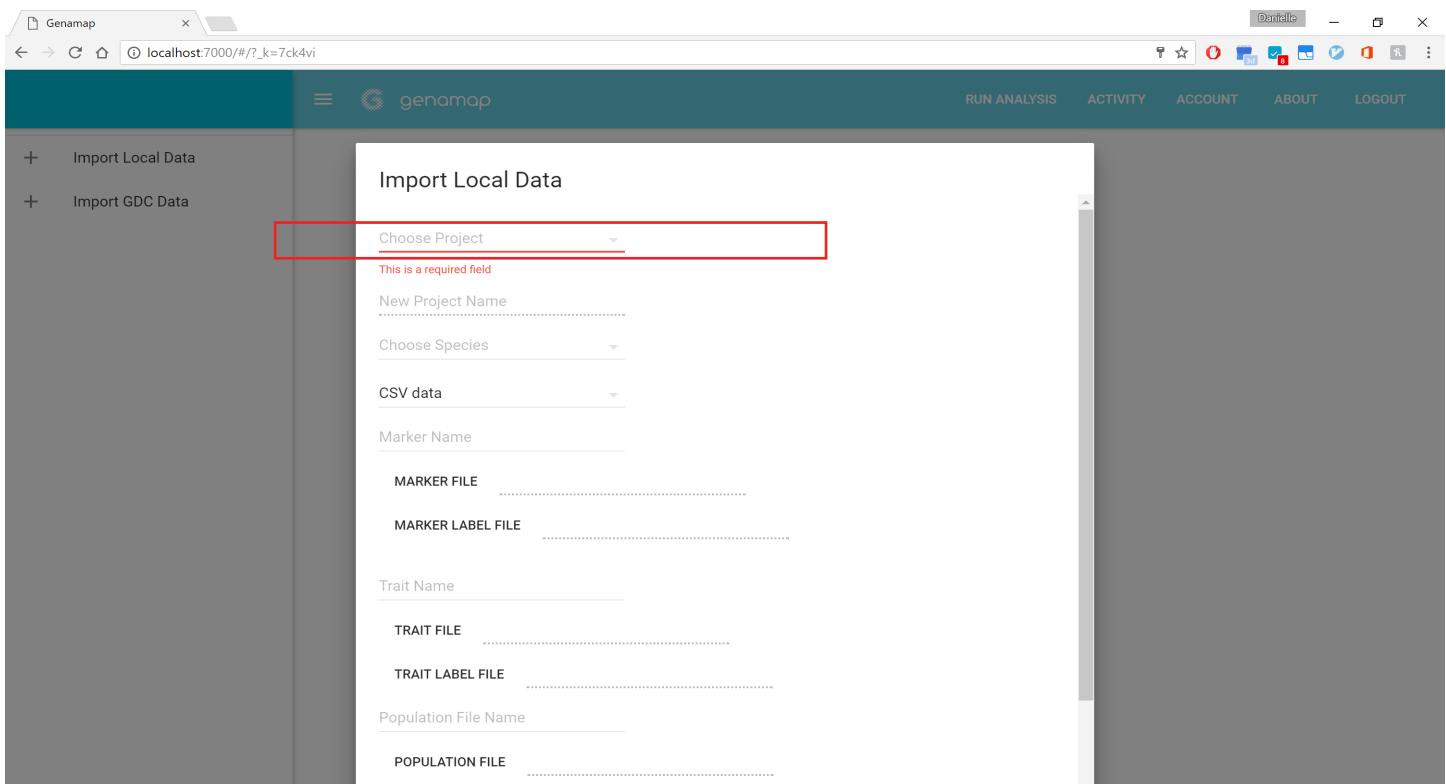


Once you have been verified, you can log into GenAMap with the account you just created. All you have to do is to start importing data!

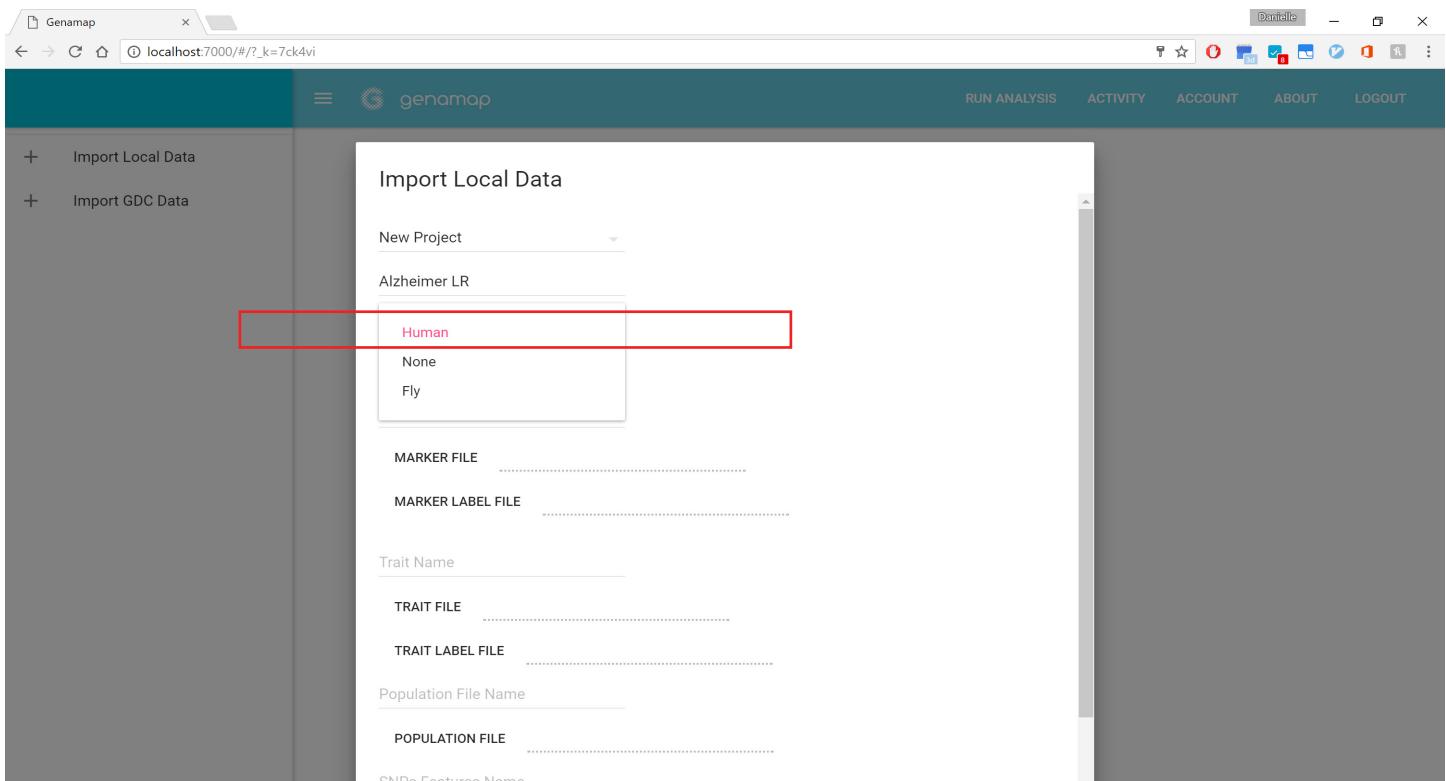
There are two options for this:

- 1) Import local data (from your machine)
- 2) Import GDC data (from NIH's GDC portal)

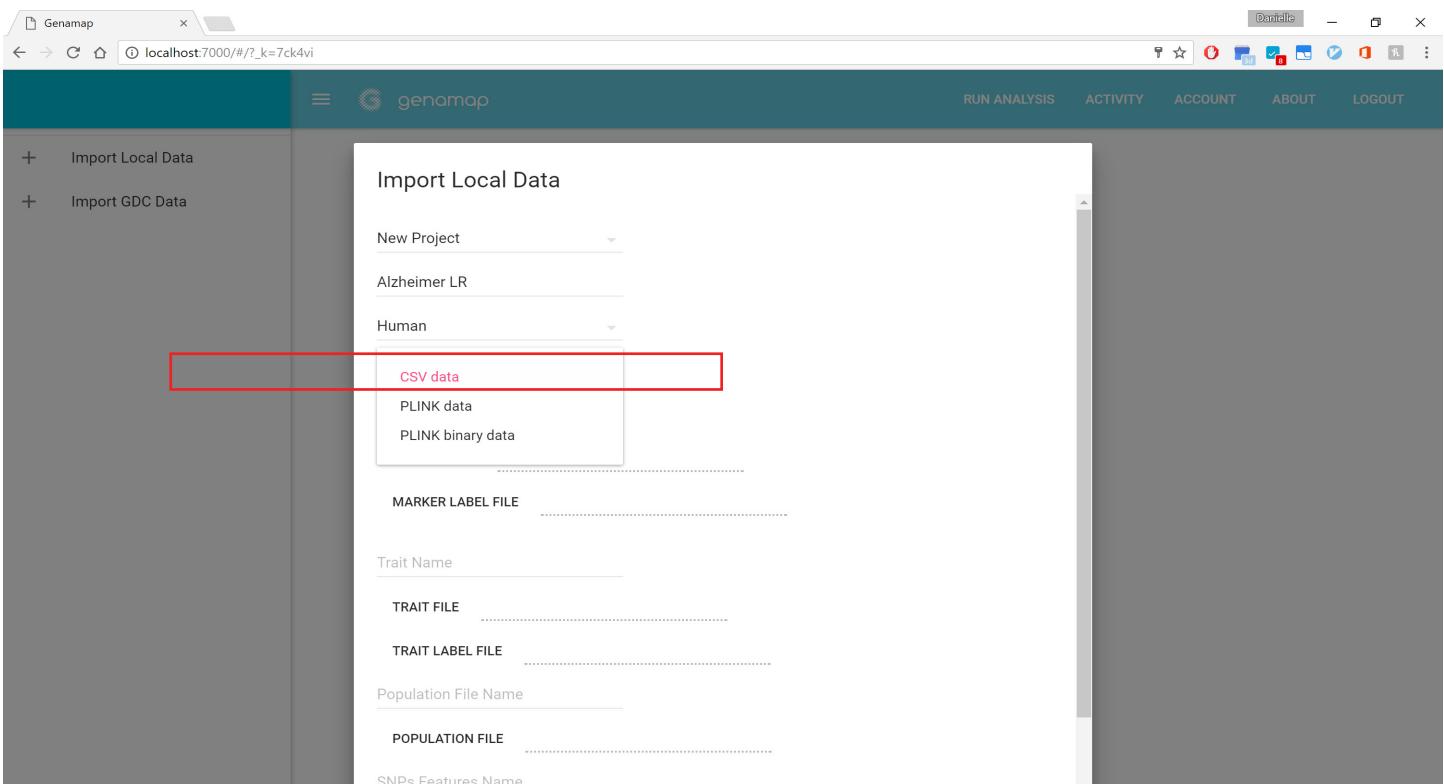
For this example, we will select “Import Local Data”



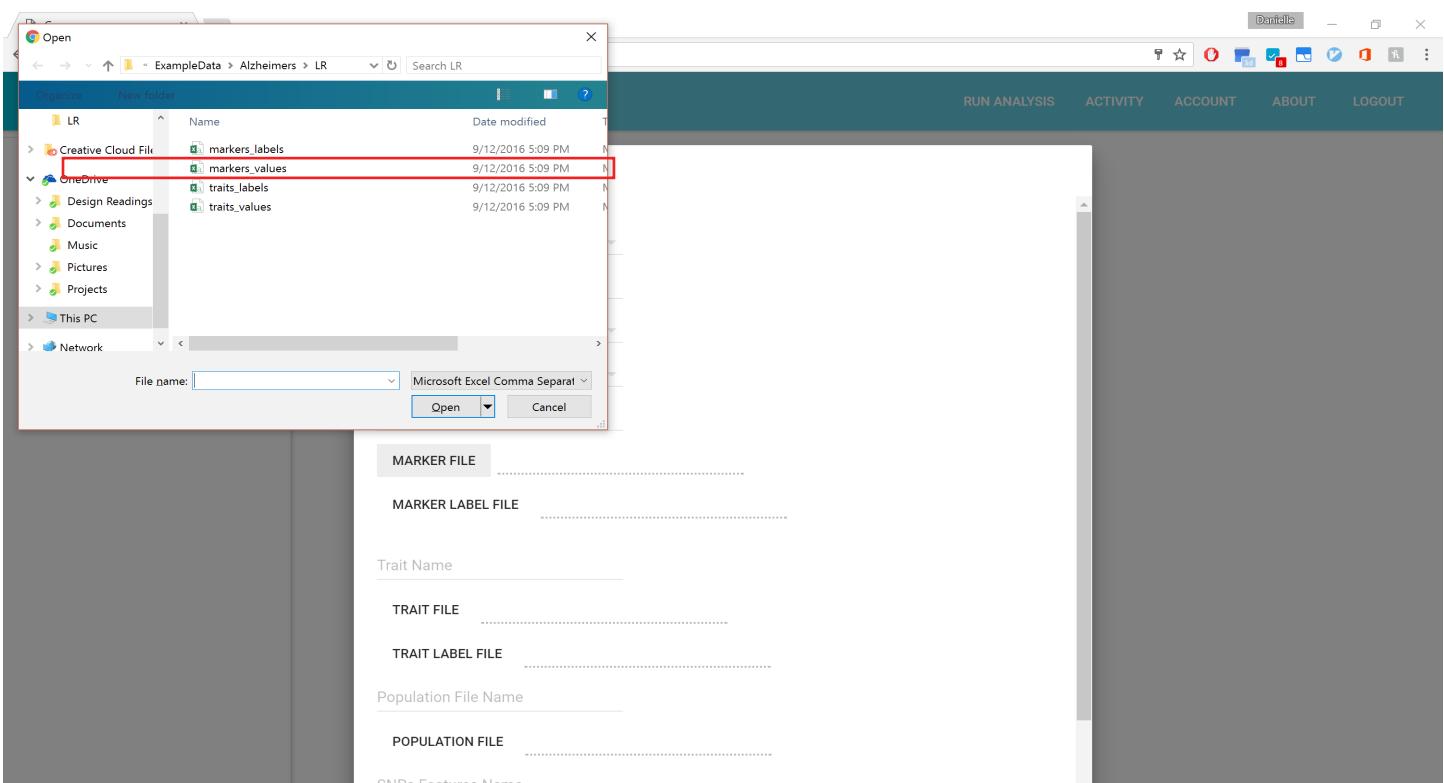
A pop-up will prompt you to insert information about your data.
Start naming the import accordingly



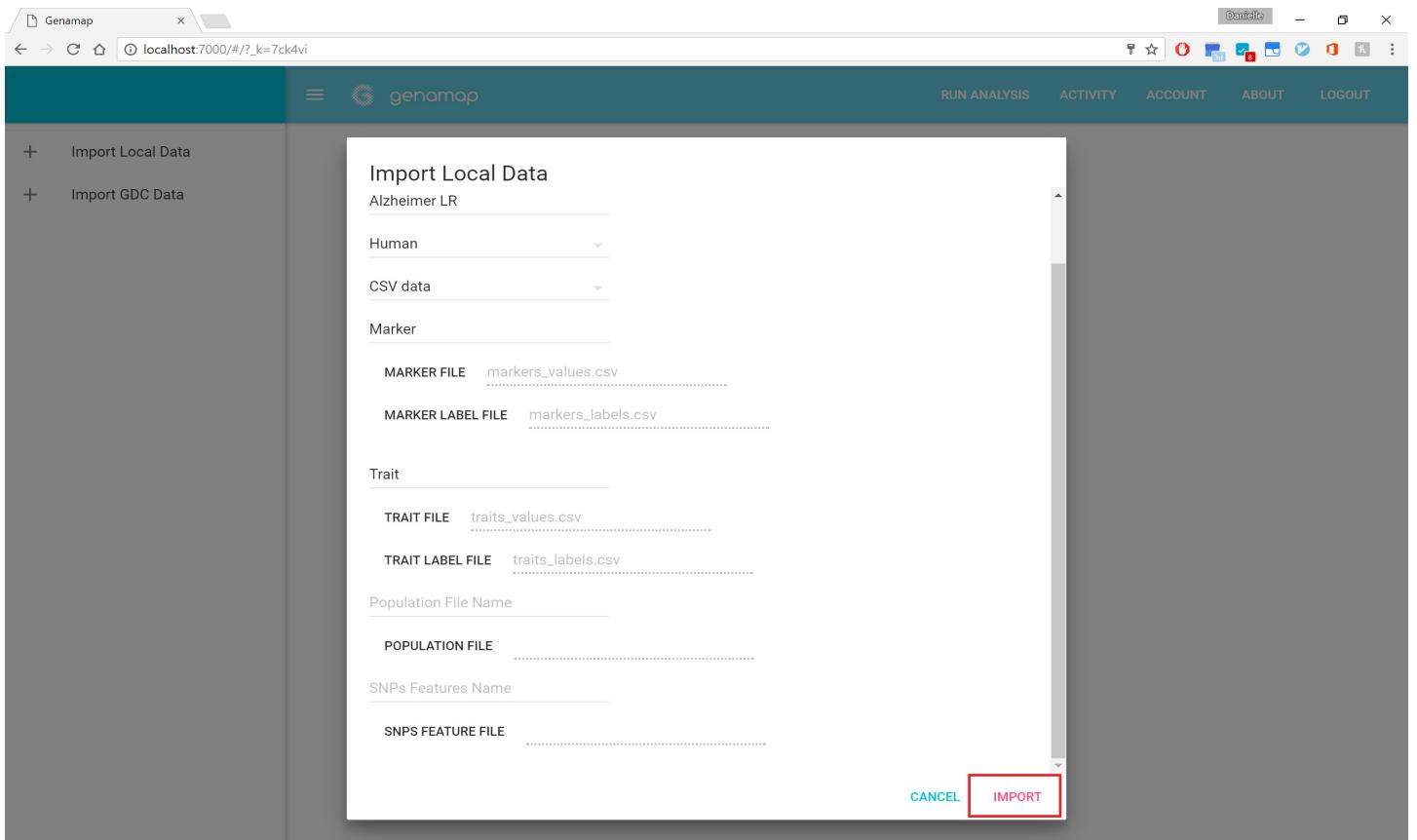
"Choose Species" allows you to choose from either "Human," "None," or "Fly"



You can also choose the type of data format from “CSV,” “PLINK,” or “PLINK binary”

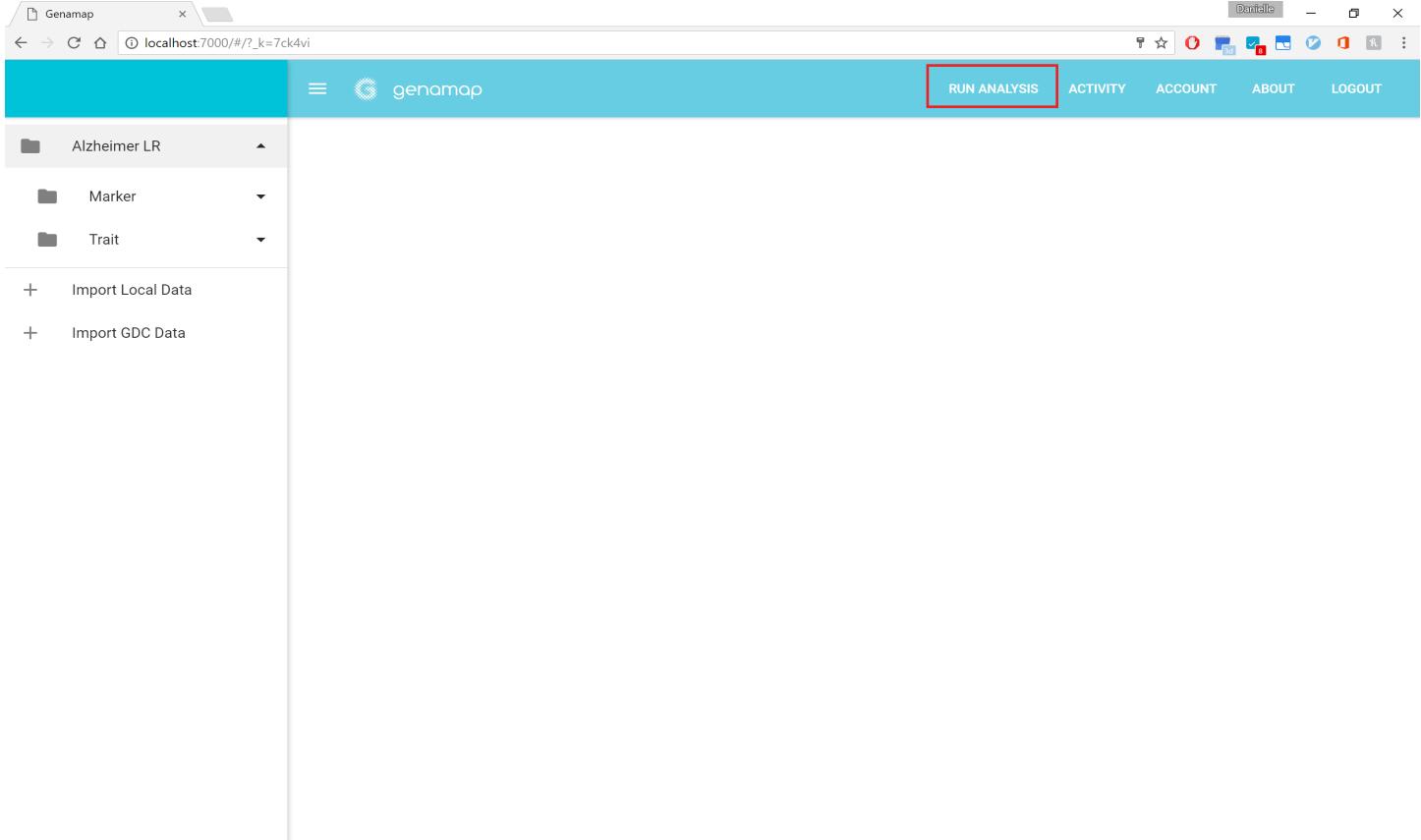


Click the button “Marker File” to pull up your file explorer, and navigate to where your data files are located. You will need (at minimum) marker labels and values, as well as trait labels and values.



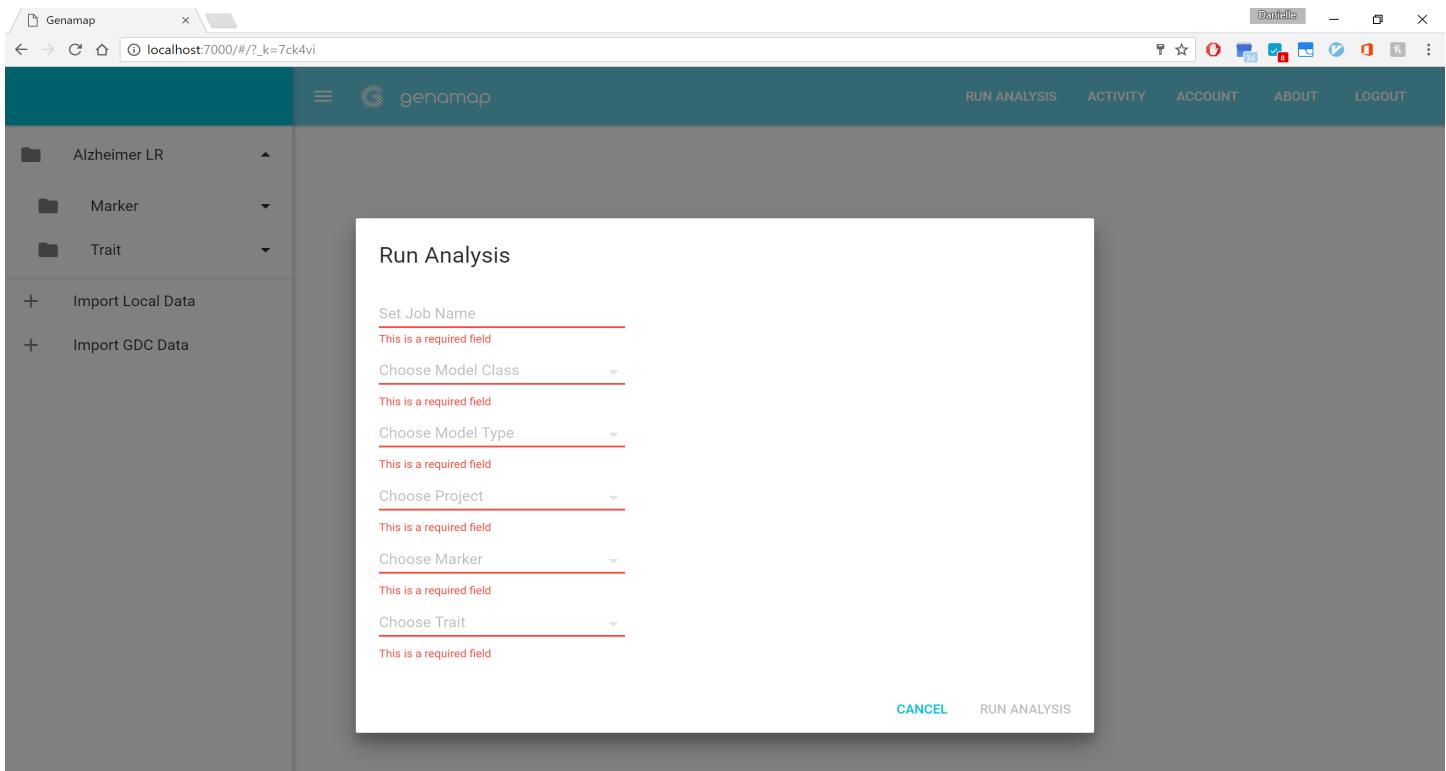
Once you have located all four files, you can proceed to upload more, or simply click to import the current files.

4) Analyze imported data

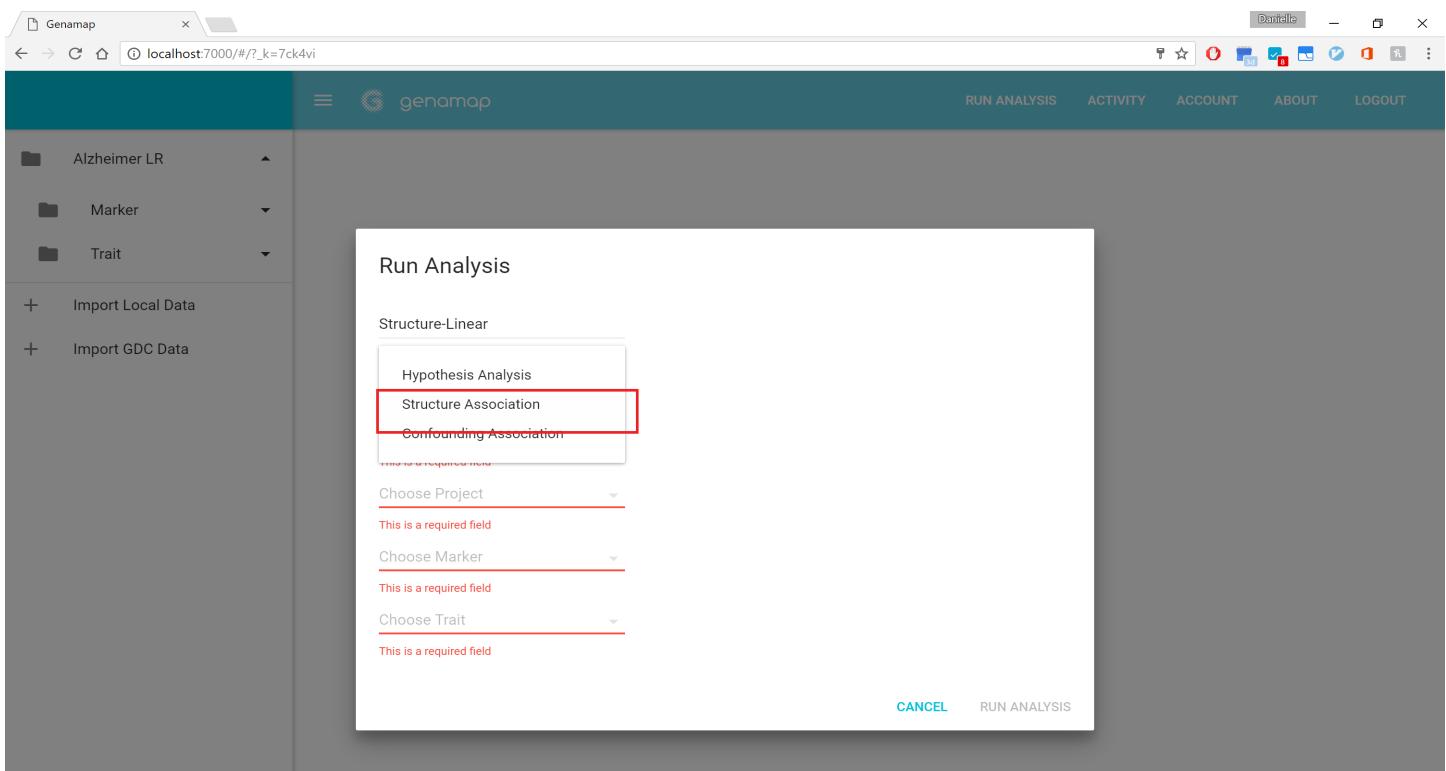


Notice our imported data is now showing on the left panel. The folder is labeled with our project name, as well as the Marker and Trait names we provided.

Now that our data is imported, we can run analyses on them to start finding interesting results! Click “Run Analysis” located in the top menu bar.



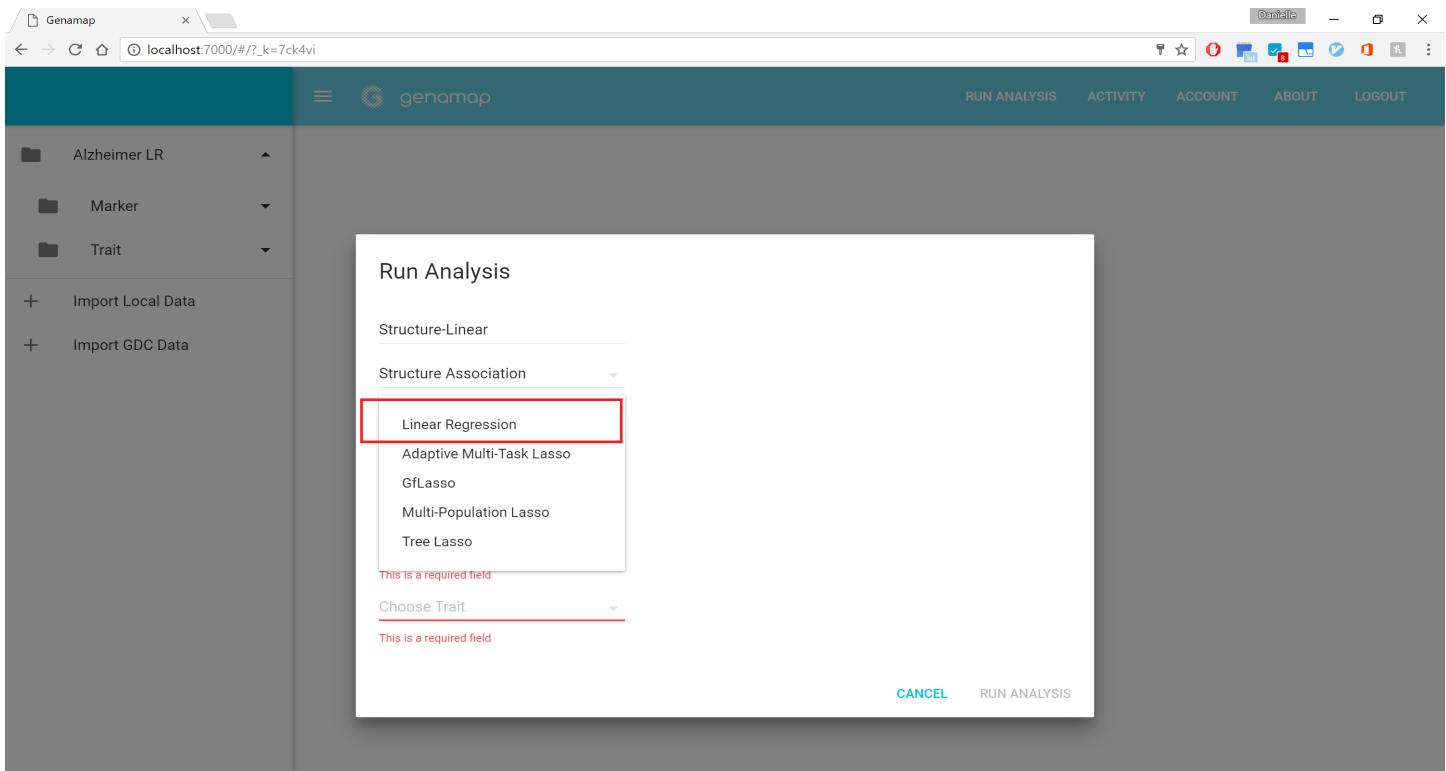
You will be prompted by a pop up again to start narrowing down the type of analysis you want to see.



You can choose between three types of model classes:

1. Hypothesis Analysis
2. Structure Association
3. Confounding Association

For this demo, we will choose “Structure Association”

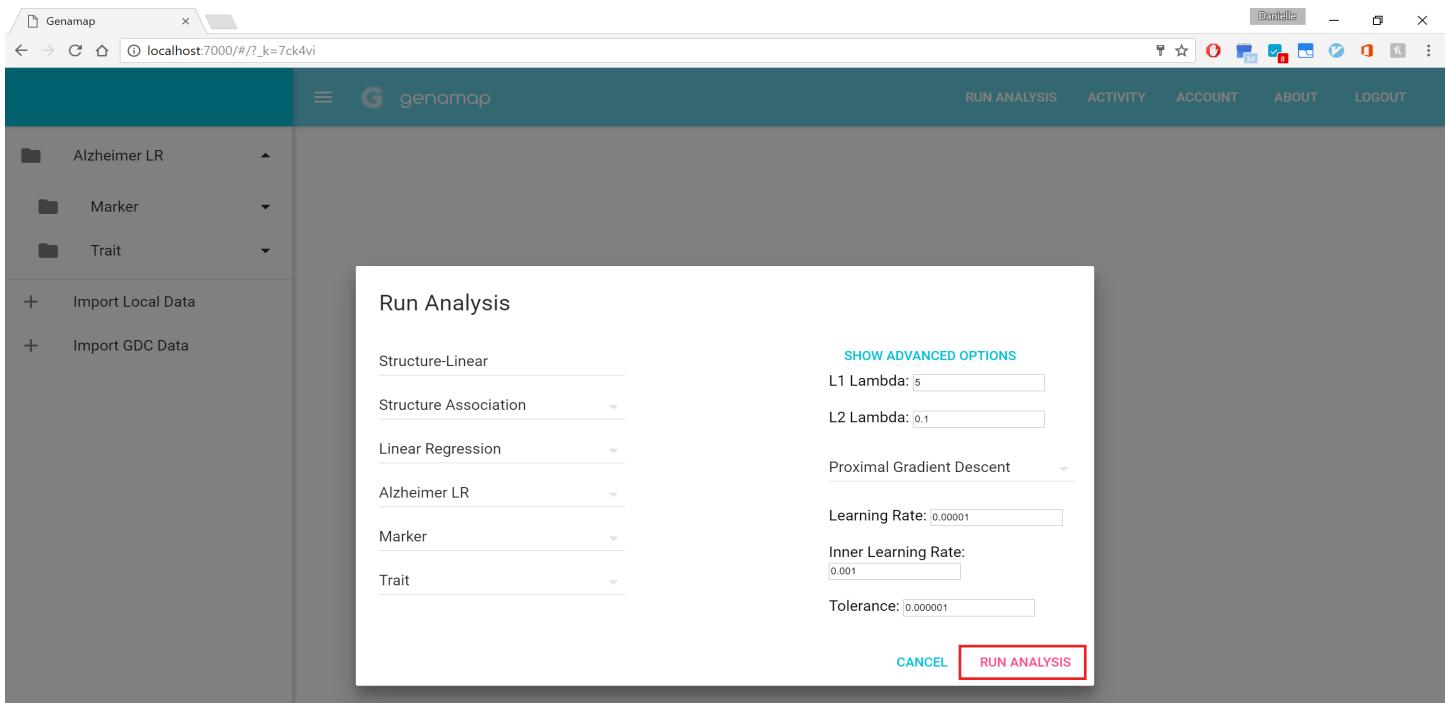


For “Structure Association,” you can choose between 5 types of model types:

1. Linear Regression
2. Adaptive Multi-Task Lasso
3. GfLasso

4. Multi-Population Lasso
5. Tree Lasso

For this demo, we will choose “Linear Regression”



Additionally, you can click “Show Advanced Options” to change various other settings.

The screenshot shows the Genemap software interface. At the top, there is a navigation bar with tabs: RUN ANALYSIS, ACTIVITY (which is highlighted with a red border), ACCOUNT, ABOUT, and LOGOUT. Below the navigation bar, there is a sidebar on the left containing a tree view of project components: Alzheimer LR, Marker, Trait, Results, Import Local Data, and Import GDC Data. On the right side, there is a progress bar panel titled "Structure-Linear" showing "100.0%" completion. The progress bar has three categories: RUNNING (blue), ALL (pink), and COMPLETED (green). A small "X" icon is located at the bottom right of the progress bar panel.

You can check on the progress of your analysis by clicking the “Activity” tab in the top menu

5) Visualize analysis

The screenshot shows a web browser window for the Genemap platform. The URL in the address bar is `localhost:7000/#/?_k=7ck4vi`. The page has a light blue header bar with the Genemap logo and navigation links for RUN ANALYSIS, ACTIVITY, ACCOUNT, ABOUT, and LOGOUT. On the left side, there is a sidebar with a tree-like structure of data projects and analysis results:

- Alzheimer LR
 - Marker
 - [Marker Values](#)
 - [Marker Labels](#)
 - Trait
 - [Trait Values](#)
 - [Trait Labels](#)
 - Results
 - [Structure-Linear Matrix View](#)

Below the sidebar, there are two buttons: "Import Local Data" and "Import GDC Data". The "Structure-Linear Matrix View" link under the Results section is highlighted with a red rectangular box.

Once the analysis finishes, the results will pop up inside your uploaded data project. To view your results, click on the “Matrix View” button.



Your analysis will upload into a matrix view, which you can scroll to see the results.



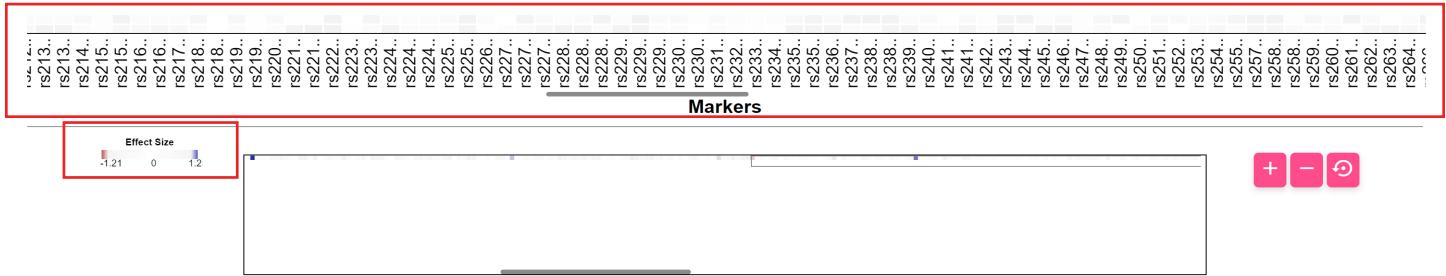
Hover over the squares in the matrix to bring up a tooltip that provides more information about each individual value in the matrix.



Below the matrix lies a miniature map of the matrix. This minimap presents you with a more broad scope and view of the analysis.

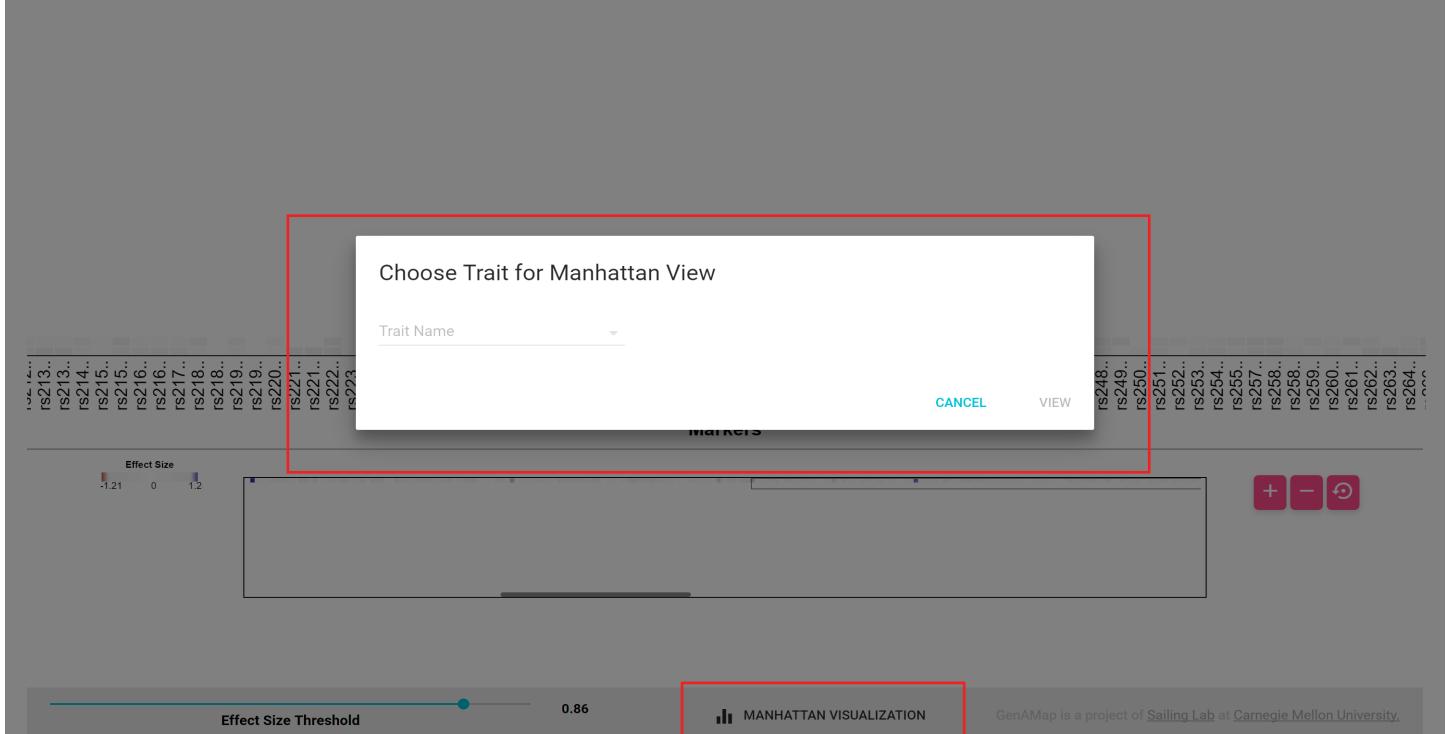


If you double click on a spot in the matrix's minimap, our above matrix will jump to that position and allow you to view that space from our main view.

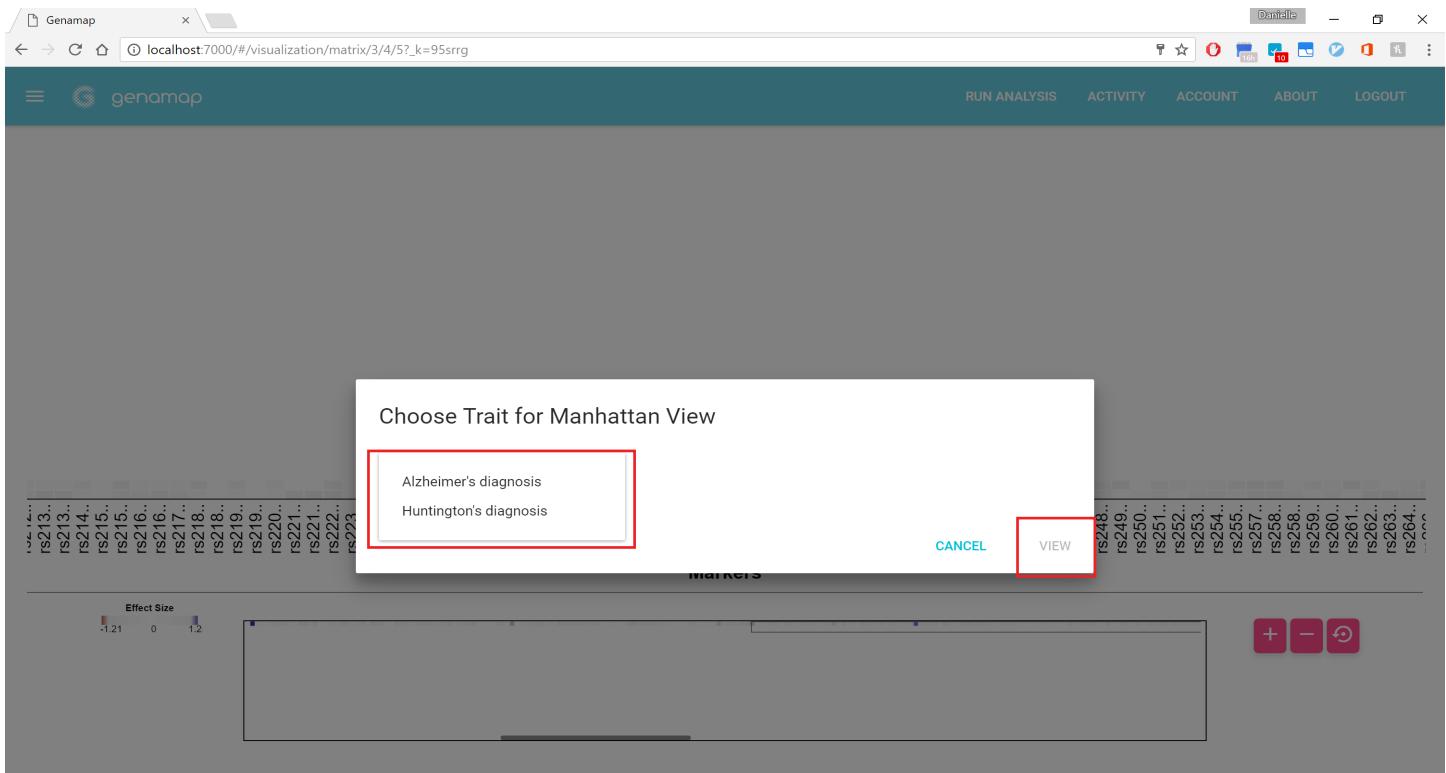


Effect Size Threshold 0.86 MANHATTAN VISUALIZATION GenAMap is a project of Sailing Lab at Carnegie Mellon University.

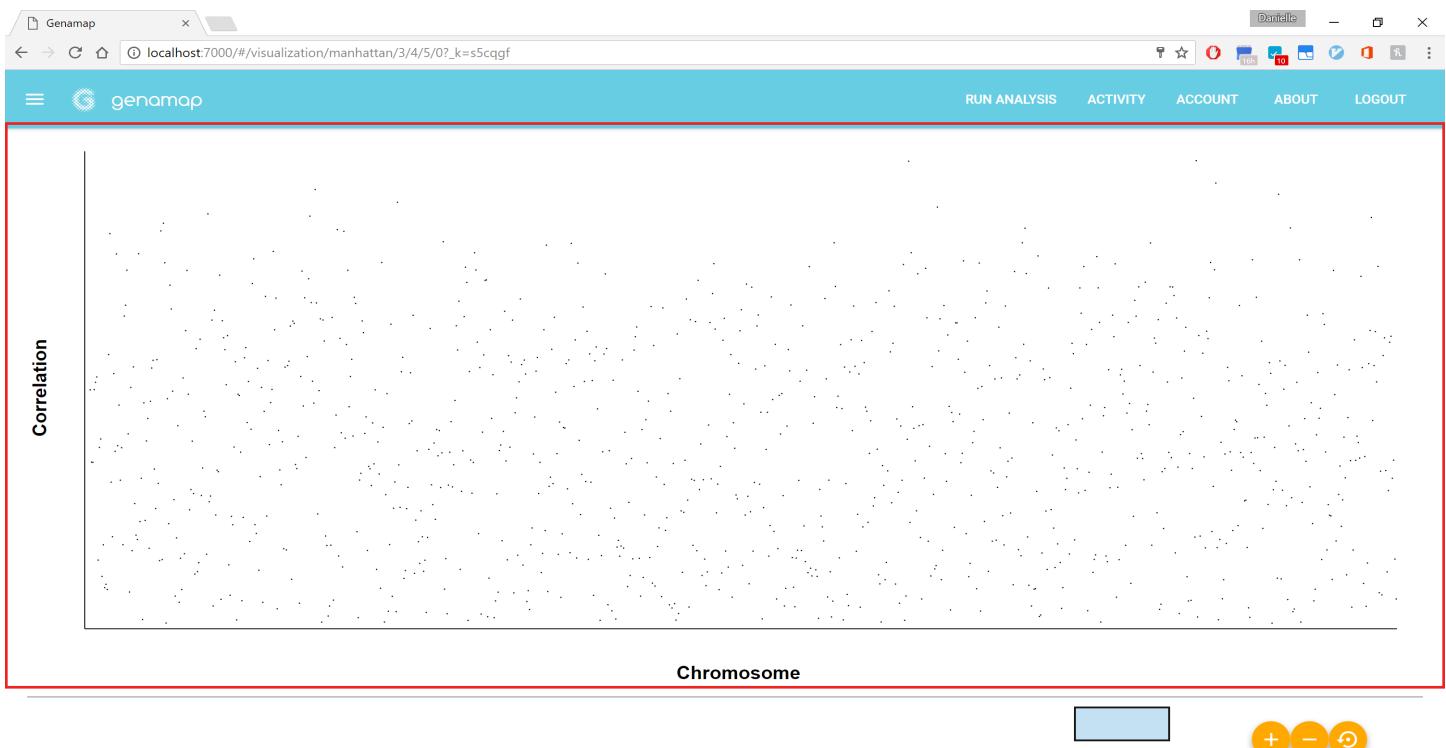
You can also play around with the “Effect Size Threshold” to filter out magnitudes in the main view. Negative effect size values are in red, while positive effect size values are in blue. As you increase the “Effect Size Threshold,” the magnitude of the values below the threshold are whited out



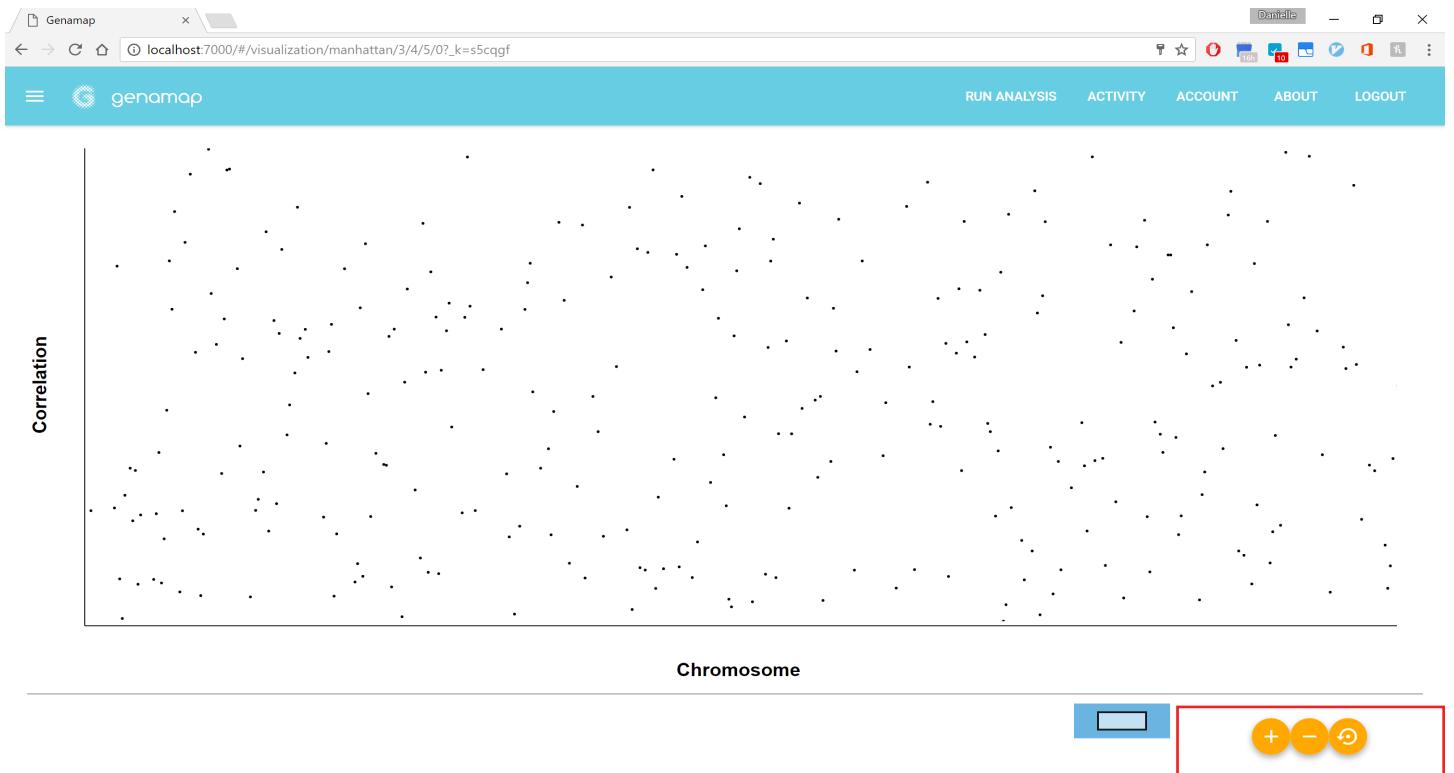
Another visualization that you can bring up is the “Manhattan Visualization.” This view transfers the visualization from a matrix to a manhattan plot. If you click “Manhattan Visualization in the bottom bar,” you will be prompted to choose a trait name to visualize.



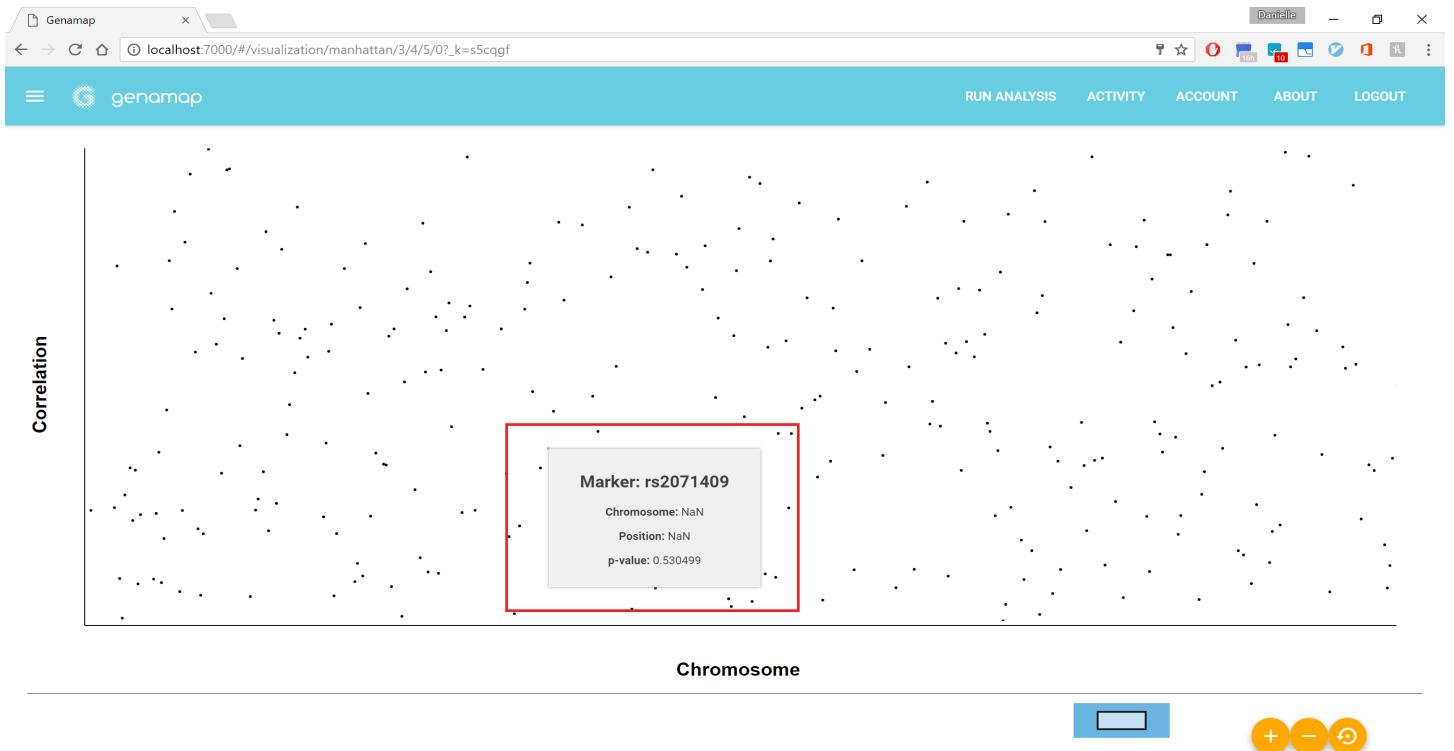
Choose one of the traits you wish to visualize with the Manhattan plot and click “View” to proceed.



The Manhattan Visualization starts out in full view of all of the data values



You can zoom into the values by using the zoom features at the bottom right.



Similar to the Matrix View, you can hover over each data value to bring up its tooltip to find out more information.