

GCP Workshop

Data Driven AI Application for Healthcare and Life Sciences

Accelerate Vaccine Research with Google Cloud

BigQuery, AI Platform and Healthcare APIs

Course overview

Duration is 2 min

The labs introduce participants to Google BigQuery, BigQuery Machine Learning and Notebook driven Data Analysis. In the labs, you learn how to analyze, and visualize data using Google BigQuery for peptidic epitope data sourced from NIH and available through BigQuery Public Dataset program. BigQuery has a [sandbox](#) through which you can try it out without having to sign up for Google Cloud (or having to provide a credit card).

- <https://towardsdatascience.com/bigquery-without-a-credit-card-discover-learn-and-share-199e08d4a064>
- To learn more about BigQuery Public Dataset and how to take advantage of free processing, you can visit: <https://cloud.google.com/bigquery/public-data>
- To learn more specific about Google Cloud for Healthcare and Life Sciences visit: <https://cloud.google.com/solutions/healthcare-life-sciences>

Lab Setup and Requirements

Qwiklabs setup

Duration is 2 min

Before you click the Start Lab button

Read these instructions. Labs are timed and you cannot pause them. The timer starts when you click Start Lab, shows how long Cloud resources will be made available.

This Qwiklabs hands-on lab lets you do the lab activities yourself in a real cloud environment, not in a simulation or demo environment. It does so by giving you new, temporary credentials that you use to sign in and access the Google Cloud Platform for the duration of the lab.

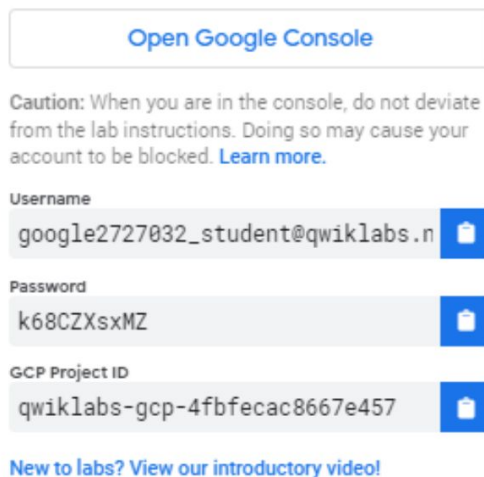
What you need

To complete this lab, you need:

- Access to a standard internet browser (Chrome browser recommended).
- **Note:** If you already have your own personal GCP account or project, do not use it for this lab.

How to start your lab and sign in to the Console

1. Click the **Start Lab** button. If you need to pay for the lab, a pop-up opens for you to select your payment method. On the left is a panel populated with the temporary credentials that you must use for this lab.



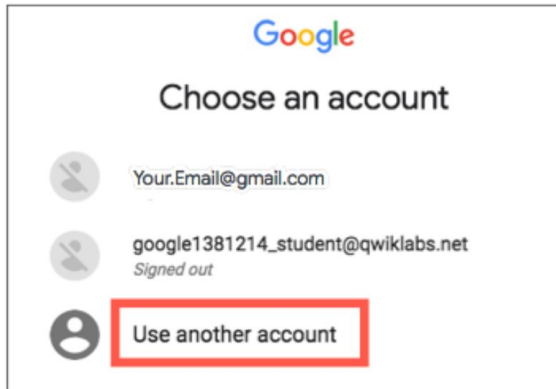
The screenshot shows a login panel with the following elements:

- A button labeled "Open Google Console".
- A caution message: "Caution: When you are in the console, do not deviate from the lab instructions. Doing so may cause your account to be blocked. [Learn more.](#)"
- Three input fields, each with a copy icon to its right:
 - Username:** google2727032_student@qwiklabs.n
 - Password:** k68CZXsxMZ
 - GCP Project ID:** qwiklabs-gcp-4fbfecac8667e457
- A link at the bottom: "New to labs? View our introductory video!"

2. Copy the username, and then click **Open Google Console**. The lab spins up resources, and then opens another tab that shows the **Choose an account** page.

Tip: Open the tabs in separate windows, side-by-side.

3. On the Choose an account page, click **Use Another Account**.



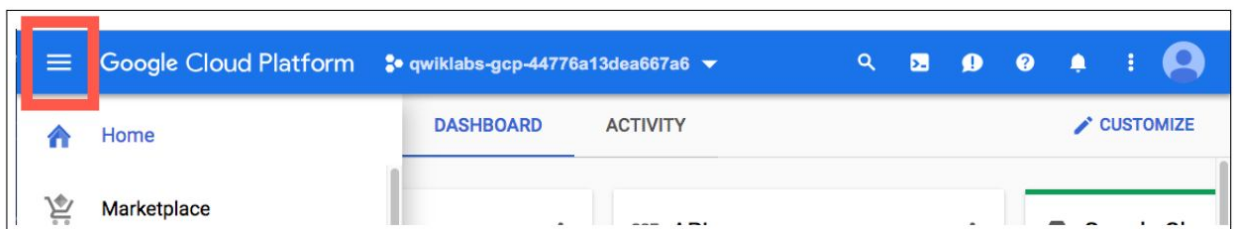
4. The Sign in page opens. Paste the username that you copied from the Connection Details panel. Then copy and paste the password.

Important: You must use the credentials from the Connection Details panel. Do not use your Qwiklabs credentials. If you have your own GCP account, do not use it for this lab (avoids incurring charges).

5. Click through the subsequent pages:
 - Accept the terms and conditions.
 - Do not add recovery options or two-factor authentication (because this is a temporary account).
 - Do not sign up for free trials.

After a few moments, the GCP console opens in this tab.

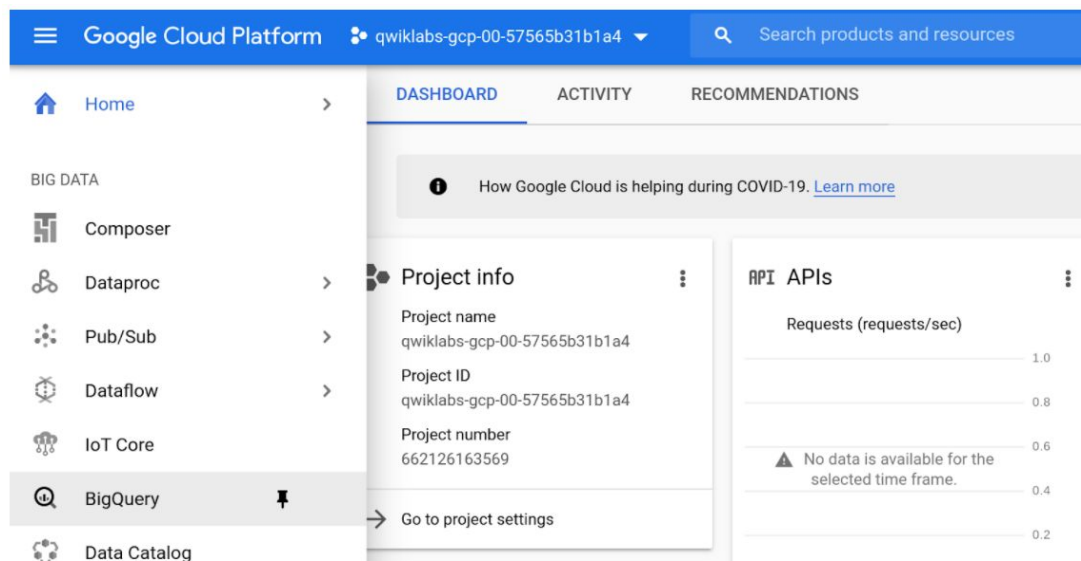
- **Note:** You can view the menu with a list of GCP Products and Services by clicking the **Navigation menu** at the top-left, next to “Google Cloud Platform”.



Lab 1: Using BigQuery Interfaces

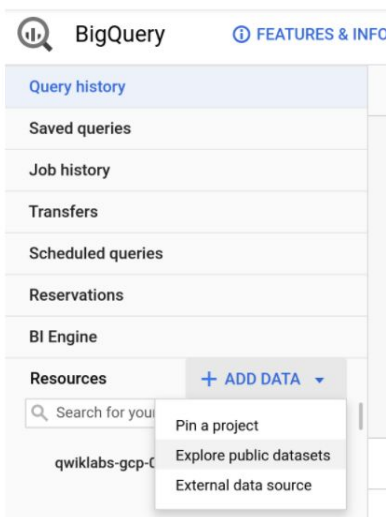
Duration is 7 min

Task: In this section, you explore the epitope public dataset using the query builder in the BigQuery web UI. Scroll down to the BIG DATA services to select BigQuery.



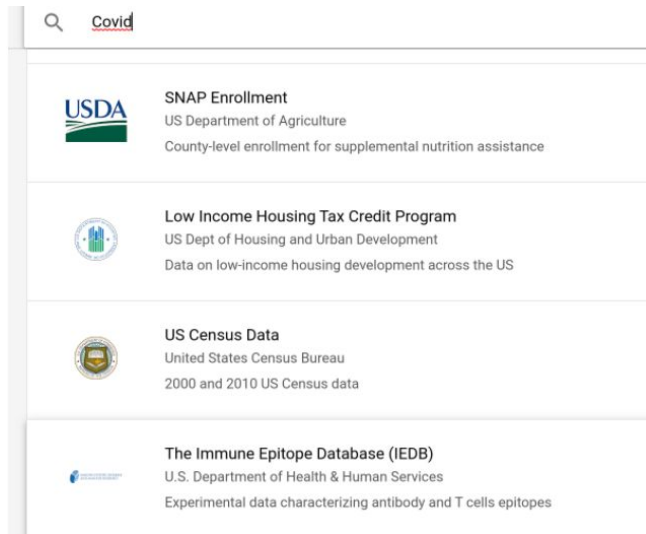
Step 1

While on BigQuery, click on **+ ADD DATA** and select Explore **public datasets**. BigQuery provides many public datasets that you can leverage for your analysis. Explore all different datasets available.



Step 2

Search for Covid on the search box for the Public Dataset page and scroll down to select The Immune Epitope Database.



Step 3

Read about the IEDB dataset that is sourced from NIH. Scroll down to sample queries and **click on the first example of “Run this Query”**. This query provides results for epitopes in a dataset for a given organism of interest, for example ‘coronavirus’.

Samples

Try the sample queries below in the BigQuery UI.

Try the sample queries below in the BigQuery UI.

Which antigen has the most number of epitopes in a dataset for organisms of interest, for example ‘coronavirus’?

This query examines which antigen has the largest number of epitopes contained in the dataset for a given organism. It specifically looks at "coronavirus". [Run this query.](#)

Selecting ‘Run this query’ will bring you back to BQ Analysis UI with the query already displayed for you. Click on the **Run** button to see the query result.

The result shows Antigen Name with total counts of epitopes assays for coronavirus available in our dataset, ordered by most number of epitopes.

For example, the resulting query shows we have 1623 epitopes for the Spike glycoprotein from an organism coronavirus.

The Immune Epitope Database (IEDB): Which antigen has the most number o... [↗](#) [+](#) [HIDE EDITC](#)

```
1 SELECT
2   Antigen_Name,
3   SUM(number_of_epitopes) AS epitopes
4 FROM
5   bigquery-public-data.immune_epitope_db.antigen_full v3
6 WHERE
7   organism_name LIKE '%coronavirus%'
8 GROUP BY
9   Antigen_Name
10 ORDER BY
11   epitopes DESC
```

[Run](#) [Save query](#) [Save view](#) [Schedule query](#) [More](#) This query will process 3.8 MB when run. [✓](#)

Query results [SAVE RESULTS](#) [EXPLORE DATA](#)

Query complete (0.4 sec elapsed, 3.8 MB processed)

Job information [Results](#) JSON Execution details


Row	Antigen_Name	epitopes
1	Spike glycoprotein	1623
2	Replicase polyprotein 1ab	1607
3	Nucleoprotein	937
4	Membrane protein	299

Rows per page: 100 1 - 27 of 27 [First page](#) [|<](#) [>](#) [| Last page](#)

Step 4

On a different tab, where you had a public dataset information page for IEDB data, click on 'VIEW DATASET' to see a full list of tables for epitopes.

On BigQuery UI, you would see IEDB public dataset and all the tables within. Click on any table and select preview on the right side to see sample data, for an example, select mhc_ligand_full table and click preview.

 **The Immune Epitope Database (IEDB)**
U.S. Department of Health & Human Services
Experimental data characterizing antibody and T cells epitopes

[VIEW DATASET](#)

[OVERVIEW](#) [SAMPLES](#)

Step 5

Lets run few more queries to get answer for key data insights

In the Query Editor section on the right, copy or write the following query to identify which mhc allele has most references in a binding affinity data for coronavirus?

```
SELECT
  allele_name as allele,
  count(*) as counts
FROM `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
WHERE
  object_type = 'Linear peptide'
  AND organism_name like '%coronavirus%'
  AND antigen_name like 'Spike%'
GROUP BY allele_name
ORDER By counts desc
```

Click **Run** to review the result.

Query editor

```

1 SELECT
2   allele_name as allele,
3   count(*) as counts
4 FROM `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
5 WHERE
6   object_type = 'Linear peptide'
7   AND organism_name like '%coronavirus%'
8   AND antigen_name like 'Spike%'
9 GROUP BY allele_name
10 ORDER BY counts desc
11

```

[Run](#)
[Save query](#)
[Save view](#)
[Schedule query](#)
[More](#)

Query results

[SAVE RESULTS](#)
[EXPLORE DATA](#)

Query complete (0.6 sec elapsed, 125.7 MB processed)

[Job information](#)
[Results](#)
[JSON](#)
[Execution details](#)

Row	allele	counts
1	HLA-A*01:01	95
2	HLA-DRB1*01:01	87
3	HLA-A*02:01	85
4	HLA-A*26:01	82
5	HLA-A*24:02	80
6	HLA-A*03:01	75
7	HLA-A*30:02	67
8	HLA-A*23:01	67
9	HLA-A*22:01	67

In the Query Editor section on the right, replace the query with a new query as shown below to identify what is the most effective length of linear peptide of spike protein for ligand-peptide binding reference? Click on [Run](#) to review the result.

```

SELECT
length(Description) as peptide_mers,
count(*) as counts
FROM `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
WHERE
object_type = 'Linear peptide'
AND organism_name like '%coronavirus%'
AND antigen_name like 'Spike%'
GROUP BY 1
ORDER BY counts desc

```


Query editor

```
1 SELECT
2 length(Description) as peptide_mers,
3 count(*) as counts
4 FROM `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
5 WHERE
6 object_type = 'Linear peptide'
7 AND organism_name like '%coronavirus%'
8 AND antigen_name like 'Spike%'
9 GROUP BY 1
10 ORDER BY counts desc
```



Run



Save query



Save view



Schedule query



More

Query results

SAVE RESULTS

EXPLORE DATA

Query complete (0.7 sec elapsed, 125.3 MB processed)

Job information

Results

JSON

Execution details

Row	peptide_mers	counts
1	9	874
2	10	407
3	15	87

In the Query Editor section on the right, replace the query with a new query as shown below to identify what is the strong binding affinity between 9 or 10 mer peptide of spike protein with HLA allele? List results in order of high positive binding to negative based on quantitative measure. Click on **Run** to review the result.

```
SELECT
antigen_name,
Description as peptide,
Parent_protein,
assay_group as binding_type,
allele_name as allele,
qualitative_measure,
quantitative_measurement as result_score
FROM `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
WHERE
object_type = 'Linear peptide'
AND organism_name like '%coronavirus%'
AND assay_group != 'qualitative binding'
AND allele_name like 'HLA-%'
AND antigen_name like 'Spike%'
AND length(Description) IN (9,10)
ORDER BY result_score
```

Query editor + COMPOSE NEW QUERY HIDE E

```

1 SELECT
2 antigen_name,
3 Description as peptide,
4 Parent_protein,
5 assay_group as binding_type,
6 allele_name as allele,
7     qualitative_measure,
8 quantitative_measurement as result_score
9 FROM `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
10 WHERE
11 object_type = 'Linear peptide'
12 AND organism_name like '%coronavirus%'
13 AND assay_group != 'qualitative binding'
14 AND allele_name like 'HLA-%'
15 AND antigen_name like 'Spike%'
16 AND length(Description) IN (9,10)
17 ORDER BY result_score

```

Run
Save query
Save view
Schedule query
More
This query will p

Query results SAVE RESULTS EXPLORE DATA

Query complete (0.4 sec elapsed, 248.6 MB processed)

Job information Results JSON Execution details

Row	antigen_name	peptide	Parent_protein	binding_type	allele	qualitative_measure	result_score
1	Spike glycoprotein precursor	SWFITQRNFF	Spike glycoprotein	dissociation constant KD (~IC50)	HLA-A*24:02	Positive-High	0.035
2	Spike glycoprotein precursor	SWFITQRNFF	Spike glycoprotein	dissociation constant KD (~IC50)	HLA-A*23:01	Positive-High	0.0458
3	Spike glycoprotein precursor	HTSSMRGVY	Spike glycoprotein	dissociation constant KD (~IC50)	HLA-A*30:02	Positive-High	0.131
4	Spike glycoprotein precursor	SWFITQRNF	Spike glycoprotein	dissociation constant KD (~IC50)	HLA-A*30:02	Positive-High	0.215
5	Spike glycoprotein precursor	KISNCVADY	Spike glycoprotein	dissociation constant KD (~IC50)	HLA-A*30:02	Positive-High	0.221
6	Spike glycoprotein precursor	VVFLHVTYV	Spike glycoprotein	dissociation constant KD (~IC50)	HLA-A*02:03	Positive-High	0.281

Step 6

Important: This step is necessary to build and run machine learning models within BigQuery.

You will create a new dataset named 'corona' for your BigQuery project. This dataset will hold your own tables and models as you need them. On the BigQuery UI left panel, highlight the name of your project and then click on **+ CREATE DATASET** from right panel middle toolbar section.

Resources + ADD DATA

Search for your tables and datasets

qwiklabs-gcp-00-57565b31b1a4

qwiklabs-gcp-00-57565b31b1a4

Run
Save query
Save view
Schedule query
More
This query will process 3.8 MB when run. ✔

qwiklabs-gcp-00-57565b31b1a4

CREATE DATASET PIN PROJECT

No datasets available

Use the controls above to create a dataset and start building out your Resources tree, or check your permissions for this resource

Give the dataset a name 'corona', leave the rest of the parameters to defaults and click on the **Create Dataset** button.

Create dataset

Dataset ID

Data location (Optional) ?

Default table expiration ?

- ☒ Never
☐ Number of days after table creation:

Encryption

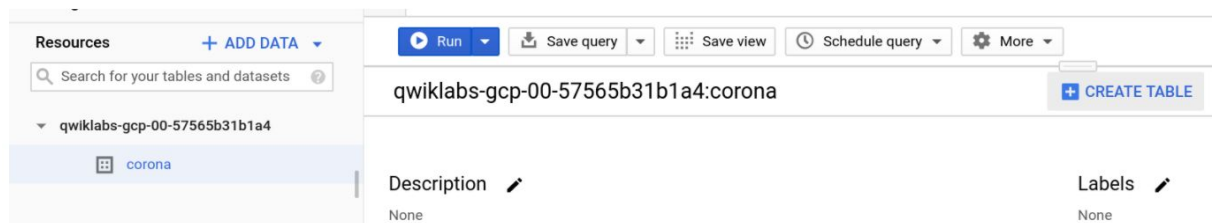
Data is encrypted automatically. Select an encryption key management solution.

- ☒ Google-managed key
No configuration required
☐ Customer-managed key
Manage via Google Cloud Key Management Service

Create dataset

Cancel

Newly created dataset 'corona' is visible on the left panel under your project. Think of a dataset as equivalent to 'schema' of training databases.



Step 7

To create a table within a dataset, you have multiple options such as creating a table manually, create a data transfer job or even just point to a file on Google storage or from your own local machine. You will download the following file, click on the url below to get a csv file that describes the amino acids basic properties.

https://storage.cloud.google.com/bq_epitope_workshop/files/amino_acids.csv

Once you have downloaded the file, highlight the 'corona' dataset from the left panel and click on **+CREATE TABLE** button from the middle toolbar on the right panel.

On the create table wizard, select as following:

Create table from: **Upload**

Select file: browse and select the **csv** you just downloaded

File format: **CSV**

Table name: **amino_acid**

Scheme - Auto detect: **check** to auto create table from CSV

Expand Advanced Options to set

- Header rows to skip: 1

Leave the rest of the parameters to default values and click on the **Create table** button.

Create table

Source

Create table from: Upload Select file: amino_acids.csv Browse File format: CSV

Destination

☒ Search for a project ☐ Enter a project name

Project name: qwiklabs-gcp-00-4bf2aa883446 Dataset name: corona Table type: Native table


Table name: amino_acid

Schema

Auto detect

☒ Schema and input parameters

1 Schema will be automatically generated.

Advanced options 

Write preference: Write if empty

Number of errors allowed: 0 Unknown values: ☐ Ignore unknown values

Field delimiter: Comma

Header rows to skip: 1 Quoted newlines: ☐ Allow quoted newlines Jagged rows: ☐ Allow jagged rows

Encryption

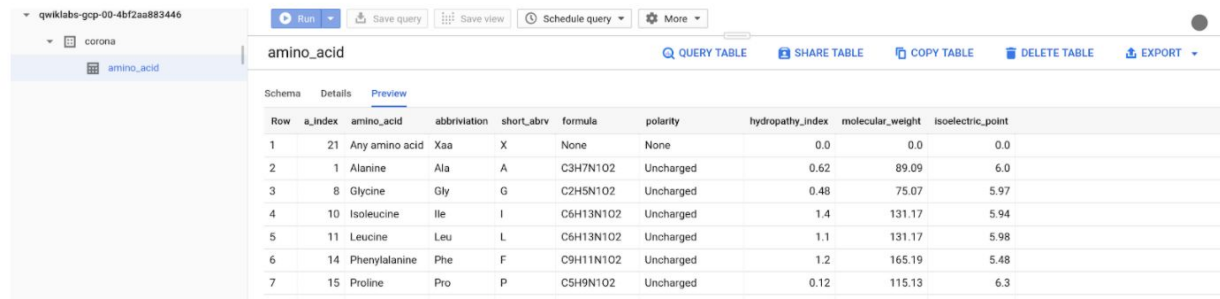
Data is encrypted automatically. Select an encryption key management solution.

☒ Google-managed key
No configuration required

☐ Customer-managed key
Manage via Google Cloud Key Management Service

Create table Cancel

If you do not see the table created, refresh the page to make sure and review the table by selecting it.



The screenshot shows the Google Cloud Platform BigQuery interface. On the left, a sidebar displays the project 'qwklabs-gcp-00-4bf2aa883446' and a folder 'corona' containing a table 'amino_acid'. The main panel shows the 'amino_acid' table with tabs for 'Schema', 'Details', and 'Preview'. The 'Preview' tab is active, displaying a table with 10 columns: 'Row', 'a_index', 'amino_acid', 'abbreviation', 'short_abrv', 'formula', 'polarity', 'hydropathy_index', 'molecular_weight', and 'isoelectric_point'. The table contains 7 rows of data for various amino acids.

Row	a_index	amino_acid	abbreviation	short_abrv	formula	polarity	hydropathy_index	molecular_weight	isoelectric_point
1	21	Any amino acid	Xaa	X	None	None	0.0	0.0	0.0
2	1	Alanine	Ala	A	C3H7N1O2	Uncharged	0.62	89.09	6.0
3	8	Glycine	Gly	G	C2H5N1O2	Uncharged	0.48	75.07	5.97
4	10	Isoleucine	Ile	I	C6H13N1O2	Uncharged	1.4	131.17	5.94
5	11	Leucine	Leu	L	C6H13N1O2	Uncharged	1.1	131.17	5.98
6	14	Phenylalanine	Phe	F	C9H11N1O2	Uncharged	1.2	165.19	5.48
7	15	Proline	Pro	P	C5H9N1O2	Uncharged	0.12	115.13	6.3

End of Lab 1. Congratulations!

Lab 2:

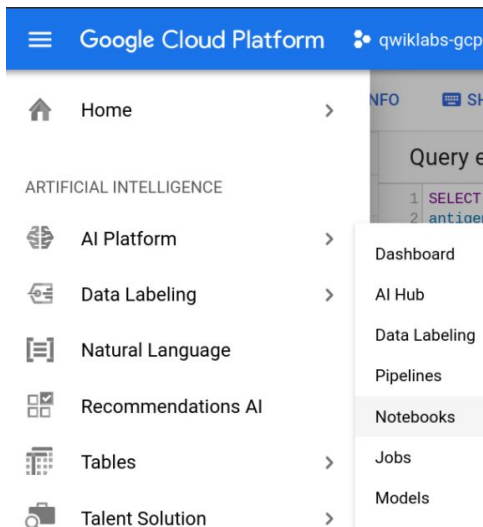
Data Analysis with Data Science Notebook

Duration is 8 min

Task: In this section, you will wear a hat of data scientist and will perform analysis on epitope dataset to identify and narrow down the possible attributes of peptides to build machine learning models. You will perform analysis using Jupyter notebook as a datalab from Google AI Platform.

Step 1

First create a notebook environment within Google Cloud. GCP provides quick access to many frameworks and tools as well as choice of CPUs and GPUs for a notebook runtime environment. You will create a notebook with PyTorch 1.4 without GPU.



From the Home menu on Google Cloud panel, select Notebook within Artificial Intelligence services.

PyTorch 1.4

Includes scikit-learn, pandas, NLTK and more

Without GPUs

With 1 NVIDIA Tesla T4

Click on **+ NEW INSTANCE** and select PyTorch 1.4 Without GPU.

New notebook instance

Instance name	python-20200716-145742
Region *	us-central1 (Iowa)
Zone *	us-central1-b
Environment ?	Intel® optimized Base (with Intel® MKL)
Machine type	4 vCPUs, 15 GB RAM
Boot disk	100 GB Disk
Subnetwork	default(10.128.0.0/20)
External IP	Ephemeral(Automatic)
Permission	Compute Engine default service account
Estimated cost ?	\$99.89 monthly, \$0.137 hourly

CUSTOMIZE CANCEL

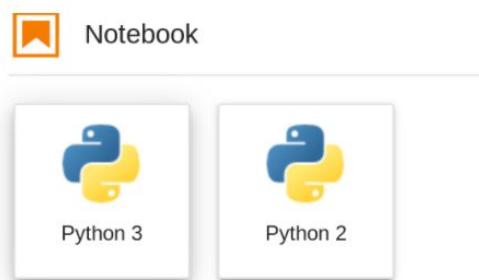
CREATE

You can leave default settings or select a region close to your data, usually for these labs, you can keep region settings to us-central1. Click on the **CREATE** button. In about 30 seconds your notebook environment will be ready to use.

Notebook instances							
+ NEW INSTANCE REFRESH ▶ START ■ STOP ⏮ RESET							
Filter table ?							
<input type="checkbox"/>	<input type="radio"/>	Instance name		Region	Environment	Machine type	GPUs
<input type="checkbox"/>	<input checked="" type="radio"/>	python-20200716-145742	OPEN JUPYTERLAB	us-central1-b	Python	4 vCPUs, 15 GB RAM	None ▼

Once ready, open the notebook instance by clicking on **OPEN JUPYTERLAB**.

Click on Python 3 Notebook to launch the notebook editor panel.



Make sure, you have completed Lab 1 to create a dataset named 'corona', which is required for hosting the machine learning model you will create in the lab 3.

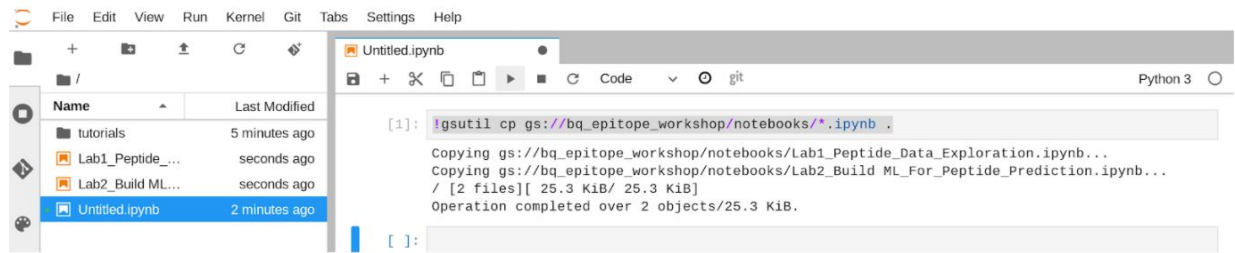
Step 2

From file menu, create New → Notebook

Enter the following command in a section as shown below and click on the 'Run' / Play button to execute. Alternatively, you can execute any selected cell in a notebook by pressing shift+enter.

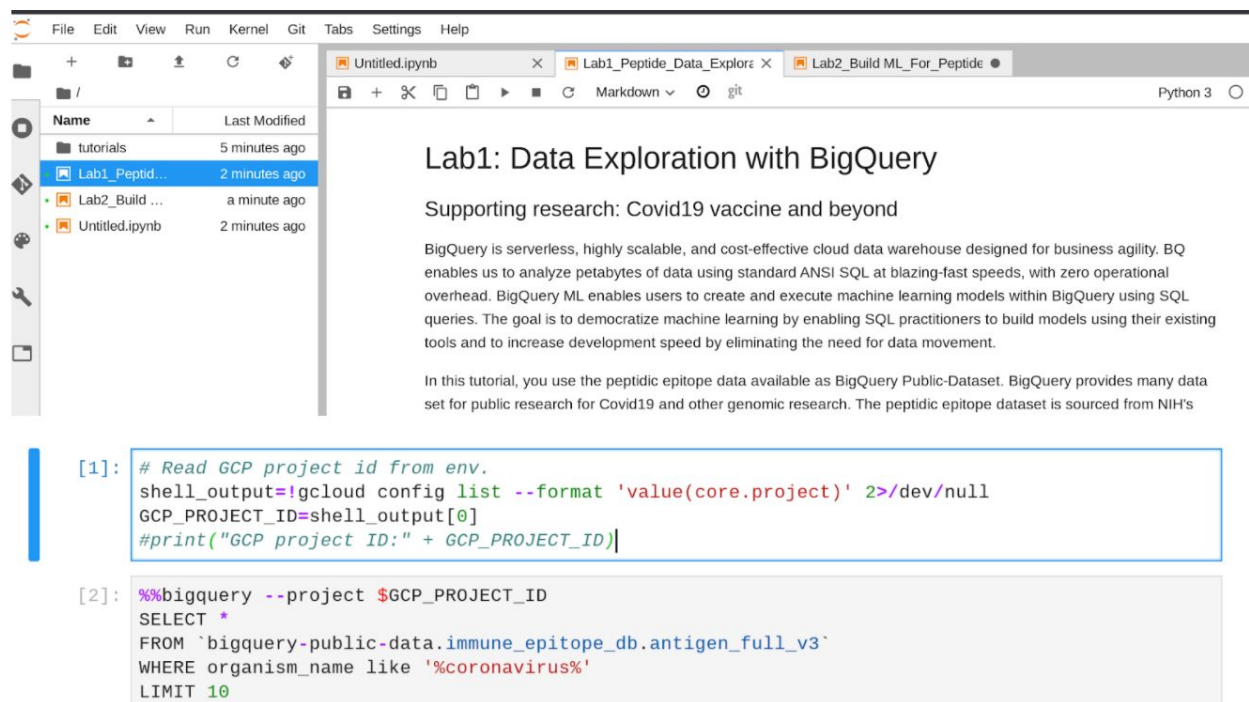
```
!gsutil cp gs://bq_epitope_workshop/notebooks/*.ipynb .
```

Command will copy two lab notebook files to your environment as shown below.



Step 3

Double click on Lab1_Peptide_Data_exploration notebook to open it in an editor panel. The notebook cells have informational sections as well as executional sections. Notebooks are designed to be self-explanatory, hence read through it carefully and execute a cell in the order it is presented. To execute a cell, click on a play icon on the tool-bar of the notebook or press shift+enter. Observe the result of the cell you execute before proceeding to the next cell.



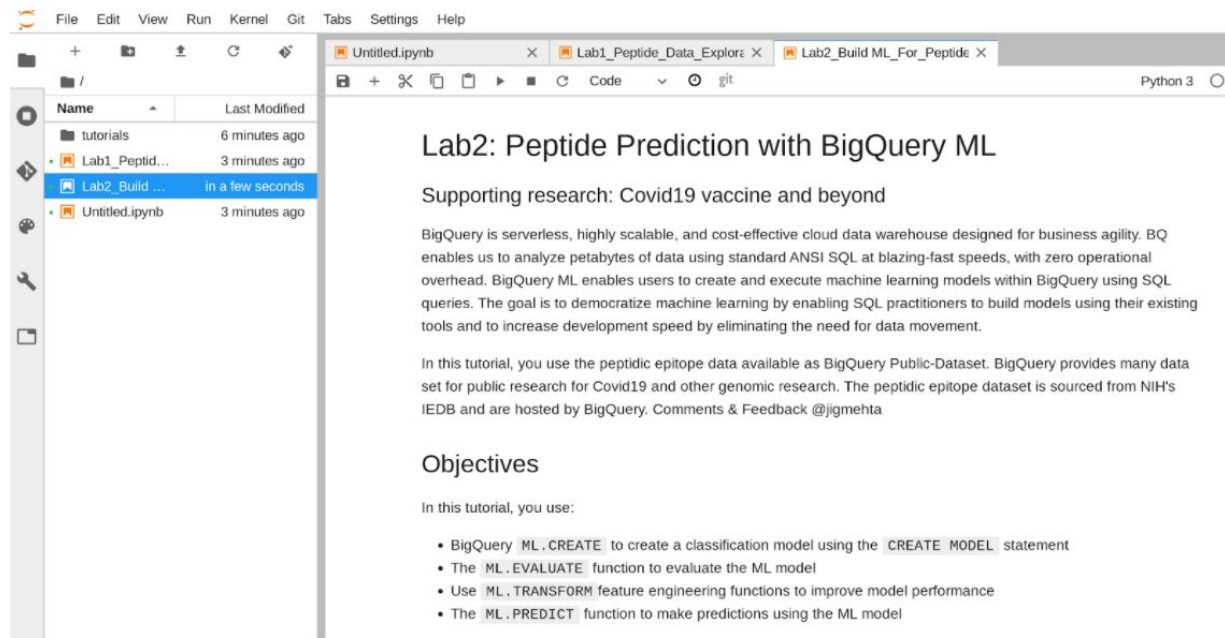
This completes Lab 2! Congratulations!

Lab 3:

Machine Learning Model with BigQuery

Duration is 7 min

Task: In this section, you will build a machine learning model with data already available in bigquery, by leveraging simple SQL statements. Then, you will evaluate the model and create another model to get better results from machine learning. At last, you will use the machine learning model you created to predict binding affinity of a peptide to a mhc ligand. Carefully execute cells in the order it is presented. To execute a cell, click on a play icon on the tool-bar of the notebook or press shift+enter. Observe the result of the cell you execute before proceeding to the next cell.



The screenshot shows a Jupyter Notebook interface. On the left is a file explorer with a table of files:

Name	Last Modified
tutorials	6 minutes ago
Lab1_Peptid...	3 minutes ago
Lab2_Build ...	In a few seconds
Untitled.ipynb	3 minutes ago

The main notebook area displays a cell titled "Lab2: Peptide Prediction with BigQuery ML". The content of the cell is as follows:

Lab2: Peptide Prediction with BigQuery ML

Supporting research: Covid19 vaccine and beyond

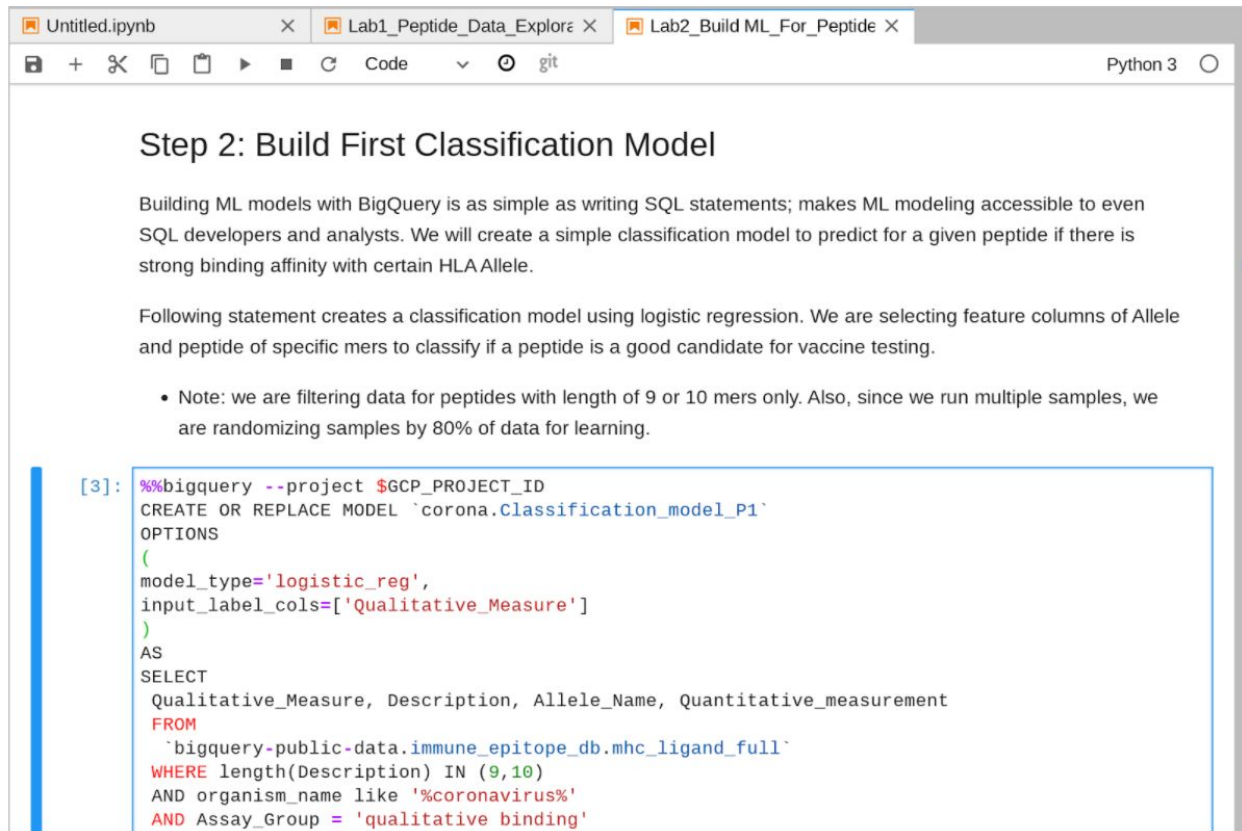
BigQuery is serverless, highly scalable, and cost-effective cloud data warehouse designed for business agility. BQ enables us to analyze petabytes of data using standard ANSI SQL at blazing-fast speeds, with zero operational overhead. BigQuery ML enables users to create and execute machine learning models within BigQuery using SQL queries. The goal is to democratize machine learning by enabling SQL practitioners to build models using their existing tools and to increase development speed by eliminating the need for data movement.

In this tutorial, you use the peptidic epitope data available as BigQuery Public-Dataset. BigQuery provides many data set for public research for Covid19 and other genomic research. The peptidic epitope dataset is sourced from NIH's IEDB and are hosted by BigQuery. Comments & Feedback @jgmehta

Objectives

In this tutorial, you use:

- BigQuery `ML.CREATE` to create a classification model using the `CREATE MODEL` statement
- The `ML.EVALUATE` function to evaluate the ML model
- Use `ML.TRANSFORM` feature engineering functions to improve model performance
- The `ML.PREDICT` function to make predictions using the ML model



The screenshot shows a Jupyter Notebook with three tabs: 'Untitled.ipynb', 'Lab1_Peptide_Data_Explor...', and 'Lab2_Build ML_For_Peptide X'. The active tab is 'Lab2_Build ML_For_Peptide X'. The notebook content includes a section titled 'Step 2: Build First Classification Model'. Below the title, there is a paragraph explaining that building ML models with BigQuery is as simple as writing SQL statements. This is followed by another paragraph stating that the following statement creates a classification model using logistic regression. A bulleted note mentions filtering data for peptides with length of 9 or 10 mers and randomizing samples by 80%. The code cell [3] contains a BigQuery SQL query to create or replace a model named 'corona.Classification_model_P1' using logistic regression. The query selects 'Qualitative_Measure', 'Description', 'Allele_Name', and 'Quantitative_measurement' from the 'bigquery-public-data.immune_epitope_db.mhc_ligand_full' dataset, filtering by peptide length (9 or 10), organism name (containing 'coronavirus'), and assay group ('qualitative binding').

Step 2: Build First Classification Model

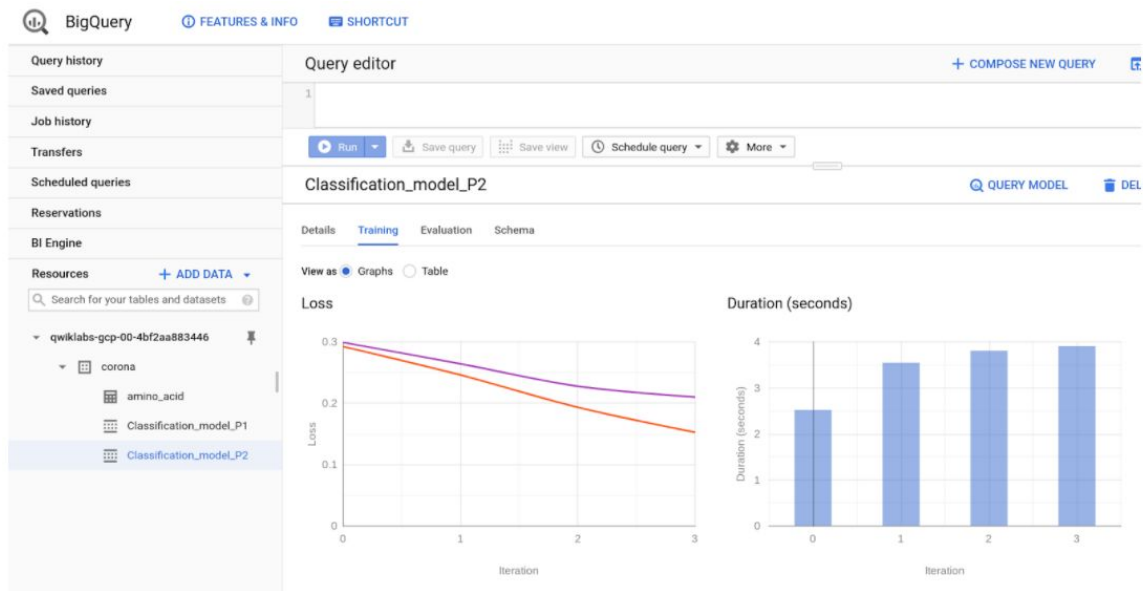
Building ML models with BigQuery is as simple as writing SQL statements; makes ML modeling accessible to even SQL developers and analysts. We will create a simple classification model to predict for a given peptide if there is strong binding affinity with certain HLA Allele.

Following statement creates a classification model using logistic regression. We are selecting feature columns of Allele and peptide of specific mers to classify if a peptide is a good candidate for vaccine testing.

- Note: we are filtering data for peptides with length of 9 or 10 mers only. Also, since we run multiple samples, we are randomizing samples by 80% of data for learning.

```
[3]: %%bigquery --project $GCP_PROJECT_ID
CREATE OR REPLACE MODEL `corona.Classification_model_P1`
OPTIONS
(
  model_type='logistic_reg',
  input_label_cols=['Qualitative_Measure']
)
AS
SELECT
  Qualitative_Measure, Description, Allele_Name, Quantitative_measurement
FROM
  `bigquery-public-data.immune_epitope_db.mhc_ligand_full`
WHERE length(Description) IN (9,10)
AND organism_name like '%coronavirus%'
AND Assay_Group = 'qualitative binding'
```

Once you complete the notebook, you can monitor model artifacts and additional details such as evaluation and confusion matrix for a model within a BQ UI. Simply select a model from your project dataset and click on the right panel for Training and Evaluation tabs to review details of model characteristics.



CONFUSION MATRIX

This table shows the percentage of actual labels that were classified correctly (in blue) and incorrectly (in grey). The last column shows the percentage of total samples for the corresponding actual label.

Actual labels	Predicted labels					% samples
	Negative	Positive	Positive-High	Positive-Intermediate	Positive-Low	
Negative	88.71%	0.24%	2.06%	3.03%	5.95%	40.31%
Positive	58.97%	15.38%	23.08%	-	2.56%	1.91%
Positive-High	15.9%	-	62.96%	12.42%	8.71%	22.46%
Positive-Intermediate	24.78%	-	30.32%	26.24%	18.66%	16.78%
Positive-Low	34.04%	0.26%	14.78%	19.53%	31.4%	18.54%

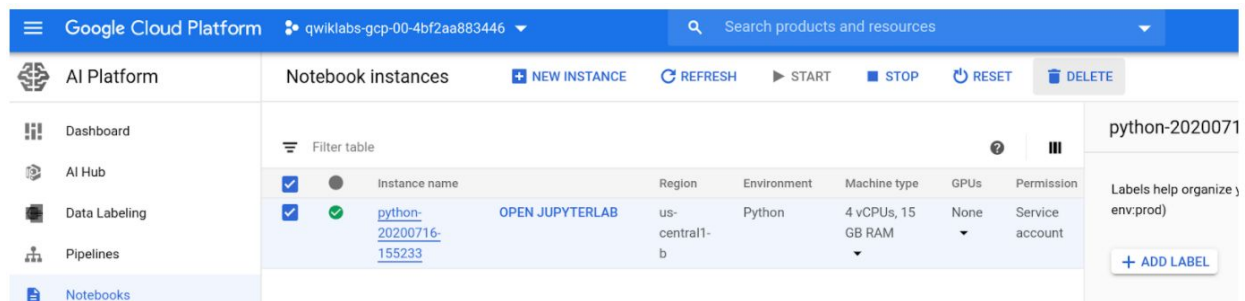
This completes Lab 3! Congratulations!

End your lab environment

Duration is 1 min

Step 1

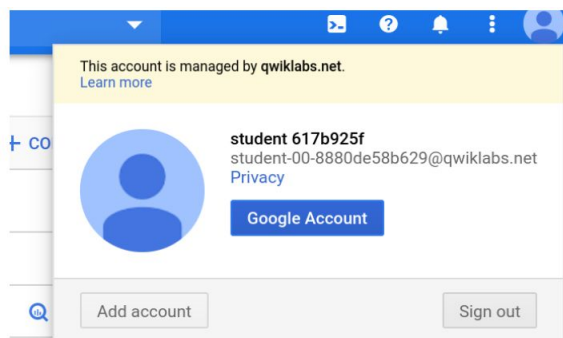
From Google Cloud Console Home menu, select Notebooks from AI Platform services. Select the notebook instance you have created, click on **DELETE** to close and remove it.



Step 2

Sign out from your Google Cloud lab console.

When you've completed your lab, click **End**. Qwiklabs removes the resources you've used and cleans the account for you.



Step 3

You'll be asked to rate the lab experience. Select the applicable number of stars, enter a comment, and then click **Submit**.

Note: When you have completed your lab, click **End**. Qwiklabs removes the resources you've used and cleans the account for you.

You will be given an opportunity to rate the lab experience. Select the applicable number of stars, type a comment, and then click **Submit**.

Note: The number of stars indicates the following:

- 1 star = Very dissatisfied
- 2 stars = Dissatisfied
- 3 stars = Neutral
- 4 stars = Satisfied
- 5 stars = Very satisfied

You may close the dialog if you don't want to provide feedback.

Additional Resources

- For more information about Google Cloud Training and Certification, see <https://cloud.google.com/training/>
- For more Google Cloud Platform Self-Paced Labs, see <http://run.qwiklabs.com>

For feedback, suggestions, or corrections, please use the **Support** tab.