

Gene Prioritization Pipeline

Cancer Genomics Cloud (CGC) version
QUICKSTART GUIDE

knoweng 

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This Quickstart guide describes how to run the Gene Prioritization (GP) pipeline/workflow on the Cancer Genomics Cloud (CGC).

In this pipeline, the user submits a spreadsheet of gene-level transcriptomic (or other omics) profiles of a collection of biological samples. Each sample is also annotated with a numeric phenotype (e.g., drug response) or binary phenotype (e.g., metastatic status). This pipeline scores each gene by the correlation between its “omic” value (e.g., expression) and the phenotype, and reports the top phenotype-related genes. Gene prioritization can be done in a Knowledge Network-guided mode (using ProGENI, PMID:28800781), and with optional use of bootstrapping to achieve robust prioritization.

Initial Steps

1. Login to the CGC at <https://cgc.sbgenomics.com/>.
If you don't have a CGC account, create one using the "Create a free account" link on this page just below the login box.
2. Click on the project's link to go to the project dashboard.
If you don't have a project to use, create one using the "Create a project" button.
3. Click on the "Apps" tab on the project dashboard.
If you don't have the KnowEnG Gene Prioritization Workflow app in your project, add it using the "Add app" button:
 - a. Click on the green "Add app" button.
 - b. Search for the app, e.g., enter "gp" or "gene prioritization" in the search box.
 - c. Click on the "Copy" button in the app box.
 - d. Click on the green "Copy" button.
 - e. Click on the "X" in the top right of the window to close it.
4. Click on the KnowEnG Gene Prioritization Workflow link to go to the app page and view information about the app.

Run the App

5. Click on the Run button to run the app.

Data Files

6. These instructions use sample input files already available in this project ([demo_GP.genomic.txt](#) and [demo_GP.phenotypic.txt](#)). For information on uploading your own data to the CGC, see the section "Uploading Files to the CGC" further down in this document.
 - a. **Genomic Spreadsheet File:**
 - i. Click on the "Select file(s)" button.
 - ii. Enter "demo" in the search box.
 - iii. Find the input file in the list of files returned (the file's name is "demo_GP.genomic.txt").
 - iv. Click on the checkbox to the left of the file name.
 - v. Click on the "Save selection" button.
 - b. **Phenotypic Spreadsheet File:**
 - i. Click on the "Select file(s)" button.
 - ii. Enter "demo" in the search box.
 - iii. Find the input file in the list of files returned (the file's name is "demo_GP.phenotypic.txt").
 - iv. Click on the checkbox to the left of the file name.
 - v. Click on the "Save selection" button.

Parameters

7. Click on the "Next: Define App Settings" button (or the "Define App Settings" tab).
The parameters are listed below in their suggested order of entry, although they may be listed in a different order on this page. For each parameter, the "?" link contains a description of what the parameter is used for and what type of value is expected, including a sample value and a link to a page that lists the possible values, <https://knoweng.org/kn-data-references/> (the values are listed within parentheses in the sections on that page; these values can be copy-n-paste'd into the parameter input boxes).
 - a. **Species Taxon ID:** the values are listed in the section [KN](#)

Running Apps

There are actually several ways to run apps on the CGC; for example, on the Apps tab, each app has some Actions, one of which is a green arrow run button; in addition, if you have run the app before, you can go to the Tasks tab, and each task includes an Action to re-run the task; and if you are on a task page, there is a green "Edit and rerun" button.

About the Demo File:

Transcriptomic file

The genomic spreadsheet preprocessed for this demo, [demo_GP.genomic.txt](#), contains basal gene expression profiles (all genes) of 491 cancer cell lines originally obtained from CCLE [PMID: 22460905].

About the Demo File:

Phenotypic file

The sample phenotypic file for this demo, [demo_GP.phenotypic.txt](#), contains values of 24 different phenotypes for each cell line in the demo transcriptomics file. Each phenotype here is the cell line's cytotoxicity in response to a drug, measured as IC50 values.

[Contents by Species.](#)

"9606" (for human) is a sample value.

(Species Taxon ID is listed twice on this page, but the input boxes are linked together so that when you enter the value in one text box it appears in the other.)

- b. **Correlation Measure:** choose a value from the pull-down menu. Choose **pearson** if your spreadsheets have continuous values; choose **t_test** if they have binary values. (The sample input files contain continuous values.)
- c. **Number of Top Genes:** enter an integer value. This value is optional; if not specified, the default value is 100.
- d. **Knowledge Network Edge Type:** the values are listed in the section [KN Contents by Gene-Gene Edge Type.](#) "STRING_experimental" is a sample value. Leave this value blank if you do not wish to use the Knowledge Network.
- e. **Amount of Network Influence:** enter an integer value between 0 and 100 (inclusive). This value is optional; if you do not enter a value, 50% will be used. A greater value means greater contribution from the network interactions. (This value is only relevant if the Knowledge Network is used.)
- f. **Number of Bootstraps:** enter an integer value; if you want to use bootstrapping, enter a value greater than 1. This value is optional; if not specified, the default value is 0 (i.e., no bootstrapping).
- g. **Bootstrap Sample Percent:** enter an integer value between 0 and 100 (inclusive). This value is optional; if you do not enter a value, 80% will be used. (This value is only relevant if bootstrapping is done.)

Launch the App

8. When the parameters are all entered, click on the green Run button to start the workflow running.

The app generally takes a few minutes to run (e.g., 4 to 9 minutes).

Results and Download

9. When the task is finished, the task page will show a green "COMPLETED" image to the left of the task name. The page shows the input files, the parameter settings, and the output files. There are several output files that give information about the run, but the main output files are the **Ranked Genes File** and the **Top Genes File**. The **README** file describes the output files.

To view an output file, click on the file name, and scroll down to the bottom of the page to view the file's contents (or just a portion of the contents, for large files). (You may need to click on the "Display raw data" button to view the contents.) From that page, you can also Download the file (the "Download" link is available under the "... "More actions" button).

You can also download a file, or multiple files, one at a time, from the task page by clicking the folder image "Browse files" button next to a particular file, or the "Outputs" header.

Using the Knowledge Network

In a nutshell, using the Knowledge Network widens your ability to infer connections via network neighbors for sparsely annotated genes.

If you do not wish to use the Knowledge Network, simply leave the Knowledge Network Edge Type parameter blank.

Links

[KnowEnG Main Website](#)
[KnowEnG Analytics](#)
[Knowledge Network Overview](#)
[Knowledge-Guided Pipelines](#)
[GP Pipeline](#)
[Pipeline Quickstart Guides](#)
[GP Pipeline Quickstart](#)
[CGC GP Pipeline Quickstart](#)
[KnowEnG YouTube Channel](#)

Uploading Files to the CGC

There are several ways to upload files to the CGC, as described on this page:

<https://docs.cancer-genomicscloud.org/docs/upload-to-the-cgc>

The best way will depend on where the files are, how you access them.

If they are on your personal computer, you can use the [CGC Uploader GUI tool](#).

If they are on a server, you can use the [Command Line Uploader](#).

If they are accessible via FTP or the web, you can use the [FTP/HTTP\(S\) import tool](#).

And you can also [upload from a cloud volume](#), such as Amazon Web Services (AWS) or Google Cloud Storage (GCS).