**DISCRIMINATOR Quick Start Manual**

**Version 1.0**

**April 2022**

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The purpose of this Quick Start Manual is to get DISCRIMINATOR up and running and process the provided example dataset. If you are interested in configuring DISCRIMINATOR to assign provisional pathogenicity classifications to your own dataset, please refer to the User Manual.

# **REQUIREMENTS:**

DISCRIMNATOR requires Python (2.7.X) in a Linux operating system to run. Python3 is currently not supported. A list of the required Python modules is listed below. If you want to run the pre-processing script, bedtools is also required.

Required Python Modules:

* progress
* networkx; version 1.8.1
* intervaltree

# **INSTALLATION:**

After you have downloaded the DISCRIMINATOR\_X.X.tar.gz file, move zipped file to the directory in which you want to run DISCRIMINATOR. Then, decompress the file.

|  |
| --- |
| tar -xzvf DISCRIMINATOR\_1.0.tar.gz --one-top-level=DISCRIMINATOR --strip-components 1 |

Diagram

Description automatically generated

**RUNNING DISCRIMINATOR:**

Enter the DISCRIMINATOR directory, and use the following command to run DISCRIMINATOR:

|  |
| --- |
| cd ~/PATH/DISCRIMINATOR  python CODE/INTERFACE\_DISCRIMINATOR.py |

If all the required Python modules are installed DISCRIMINATOR will run and you will get the following output to the console:

|  |
| --- |
| BUILDING PATIENT MERGED DATA FILES...  Processing |################################| 100% COHORT1.txt  BUILDING BENIGN MERGED DATA FILES...  Processing |################################| 100%  ASSIGNING PROVISIONAL PATHOGENICITY CLASSIFICATIONS  Processing |################################| 100% COHORT1\_PrimaryCNVs\_0.4.txt |

# **COMMON ERROR:**

Use of Python3 instead of Python2 (2.7.X):

|  |
| --- |
| File "CODE/INTERFACE\_DISCRIMINATOR.py", line 13  print 'BUILDING PATIENT MERGED DATA FILES...'  ^  SyntaxError: Missing parentheses in call to 'print'. Did you mean print('BUILDING PATIENT MERGED DATA FILES...')? |