PARGT User’s Guide for Mac

(Version 1.0)

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School of Electrical Engineering and Computer Science,

Washington State University, Pullman, USA

For more information, please contact Abu Sayed Chowdhury (Email: abu.chowdhury@wsu.edu, abu.chowdhury2005@gmail.com)

**PARGT** is a standalone software package developed to predict antimicrobial resistance proteins in bacteria. It is written mainly in python3 though some modules are implemented in R and called from main python script.

1. To install and use PARGT on Windows:

* Download “PARGT\_Mac.zip” from Github link- <https://github.com/abu034004/PARGT> . Unzip it and save it in a directory.
* Download “Materials\_PARGT\_Mac.zip” from <https://drive.google.com/file/d/1f1WWxAkPvaX9ikXkhziU4FQv39JPwSW8/view?usp=sharing> . Unzip it and save it in the “PARGT\_Windows” folder.
* To install “Jupyter Notebook”, visit the link- <https://www.anaconda.com/download/> and install anaconda for python 3. To install it from terminal, please visit the link- <https://jupyter.org/install> .
* It may happen that you may get an error noticing permission denied while running legacy BLAST and PSIPRED executive files. In this situation, please consider the following steps.

Step-1: Run the command “sudo chmod 755 psipred”.

Step-2: use ‘cd’ command to go the directory where “PARGT\_Mac/blast/bin” folder is saved and run the command “sudo chmod 755 blastpgp\_universal-macosx” and “sudo chmod 755 makemat”.

* Provide the test fasta sequences in the file “input\_seq.fasta”. Please note that there are some example test sequences available in the folder- “test examples”.
* Now, use ‘cd’ command to go the directory where “PARGT\_Mac” folder is saved and then type command- “Jupyter notebook”.

Then after couple of seconds, a new page for Jupyter Notebook will appear in your default browser. A screenshot is given below.

A screenshot of a social media post

Description automatically generated

Now, click on PARGT.ipynb (marked by red circle in the above figure). Then it will be open up in a new browser. A screenshot is given below. Please note that PARGT.py script is given if a user wants to use it instead of notebook (.ipynb) version.

A screenshot of a social media post

Description automatically generated

**Before running the script, please install rpy2 package using command “conda install -c r rpy2” from Anaconda command prompt. Also, please install tzlocal package using command “conda install -c conda-forge tzlocal” if needed. For details, please visit** <https://anaconda.org/r/rpy2> **and** <https://anaconda.org/conda-forge/tzlocal> **for rpy2 and tzlocal packages, respectively. It may happen that your system cannot find ‘psipred’ executable file. In that case, please install psipred package using command “conda install -c biocore psipred”. Also, if your system cannot locate e1071 package, please install psipred package using command “conda install -c r r-e1071”. For details, please visit** <https://anaconda.org/biocore/psipred> **and** <https://anaconda.org/r/r-e1071> **for psipred and e1071 packages, respectively. All of the remaining packages should come with Jupyter Notebook by default. In the worst case, if any package is missing, please use ‘conda install’ command to install the required packages. Also, users can consider ‘pip install’ command to install necessary packages as an alternative option.**

Now, click inside a code cell and then click on “Run” button (red marked in the following screenshot).

A screenshot of a cell phone

Description automatically generated

If you want to stop running the script, please click on the “Interrupt the kernel” (i.e., stop button) (red marked in the following figure).

A screenshot of a cell phone

Description automatically generated

If you want to restart the kernel after facing an error, please click on “restart the kernel” button (red marked in the following figure).

A screenshot of a cell phone

Description automatically generated

After running the script, a GUI should appear as below.

A screenshot of a cell phone

Description automatically generated

Please click on the option menu to see all options available in the tool (please see below the figure).

A screenshot of a cell phone

Description automatically generated

Brief description of the options is given below.

1. **Predict aac/bla/dfr/bac/van resistance sequences**: This option is for predicting acetyltransferase (*aac*), beta-lactamase (*bla*), dihydrofolate reductase (*dfr*), bacitracin (*bac*) and vancomycin (*van*) antimicrobial resistance (AMR) proteins from the input fasta sequences in the “input\_seq.fasta” file.
2. **Include new aac/bla/dfr/bac/van resistance sequences:** These options are for a user who wants to include new known AMR sequences to the original training data comes with this tool. Again the sequences that a user wants to add need to be given in the “input\_seq.fasta” file.
3. **Include new aac/bla/dfr/bac/van non-resistance sequences:** These options are for a user who wants to include new known non-AMR sequences to the training data that comes with this tool. Again the sequences that a user wants to add need to be given in the “input\_seq.fasta” file.
4. **Restore training sets:** This option is to reset all training datasets back to the original version came with this tool.

If you find our tool useful, please cite our following papers.

**Citations:**

1. Chowdhury, A.S., Call, D.R and Broschat, S.L., To be submitted. PARGT: A Standalone Software Tool for Predicting Antimicrobial Resistance in Bacteria. Nature Microbiology.
2. Chowdhury, A.S., Call, D.R and Broschat, S.L., 2019. Antimicrobial Resistance Prediction for Gram-Negative Bacteria via Game Theory-Based Feature Evaluation. Scientific Reports.
3. Chowdhury, A.S., Khaledian, E. and Broschat, S.L., 2019. Capreomycin resistance prediction in two species of Mycobacterium using a stacked ensemble method. Journal of applied microbiology.