

Cogent™ NGS Immune Profiler v1.0 Quick Start Guide

The following information is provided as a high-level introduction to the software. For more detailed information, please see the [Cogent NGS Immune Profiler Software v1.0 User Manual](#).

Before You Begin

- A. Review the [End User License Agreement](#)

IMPORTANT: See note on page 2 of this document.

- B. Supported operating systems
- Mac OS X: El Capitan (Version 10.11 and up)
 - Linux: CentOS 6 or higher, RedHat 7.5 or higher
- C. Hardware requirements
- Memory: 16 GB RAM
 - Free disk space: at least 100 GB available hard drive space
- D. Additional software dependencies
- Java 1.8 or higher
 - Python 3.6 or higher
- E. Required input files
- FASTQ files generated by an Illumina® sequencing platform
 - CSV metadata file

Confirm Java & Python versions

NOTE: To bring up a terminal window on a Mac, go to the search box, type in 'Terminal' and press [Enter].

- Verify Java is installed and meets or exceeds the required version by typing the following into a terminal window:

```
java -version
```

- Verify Python3 is installed and the default version by typing the following into a terminal window:

```
python3 -V or python3 -version
```

NOTE: If Python3 is installed and this command returns an error, please contact [technical support](#) for additional assistance.

- Verify the required Python modules are installed by typing the following into a terminal window:

```
python3 required_python_module_check.py
```

If any modules are listed as missing, install them before proceeding. For help, go to:

<https://docs.python.org/3/installing/>

Installation

1. Download the Immune Profiler software from takarabio.com/ngs-immune-profiler

NOTE: Make sure to download the version for the operating system it will be installed on.

- If the Takara Bio Immune Profiler was previously installed on the same computer as the Cogent NGS Immune Profiler will be installed, proceed to step 2
- If this is a new install, skip to step 3

2. (Uninstall the previous version)
 - a. If you want to save any previous output files stored in the `immune_profiler/` directory, make sure to move them to another folder location before continuing.
 - b. Delete the `immune_profiler/` directory and all subfolders.
3. (Install the new version): On the computer on which Immune Profiler is to be installed, unzip the Immune Profiler software package downloaded in Step 1 into the folder location of your choice.

To run the Immune Profiler:

UI (Mac-only):

1. Double-click on the executable (Immune Profiler)
2. Fill out the fields in the interface
3. Click [Start]

Command line (Mac and Linux):

```
python3 immune_profiler.py -r <RECEPTOR>
-f <FASTQ> -m <METADATA> -o <OUTPUT>
-t CDR3
```

where:

- <RECEPTOR> is the immune cell receptor type of the data being processed (options: TCR -or- BCR)
- <FASTQ> is the full path of the FASTQ folder
- <METADATA> is the filename (including the full path) of the metadata file
- <OUTPUT> is a string; it will be the name of the output folder created by the analysis AND the prefix of all the results files
- CDR3 is the target regions reads should map to

End User License Agreement

Immune Profiler incorporates two third-party programs, MIGEC and MiXCR, packaged and included for use only with this software under an [end-user license agreement \(EULA\)](#), acceptance of which requires the Immune Profiler user to be bound by and to comply with the terms before downloading and using Profiler.

IMPORTANT: Checking the box next to the [EULA](#) acceptance statement before submitting the completed form constitutes accepting and legally binding the Immune Profiler user to the terms of the EULA.

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