



DNAMIC ANALYSIS USER GUIDE

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1 INSTALLATION

1.1 Windows

1. Download & install the latest version of [Python 3 for Windows executable installer](#).
2. Download the source code zip of the [latest DNAmic Analysis release](#).
3. Unpack the source code zip file and start a command prompt from within the directory.
4. **pip3 install -r requirements.txt**
5. Run the application with valid arguments as outlined in the [Usage](#) section below.

1.2 Linux

1.2.1 RHEL/CentOS

1. Install EPEL Release repository:
sudo yum install epel-release -y
2. Install Python 3.6 from EPEL:
sudo yum install python36 -y
3. Upgrade pip to latest version:
sudo python3 -m pip install --upgrade pip
4. Clone GitHub repository for DNAmic Analysis:
git clone <https://github.com/infamousjoeg/DNAmicAnalysis.git>
5. Change directory to the newly cloned GitHub repo directory:
cd DNAmicAnalysis/
6. Install requirements.txt dependencies:
sudo python3 -m pip install -r requirements.txt
7. Run DNAmicAnalysis with proper arguments as outlined in the [Usage](#) section below.

1.2.2 Ubuntu/Debian

1. Install Python 3.6:
sudo apt install python3.6 -y
2. Install pip for Python 3.6:
sudo python36 -m ensurepip
3. Upgrade pip to latest version:
sudo python36 -m pip install --upgrade pip
4. Clone the GitHub repository for DNAmic Analysis:
git clone <https://github.com/infamousjoeg/DNAmicAnalysis.git>
5. Change directory to the newly cloned GitHub repo directory:

```
cd DNAmicAnalysis/
```

6. Install requirements.txt dependencies:

```
python36 -m pip install -r requirements.txt
```
7. Run DNAmicAnalysis with proper arguments as outlined in the [Usage](#) section below.

1.2.3 MacOS

1. Install the latest Python 3:

```
brew install python
```
2. Clone GitHub repository for DNAmic Analysis:

```
git clone https://github.com/infamousjoeg/DNAmicAnalysis.git
```
3. Change directory to the newly clone GitHub repo directory:

```
cd DNAmicAnalysis/
```
4. Install requirements.txt dependencies:

```
pip3 install -r requirements.txt
```
5. Run DNAmicAnalysis with proper arguments as outlined in the [Usage](#) section below.

2 USAGE

2.1 Pre-Requisites

- A DNA database file from a CyberArk Discovery & Audit (DNA) scan
 - > Must **NOT** be obfuscated
 - > To disable auto-deletion of the DNA db file, open **dna.exe.config** and edit:
DeleteDB=yes to **DeleteDB=no**

2.2 Create Configuration Template

- A configuration template must be created for DNAmic Analysis to use for analysis.
- You should create one configuration template per customer account.
- You should keep all configuration templates in the **config/** directory located in the root directory where **DNAmicAnalysis.py** exists.
 1. Copy **config/template_config.yml** and rename it to something like **customer_config.yml**.
 2. Update the values within the YAML config file to match those given to you by the customer for the scan analysis.
 - a. **database_file**
 - i. The path where the DNA database file is located on the local filesystem.

- ii. The file path can be in Linux or Windows format.
- b. **domain**
 - i. A domain name that is included in the scan.
 - ii. This is for your protection to ensure analysis is being done on the proper customer scan.
- c. **account_regex**
 - i. **service_account**
 - 1. A YAML array containing the naming convention used in the scan for service accounts.
 - 2. ^ is the wildcard character. **svc^** will look for accounts starting with **svc**. **^service** will look for accounts ending with **service**. **^svc^** will look for accounts starting, ending, or containing **service**.
 - ii. **admin_account**
 - 1. A YAML array containing the naming convention used in the scan for admin accounts (domain, personal privileged, etc).
 - 2. ^ is the wildcard character. **a_^** will look for accounts starting with **a_**. **^admin** will look for accounts ending with **admin**. **^admin^** will look for accounts starting, ending, or containing **admin**.
- d. **include_disabled_accts**
 - i. Yes or no on whether you want to include disabled accounts in the report. (I recommend keeping no.)
- e. **test_mode**
 - i. For testing only.
- f. **scan_datetime**
 - i. **override**
 - 1. Yes or no on whether to override detecting scan datetime from the DNA database filename and use **manual_scan_datetime** below instead.
 - ii. **manual_scan_datetime**

1. Use 24h format for the time.
2. Example: **2019-05-21 20:47:43**

2.2.1 Example Configuration Template

2.2.1.1 config/customer_config.yml

```
---
# path to where the DNA database file is located
database_file: /Users/joegarcia/Git/infamousjoeg/DNAmicAnalysis/data/test/DNA_2019-05-21_08-57-43-PM.db
# domain name of one scanned domain that can be detected
domain: cyberarkdemo.com
# privileged account patterns to match
account_regex:
  service_account:
    - svc^
    - ^service
  admin_account:
    - adm^
    - ^admin
# yes or no: whether to include disabled accounts in metrics
include_disabled_accts: no
# yes or no: activate test mode... do not adjust unless you
# know what you are doing
test_mode: yes
# DNA scan date & time settings
scan_datetime:
  # yes or no: override the timestamped DNA.db filename with the manual_scan_datetime
  override: yes
  # Use 24-hour format for the time e.g. 2019-05-21 20:57:43 for 08:57:43 PM
  manual_scan_datetime: "2019-05-21 20:57:43"
```

2.3 Run DNAmicAnalysis.py

2.3.1 Windows

- python.exe not in \$PATH:
 - > python.exe DNAmicAnalysis.py customer_config.yml
- python.exe in \$PATH:
 - > .\DNAmicAnalysis.py customer_config.yml

2.3.2 *Nix or MacOS

- ./DNAmicAnalysis.py customer_config.yml

3 OUTPUT

3.1 Excel Workbook

A Microsoft Excel workbook is created in the **reports/** directory where **DNAmicAnalysis.py** was ran from. It contains all the metric data needed for analysis and includes the relevant underlying data, as well.

3.2 Logs

A log file is generated at every runtime in **logs/** that includes every action taken by DNAmic Analysis. If an error occurs, this is a good place to start troubleshooting.

4 SUPPORT

E-Mail PASProgramsOffice@cyberark.com and be sure to include the log file from **logs/** that was generated during the analysis and any relevant screenshots.