DTarray_pro installation and basic usage

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Contents

1	Inti	roduction	1
2	Installation		1
	2.1	Download and unpack DTarray_pro archive file from GitHub .	4
	2.2	Build DTarray_pro executable	2
	2.3	Adding a shortcut for DTarray_pro (optional)	
3	Usa	age	ŀ

1 Introduction

DTarray_pro extracts Uniprot ID numbers, molecular weights, and spectral counts from .dtafilter files stored in the working directory. Protein data is combined into one dataset and written to the working directory as a tab delimitated text file (.tsv). This document will describe how to install the latest version of DTarray_pro step by step. Some experience using a unix shell is assumed.

2 Installation

DTarray_pro is hosted at GitHub, which is a free hosting service for distributed version control in software development. The latest stable version of DTarray_pro will be posted at https://github.com/ajmaurais/DTarray_pro/releases

2.1 Download and unpack DTarray_pro archive file from GitHub

- Navigate to the releases tab on the DTarray_pro GitHub page.
- The files for the latest release should be at the top of the page.
- Download the file: Source code (tar.gz) for the latest release, to you computer.
- DTarray_pro expects to be installed in ~/local. The program needs data stored in text files in ~/local/DTarray_pro-1.7.4/db for some features to work. First make the directory ~/local on your pleiades account if it doesn't already exist.
- Transfer the source code archive (should be named something like DTarray_pro-1.7.4.tar) to your pleiades account using your FTP client of choice.
- The source code archive has to be unpacked before you can access it. To unpack the .tar type the following commands in your terminal.

```
$ cd ~/local
$ tar -xfv DTarray_pro-1.7.4.tar
```

- As a result, a new directory should be created in /local named DTarray_pro-1.7.4
- Once you have unpacked the archive, you no longer need the .tar file and can delete if of you wish.

2.2 Build DTarray_pro executable

- Before you can use DTarray_pro, you have to build the executable from source. Fortunately DTarray_pro is configured to work with a build automation tool called make so the process should be straightforward.
- To build DTarray_pro run the following commands in your terminal.

```
$ cd ~/local/DTarray_pro-1.7.4/
$ ./configure
$ make
```

• After you have run make, there should be several new files in the DTarray_pro-1.7.4 directory. If everything worked, the executable file should be located at DTarray_pro-1.7.4/bin/DTarray

2.3 Adding a shortcut for DTarray_pro (optional)

To run DTarray_pro you have to navigate on your terminal to a folder which contains DTASelect-filter files then type the full path to the executable file relative from the directory you are currently in. Its possible to install a program system wide so you don't have to type the path every time, but without administrative privileges, its a bit complicated. A workaround is to create a shortcut or alias to the executable file. This section will explain how to add an alias for DTarray_pro to your shell profile on pleiades

- To add an alias for DTarray_pro, you will have to edit your shell profile, which is a file stored in your home directory named .tcshrc.
- To edit your shell profile, you will use a command line text editor called nano. To open .tcshrc in nano, type:

```
$ cd
$ nano .tcshrc
```

• After starting nano, your terminal window should look something like this:

• Scroll to the bottom of the file and add the line: alias DTarray "~/local/DTarray_pro-1.7.4/bin/DTarray"

```
GNU nano 2.0.9

File: .tcshrc

Modified

alias cim_combine_byProtein "cimage_combine by_protein output_rt_10_sn_2.5.to_excel.txt dta"
alias scanExtract "bash ~/scripts/precursorScanExtractor/precursorScanExtractor.sh"
alias expandSupInfo "~/scripts/precursorScanExtractor/precursorScanExtractor.sh"
alias cimsetup "bash ~/scripts/cimage_scripts/cimage_setup.sh"
alias cimsetup "bash ~/scripts/cimage_scripts/cimage_stup.sh"
alias purgecimage "bash ~/scripts/cimage_scripts/purgeCimage.sh"
alias fdh! "foreach d (heavy/ light/)"
alias fsh! "foreach s (heavy/ light/)"
alias ssetup "bash ~/scripts/cimage_scripts/py_realpath/src/main.py"
alias qstaffist "python /home/mauraisa/scripts/py_realpath/src/main.py"
alias anotateNE2" "/scripts/ms2_anotator/bin/anotate_ms2"
alias nlutil "python /home/mauraisa/scripts/py_nlutil/src/py_nlutil.py"
alias spaceCimage "python ~/scripts/parseCimage/src/parseCimage.py"
alias paseCimage "python ~/scripts/parseCimage/src/parseCimage.py"
alias gdel_all "python /home/mauraisa/local/del_all.py"
alias getResidueNumbers "python /home/mauraisa/local/gdetResidueNumbers/src/getResidueNumbers.py"
alias DTarray "~/local/DTarray_pro-1.7.4/bin/DTarray"
```

• To save and exit the file, hit ^+ X. A dialog should show up at the bottom which says:

```
Save modified buffer (ANSWERING "No" WILL DESTROY CHANGES) ?
```

- Hit y
- Next a dialog should show up at the bottom which says

```
File name to write: .tcshrc
```

- Hit enter to exit.
- Finally you have to tell the computer to reload your shell profile after you have modified it with the command:

```
$ source .tcshrc
```

• You can test your alias by typing the following command from your home directory:

```
$ DTarray --version
```

• If the alias is recognized by the computer, it should display something like:

```
DTarray_pro 1.7
Last git commit: Sat Sep 22 20:28:17 2018
git revision: 04
d30f4fd7790abfca60197d85cefc9d2a877cfc
```

3 Usage