

DTarray_pro-1.8.0 User Guide

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1 Introduction

DTarray_pro extracts Uniprot ID numbers, molecular weights, and spectral counts from DTASelect-filter files. Protein data is combined into one dataset and written to the working directory as a tab delimited text file (.tsv). This document will describe how to install and use 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 your computer.
- DTarray_pro expects to be installed in `~/local`. The program needs data stored in text files in `~/local/DTarray_pro-1.8.0/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-1.8.0.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 -xvf DTarray_pro-1.8.0.tar
```

- As a result, a new directory should be created in `/local` named `DTarray_pro-1.8.0`
- Once you have unpacked the archive, you no longer need the `.tar` file and can delete it if 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-1.8.0/
$ ./configure
$ make
```

- After you have run `make`, there should be several new files in the `DTarray_pro-1.8.0` directory. If everything worked, two executable files should be located at `DTarray_pro-1.8.0/bin/`

```
$ ls bin
DTarray          DTsetup
```

- `DTarray` is the executable for `DTarray_pro`
- `DTsetup` is the executable for a script which will automatically setup `DTASelect-filter` to be read into `DTarray_pro`.

2.3 Adding a shortcut for DTarray_pro and DTsetup (optional)

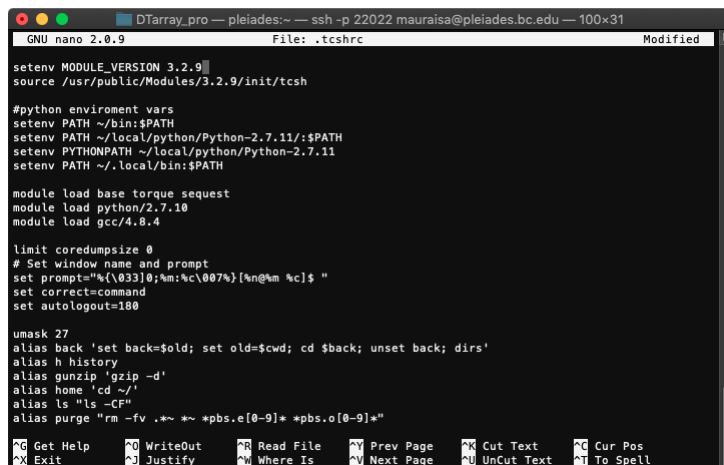
To run `DTarray_pro` you have to navigate on your terminal to a folder which contains `DTASelect-filter` files then type the full path to the executable file relative from the directory you are currently in. It's possible to install a program system wide so you don't have to type the path every time, but without administrative privileges, it's 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 and DTsetup to your shell profile on pleiades

- To add an alias for DTarray_pro and DTsetup, 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 Figure 1.



```
DTarray_pro — pleiades:~ — ssh -p 22022 mauraia@pleiades.bc.edu — 100x31
GNU nano 2.0.9 File: .tcshrc Modified

setenv MODULE_VERSION 3.2.9
source /usr/public/Modules/3.2.9/init/tcsh

#python enviroment vars
setenv PATH ~/bin:$PATH
setenv PATH ~/local/python/Python-2.7.11/:$PATH
setenv PYTHONPATH ~/local/python/Python-2.7.11
setenv PATH ~/.local/bin:$PATH

module load base torque sequest
module load python/2.7.10
module load gcc/4.8.4

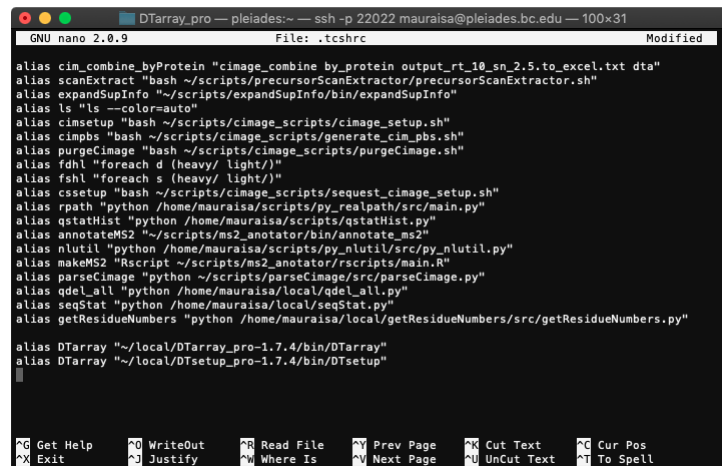
limit coredumpsizes 0
# Set window name and prompt
set prompt="%{\033}0;nm:%c\007%)[n@%m %c]$ "
set correct=command
set autologout=180

umask 27
alias back 'set back=$old; set old=$cwd; cd $back; unset back; dirs'
alias h history
alias gunzip 'gzip -d'
alias home 'cd ~/'
alias ls "ls -C"
alias purge "rm -fv .*~ *~ *pbs.e[0-9]* *pbs.o[0-9]*"

Get Help WriteOut Read File Prev Page Cut Text Cur Pos
Exit Justify Where Is Next Page UnCut Text To Spell
```

Figure 1: Example terminal window after opening `.tcshrc` with `nano`

- Scroll to the bottom of the file and add the lines:
alias DTarray "~/local/DTarray_pro-1.8.0/bin/DTarray"
alias DTsetup "~/local/DTarray_pro-1.8.0/bin/DTsetup"
(See Figure 2 for an example).
- To save and exit the file, hit `^+ X`. A dialog should show up at the bottom which says:



```
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/expandSupInfo/bin/expandSupInfo"
alias ls "ls --color=auto"
alias cimsetup "bash ~/scripts/cimage_scripts/cimage_setup.sh"
alias cimps "bash ~/scripts/cimage_scripts/generate_cim_pbs.sh"
alias purgeCimage "bash ~/scripts/cimage_scripts/purgeCimage.sh"
alias fdhl "foreach d (heavy/ light/)"
alias fshl "foreach s (heavy/ light/)"
alias cssetup "bash ~/scripts/cimage_scripts/sequest_cimage_setup.sh"
alias rpath "python /home/mauraisa/scripts/py_realpath/src/main.py"
alias qstatHist "python /home/mauraisa/scripts/qstatHist.py"
alias annotateMS2 "~/scripts/ms2_annotator/bin/annotate_ms2"
alias nutil "python /home/mauraisa/scripts/py_nutil/src/py_nutil.py"
alias makeMS2 "Rscript ~/scripts/ms2_annotator/rscrip/main.R"
alias parseCimage "python ~/scripts/parseCimage/src/parseCimage.py"
alias qdel_all "python /home/mauraisa/local/qdel_all.py"
alias seqStat "python /home/mauraisa/local/seqStat.py"
alias getResidueNumbers "python /home/mauraisa/local/getResidueNumbers/src/getResidueNumbers.py"

alias DTarray "~/local/DTarray_pro-1.7.4/bin/DTarray"
alias DTsetup "~/local/DTsetup_pro-1.7.4/bin/DTsetup"
```

Figure 2: .tcshrc with new aliases for DTarray_pro and DTsetup

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: 04d30f4fd7790abfca60197d85cefc9d2a
```

3 Usage

3.1 Setting up filter files with DTsetup

DTsetup searches all directories one level below where it is run for a file named DTASelect-filter.txt. If a matching file is found, it is copied into a folder named <date>.<time>.dtarraySetup with the name <sample.name>.dtafilter. Once DTsetup is run, DTarray_pro can be run from the newly created directory to compare spectral counts for proteins found in multiple runs.

To run DTsetup, first navigate to a directory containing subdirectories with DTASelect-filter.txt files and run the command:

```
$ DTsetup
Creating dtarraySetup folder in parent dirrectory...
Copying DTA filter files to 18-09-28_121625_dtarraySetup
    Adding ./sample_1...
    Adding ./sample_2...
    Adding ./sample_3...
    Adding ./sample_4...
Done
```

3.2 DTarray_pro Input format options

Users have two options for how the input DTASelect-filter files read in by DTarray_pro are structured.

3.2.1 std mode

In std mode, DTASelect-filter are stored in a common directory and the files are named with the format <sample.name>.dtafilter (This is the default input mode for DTarray_pro.)

```
$ ls
sample_1.dtafilter      sample_2.dtafilter
sample_3.dtafilter      sample_4.dtafilter
```

The user can either manually setup the folder, or use `DTsetup` to automatically generate the folder. To run `DTarray_pro` in `std` mode, run the commands:

```
$ cd <path_to_directory_with_filterfiles>
$ DTarray

DTarray_pro v1.7

Adding sample_1...
Adding sample_2...
Adding sample_3...
Adding sample_4...

4 files combined.

Writing protein data... done!
Protein data written in wide format to: DTarray_pro.tsv
```

If `DTarray_pro` was successful, two files should have been generated. `DTarray_pro.tsv` is a tab delimited text file (.tsv) which contains a row for each protein and a column for the spectral counts of that protein in each sample. `dtarray_pro_flist.txt` is a list of valid `.dtafilter` files found in the directory. If a file list already exists in the folder, the existing file list is used. The user can edit the file list to change the order of the columns in the output file and add additional files to the list.

3.2.2 subidr mode

In `subidr` mode, DTASelect-filter files are stored in a separate directory, the directory name is the sample name, and the filter files are named `DTASelect-filter.txt` (This is the default input mode for `dtarray.pl`.)

```
$ find */*.txt
sample_1/DTASelect-filter.txt
sample_2/DTASelect-filter.txt
sample_3/DTASelect-filter.txt
sample_4/DTASelect-filter.txt
```

To run `DTarray_pro` in `subidr` mode, the user has to include the `-i subidr` option, because `subidr` is not the default behavior.

```
$ cd <path_to_parent_directory>
$ DTarray -i subidr
```

Upon completion, a files named `DTarray_pro.tsv` and `dtarray_pro_flist.txt` are generated formatted the same as in `std` mode.

3.3 DTarray_pro Output file options

This document will not provide an exhaustive list of options for `DTarray_pro`. Instead, this section will provide examples of options will likely find useful. For the full list of optional arguments see `DTarray_pro-1.8.0/helpFile.pdf` or use `DTarray -h` to see the help file from the terminal.

3.3.1 Get spectral counts for unique peptides by protein

the `-u` option is used to include a column for the total counts for unique peptides in the `DTarray_pro.tsv` output file.

```
$ DTarray -u
```

By default, the columns for spectral counts and unique peptide spectral counts are grouped by sample. See section [3.3.2](#) to change this behavior.

3.3.2 Specify how to group supplementary information columns in output file

The examples in this section are use the `-u` option (section [3.3.1](#)), but the `-u` option is also compatible with other `DTarray_pro` options including the

`-lr` option (see section 3.3.5)

By default, the columns for sample specific supplementary information are grouped by sample as shown in table 1.

Protein	Sample_1		Sample_2	
	SC	Unique_SC	SC	Unique_SC
ALBU	2149	2149	3092	3092
TRFE	661	661	698	698
IGHG1	573	152	382	52

Table 1: Default column arrangement

The `-s` option can be used to control this behavior. To group the columns by sample (table 2, then observation add the `-s 1` option.

```
$ DTarray -u -s 1
```

Protein	SC		Unique_SC	
	Sample_1	Sample_2	Sample_1	Sample_2
ALBU	2149	3092	2149	3092
TRFE	661	698	661	698
IGHG1	573	382	152	52

Table 2: Grouping columns by sample

3.3.3 Get spectral counts for peptides

By default no peptide file is generated. To also generate a file containing spectral counts for peptides in each sample, use the `-p 1` option.

```
$ DTarray -p 1
```

An additional file should be generated named `peptideList.tsv` containing peptide data.

3.3.4 Modify how peptides are grouped in output file

By default, peptides are grouped by sequence and parent protein. A separate entry for each charge state of a given peptide will be included in peptide output files. If the `-g 2` option is set, peptides will also be grouped by charge; i.e., the spectral counts for each peptide will be the sum of all charge states identified for that peptide.

```
$ DTarray -p 1 -g 2
```

The `-modG <group_method>` specifies how to group modified peptides in `peptideList.tsv`. By default peptides with the same sequence, but different modification status will not be grouped. A separate entry will be included for each modification status found for a peptide. To ignore modification status when grouping peptides, use the `-modG 1` option.

```
$ DTarray -p 1 -modG 0
```

If the `-p 1` option is not set, the `-g` and `-modG` will be ignored. The `-g` and `-modG` options can also be combined as desired.

3.3.5 Get subcellular location data for proteins

`DTarray_pro` can use `DTarray_pro-1.8.0/db/humanLoc.tsv` to lookup subcellular localization information for proteins. `humanLoc.tsv` contains Uniprot annotations for subcellular localization by Uniprot ID, updated as of Jan 18 2017. Currently, sub cell location information is available for human proteins only.

There are two ways in which subcellular location information can be compiled.

1. The `-loc` option will add a column for the location of each protein in `DTarray_pro.tsv`. To include the subcellular location column in `DTarray_pro.tsv` run the command:

```
$ DTarray -loc
```

2. The `-lr 1` option will create a file named `loc_summary.tsv` with the sum of spectral counts, sequences, and proteins identified for each subcellular location. To generate `loc_summary.tsv` run the command:

```
$ DTarray -lr 1
```

By default, columns are arranged by sample. The `-s 1` option can be used to arrange the columns by observation. See section [3.3.2](#) for an explanation of the `-s` option.

3.3.6 Calculate molecular weights for peptides and proteins

DTarray_pro will calculate protein/peptide molecular weights and molecular formulas when the `-mw` option is provided. Columns will be included in output files for average mass, monoisotopic mass and molecular formula.

Three files are required for the calculation:

1. An atom count table, named `atomCountTable.txt` which contains the number and types of atoms found in each amino acid (similar to Cimage table).
2. An atom mass table, located at `DTarray_pro-1.8.0/db/atomMasses.txt`, containing the masses of each atom.
3. A `.fasta` file to lookup protein sequences located at `DTarray_pro-1.8.0/db/humanProteome.fasta` (required for proteins only) Currently, the `-mw` option is supported for human proteins only.

By default the atom count table located at `DTarray_pro-1.8.0/db/atomCountTable.txt` is used. The default atom count table includes a static modification for iodoacetamide alkylation. To calculate peptide and protein masses with default residue masses, run:

```
$ DTarray -p 1 -mw
```

The user can also supply a custom `atomCountTable.txt` file with the `-act <file_name>` option. A copy of the default atom count table can be generated in the working directory with the `-mact` option.

```
# make default atomCountTable.txt in working directory
$ DTarray -mact
# run DTarray with custom atomCountTable.txt
$ DTarray -act ./atomCountTable.txt -p 1 -mw
```

The user can also edit the default atom count table as at `DTarray_pro-1.8.0/db/atomCountTable.txt` as desired, but editing `DTarray_pro-1.8.0/db/atomMasses.txt` is not recommended.