
DrHelp Documentation

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CHAPTER 1

Description:

This tool is an interactive command line framework kinda tool, which is use to get biological sample with scraping. it does not requires any programming skill to run. evry module is explained and available in help menu. Note that this tool is completely based on web-scraping from trusted websites. any changes occurance on that website will make this tool completely useless. so, basically this tool is not stable for forever. but still i will keep maintaining this tool.

CHAPTER 2

Options

Features	Details	Examples
Set	use for setting id, item type, doc type etc <i>Options.set</i> .	set id=1798174254 type=nucore doc=html report=genbank
Get	use for getting the data after setting creds with set. <i>Options.get</i> .	get gene , get sequence , get comment , get all
Search	use for searching for any term available <i>Options.search</i> .	searchd /roma52 or searchl /roma52
Clear	use for clearing the console as usual	cls
FTP*	use for getting any data files from http://ncbi.nlm.nih.gov	ftp
Options	use to get options for selected module	options
Help	use to get all available help options	help
Visualize+	use to open the scrapping page on browser if something is not working	visualize
Exit	use to exit the console	exit

(+) options are under development

2.1 Set Options

Options	Details	Examples
ID	NCBI use separate IDs for all data, so we can use the IDs to get required data, You can get the IDs of any species by <code>search1</code> command.	<code>set id=<ID here></code>
Item Type	NCBI use specific name for every category of species data you want to get. <i>Item.type</i> .	<code>set <Item Value></code>
Report Type	NCBI use specific report type for different purposes <i>Item.report</i> .	<code>set <Report Name></code>
Document Type	NCBI use html and text format. NOTE: <i>there is no CUSTOM get option available for text format. it will give whole page at once.</i>	<code>set <doc type></code> <code>html(custom options) or</code> <code>text(all)</code>

2.2 Item-type Informations

Item	Details	Values
Nucleoid	use to get nucleotide samples and other infos.	nucore
Genes	use to get Genes samples and other infos.	gene
Protein	use to get Protein samples and other infos.	protein
Probe	use to get Probes infos.	probe
Popset	use to get Popset infos.	popset

2.3 Report-type Informations

Reports	Details	Values
Genbank	use to get nucleotide samples and other infos.	genbank
FASTA	use to get Genes samples and other infos.	fasta

2.4 Get Options

Options	Details	Examples
Name	Use to get db based name of species.	<code>get name</code>
Introduction	Use to get introduction of species.	<code>get intro</code>
Comments	Use to get comment on the report.	<code>get comment</code>
Gene	Use to get gene of the selected species.	<code>get gene</code>
Stem Loop	Use to get Stem Loop of the report.	<code>get stem-loop</code>
Peptide	Use to get Peptide of the report.	<code>get peptide</code>
CDS	Use to get CDS of the report.	<code>get cds</code>
Source	Use to get Source of the report.	<code>get source</code>
All	Use to get complete page in text format of report.	<code>get all</code>

2.5 Search options

To search All detailed summary of search term:

```
searchl <ITEM VALUE> <TERM>
```

To search All IDs of search TERM:

```
searchd <ITEM VALUE> <TERM>
```

Item	Details	Values
Nucleoid	Use to search nucleotide samples and their list.	nucore
Genes	Use to search samples and other infos.	gene
Protein	Uses to search Protein samples and other infos.	protein
Probe	Uses to search Probes lists.	probe
Popset	Uses to search Popset lists.	popset