



Instructions to Install and Configure BaseSpace CLI

The BaseSpace Sequence Hub CLI (command-line interface) allows you to directly interact with your data in BaseSpace. You can use various commands to download data directly from a BaseSpace project to HiPerGator.

Please see <https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview> for the official documentation from Illumina.

1. Login to HiPerGator via Putty or a terminal. You will be in your home directory (/home/<user>).
2. Make a new directory, called "bin". (Don't include the \$ sign).

```
$ mkdir $HOME/bin  
$ ls  
#If you see "bin", then your new directory was successfully created.
```

3. Type (or copy/paste) and execute the following.
 - a. Note – when using Putty, Control-C and Control-V do not work for copy/paste. They have very different meanings. To paste something into Putty, just right click once you've already copied from your source. To copy from Putty, highlight the text (that's it...it's now copied). Now you can paste in your word doc, browser, etc.

```
$ wget "https://api.bintray.com/content/basespace/BaseSpaceCLI-EarlyAccess-BIN/latest/  
/\$latest/amd64-linux/bs?bt_package=latest" -O $HOME/bin/bs
```

4. Make the downloaded binary executable.

```
$ chmod u+x $HOME/bin/bs
```

5. Install a separate binary to use the bs cp command.

```
$ wget https://api.bintray.com/content/basespace/BaseSpace-Copy-BIN/\$latest/linux/bs  
cp?bt_package=develop -O $HOME/bin/bs-cp
```



6. Authenticate

```
$ bs auth
```

- a. Follow the prompt by going to the displayed URL and follow the instructions. You will have to input your BaseSpace username and password.
 - i. If you receive a server error/warning, just wait and try again later.
 - ii. You only have to authenticate once per Workgroup. If you change your BaseSpace password after authentication, the BaseSpace CLI will still continue to work.
 - iii. If you have more than one Workgroup in your BaseSpace account, you need to authenticate for each Workgroup. Your default Workgroup will automatically be configured with the above command. To authenticate an additional workgroup, use the following command:

```
$ bs auth -c <name_of_second_non-default_workgroup>
```

You have now installed BaseSpace CLI and can now download/transfer data directly from your BaseSpace account to HiPerGator. See below for a list of helpful commands. (Go to <https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview> for a list of all commands and options).

```
$ bs list run --terse      #list runIDs
```

```
$ bs list project        #list project names and size in default workspace (in table format)
```

```
$ bs -c <workgroup_name> list project    #lists projects and size under specified,  
non-default workgroup (in table format) (can use -c for any bs option and sub-option)
```

```
$ bs list project --template='{{.Name}}'    #List just project names (non-table format)
```

```
$ bs list biosample --help    #lists all flag options (can use for any bs option)
```

```
$ bs list biosample --project-name=<projectname> --template='{{.Name}}'  
#List all biosamples for a particular project name
```



```
$ bs download project -n <projectname> --extension=fastq.gz -o <output dir>
#Download just the fastqs from a project using project name

$ bs download project -i <projectID> --extension=fastq.gz -o <outputs>
#Download just the fastqs from a project using id

$ bs download biosample -n <biosampleID> -o <output dir>
#Download data from a specific biosample
```