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BaseSpace CLI
January 17, 2023
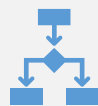
Outline

- BaseSpace CLI

- Installing BaseSpace CLI

- Interacting with your data via BaseSpace CLI

- Data Transfers from BaseSpace to HiPerGator

- Available pipelines and tools on HiPerGator

BaseSpace Command Line Interface (CLI)

- Work with your data in BaseSpace via command-line from HiPerGator

- Overview and documentation
    - https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview

- CLI examples/use cases
    - https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-examples
    - Retrieve basic run and project information
    - Create biosamples, projects, etc.
    - Download files
    - Upload files
    - ….and more

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Benefits of BaseSpace CLI

- Directly transfer data from BaseSpace to HiPerGator for analysis
  - Command line and Galaxy

- No need to download files locally and then reupload to HiPerGator
  - Avoid slow downloads to your local machine due to state firewalls

Install and Configure BaseSpace CLI

- Login to HiPerGator via Putty or a terminal
  - You will be in your home directory (/home/<user>/)

- Make a new directory, called "bin"

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

- Type (or copy/paste) and execute the following:
  - Note – Control-C and Control-V do not work for copy/paste in Putty. To paste, right click once you've copied from your source. To copy, highlight text (that's it).

```
[usr@login]$    wget "https://launch.basespace.illumina.com/CLI/latest/amd64-linux/bs" -O $HOME/bin/bs
```


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Install and Configure BaseSpace CLI

- Make the downloaded binary executable.

```
[usr@login]$   chmod u+x $HOME/bin/bs
```

Authenticate

- Authenticate your BaseSpace account

```
[usr@login]$   bs auth
```

- Follow the prompt by going to the displayed URL and follow the instructions. You will have to input your BaseSpace username and password.

  - If you receive a server error/warning, just wait and try again later.
  - You only have to authenticate once per Workgroup. If you change your BaseSpace password after authentication, the BaseSpace CLI will still continue to work.
  - 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:

```
[usr@login]$   bs auth –c <name_of_second_non-default_workgroup>
```

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Installation Complete!

- You can now start to work directly with your BaseSpace data and transfer data to HiPerGator.

- Go to https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-examples to see a list of all commands and options for use cases.

BaseSpace CLI Commands and Use Case Examples

- bs list

```
[usr@login]$ bs list run --terse     #list run IDs

[usr@login]$ bs list project     #list project names and size in default workspace (in table format)

[usr@login]$ bs –c <workgroup_name> list project     #lists projects and size for specified, non-default workgroup (in table format) (can use –c for any bs option and sub-option)

[usr@login]$ bs list project --template='{{.Name}}'     #list just project names (non-table format)

[usr@login]$ bs list project --filter-term=<projectname> --template='{{.Id}}'     #Get project ID based on project name

[usr@login]$ bs list biosample --help     #list all flag options (can use for any bs option)

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

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BaseSpace CLI Commands and Use Case Examples

- bs download

[usr@login]$ bs download project –n <projectname> --extension=fastq.gz –o <output_dir>   **#Download just the fastqs from a project using project name**

[usr@login]$ bs download project –i <projectID> --extension=fastq.gz –o <output_dir>   **#Download just the fastqs from a project using project ID**

[usr@login]$ bs download biosample –n <biosampleID> -o <output_dir>   **#Download data from a specific biosample**

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BaseSpace CLI Commands and Use Case Examples

- bs create and bs upload

```
[usr@login]$ bs create project –n <projectname>     #Create new project in BaseSpace

[usr@login]$ bs create biosample –n <biosamplename> -p <projectname>    #Create new biosample in project

[usr@login]$ bs upload dataset –p <projectID> <fastqR1> <fastqR2>    #Upload a pair of fastq files to a project; creates biosample automatically

[usr@login]$ bs upload dataset –p <projectID> --recursive <fastqs_dir>    #Upload an entire directory of fastqs to a project
```

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Questions???

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