

Genomics from a portable external drive

About this Protocol

This protocol is for users who have a Windows Subsystem for Linux, but have their data saved onto a portable external hard drive. This will allow you to access your external drive through your home directory, and save large genomic files onto the external hard drive instead of your C: drive. This method is a great alternative for those that do not have a computer that can be expanded with an additional internal hard drive. However, external hard drives do fail and any important files should be backed up frequently to an additional location.

BLUF

Computer requirements and recommendations:

- A portable external hard drive, with ~3 TB of space, although this depends on your needs
- A secondary external hard drive to back up the first
- A computer with a Linux subsystem (How To: <https://docs.microsoft.com/en-us/windows/wsl/install-win10>)

Let's get started

1. Check properties of your external hard drive

For a rough estimate, it is recommended that you have at least 3 TB of space available for each major project or analysis. It is also recommended that you have an additional external hard drive, with more space than the first, to periodically backup the original files to. Look for a drive with a USB 3.0 as this connection will be faster and incur less performance costs.

2. Create a symbolic link from your home directory to your external hard drive

Once plugged in, a symbolic link should be created between your home directory and your external hard drive. This allows you to easily access all the genomics data that will be saved on the external drive. Start by creating a folder on your external hard drive. In this example, I create a folder named, "shared_folder".

> ln -s /mnt/path/to/folder

Example: > ln -s /mnt/d/Users/Bernadette/shared_folder

3. Test the symbolic link

Create an empty text document within the "shared_folder" of your external hard drive. Name it "test.txt". Close any terminal windows that might be open. Now open a new terminal window, and check to see if you can access the shared folder and this file.

> ls

The function *ls* should list the names of everything in the home directory. Your "shared_folder" should be present. We can change our directory to be inside this shared folder to check for "test.txt".

> cd shared_folder

>ls

Here the text document "test.txt" should be listed as well.