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Preparing the data you're getting

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    - How much storage space will I need to complete the analyses?
        - E.g. if running AMR++, you could try running the entire pipeline at once which will require 2-3X the storage space compared to the raw data, or you can run each piece of the pipeline individually to better manage your space.

Downloading samples from sharepoint (onedrive) using Globus

The TAMU HPRC has more information about ways to transfer files here, but generally we recommend using Globus to transfer files between onedrive and TAMU's servers.

You'll need to log into globus and can follow these instructions for more information.

In short, you'll go to the File Manager and select the "TAMU AIP Azure OneDrive Globus Storage Collection" as one of your endpoints. From the starting point, you'll have to click the "up one folder" button to then see the "Shared" folder where you'll find the folders that were shared with you.

Set up your second endpoint as either "TAMU Grace - dnt" or "TAMU Terra - fnt", navigate to the right folder, and click "Start" on the side with the OneDrive folder to begin transfer toward the TAMU server. On the server, you'll typically use directory in your scratch space, like this "/scratch/user/enriquedoster/".

Next steps

Depending on whether you're analyzing 16S reads or shotgun metagenomic reads (including target enriched reads), you'll be following similar steps but using different software.

Generally, the bioinformatics steps you are performing are:

1. QC evaluation
2. QC trimming

3. Contaminant removal (e.g. host DNA, mitochondrial DNA, etc)
4. Read classification (e.g. taxonomic, antimicrobial resistance, functional genes, etc)

Follow the relevant tutorials to use qiime2 for 16S analysis and AMR++ for the resistome.