

- how much space your project will need and what will be the file limit (i.e. what kind of file count do you expect)

I apply for 10 TB in total (i.e. additional 5 TB). Now I need to download 5.5 TB data (30 high-coverage whole genome sequencing BAM files). The final number of files I need to use is around 50, so 10 TB is requested for both data storage and intermediate data processing in the analysis.

- what measures you are and will continue to take to optimize the space usage (deleting unneeded data, compressing data, moving infrequently used data to archive)

Yes, I will delete unneeded data, compress data, and move data to archive if not frequently used.

- why you need the space

I need the space for downloading and analyzing whole genome sequencing data generated in my project.

- how long you need the space

Two years for my current project. It may be extended if I need to use the data for my following projects.