**Explore samples**

▶ Open terminal
cd users/HGXXX/id22

▶ List of files
ls \_lrt

▶ For each sample, a directory was created during data acquisition
cd sample\_name

▶ In this sample folder, data are in .h5 (data are also available as .dat in the « datfiles» folder)

**Binning procedure**

▶ In the id22 folder, in order to use beamline specific softwares such as id22sum, connect to diffract22new: ssh -X opid22@diffract22new (pwd tonic22)

▶ You are now connected to diffract22
Go in the « users » folder
cd users

▶ Go in your experiment folder
cd hg172

▶ Go in the id22 folder
cd id22

▶ Go in the « processing » folder (HGXXX/id22/processing)
cd processing

▶ Create a directory for your sample :
mkdir UN\_sample\_name (UN = User Name)

▶ Go in this directory
cd UN\_sample\_name

▶ Copy file to correct offset between the Si detectors
cp ../temp.res .

▶ Create a .xye « total » file (sum of all scans)
id22sum ~/data1/UN\_sample\_name\_0001.dat 0.002 1 7 lowtth=0 scalmon ed=12
*0.002 = binning size
1 7 number of scans you average. If only 2 scans were collected, 1 2
ed=12 : exclude detector 12 (ONLY FOR 1st run of HG172 – September 2021)*▶ Extract one .xye file per scan
id22sumall ~/data1/UN\_sample\_name.dat 0.0007 1 7 lowtth=0 scalmon

▶ To visualize patterns, in processing/HGXXX/...
plmany UN\_sample\_name.xye

**Data transfer**

Please follow instructions on :

<https://www.esrf.fr/home/UsersAndScience/support-and-infrastructure/Computing/ComputingOffsite/accessing-experimental-data.html>

We recomand using the Globus solution