Navigating the CAIR internal environment – Command Line Method

The following guide describes how to open the Terminal window and log in to Sched1, login1 and login2 to navigate CAIR's file management system (LSF) using a command line interface. The instructions are broken down by Operating System (Linux, Mac or Windows).

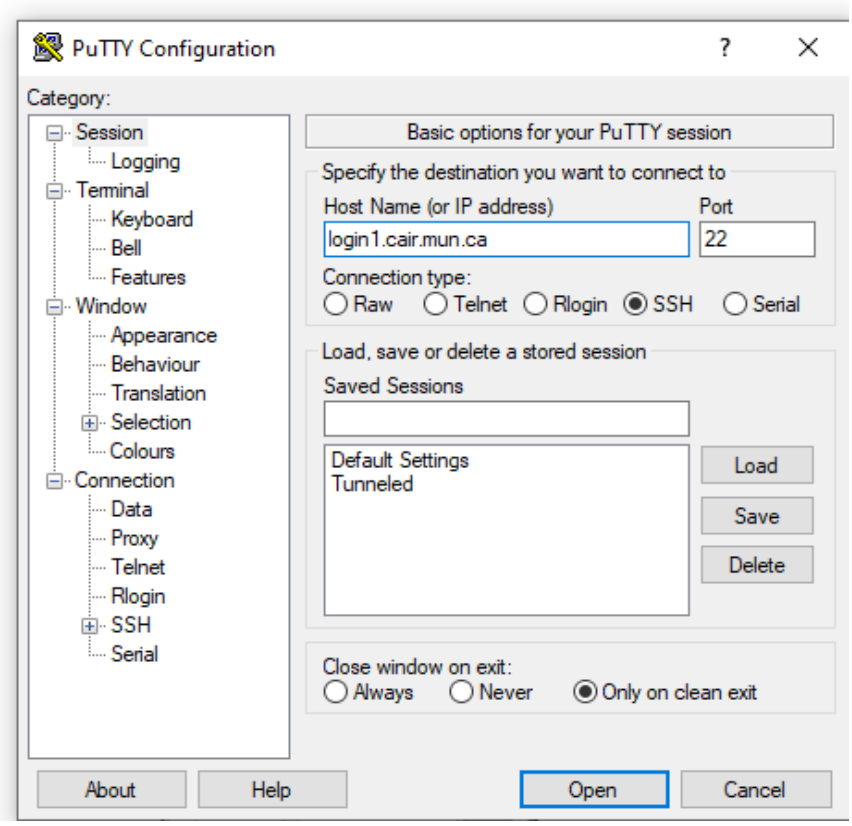
Logging in - Windows Operating System

Please note: To login to the CAIR computing environment using the command line, an Open SSH client is required if you do not already have one. One such program is called PuTTY:
Download PuTTY - a free SSH and telnet client for Windows

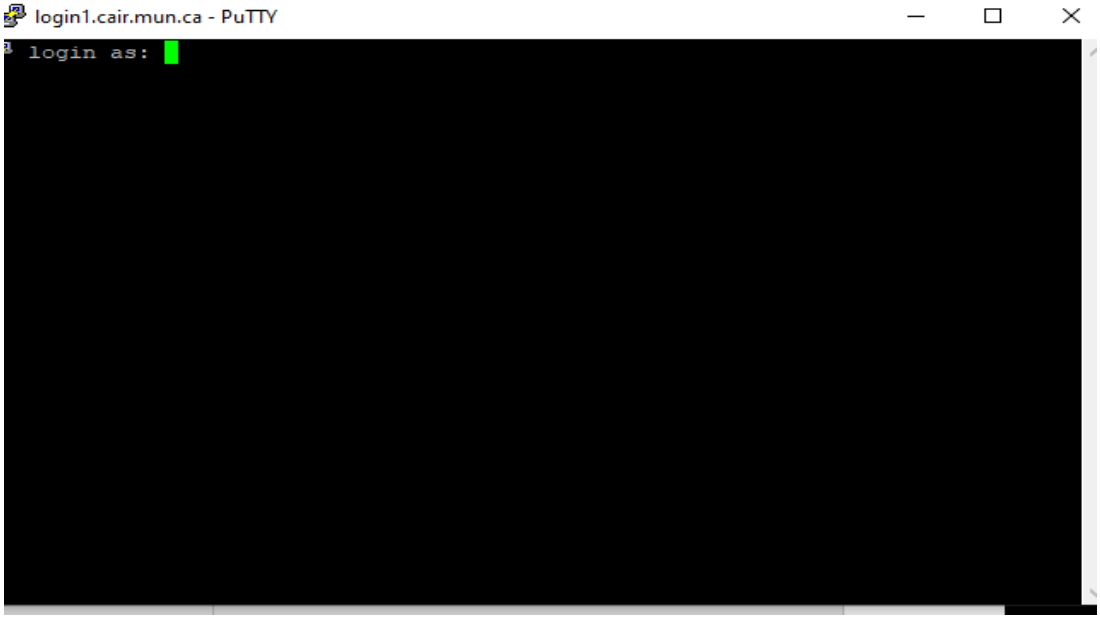
Please be sure to download the latest version, which is normally the first link listed under "For Windows on Intel x86"

Click on putty.exe. Click "Save File". PuTTY is now found in your Downloads.

1. Open PuTTY and type login1.cair.mun.ca or login2.cair.mun.ca for Host Name (or IP Address) of the resource you want to use. Enter 22 under Port to begin ssh session. In the below example we are logging into login1.cair.mun.ca



2. Click open. You should now see this screen:



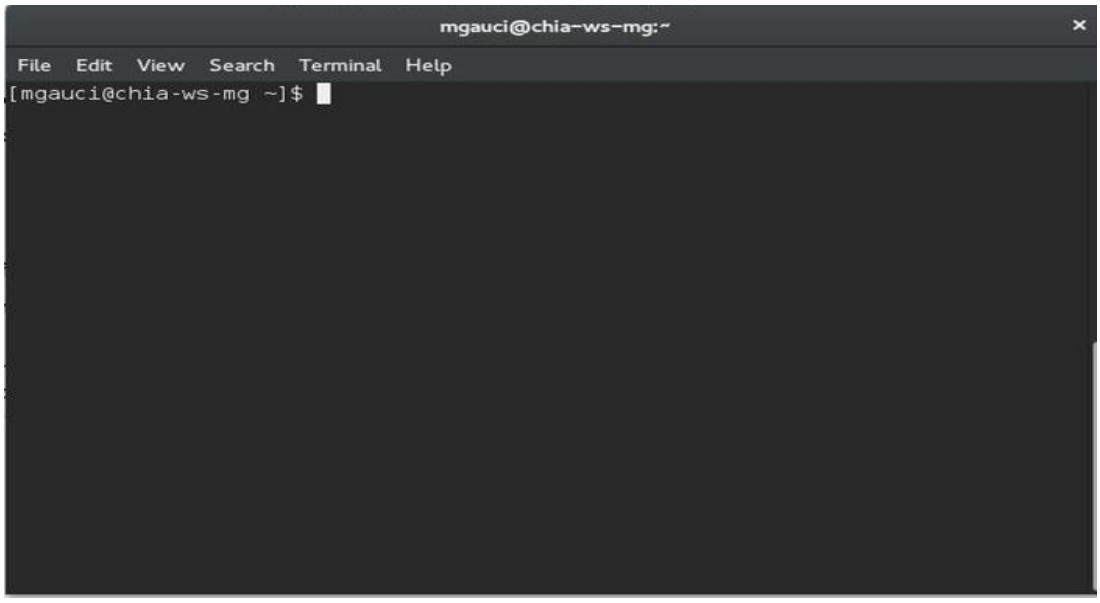
3. Enter your Username at the login and hit Enter. Then type your password and Enter (your password may not appear on screen as you type but if entered correctly will still work).

4. You should now be logged in to login1 and can type in your desired commands.

5. To end your ssh session, type logout at the prompt and hit enter.

Logging in – Linux or MAC OS

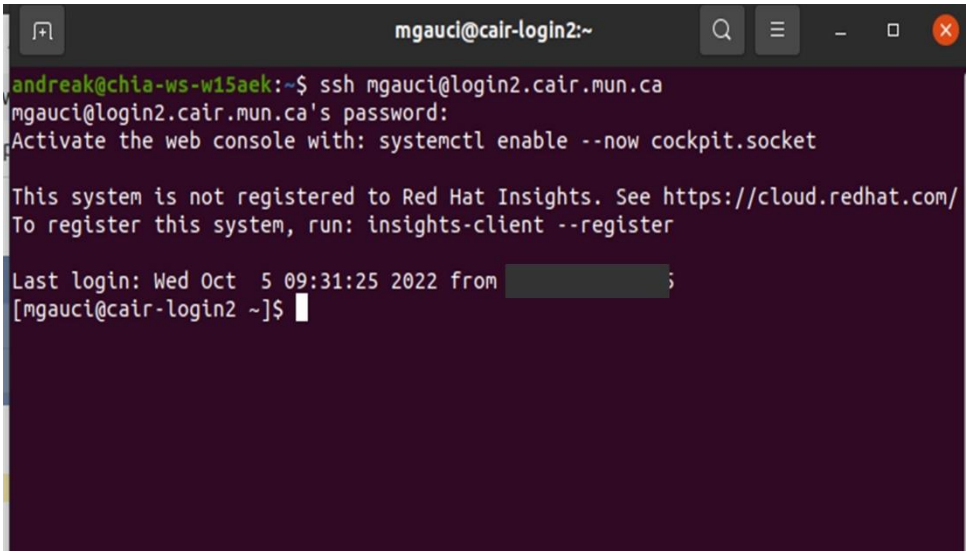
1. Open a terminal window



   Type ssh username@login1.cair.mun.ca or ssh username@login2.cair.mun.ca

2. The user will be asked for their password.

3. Upon entering the correct password, the user's terminal window will show which node they are logged into. Below is an example of a login to login2.cair.mun.ca



Transferring a job to LSF – command line method

Before submitting a job to LSF, you must first upload the required file to your user directory. Using terminal window or PuTTy

1. Type scp filepath/filename username@server.
   Example: scp Documents/testdata.bash username@login1.cair.mun.ca:
2. Enter your password when prompted

Submit Jobs and Navigate LSF – command line method

The following instructions describes how to submit jobs and navigate around to CAIR's file management system (LSF) using the Terminal Window or PuTTy.

1. Open terminal window

2. Type ssh username@login1.cair.mun.ca or ssh username@login2.cair.mun.ca

3. Enter your password as prompted

4. The following are the main job submission and control commands you need to know for using LSF in command:
   - bsub [options] command [cmdargs] (common bsub options are –J to name the job, -q to submit job to specified queue, -n for number of CPUs needed for the job,-cwd *dir-path* specifies the current working directory for the job, -i *filename* to use standard file as standard input for job, -I submits an interactive batch. *All options associated with bsub can be viewed by typing man bsub on the command line.)*
   - bjobs [-a][-J jobname][-u usergroup|-u all][...] jobID
   - bhist [-a][-J jobname][-u usergroup|-u all][...] jobID

- bbot/btop [jobID | "jobID[index_list]“] [position]
- bkill [-J jobname] [-m] [-u] [-q] [-s signalvalue]
- bmod [bsub_options] jobID
- bpeek [-f] jobID
- bstop/bresume jobID
- bswitch destination_queue jobID

5. The following example submits a job called ‘jobname’ to the normal queue using 4 CPUs in the current working directory of jobname. /my_job_launcher.sh:

   bsub -J `jobname` -q normal -n 4 -cwd `jobname` ./my_job_launcher.sh

6. Once a job has been created you should see something like this:
   - Job <4>, Job Name </gpfs/home/username/regression/chip1>, User <username>
     Project <default>, Status <RUN>, Queue <normal>,
     Command <./my_job_launcher.sh>
     Thu Mar 1 17:48:43: Submitted from host <cair-sched1>,
     CWD </gpfs/home/username/regression/chip1>;

     Thu Mar 1 17:51:55: Started on <cair-cair->,
     Execution Home </home/username>,
     Execution CWD </gpfs/home/username/regression/chip1> ;
     Thu Mar 1 17:52:12: Resource usage collected.
     MEM: 2 Mbytes; SWAP: 5 Mbyt

7. To terminate a job type bkill. To terminate all jobs of the current user: bkill –b 0

8. The bjobs command displays information about pending, running and suspended jobs. To view all jobs use bjobs –a. To see pending jobs type bjobs –p. For running jobs use bsub –r. To see jobs for a specific use type bjobs –u *user_name.*

   Further information on options for the bsub command can be viewed by typing man bjobs on command line interface.

9. An example of the type of information displayed from the command bjobs –u all –a:

JOBID	USER	STAT	QUEUE	FROM_HOST	EXEC_HOST	JOB_NAME	SUBMIT_TIME
1233	test1	DONE	normal	mac1	mainmac	testjob	Feb 27 10:00
1234	test1	RUN	priority	mac1	mainmac	logger	Feb 27 10:00
1235	test2	PEND	normal	win2		ranalysis	Feb 27 10:03
1236	test	PEND	night	win2		jobname	Feb 27 10:06
1237	test3	RUN	GPU	cair-sched1			

For more information on working with Jobs in LSF please refer to this document:
https://www.bsc.es/support/LSF/9.1.2/lsf_users_guide/index.htm?clusters_jobs_about.html~main

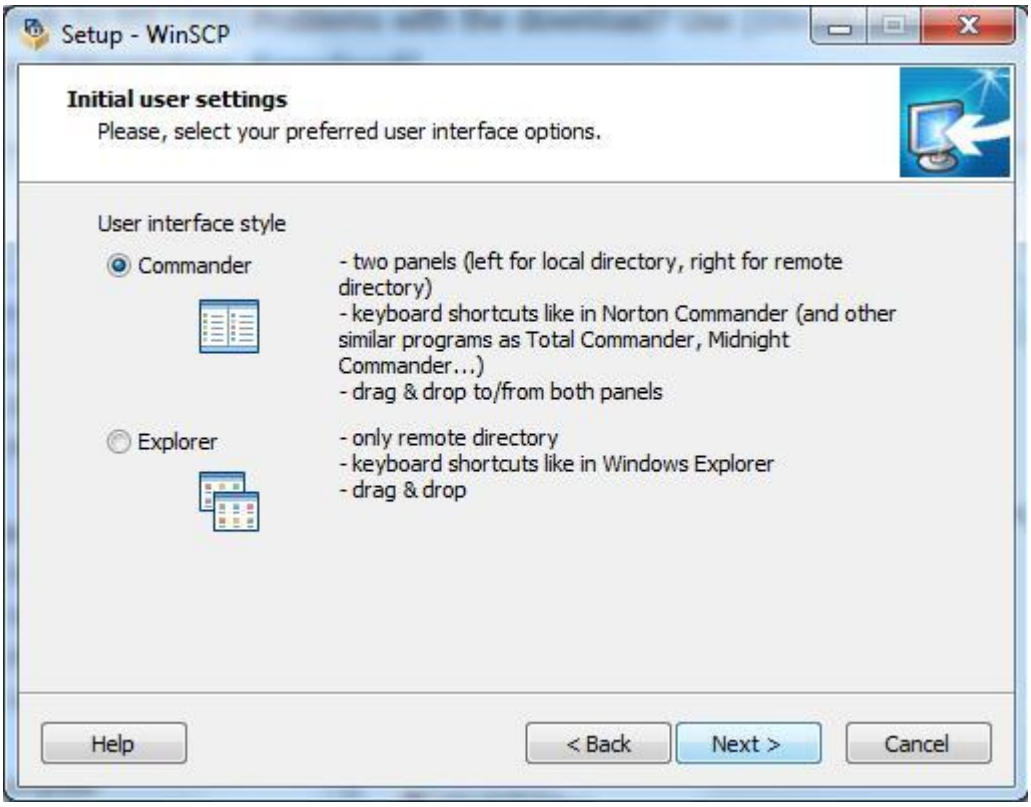
Uploading Files to the CAIR computing environment using transfer client

1. Download a sftp program such as WinSCP (download link: https://winscp.net/eng/download.php#download2)

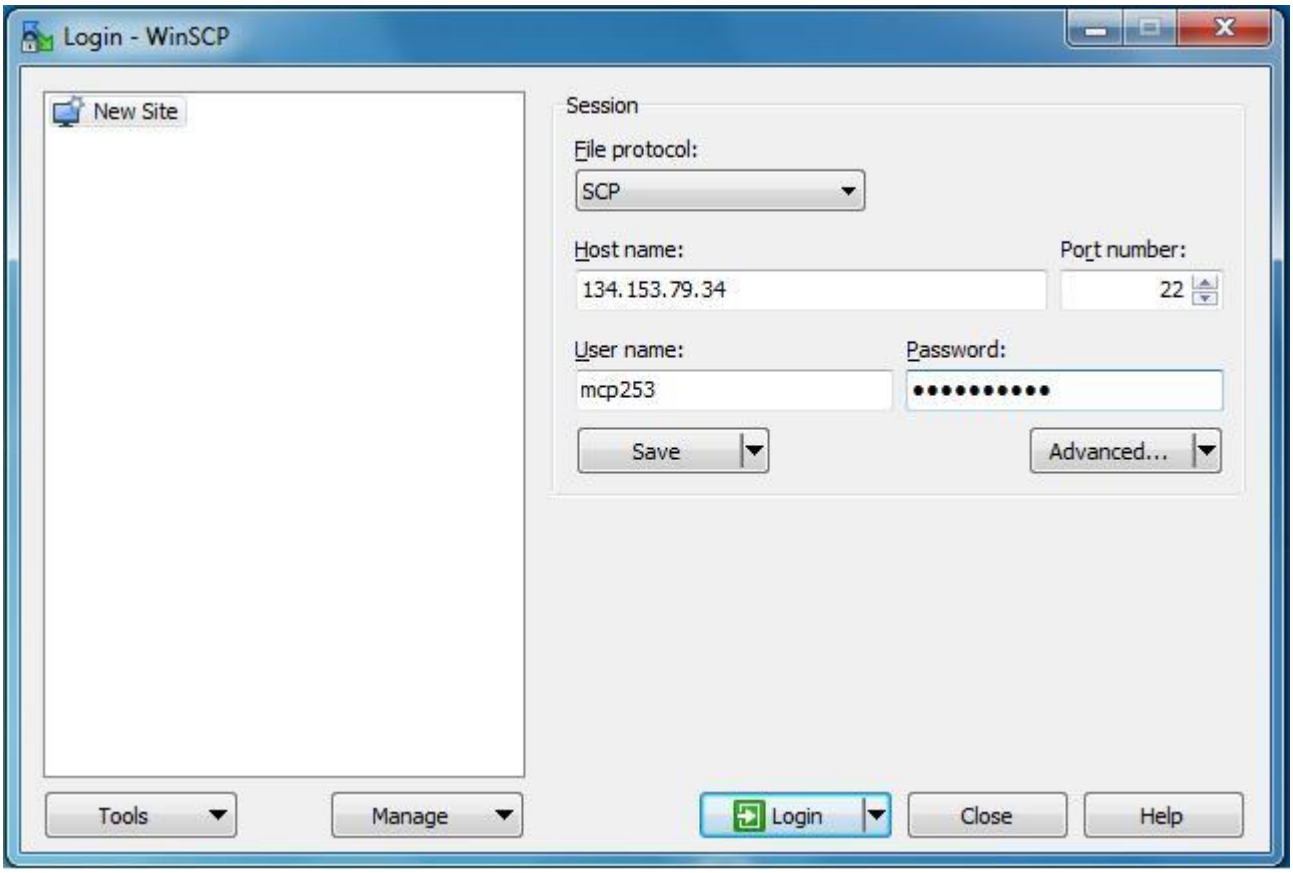
2. Download the version nearest the top of the page.

3. Follow the Setup Wizard Instructions. Select “Typical installation.”

4. Select “Commander” for User interface style. Complete the installation

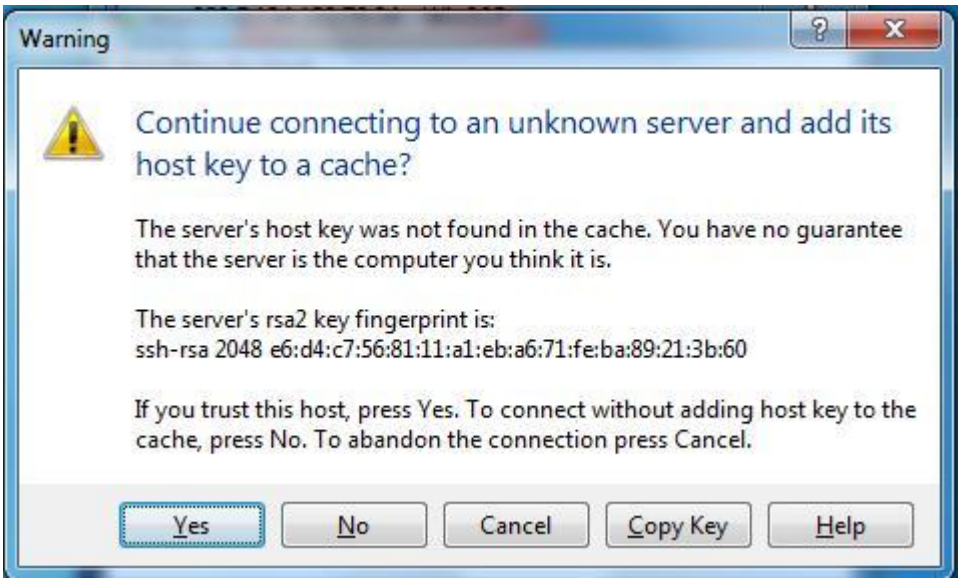


5. Open WinSCP
6. Click on New Site and enter Host name (134.153.79.34), user name and password. Choose SCP from the File protocol list (see below).

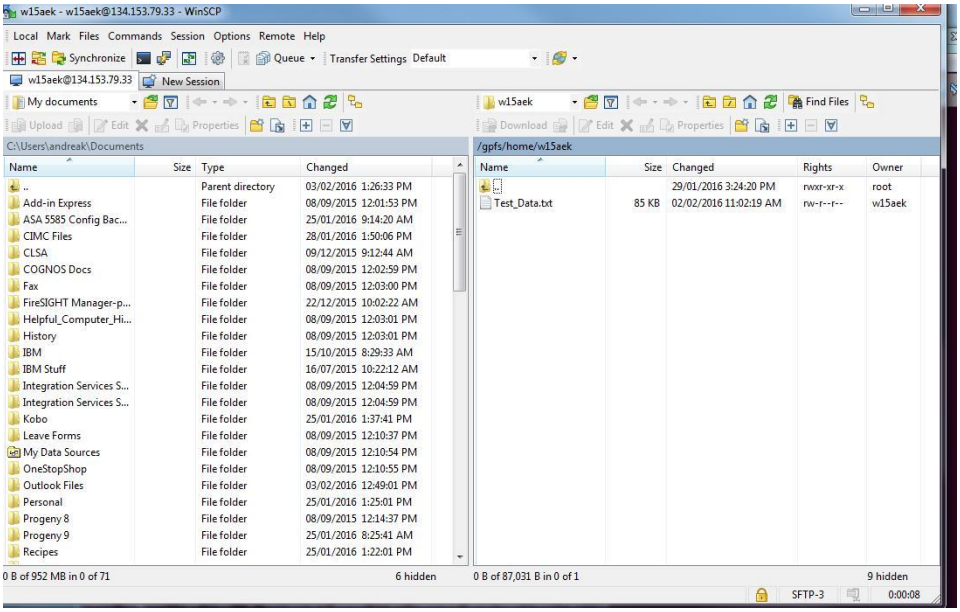


7. Click Login

You may see this warning message:



8. Click Yes. You should now see a screen similar to this:

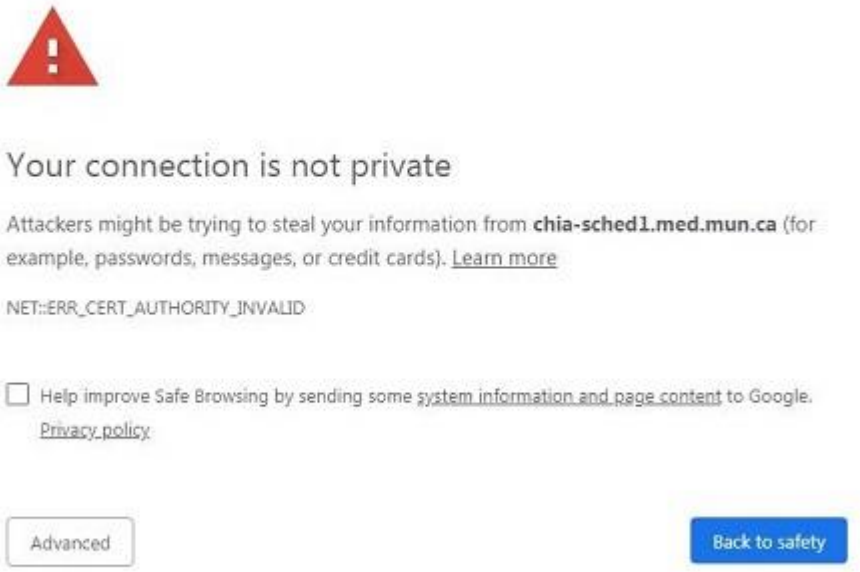


Find the file you need to upload on the left and drag it to your home directory on the right. This file should now appear in your /gpfs/home/username directory

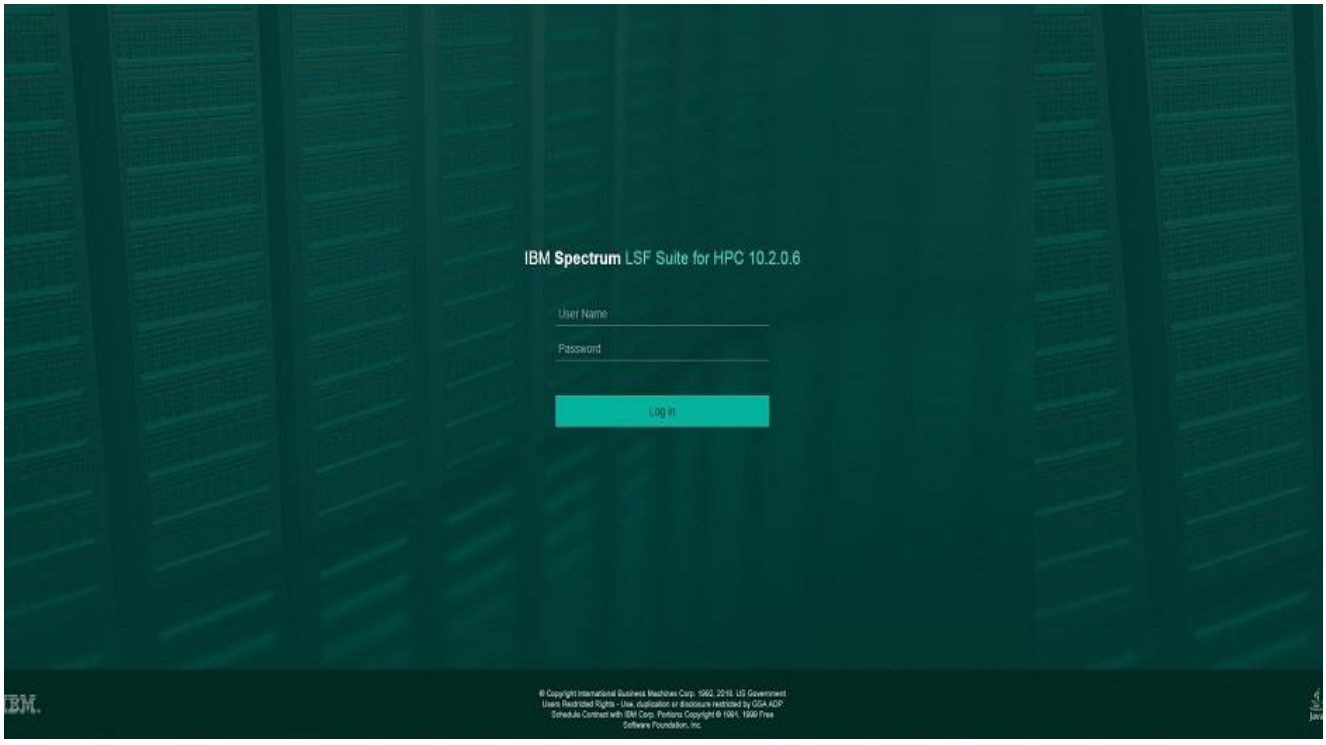
Navigating the CAIR internal environment – Web Method

The LSF web interface is an alternative way to submit jobs to the CAIR internal environment that does not require users to use the command line interface. This is the recommended interface for most users.

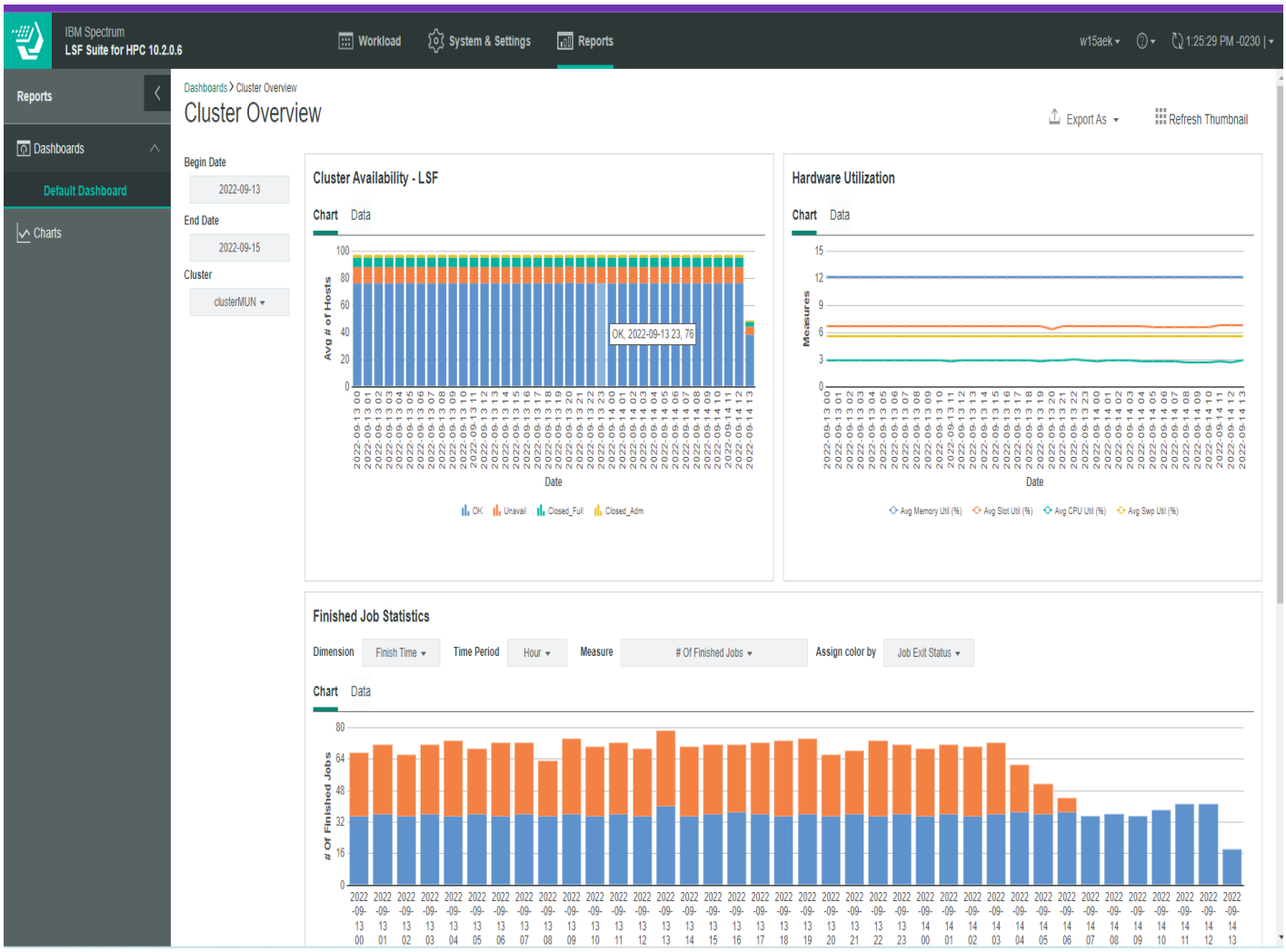
1. Open your browser and type in**https://sched1.cair.mun.ca.** If you get the following message (or something similar) please choose advanced tab and select the option to proceed to page or add exception, depending on browser used :



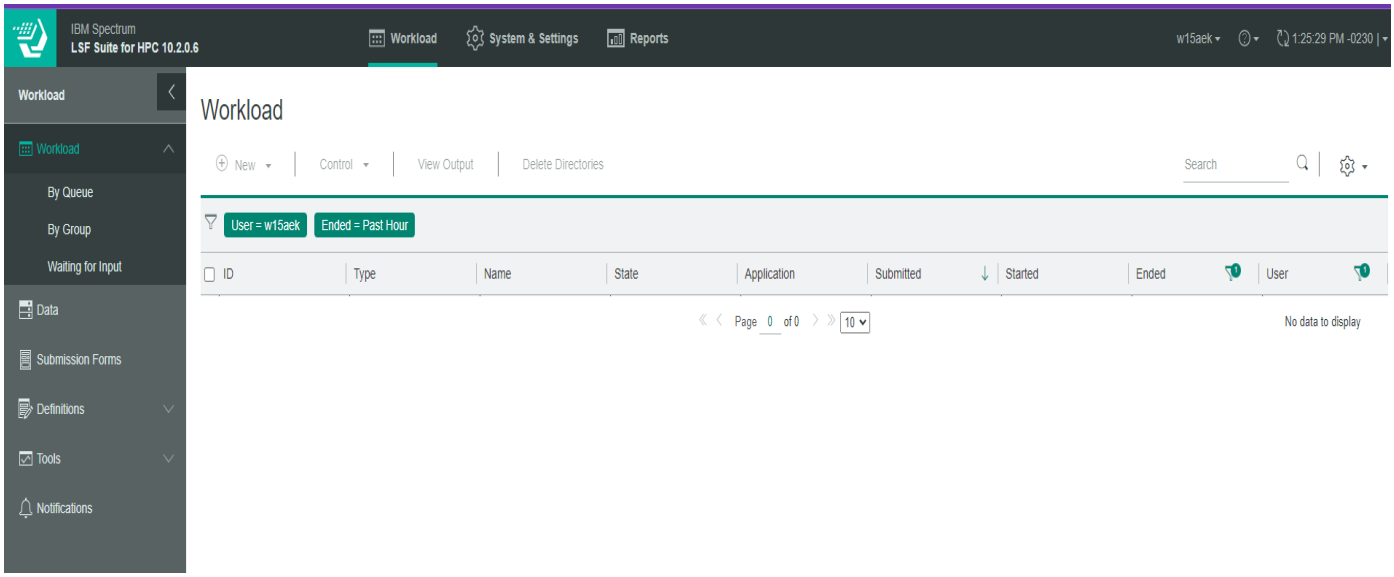
2. On the LSF login screen, enter your CAIR provided username and password and click Log In:



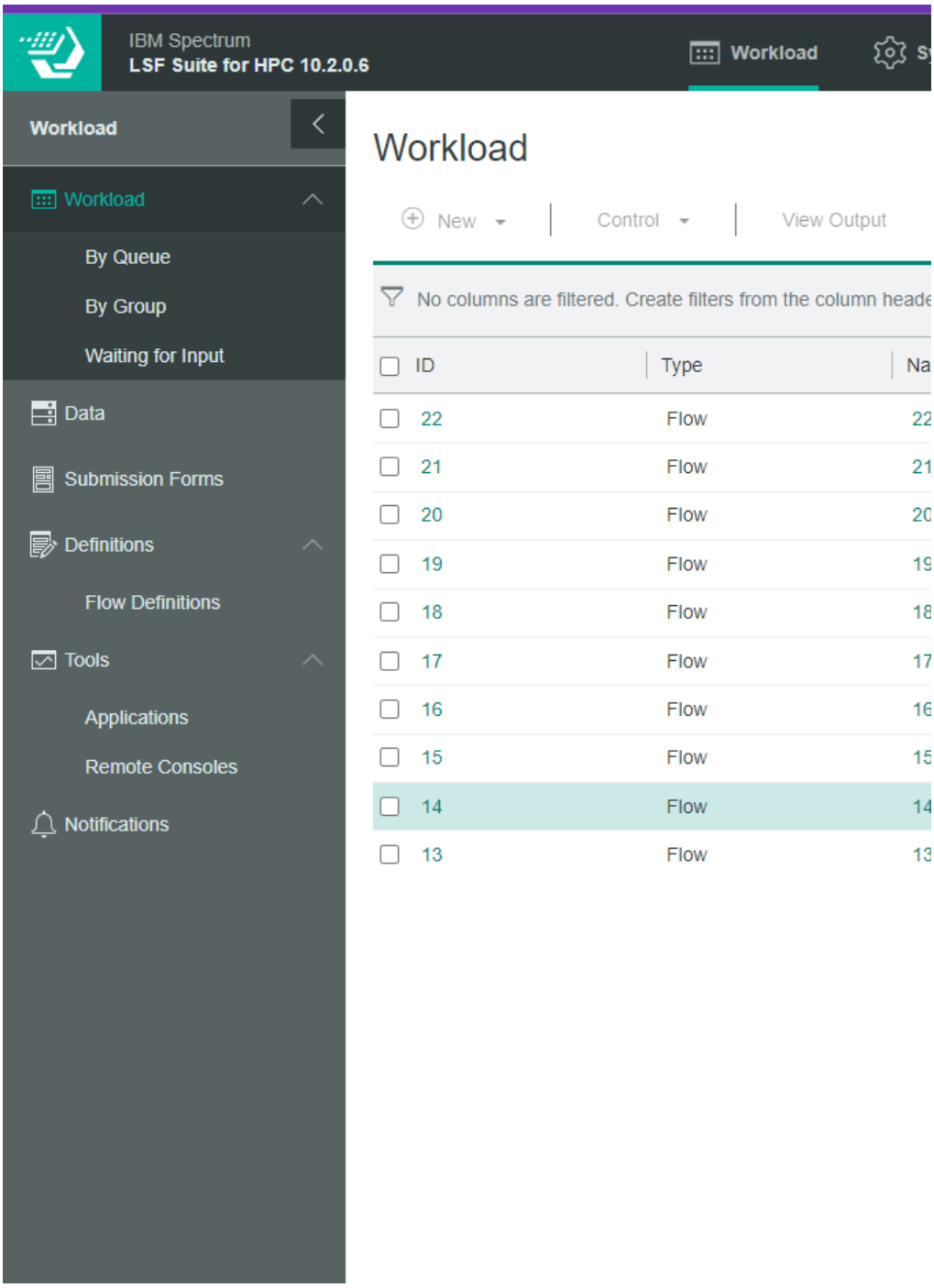
3. You should see a screen like this:



4. To view existing jobs, view data results, or to submit new data, please click the Workload icon at the top of the screen. The resulting screen will look like this:

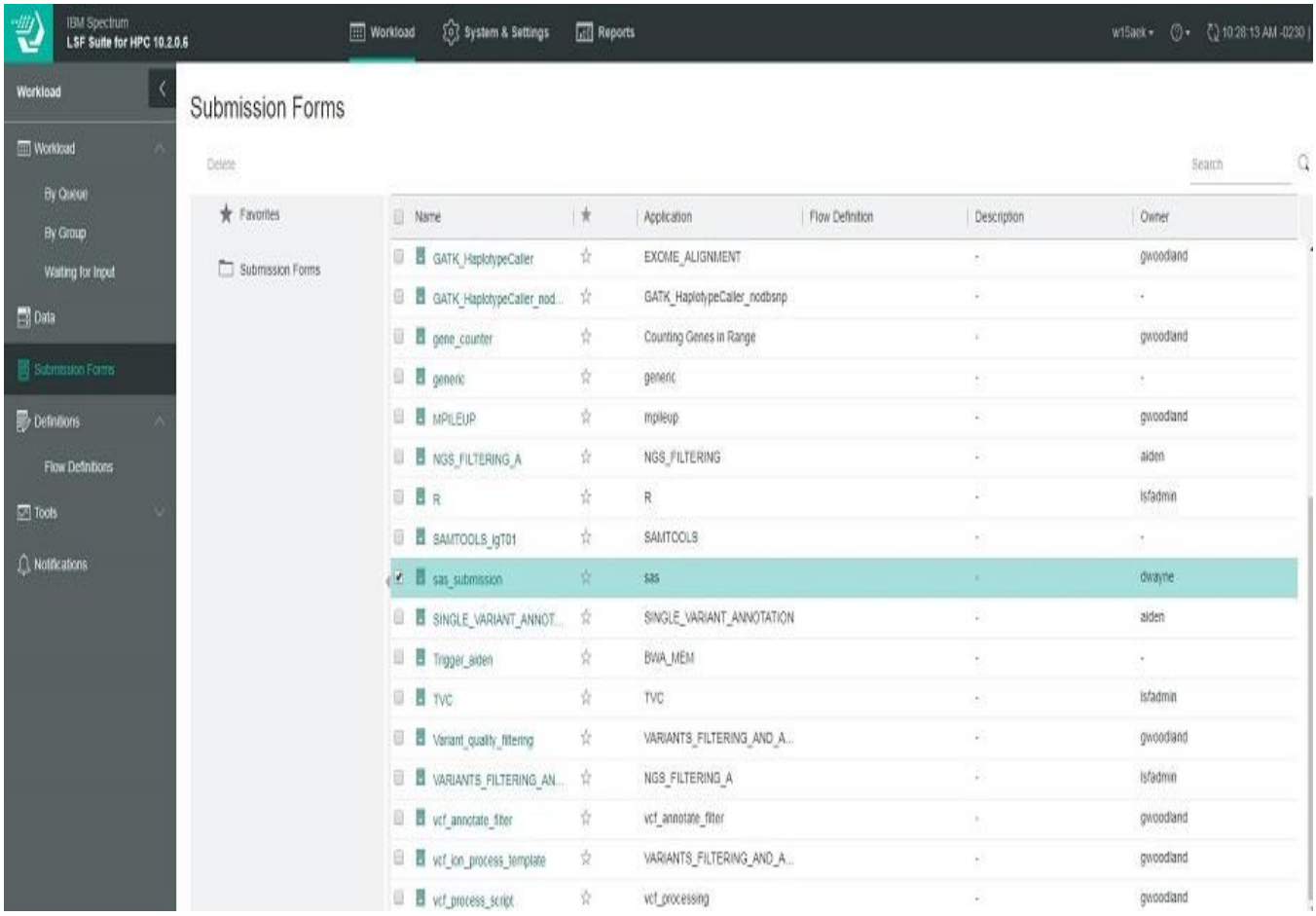


5. The navigation menu on the left allows you to view existing submission under the Workload section, view any existing data on the cluster under the Data section, submit new data to the cluster using Submission Forms, etc.

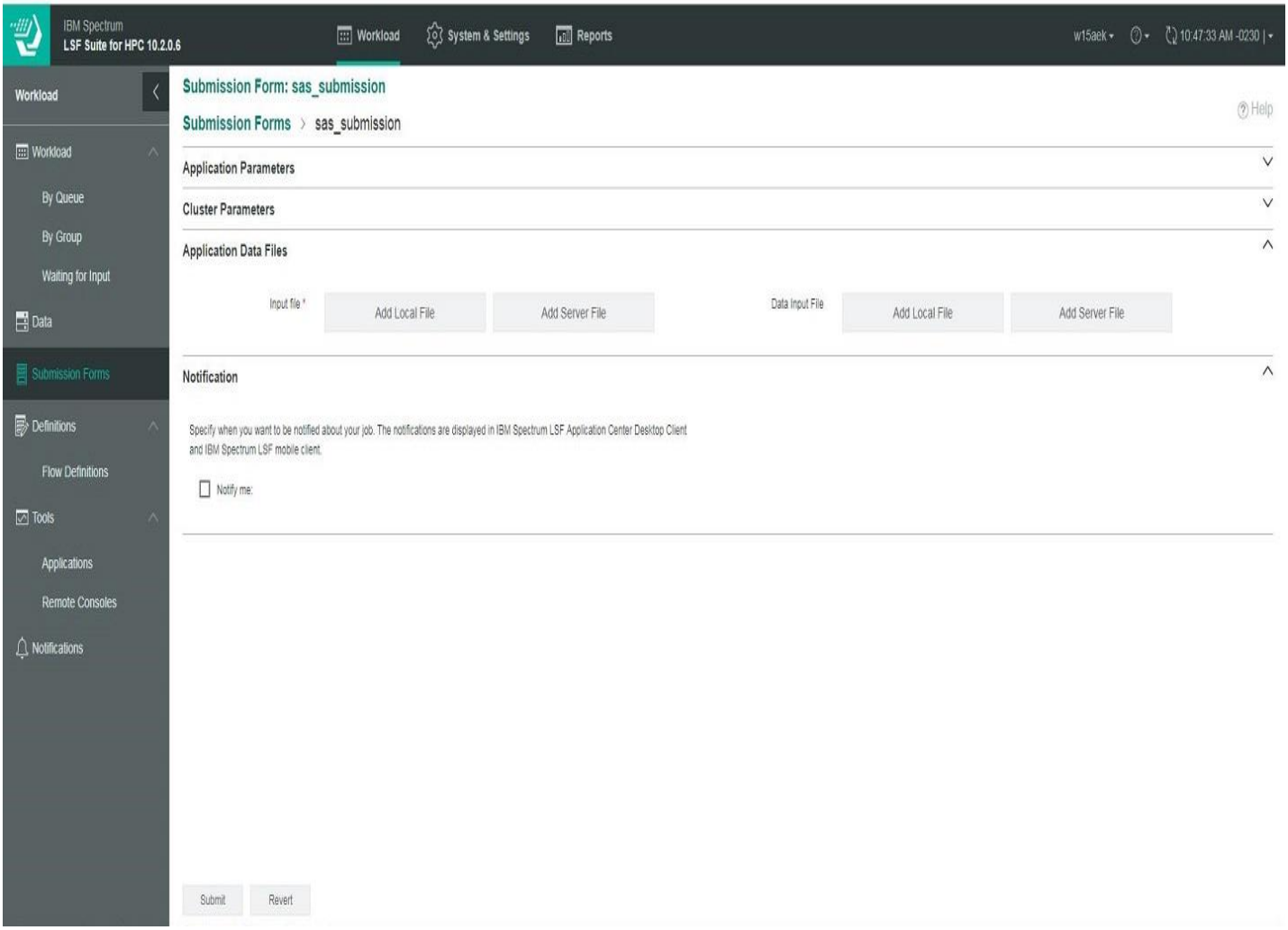


To Submit new data:

1. Having clicked Workload from the top Menu, select Submission Forms from the left menu, and a list of available forms for submitting various jobs will appear:

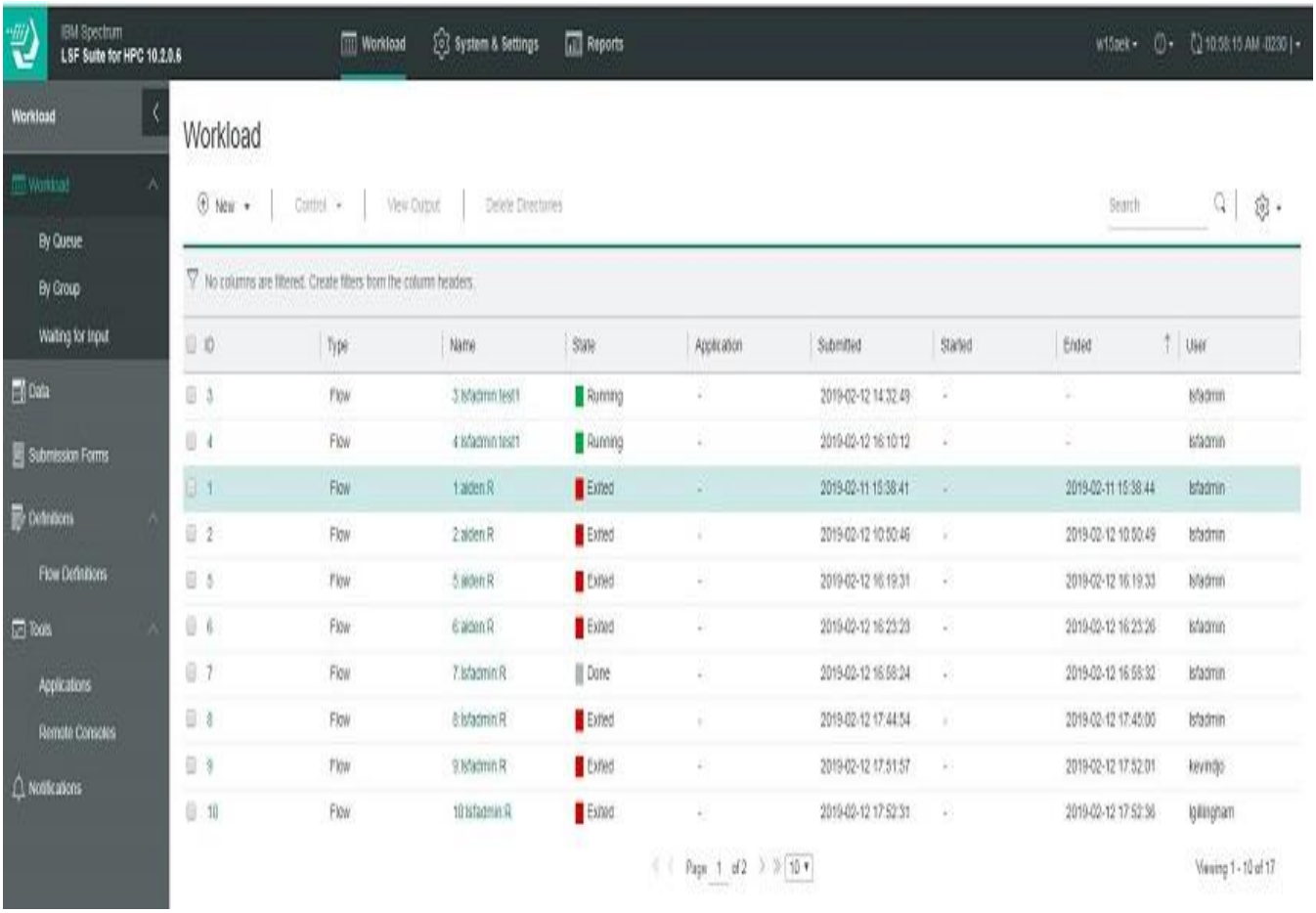

IBM Spectrum
LSF Suite for HPC 10.2.0.6
Workload
System & Settings
Reports
w15aek
10:28:13 AM -0230
Workload
Workload
By Queue
By Group
Waiting for Input
Data
Submission Forms
Definitions
Flow Definitions
Tools
Notifications
Submission Forms
Delete
Search
Favorites
Submission Forms
Name
Application
Flow Definition
Description
Owner
GATK_HaplotypeCaller
EXOME_ALIGNMENT
gwoodland
GATK_HaplotypeCaller_nod...
GATK_HaplotypeCaller_nodbsnp
gene_counter
Counting Genes in Range
gwoodland
generic
generic
MPILEUP
mpileup
gwoodland
NGS_FILTERING_A
NGS_FILTERING
aiden
R
R
lsfadmin
SAMTOOLS_IgT01
SAMTOOLS
sas_submission
sas
dwayne
SINGLE_VARIANT_ANNOT...
SINGLE_VARIANT_ANNOTATION
aiden
Trigger_aiden
BWA_MEM
TVC
TVC
lsfadmin
Variant_quality_filtering
VARIANTS_FILTERING_AND_A...
gwoodland
VARIANTS_FILTERING_AN...
NGS_FILTERING_A
lsfadmin
vcf_annotate_filter
vcf_annotate_filter
gwoodland
vcf_ion_process_template
VARIANTS_FILTERING_AND_A...
gwoodland
vcf_process_script
vcf_processing
gwoodland

2. Select the desired submission type and a job submission form will appear. For example, to submit data for SAS analysis, choose sas_submission by clicking on it.

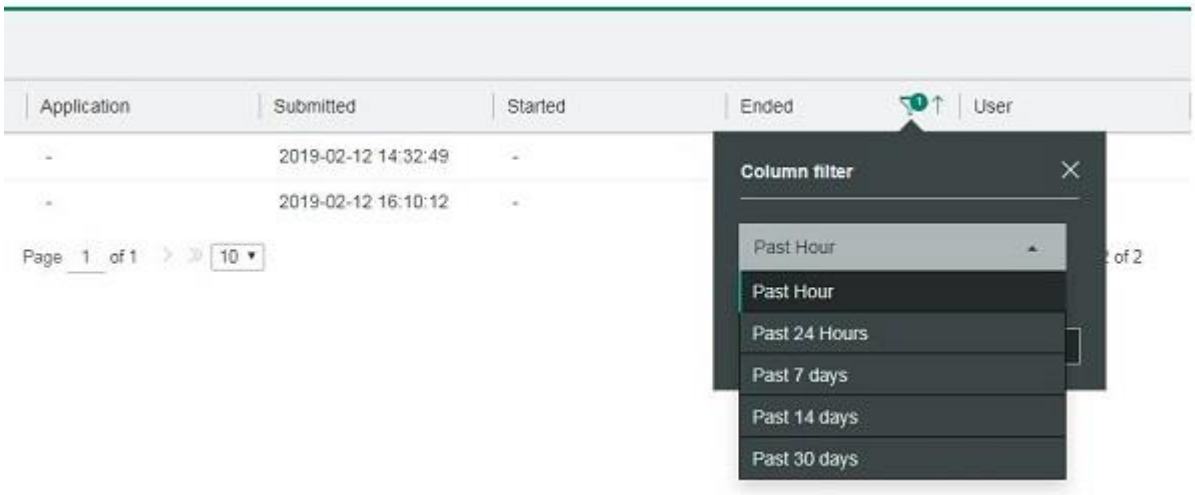


Choose the data file you wish to analyse either from your local computer (click Add Local File and browse to data location) or from a folder inside the CAIR cluster (click Add Server File and locate data). Click on Submit to begin.

3. To check the status of your job, click Workload on the left menu. All jobs will be listed with their status

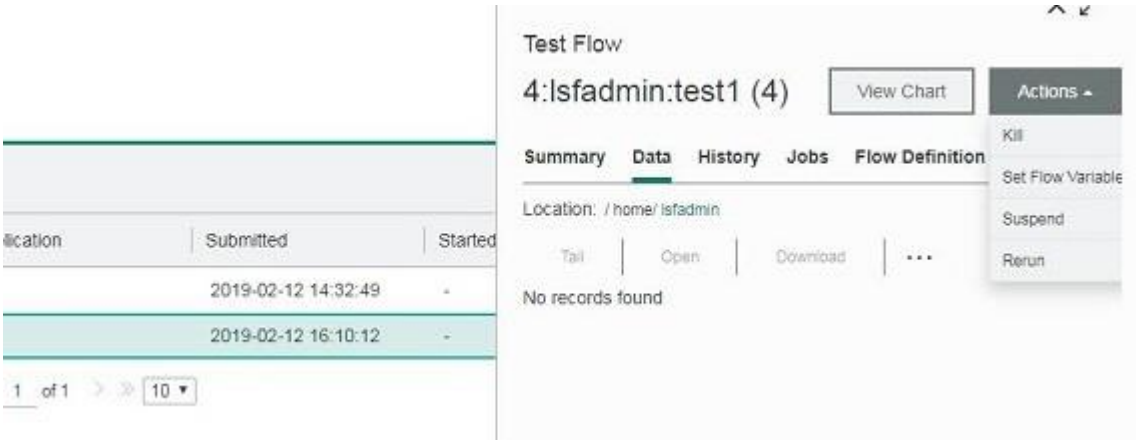


4. If no jobs appear, try changing the Ended period to a larger time frame by clicking the filter icon on the Ended Column. The available options are Past Hour, Past 24 Hours, Past 7 days, Past 14 Days and Past 30 Days.

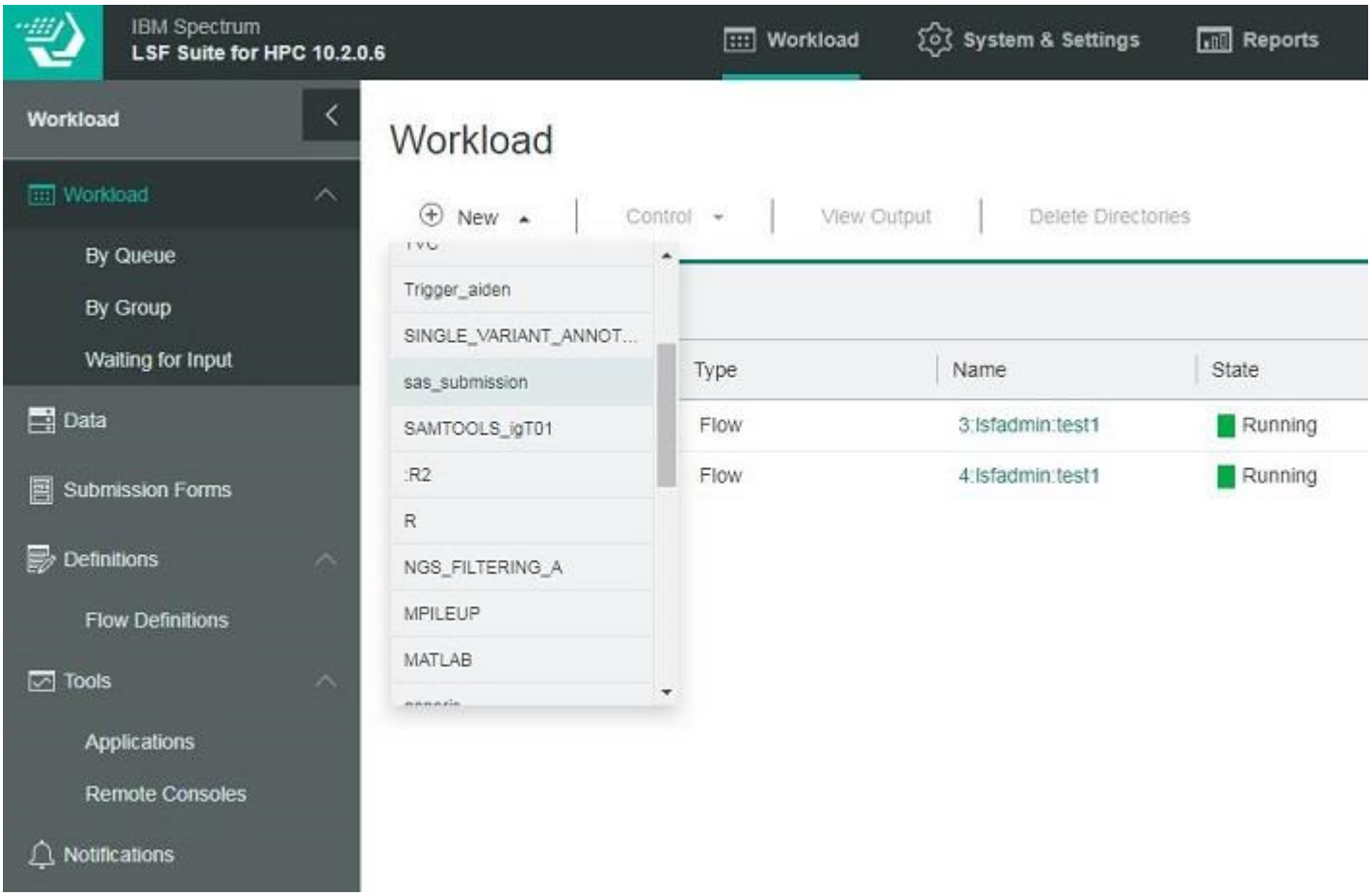


5. Clicking the left box at the beginning of a job record gives some additional control of the specified job - options to kill process, set flow variables, suspend job or rerun job.

6. Clicking on a job brings up a side menu with some additional job options



7. New jobs can be submitted from the Workload section as well by clicking New and choosing the required submission form from the dropdown list:



Submission screen will appear as in the above steps to Submit New Data.