

# TX-E1 REFERENCE GUIDE

## Getting Help

Website: <https://supercloud.mit.edu/>

Email: [supercloud@mit.edu](mailto:supercloud@mit.edu)

To help us resolve your issue more quickly, when emailing us, include the following information, where applicable:

- Whether you are submitting your jobs from a Jupyter Notebook running on your desktop system, or if you are using an ssh session to the login node
- The command that you used to launch your job
- The job id of your job
- The full error message you received
- Any supporting files (code, submission scripts, screenshots, etc.)

## Accessing TX-E1

- Via SSH (for access to the command line):  
`ssh <username>@txe1-login. mit.edu`
- Via Web Portal:  
<https://txe1-portal.mit.edu/>

## Policies

- Standard MIT Acceptable Use Policies apply to all accounts on the SuperCloud systems
- **We do not back up files on the SuperCloud** and strongly recommend that you regularly move files back to your local workstation
- **Regular System Maintenance**  
Routine maintenance on TX-E1 is performed on the third Thursday of the month. If the scheduled maintenance day falls on a campus holiday, the downtime will occur on the same day the following week.  
We usually start carefully draining the scheduler of jobs on Wednesday evening. When the maintenance is complete, an email will be sent informing users that the system has been returned to service.  
During the maintenance period, the Jupyter Portal, the Database Portal, and all of the compute nodes are unavailable.

## Group Shared Directories

### Requesting a Group Shared Directory

Email your request to [supercloud@mit.edu](mailto:supercloud@mit.edu) and provide the following information:

- The name you'd like for the directory (shorter is better, and it should not contain spaces)
- The list of users who should be allowed to access the directory
- Whether you'd like the directory to be read-only once your data have been moved into the directory (to prevent accidental deletion)
- Whether this is a public dataset

### Using Group Shared Directories Safely

- When uploading files to the group shared directory, always use the "scp" or "rsync" tools
- In scripts and code, when referencing the shared directory, always use this path as the leading prefix to point to files when sharing with other members:  
`/home/gridsan/groups/<shared_directory_name>`  
Note that a username does not appear in this pathname

## TX-E1 Web Portal

<https://txe1-portal.mit.edu/>

### How to Log In to TX-E1 Web Portal

Log in to the TX-E1 Web Portal with one of the following:

- PKI Certificate/SmartCard
- MIT Touchstone/InCommon Federation
- Username and password

### What You Can Do From the TX-E1 Portal Home Page

- Edit your SSH keys
- Browse the file system
- Access the Databases system
- Access the Jupyter Notebook system
- Access the Online Courses
- End your grid portal session

## Jupyter Notebooks

Once you are connected to the Jupyter Notebook system, you can launch a session with default settings, or use the Advanced Launch Options to select alternate Jupyter environment settings, and allocate more cores and other resources. In most cases, the default settings are sufficient for a Jupyter instance.

### Advanced Options

- Partition : Normal | GPU
- CPU Type : Intel Xeon-E5 | AMD Opteron
- GPU Resource flag : Volta V100
- GPU Resource Count : 1—4
- Ncpu : number of cores
- Exclusive mode : allocates a full node
- Anaconda/Python version
- Application : Jupyter Notebook | Jupyter Lab

When you first enter the Jupyter environment, you will see the files and directories in your home directory. You can navigate through these by clicking.

By clicking on the "New" button in the top right, you can:

- Start a new notebook (Julia, Python, Matlab, Octave, R)
- Open a terminal window
- Create a new text file with a simple text editor

## Online Courses

We offer courses about high performance computing and related topics. The courses are built with hands-on exercises that can be run on the SuperCloud.

Access to Online Courses is through the TX-E1 Web Portal.

To see the courses that we offer, click on "Explore Courses" in the upper left corner.

Email [bwx-help@bwsix.mit.edu](mailto:bwx-help@bwsix.mit.edu) if you have issues with the course platform.

## General Job Management Commands

### Check System Status

```
$ LLGrid_status [opteron | xeon-e5 | gpu | all]
```

```
$ LLfree
```

### Monitor Your Job

```
$ LLstat
```

### Stop Your Job

```
$ LLkill [options] <job_id_list>
```

job\_id\_list      Comma separated list of job number(s)

Options:

- version      Show program's version number and exit
- h, --help      Show this help message and exit
- t <task\_list>      Specify selected job array elements to delete  
task\_list syntax: start[-end[:step]]
- u <username>      Delete all jobs owned by username  
No effect if job\_id\_list is specified

## Copying Files to the TX-E1

### scp

```
scp [options] <src> <user>@txe1-login.mit.edu:<dest>
```

Most commonly used options:

- r      Recursively copy files in all subdirectories
- v      Verbose

### rsync

```
rsync [options] <src> <user>@txe1-login.mit.edu:<dest>
```

Most commonly used options:

- r      Recursively copy files in all subdirectories
- l      Copy and retain symbolic links
- u      Skip files that are newer on the LLSC system
- g      Preserve group attributes (use with shared groups)
- v      Verbose

### LLcopy2tmp

```
LLcopy2tmp [-gCopyGroup] <src-1> [src-2 ...]
```

Copy <src-#> and its contents to the local directory pointed to by the TMPDIR environment variable

- Copies once per node for the same CopyGroup, which defaults to the environment variable SLURM\_JOB\_ID
- Dereferences symlinks

## LLsub

### Submit a job

```
$ LLsub <command> [<N>] [options] [-- <command_args>]
```

Options for job submission only:

- command      Specify the program file to execute
- N              Specify the number of tasks/processes

### Request an interactive session

```
$ LLsub -i [full | -s <slots_per_task> | -N <num_nodes>]
[-c opteron | xeon-e5] [-q <queue_name>]
[-g volta:<count>] [--x11]
```

Options for interactive session only:

- full      Request exclusive node access
- N <num\_nodes>      Number of nodes to allocate
- x11      Enable X11 forwarding

Most commonly used options for job submission or interactive session (see website for full list of options):

- h      Show this help message and exit
- g volta:<count>      Number of GPU units to be used: 1–4
- s <slots\_per\_task>      Number of slots (cores) per task (default: 1)
- a mpi      Indicates the command is an MPI application  
mpirun command will be selected from your PATH

## Launching MATLAB®/Octave Jobs

Use these commands at the MATLAB®/Octave prompt or in a MATLAB®/Octave function or script.

### pMatlab Job

- Launch your pMatlab job from a MATLAB®/Octave session:  
eval(pRUN('myScriptName', <num proc>, 'grid&'))

### Single MATLAB®/Octave Job

- Launch your serial functions on LLSC systems:  
launch\_status = LaunchFunctionOnGrid(m\_file)  
launch\_status = LaunchFunctionOnGrid(m\_file, <variables>)
- Launch your MATLAB® functions that call the parfor() function on LLSC systems:  
launch\_status = LaunchParforOnGrid(m\_file)  
launch\_status = LaunchParforOnGrid(m\_file, <variables>)

## LLMapReduce

```
LLMapReduce --mapper <script> --input <input_dir>
--output <output_dir> [options]
```

Most commonly used options (see website for full list of options); default values are shown in **bold**:

- h, --help      Show the full help message and exit
- apptype=siso | mimo      Specify the application type
- cpuType=opteron | xeon-e5      Request compute nodes with a specific CPU type
- exclusive=true | **false**      Enable exclusive mode
- gpuNameCount=volta:<count>      Number of GPU units to be used: 1–4
- input=<input\_dir>      Path to input files, or file containing list of input files
- keep=true | **false**      Keep temporary MAPRED.PID directory
- mapper=<mapper>      Specify the mapper program to execute
- ndata=<count>      # input data files to be processed per task (default: 1)
- np=<nprocs>      # processes to run concurrently (default: # input files)
- output=<output\_dir>      Path for the output files
- reducer=<reducer>      Specify the reducer program to execute
- slotsPerTask=<num\_slots>      Number of slots (cores) per task (default: 1)
- slotsPerTaskType=**1** | 2 | 3      How the number of slots per task value is applied  
1 = Map only; 2 = Map and Reduce; 3 = Reduce only

## Slurm Resources

- Native Slurm commands and options can be used for job submission and monitoring
- A two-page Command Summary can be found here:  
<https://slurm.schedmd.com/pdfs/summary.pdf>

## Module Commands

```
module avail
module show <module>
module load <module>
module unload <module>
module list
```

## Loading Modules in a Script

```
#!/bin/sh
# Initialize the module command
source /usr/share/Modules/init/sh
# Load the desired module
module load <module>
...
```