ECE253: Lab Submission Instructions

File Transfer, Sanity Check, Submit and Checking Marks

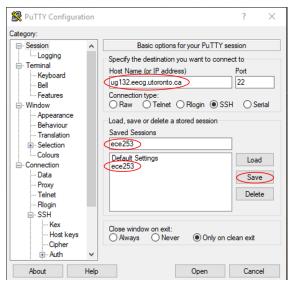
The goal of this document is to provide step-by-step instructions on how to submit the lab assignments for automarking in ECE253.

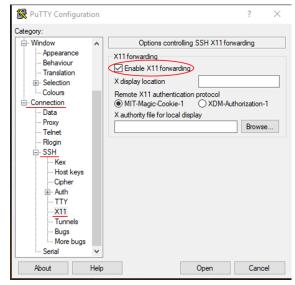
Prerequisite 1: UG Machine Login

The UG machines are Linux-based machines located in the ECE Workstations Labs. The address of these machines range from ug132.eecg.utoronto.ca - ug180.eecg.utoronto.ca. You should make sure that you can log into your ECE account on these machines. You can use SSH to access the UG machines remotely.

Note: If this is the first time you are logging into these machines, your username is your UTORID and your default password is your student number. Once you log in (after following the instructions below), make sure to secure your account by changing your password with the passwd command.

For Windows users: You can install PuTTY, which is a an SSH client. The first time you open up PuTTY, you will have to configure your connection to a UG machine. Pick a machine from the range of ug132 - ug180 and enter the address in the Host Name field (Figure 1a). You can save the configuration by giving it a name and pressing Save, and it should appear in your list of Saved Sessions. Double click on the saved session or click Open to initiate a connection. You may get a warning message saying the server's host key is not cached in the registry, click Yes. You can now enter your username and password to log into your account on this machine.





(a) PuTTY configuration.

(b) X11 forwarding.

Figure 1: PuTTY set up to connect to UG machines.

Optional: forward graphics. You may also want to install Xming if you want to remotely run graphical applications (e.g. ModelSim) remotely. You can update your PuTTY configuration to support graphical applications by doing the following (Figure 1b):

- 1. left click on your saved session and click Load
- 2. go to Connection \rightarrow SSH \rightarrow X11 and click Enable X11 forwarding

3. go back to Session and click Save

Make sure you have Xming running in the background and you can now open a connection on PuTTY that supports graphical applications.

For Mac users: Open the Terminal app and type: ssh username@ug132.eecg.utoronto.ca. Make sure to replace username with your actual username and change ug132 to any machines between the range of ug132 - ug180. You may get a warning message saying the remote host identification has changed, type yes. You should now be able to enter you password and log into your account on the UG machine.

Optional: forward graphics. You may want to install XQuartz if you want to run graphical applications (e.g. ModelSim) remotely. To be able to run graphical applications remotely, you want to enable X11 forwarding when you connect to the UG machines. You can do this by adding the -X option when you connect: ssh -X username@ug132.eecg.utoronto.ca.

Prerequisite 2: Using the Terminal on UG Machines

The UG machines run on Linux and you need to be able to navigate through the file system using the terminal (a.k.a. command line) to submit your lab assignments. This section gives a brief review of the Linux file system and different commands you can type into the terminal.

File System Structure. Everything in Linux is stored as a file, whether it be a program you run or a piece of code you wrote. These files all have a name and are stored in some **directory**. The entire file system starts at the **root** directory (denoted by the / symbol). Since each directory can contain zero or more files and/or subdirectories, you can have a file called labo.sv that resides in a directory called ece253, which is in a directory called fall2022 under the root directory. To refer to this file, you would provide the **path** to this file: /fall2022/ece253/labo.sv. In addition to the root directory, there are a few more shorthand symbols for specifying the path of a file listed in Table 2.

Symbol	Meaning
/	root directory
~	home directory
•	current directory
• •	parent directory

Table 1: Linux path shorthand.

Navigating Directories Using the Terminal. When you log into a UG machine using SSH, you start with a terminal that allows you to type command into it. A terminal is always "working" in a directory – to print the working directory, type pwd and press enter. You should see something along the lines of /homes/t/teststudent. By default, you start at your home directory. This is a directory that belongs to you – you are free to create files and directories under your home directory as you wish. To list what files are under the current directory, type 1s. If this is your first time logging into a UG machines, your home directory (shown with a ug###: "% in the terminal, where ### is the number of the computer you connected to) will be empty.

To change into a different directory, type cd <path to directory>. You can either supply the absolute path of the directory (e.g. cd /home/t/teststudent/Documents) or you can supply the relative path of the directory (e.g. cd Documents). The relative path is always relative to the current working directory. After the cd command, you should now be in the Documents directory. Check that you changed directory successfully using the pwd command to print out the working directory.

If you want to make a new directory, you can type mkdir <path to new directory>. Again, the path can be absolute or relative - typing mkdir /homes/t/teststudent/Documents/tmpdir and typing mkdir

tmpdir while inside the Documents directory both creates the tmpdir directory at the same location. Try creating a directory and use the ls command to check that the new directory is created. Similar to mkdir, if you want to remove a directory, you can type rmdir path to directory>. Try removing the newly created directory and use the ls command to check that the new directory is removed.

If you want to copy a file, type cp <path to source file> <path to destination file>. Try the cp command and use ls to make sure the copy was successful. If you want to move a file to a different location, type mv <path to source file> <path to destination file>. The mv command can be used to rename a file if the source and destination directories are the same. Again, try the mv command and use ls to make sure the move was successful. If you want to remove a file, type rm <path to file>. Files removed using the rm command cannot be recovered, so be sure that you want to remove the file before typing this command.

Command	Meaning
pwd	print working directory
ls	list all files in the working directory
cd <path dir="" to=""></path>	change working directory to <path dir="" to=""></path>
mkdir <path dir="" to=""></path>	make a new directory at <path dir="" to=""></path>
rmdir <path dir="" to=""></path>	remove a directory at <path dir="" to=""></path>
cp <path src="" to=""> <path dst="" to=""></path></path>	copy the file at <path src="" to=""> to <path dst="" to=""></path></path>
mv <path src="" to=""> <path dst="" to=""></path></path>	move the file at <path src="" to=""> to <path dst="" to=""></path></path>
rm <path file="" to=""></path>	remove the file at <path file="" to=""></path>

Table 2: List of Linux commands to navigate the file system.

How to Submit Labs

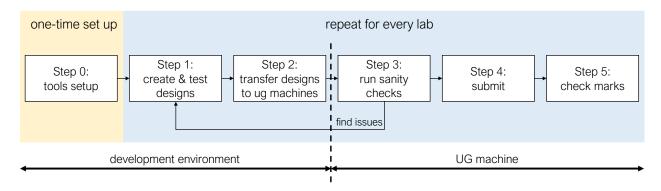


Figure 2: Process in completing each lab assignment.

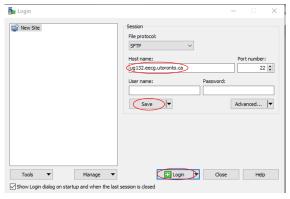
Figure 2 shows a flow chart of the design cycle for completing each lab assignment. Here, the development environment refers to where you write, compile and simulate your design using ModelSim. The UG machine is where you need to send the designs to in order to submit your lab assignments. This document describes **Steps 2 to 5** in this design process. By the end of this document, you should know how to:

- transfer files between the UG machines and your development environment
- run a format check on your design
- submit your design for each lab
- check what files you have submitted for each lab
- check what tests you've passed/failed after receiving your grade

1 Transfer Designs to UG Machine

At this point in the design process, you should have completed and tested your designs and are ready to submit. In this document, we will use examples where you are submitting SystemVerilog files. Depending on the lab, you may be required to submit files of different formats. The same submission procedure applies. If your development environment is on the UG machines themselves, you can ignore this and proceed to the next step.

For Windows users: You can install WinSCP, which is a an SCP/SFTP client. The first time you open up WinSCP, you will have to configure your connection to a UG machine. Pick a machine from the range of ug132 - ug180 and enter the address in the Host name field (Figure 3a). You can save the configuration so you don't have to type in the address every time by pressing Save. Click Login and you should be able to, depending on the WinSCP version, either see the file system on the UG machines on the right panel, while the left panel is your home machine (Figure 3b), or you will see just the file system on the remote machine. (Figure 3c). You should now be able to drag and drop files between the two panels or drag and drop to windows file explorer to transfer files between your home computer and the UG machine.



(a) WinSCP configuration.

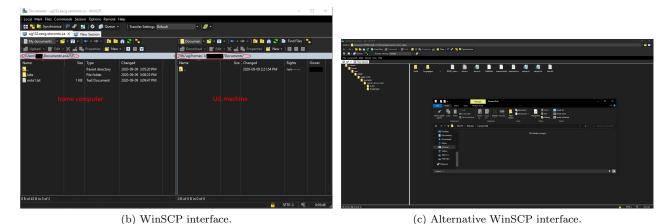


Figure 3: WinSCP set up to transfer files to and from UG machines.

For Mac users: You can use the scp command in the terminal to transfer files to and from the UG machines. The scp command is in the form: scp /path/to/source/file /path/to/destination. If any of the source or destination path is on a remote machine, the path should be prepended with username@remote.machine.address: (note the: at the end). For example, to transfer a file called lab0.sv from the Documents directory on your Mac to the home directory on the UG machine, do the following:

- 1. Open the **Terminal** app
- 2. Navigate to the location of the file you want to transfer: cd Documents

3. Issue SCP command: scp lab0.sv teststudent@ug132.eecg.utoronto.ca:~ Similarly, if you want to transfer a file called lab1.sv from the UG machine's home directory back to your Mac, you can type: scp teststudent@ug132.eecg.utoronto.ca:~/lab1.sv ~/Documents. Make sure you replace the username with your actual username and replace ug132 with any of the machines between ug132 - ug180.

2 Run Sanity Check

In this course, we provide you with a simple tester for each lab to make sure your design can be marked by the automarker. These testers serve as a sanity check to help you determine if all naming conventions have been followed. Important: passing the sanity check does not mean you pass all test cases for the lab! You need to come up with your own test cases (in Step 1 of Figure 2) to make sure your design works correctly under all inputs. The testers for each lab will be released as the semester goes on and will have the form: /cad2/ece253f/public/<lab#>/tester.

By this step, your SystemVerilog design should have been transferred to the UG machine, and you are ready to run a sanity test on your design. Do the following to run the tester:

- 1. Connect to the UG machine via terminal (see Prerequisite 1: UG Machine Login if you forgot how to do this).
- 2. Navigate to the directory containing your designs (see Prerequisite 2: Using the Terminal on UG Machines if you forgot how to do this).
- 3. Run the tester for that specific lab (e.g. /cad2/ece253f/public/0/tester for testing lab 0).

The tester may take some time to run, and you should see the terminal print out information on whether each part of your lab passed the sanity check. The same output is saved to a file called track.txt. An example of what the output looks like is in Figure 4. As a reminder, your files should be named part1.sv, part2.sv, etc. The automarker will not be able to mark your code if they are named incorrectly.

3 Submit

Once you have confirmed with the tester that your files can be marked by the automarker, you are ready to submit them. Navigate to the directory containing your files if you are not already there. The submit command follows this format:

/cad2/ece253f/public/submit <lab#> <part1 file name> [optional name to additional parts]

This command allows you to submit one or more files for a specific lab. For example, the command to submit SystemVerilog files for parts 1, 2 and 3 for lab 1 is: /cad2/ece253f/public/submit 1 part1.sv part2.sv part3.sv

Here are some things you should keep in mind when submitting:

- 1. Before submitting, make sure the files you want to submit are in the same folder where you run the command.
- 2. You do not need to submit all parts at once. Submitting one or two parts at a time will not affect prior submissions made for other part(s).
- 3. Pay close attention to the lab #. Students sometimes submit code for the wrong lab. If you do that, we won't know this and you will receive a zero. Make sure to **double check** the lab number when submitting.

For each lab, submission will open when the lab is released. You can submit files at any time before the deadline, and you may re-submit files as many times as you want before the deadline. Only the most recent submitted file will be used for marking. Submission will close after the deadline and you will see an error message if you try to use the submit command for that lab.

To check the files you have submitted, you can use the following command:

```
Model Technology ModelSim – Intel FPGA Edition vlog 2020.1 Compiler 2020.02 Feb 28 2020
Start time: 17:47:37 on Sep 09,2020
vlog part1.v
   Compiling module part1
 Top level modules:
       part1
End time: 17:47:37 on Sep 09,2020, Elapsed time: 0:00:00
Errors: Θ, Warnings: Θ
Reading pref.tcl
# 2020.1
# vsim -c -do "/cad2/ece253f/public/0/test/run.do" work.part1_tb
# Start time: 17:47:37 on Sep 09,2020
     ModelSim - Intel FPGA Edition 2020.1 Feb 28 2020 Linux 4.19.0-10-amd64
      Copyright 1991-2020 Mentor Graphics Corporation
      All Rights Reserved.
     ModelSim - Intel FPGA Edition and its associated documentation contain trade
     secrets and commercial or financial information that are the property of
     Mentor Graphics Corporation and are privileged, confidential,
      and exempt from disclosure under the Freedom of Information Act,
      5 U.S.C. Section 552. Furthermore, this information
      is prohibited from disclosure under the Trade Secrets Act,
      18 U.S.C. Section 1905.
# Loading sv_std.std
# Loading work.part1_tb
# Loading work.part1
# do /cad2/ece253f/public/0/test/run.do
# input = 0000 output = 1000000 golden_output = 1000000 PASSED
# input = 0001 output = 1111001 golden_output = 1111001 PASSED
# input = 0010 output = 0100100 golden_output = 0100100 PASSED
# End time: 17:47:37 on Sep 09,2020, Elapsed time: 0:00:00
# Errors: 0, Warnings: 1
Number of Errors by compiling the verilog code: 0
Number of Errors by running the simulation: 0
Number of PASSED: 3
Number of FAILED: 0
 part1 is done!
```

Figure 4: Example of the tester output.

/cad2/ece253f/public/check_submission <lab#>

For example, after submitting parts 1 to 3 for lab 1, /cad2/ece253f/public/check_submission 1 will output what files have been submitted and when they were submitted. It is a good idea to use this command and double check that all the files you want to submit for a lab are submitted successfully.

4 Check Marks

After your lab has been graded, we will release a marker script that you can use to see where you lost marks. The marker operates very similar to the tester:

- 1. Connect to the UG machine via terminal.
- 2. Navigate to the directory containing your designs.
- 3. Run the marker for that specific lab (e.g. /cad2/ece253f/public/1/marker for testing lab 1).

The marker may take some time to run, and the output is saved to a file called mark.txt.

5 Q&A

Q1

Q: What files do we need to submit?

A: Each lab handout should have a Submission section. This section will tell you exactly what you need to submit for each part.

$\mathbf{Q2}$

Q: How should I name my modules?

A: Please follow the module names in the Submission section.

$\mathbf{Q3}$

Q: The tester is not working!

A: Check the following:

- 1. make sure your folders do not contain a space
- 2. make sure you are in the folder containing lab files when running the tester command
- 3. all paths are case-sensitive, make sure you typed everything correctly

$\mathbf{Q4}$

Q: The submit command is not working!

A: Check the following:

- 1. make sure your folders do not contain a space
- 2. make sure you are in the folder containing the files you want to submit
- 3. all paths are case-sensitive, make sure you typed everything correctly