

## Working with saturn, the Biostat server

You may do all the computations for class using SAS on the Biostatistics machine called **saturn**. This can be done from home by modem or through any computer lab on campus that you have access to. This handout describes how to use **saturn** and save output at two places:

- Biomedical Library in Diehl Hall
- Computing Lab in A-269 Mayo

The Biomed Library is open in the evenings and on weekends. The A-269 Computing Lab will only be available to you during Lab times. The Biomed Library has both Macs and PCs; Mayo computing lab has only PCs.

**Logging into your account at the Biomed Library.** At the Reserve Desk, ask for a machine assignment: PCs Blue 21-25 or Green 20-24; Macs Red 1-5.

**On a PC:** Click on the bar marked *SAS Related Programs*, then click *Telnet to SAS*. Then type in your account number and password.

**On a Mac:** Click on the *telnet* icon, or the square marked *Public Health Statistics*. Type in the host: **saturn.biostat.umn.edu** Then your account number and password.

Some Macs have *select a set-up*. Scroll to PubH5452 and click once. Do this again after the virus check. Then click the square marked *Public Health Statistics*, and type in the host: **saturn.biostat.umn.edu** Then your account number and password.

**Logging into your account at the Mayo computing lab.** Click and hold the *Start* button in the lower left. Slide the mouse to choose this sequence from the menus:

*Start : programs : internet applications : telnet*

A **telnet** dialog box will open.

Click **New**, and type in the host: **saturn.biostat.umn.edu**. Then type in your account number and password.

**Working in your account: UNIX commands.** The Biostat server **saturn** has a UNIX operating system. There are no menus; you must type in commands. Here are a few basic UNIX commands which should get you through this course:

<b>ls</b>	lists all the files in your account
<b>cat file</b>	prints <i>file</i> on the screen; use this for screen capture
<b>more file</b>	prints <i>file</i> one screenful at a time; hit return to go to the next, <b>q</b> to quit
<b>pico</b>	starts the editor <b>pico</b> and creates a new file
<b>pico file</b>	opens <i>file</i> with the editor <b>pico</b>
<b>sas file</b>	runs the SAS program in <i>file.sas</i>
<b>rm file</b>	deletes <i>file</i>
<b>rm *.log</b>	deletes all SAS log files
<b>rm *.lst</b>	deletes all SAS listing files
<b>mv file1 file2</b>	changes the name of <i>file1</i> to <i>file2</i>
<b>cp file1 file2</b>	makes a copy of <i>file1</i> called <i>file2</i>

**Getting files from the course account:** All data files and example programs for the homework will be made available in the course account. To copy a file from the course account to your own account, use:

```
cp /home/ph5450/file file
```

The stuff preceding the name of the file is called the *path*. There is no need to copy data files to your account. Your SAS program can read a dataset directly from the course account if you include the path in the infile command:

```
data one;
  infile '/home/ph5450/data/Ch01/TA01_009.TXT' firstobs=2;
```

**Getting SAS output.** The process of working with SAS is circular: write code, examine the listing file, examine the log file to see what went wrong, correct the code, and repeat. By using *cat*, *more*, or *pico*, you can examine your output until you are sure it is OK. In order to save it or print it, you must close your connection to saturn through telnet. There are two choices:

1. Save your output or listing file on a floppy disk. This allows you to extract the pieces you want later and print them at home or elsewhere. You can open the file using MSWord or any word-processing program. Make sure the whole file is in Courier or another equally-spaced font, because SAS does not use tabs to line up columns.
2. Send your output or listing file directly to the printer. This gives you only a paper copy of the file.

### **Getting SAS output at the Biomed Library:**

**On a PC:** Quit telnet. Click on the bar marked *WS FTP*. Just as when logging in, type in the host name, your account number and password. Click OK.

Now an *ftp* dialog box will open. In the right window, under *Remote System*, all your files on *saturn* will be listed. Select a file by clicking on it. To send this file directly to the printer, select *View*. When the file opens, under the *File* menu, select *Print*.

To save the file to disk, put a disk in the disk drive. In the left window, under *Local System*, click on [-- a --]. This selects your floppy disk as the place to put the file(s) you will move. The top line above the window should say **A**:

In the right window, under *Remote System*, select a file by clicking on it. Then click the ← arrow button. This moves the file, and its name should now appear in the left window as well as the right window. Repeat for each file you wish to move.

When you have moved all the files you want to print, click *Close*, then *Exit*.

**On a Mac:** Quit telnet. Click on *fetch*, and under shortcuts select *Bio-statistics*. Type in your account and password. Your files on *saturn* should appear. Select a file by clicking on it. To send this file directly to the printer, under the *Remote* menu select *View File*. Under the *File* menu, select *Print*.

To save the file to disk, put a disk in the disk drive. Double-click on the file name.

**Getting SAS output at the Mayo Computing lab:** Click and hold the *Start* button in the lower left. Slide the mouse to choose this sequence from the menus:

*Start : programs : internet applications : WS ftp32*

Now follow the same steps as given for the PC at the Biomed Library.