



As this course is part of the Scientific Computing series of courses run by the Computing Service, all the examples that we use will be more relevant to scientific computing than to system administration, etc.

This does not mean that people who wish to learn shell scripting for system administration and other such tasks will get nothing from this course, as the techniques and underlying knowledge taught are applicable to shell scripts written for almost any purpose. However, such individuals should be aware that this course was not designed with them in mind.



bash is probably the most common shell on modern Unix/Linux systems – in fact, on most modern Linux distributions it will be the default shell (the shell users get if they don't specify a different one). Its home page on the WWW is at:

http://www.gnu.org/software/bash/

We will be using bash 3.0 in this course, but everything we do should work in bash 2.05 and later. Version 3.0 and version 2.05 (or 2.05a or 2.05b) are the versions of bash in most widespread use at present. Most recent Linux distributions will have one of these versions of bash as one of their standard packages. The latest version of bash (at the time of writing) is bash 3.2, which was released on 12 October, 2006.

For details of the "Unix Systems: Shell Scripting (II)" course, see:

http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#script2 For details of the "Unix Systems: Shell Scripting (III)" course, see:

http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#scriptwkshp

For details of the "Programming: Python for Absolute Beginners" course, see: http://www.cam.ac.uk/cs/courses/coursedesc/prog.html#python



The course officially finishes at 17.00, but the intention is that the lectured part of the course will be finished by about 16.30 and the remaining time is for you to attempt an exercise that will be provided. If you need to leave before 17.00 (or even before 16.30), please do so, but don't expect the course to have finished before then. If you do have to leave early, please leave quietly and *please make sure that you fill in a green Course Review form* and leave it at the front of the class for collection by the course giver.



For details of the "Unix Systems: Shell Scripting (II)" course, see: http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#script2

For details of the "Unix Systems: Shell Scripting (III)" course, see: http://www.cam.ac.uk/cs/coursed/coursedesc/linux.html#scriptwkshp



For details of the "Unix System: Introduction" course, see: http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#unix

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If you give the cd command without specifying directory then it will change the directory to your *home directory* (the location of this directory is specified in the HOME *environment variable* – more on environment variables later).

The chmod command changes the permissions of a file or directory (in this context, the jargon word for "permissions" is "mode"). For instance, the above example gives read access to the file treasure.txt for all users on the system. Unix permissions were covered in the "Unix System: Introduction" course, see:

http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#unix



Note that the cp command has many other options than the three listed above, but those are the options that will be most useful to us in this course.

Unix commands (3)			
date > date Fri Feb	display/set system <i>date</i> and time 16 11:52:03 GMT 2007		
echo > echo ' Hello	display text "Hello"		
env	With no arguments, display <i>env</i> ironment variables (example later)		
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Please note that if you try out the date command, you will get a different date and time to that shown on this slide (unless your computer's clock is wrong!). Also, note that usually only the system administrator can use date to set the system date and time.

Note that the echo command has a few useful options, but we won't be making use of them today, so they aren't listed.

Note also that the env command is a very powerful command, but we will not have occasion to use for anything other than displaying *environment variables* (see later), so we don't discuss its other uses.



The patterns that the grep command uses to find text in files are called *regular expressions*. We won't be covering these in this course, but if you are interested, or if you need to find particular pieces of text amongst a collection of text, then you may wish to attend the CS "Pattern Matching Using Regular Expressions" course, details of which are given here:

http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#regex

The ln command creates links between files. In the example above, we create a symbolic link to the file motd in /etc and then use cat to display both the original file and the symbolic link we've created. We see that they are identical.

There are two sort of links: *symbolic links* (also called *soft links* or *symlinks*) and *hard links*. A symbolic link is similar to a shortcut in the Microsoft Windows operating system (if you are familiar with those) – essentially, a symbolic link points to another file elsewhere on the system. When you try and access the contents of a symbolic link, you actually get the contents of the file to which that symbolic link points. Whereas a symbolic link points to another *file* on the system, a hard link points to *actual data* held on the filesystem. These days almost no one uses ln to create hard links, and on many systems this can only be done by the system administrator. If you want a more detailed explanation of symbolic links and hard links, see the following Wikipedia articles:

http://en.wikipedia.org/wiki/Symbolic_link http://en.wikipedia.org/wiki/Hard_link



If you try out the ls command, please note that its output may not exactly match what is shown on this slide – in particular, the colours may be slightly different shades and there may be additional files and/or directories shown.

Note also that the ls command has many, many more options than the three given on this slide, but these three are the options that will be of most use to us in this course.



(Note that the output of the more command may not exactly match that shown on this slide – in particular, the number of lines displayed before the "--More--(0%)" message depends on the number of lines it takes to fill up the window in which you are running the more command.)

The more and less commands basically do the same thing: display a file one screenful of text at a time. Indeed, on some Linux systems the more command is actually just another name (an *alias*) for the less command.

Why are there two commands that do the same thing? On the original Unix systems, the less command didn't exist – the command to display a file one screenful of text at a time was more. However, the original more command was somewhat limited, so someone wrote a better version and called it less. These days the more command is a bit more sophisticated, although the less command is still much more powerful.

For everyday usage though, many users find the two commands are equivalent. Use whichever one you feel most comfortable with, but remember that every Unix/Linux system should have the more command, whereas some (especially older Unix systems) may not have the less command.



Note that the mkdir command has other options, but we won't be using them in this course.



Note that the mv command has other options, but we won't be using them in this course. Note also that if you move a file or directory between different filesystems, move actually copies the file or directory to the other filesystem and then deletes the original.



Note that the rm command has other options, but we won't be using them in this course.

U rmdir > rmdir	nix co <i>rem</i> ove : /tmp/	ommands (10) e <u>empty</u> directories mydir	
touch	change if the f with th (the de current /tmp/	e the timestamp of a fil file doesn't exist create he specified timestamp efault timestamp is the t date and time) nowfile	e;
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The rmdir and touch commands have various options but we won't be using them on this course. If you try out the touch command with the example above, check that it has really worked the way we've described here by using the ls command as follows:

ls -l /tmp/nowfile

You should see that the file nowfile has a timestamp of the current time and date.



Recall that the chmod command changes the permissions on a file. chmod +x sets the executable bit on a file, i.e. it grants permission to execute the file. Unix file permissions were covered in the "Unix System: Introduction" course, see:

http://www.cam.ac.uk/cs/courses/coursedesc/linux.html#unix



A common naming convention for shell scripts is for them to have the extension .sh, and all our shell scripts will follow this convention. This has the advantage that editors like gedit will automatically recognise our files as shell scripts and highlight them appropriately.

The name of the shell script we are running is "hello.sh". Since it is in the current directory, we can tell the shell to execute it by typing "./" in front of its name, as shown on this slide. This basically means "execute the file hello.sh that is to be found in the current directory" - if there is no file of that name in the current directory, the shell returns a "No such file or directory" error. It is useful to know how to use "./" for two reasons:

- If you ask the shell to run a program by just typing the name of the program and pressing return, it looks for the program in all the directories specified in the PATH *environment variable* (more on environment variables later). If the current directory isn't one of those specified in the PATH environment variable, then it wouldn't find the hello.sh that we want it to execute. By explicitly telling the shell to look in the current directory, it finds the hello.sh that we are looking for.
- 2) There might be another program called "hello.sh" in a directory that is specified in the PATH environment variable. The shell looks for programs to execute in the directories specified in the PATH environment variable <u>in the order they are specified in that</u> <u>environment variable</u>. It then executes the *first* program it finds that matches the name given. So if there was a file called "hello.sh" in some other directory specified in the PATH environment variable, then that might be executed instead.

You can achieve the same effect by asking the shell to run a program and giving it the path to the program, e.g. if hello.sh was in the directory /home/x241, then typing:

/home/x241/hello.sh

and pressing return would execute hello.sh.



Remember that the 1s command lists the files in a directory and that it can take options that modify its behaviour. 1s -1 < file> gives us a lot of information about the particular file < file>. In particular, it shows us the file's permissions (in this case: "-rwxr-xr-x"), and we see that this file indeed has its execute bits set. Note that the exact text you see when you execute "1s -1 hello.sh" on the computer in front of you may be slightly different – in particular, the owner ("x241") and group ("x241") of the file will be different.

Recall that cat <file> displays the contents of the file <file>.

gedit <file> starts the editor gedit and loads the file <file>. The "&" tells the shell to run gedit in the background, so that we go straight back to the shell prompt and can carry on doing other things rather than waiting until we quit gedit. Note that because we're running gedit in the background, after we quit gedit the shell will print a message saying "Done" (along with some other text) to indicate that the gedit program that was running in the background has finished.

You don't have to use gedit to edit the file, you can use whatever editor you are most comfortable with.

Remember that the echo command prints out the text that it has been given on standard output (normally the screen). It is a *shell builtin command*, i.e. a command that is implemented by the shell itself as opposed to an external program that the shell runs on your behalf. For example, the ls command is *not* a shell builtin command – it is an external program that the shell executes when you type "ls".

Errors in shell scripts (1)

Change: echo "Hello! I am a shell script." to: echoq "Hello! I am a shell script." > ./hello.sh ./hello.sh: line 3: echoq: command not found Who are you? > (Now change "echoq" back to "echo".) escience-support@ucs.cam.ac.uk Unix Systems: Shell Scripting () 22

Make sure you save the file before running it again, or the changes won't take effect.

As you can see, even if there is an error in the shell script, the shell script simply reports the error and merrily continues running. There are many different sorts of errors one can make in writing a shell script, and for most of them the shell will report the error but continue running. There **is** one type of error that will stop the execution of the shell script: a *syntax error* (see next slide).

Also note that the shell tells us what the error is – "command not found" (as there is no "echoq" command) – and the line on which it occurred (line 3). This makes it easier to track down the error and fix it.

You can force the shell script to quit when it encounters an error by using the set shell builtin command like this:

set -e

as we will see later.



Make sure you save the file before running it again, or the changes won't take effect.

If there is a **syntax** error in the shell script, the shell script will abort once it encounters the error, because it doesn't understand what it should do.

Note that although the error is actually at line 4, it is not until line 5 that the shell decides something is wrong and tells us anything. **Get used to this behaviour!** – it is very annoying, as it makes debugging shell scripts painful, but that's just the way it is. When the shell tells you there is a syntax error at line n, you should take that to mean that there is a syntax error somewhere between the last command the script managed to execute and line n (inclusive).



If the shell is started with the -x option, it prints commands and their arguments as they are executed. You can also get this behaviour by using the set shell builtin command like this:

set -x

Automating repetitive tasks (1)

Imagine I'm working on a program. Every time I change it, I save it, then compile and run it. My editor makes a backup copy of the file, and the compiler produces one or more files that are of no interest to me, as well as the executable that I actually run. At some point I need to clean up these files.

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Different editors tend to backup files in different ways. gedit's backups have the same name as the original file with a ~ added to the end of the name (e.g. the backup of myprog.c would be myprog.c~). Some editors' backups will have the same name as the original file with a .bak added to the end of the name. For the sake of this example, let's suppose I sometimes use different editors as the mood takes me so I want to handle whatever backup files there might be, regardless of which editor(s) I've been using.



Instead of typing out those commands each time I want to do this, I could just put them all together...



...into a very simple shell script. Note that this shell script is just a linear list of the commands I would type at the command line in the order I would type them. Now I can just type:

./cleanup-prog-dir.sh

if I'm in my source directory, or:

~/source/cleanup-prog-dir.sh

if I'm in another directory, instead of all those separate commands. Simple, really.

(After creating the shell script in gedit (or another editor of your choice) remember to save it *and* set the executable bit on the script using chmod before trying to run it.)



Of course, my shell script is very simple, so it gives me errors if I run it more than once, or if some of the files I want to handle don't exist. I can fix some of these errors quite simply:

- If I use the -p option with mkdir, then it won't complain if the backup directory already exists.
- If I use the -f option with rm, then it won't complain if there aren't any .o files.

Unfortunately, there's no correspondingly easy way to deal with mv complaining if there aren't any files ending in ~ or .bak. We need to know more shell scripting to deal with that problem.

Note, though, that it doesn't prevent our shell script from running, it just gives us some annoying error messages when we do run it. So our shell script is still perfectly usable, if not very pretty.

(Remember to save your shell script after making these changes.)



One of the most important improvements I can make to even this simple shell script is to add some documentation, in the form of *comments*, to it.

Any line that starts with the hash character (#) is ignored by the shell. Such lines are called comments, and are used to add notes, explanations, instructions, etc to shell scripts and programs.

This is very important, because I may well have forgotten what this shell script is supposed to do in several months when I come to use it again. If I've put sensible comments in it though, then it is immediately obvious.

This also makes it easier to debug if I've made a mistake: the comment tells me what the shell script is *supposed* to be doing at that point, so if there is a discrepancy between that and what it *actually* does when I run it, then it is clear there's a bug in the script, probably somewhere around that point.

(Remember to save your shell script after adding the comments.)



The iterator program is in your home directory. It is a program written specially for this course, but this is a pretty general task you might want to do with many different programs. Think of iterator as just some program that takes some input on the command line and then produces some output in a file, e.g. a scientific simulation or data analysis program.

Know Your Enemy (1)					
> ./iterator					
Wrong number of argumen	ts!				
4 expected, 0 found.					
Usage: ./iterator Nx Ny	n_iterations epsilon				
> ls hello.sh iterator					
> ./iterator 10 10	0 100 0.1				
x dimension of grid:	10				
y dimension of grid:	10				
Number of iterations:	100				
Epsilon:	0.100000				
Output file:	output.dat				
Iterations took 0.000 seconds					
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The iterator program, which is located in your home directory, takes 4 numeric arguments: 3 positive integers and 1 floating-point number. It always writes its output to a file called output.dat in the current working directory, and also writes some informational messages to the screen, which we'll ignore for now.

Please note that the output of the 1s command may not exactly match what is shown on this slide – in particular, the colours may be slightly different shades and there may be additional files and/or directories shown.



Again, please note that the output of the 1s command may not exactly match what is shown on this slide – in particular, the colours may be slightly different shades and there may be additional files and/or directories shown.

The iterator program is not as well behaved as we might like: every time it runs it creates a file called running in the current directory, and it will not run if this file is already there (because it thinks that means it is already running). Unfortunately, it doesn't remove this file when it has finished running, so we have to do it manually if we want to run it multiple times in the same directory.

Of course, if we run it multiple times in the same directory, we will overwrite any file called output.dat each time. So if we want to keep the output of each run we'll need to rename the output.dat file or copy it to somewhere else before we run the program again.



Your task is to create a simple shell script that does the above task. Basically, you want to run the *iterator* program three times with a different parameter set each time. Note that only the last parameter changes between each run, and that is the parameter we insert into the output file name when we rename it to stop it being overwritten by the next run.

We have gone through everything you need to do this exercise (remember the shell script should be very simple, nothing fancy). You should comment your shell script, preferably as you are writing it, and you should try to avoid it producing errors if you can. (However, the important thing is to produce a shell script that completes the above task, even if it produces some error messages along the way.)

When you've finished this exercise, take a break from the computer – and I do mean "from the computer" – sitting at a computer for too long is bad for you! Don't check your e-mail, get up, stretch, move around, get something to drink.





We create shell variables by simply assigning them a value (as above for the shell variables VAR and VAR1). We can access a the value of a shell variable using the construct \${VARIABLE} where VARIABLE is the name of the shell variable. Note that there are **no** spaces between the name of the variable, the equal sign (=) and the variable's value in double quotes. This is very important as whitespace (spaces, tabs, etc) is significant in the names and values of shell variables.

Also note that although we can assign the value of one shell variable to another shell variable, e.g. VAR1="\${VAR}", the two shell variables are in fact completely separate from each other, i.e. each shell variable can be changed independently of the other. Changing the value of one will not affect the other. VAR1 is *not* a "pointer" to or an "alias" for VAR.



I can use shell variables to store (almost) any values I like, much as I can use variables in a program. I can define my program directory and backup directory in shell variables, and then use those variables in the rest of my shell script wherever I would have previously used the corresponding values. This has the huge advantage that if I want to change the location of my program directory or backup directory, I only need to do it in one place. (Whilst in this shell script I only use the location of my program directory in one place, I use the location of the backup directory in three places, and previously I would have needed to change it in all three places if I decided to store my backups somewhere else.)

Another advantage is, if I am disciplined and define all my important shell variables at the start of my shell script, I know immediately, just by looking at the start of the shell script, what values are important to my shell script. Note that I've used variable names that have some relation to what their values represent rather than generic variable names like VAR1, VAR2, etc. Using sensible variable names can be a huge help in figuring out what the shell script is supposed to do.

(Remember to save your shell script after making the changes above.)



When used with no arguments, the env command displays the *environment variables* (and their values). The environment variables are simply a collection of variables and values that are passed to a program (including the shell and any shell scripts) when the program starts up. Typically they contain information that may be used by the program or that may modify its behaviour. Two environment variables you may have already met are PATH and HOME. PATH specifies which directories the system should search for executable files when you ask it to execute a program and don't give it a path to the executable. HOME is usually set by the system to the location of the user's home directory.

The set shell builtin command (when issued with no arguments) displays all the environment variables, shell variables, various *shell parameters* and any *shell functions* that have been defined. (We'll be meeting shell parameters in context a little later, which should make clear what they are, and shell functions are covered in the "Unix Systems: Shell Scripting (II)" course.). Thus set displays many more variables than the env command.

So many more, in fact, that we probably want to *pipe* its output through the more command. (The more command displays its input on the screen one screenful (page) at a time.) Piping is the process whereby the *output* of one command is given to another command as *input*. We tell the shell to do this using the | symbol. So:

set | more

takes the the output of the set shell builtin command and passes it to the more command, which displays it for us one screen at a time.

Note that the output of env and set may be different from that shown here, and also, since both commands produce so much output, not all of their output is shown on this slide, as is indicated by the three dots on separate lines:



Recall that we create shell variables by simply assigning them a value (as above for the shell variable zzTEMP). A shell variable is **not** the same as an environment variable however, as we can see by searching for the shell variable zzTEMP in the output of the env command. However, we have indeed created a *shell* variable with that name, as we see by examining the output of the set shell builtin command.

The grep command searches for strings of text in other text. In the example above we are using it to search for the text "zzTEMP" in the output of various commands.

The export shell builtin command adds a shell variable to the shell's environment. Once we've done this, we see that if we run the env command we will find the zzTEMP variable. It is has become an *environment variable*.



We can remove a variable from the shell's environment by using the export shell builtin command with the -n option. Note that this does *not* destroy the variable, and it remains a shell variable, but is no longer an environment variable.

Once a shell variable has been added to the shell's environment, it remains an environment variable even if we change its value. Thus we do not have to keep using the export shell builtin command on a variable every time we change its value.

We can also set a shell variable and add it to the shell's environment all in one go using the export shell builtin command, as in the above example with the zzVAR variable.



Shell parameters are special variables set by the shell. Many of them cannot be modified, or cannot be directly modified, by the user or by a shell script. Amongst the most important parameters are the *positional parameters* and the other shell parameters associated with them.

The positional parameters are set to the arguments that were given to the shell script when it was started, with the exception of positional parameter 0, which is set to the name of the shell script. So, if myscript.sh is a shell script, and I ran it by typing:

./myscript.sh argon hydrogen mercury
then positional parameter 0 = ./myscript.sh

1 = argon

2 = hydrogen

3 = mercury

and all the other positional parameters are not set.



The special parameter @ is set to the value of all the positional parameters, starting from the first parameter, passed to the shell script, each value being separated from the previous one by a space. You access the value of this parameter using the construct $\{0\}$. If you access it in double quotes – as in " $\{0\}$ " – then the shell will treat each of the positional parameters as a separate *word* (which is what you normally want).

The special parameter # is set to the number of positional parameters *not counting positional parameter 0*. Thus it is set to the number of arguments passed to the shell script, i.e. the number of arguments on the command line when the shell script was run.



In the examples subdirectory of your home directory there is a script called params.sh. If you run this script with some command line arguments it will illustrate how the shell parameters introduced earlier work. Note that even if you type exactly the command line on the slide above your output will probably be different as the script will be in a different place for each user.

The positional parameter 0 is the name of the shell script (it is the name of the command that was given to execute the shell script).

The positional parameter 1 contains the first argument passed to the shell script, the positional parameter 2 contains the second argument passed and so on.

The special parameter # contains the number of arguments that have been passed to the shell script. The special parameter @ contains all the arguments that have been passed to the shell script.

Using positional parameters

```
#!/bin/bash
# Remove left over running file
rm -f running
# Run iterator with passed arguments
./iterator "${@}"
# Remove left over running file
rm -f running
# Rename output file
mv output.dat "output-${4}.dat"
```

The file run-once.sh in the scripts directory (shown above) accepts some command line arguments and then tries to run the iterator program with them. (Note that it does no checking of the arguments it is given whatsoever.) On the assumption that only the fourth argument will change between runs, it renames the output file to a new name based on that argument. Change to your home directory and try this:

scripts/run-once.sh 100 100 1000 0.05 Do an 1s of your home directory and see what it has produced.

Redirection (>) Redirect output to a file, <i>overwriting</i> file if it exists:	
command > file	
Equivalently:	
command 1>file	
Redirect standard error to a file, <i>overwriting</i> file if it exists:	
command 2>file escience-support@ucs.cam.ac.uk Unix Systems: Shell Scripting (I)	45

The > operator redirects the output from a command to a file, *overwriting* that file if it exists. You place this operator at the end of the command, after all of its arguments. This is equivalent to using 1>filename which means "redirect file descriptor 1 (*standard output*) to the file filename, *overwriting* it if it exists".

Unsurprisingly, 2>filename means "redirect file descriptor 2 (standard error) to the file filename, overwriting it if it exists". And it will probably come as no shock to learn that descriptor>filename means "redirect file descriptor descriptor to the file filename, overwriting it if it exists", where descriptor is the number of a valid file descriptor.

You may think that this "overwriting" behaviour is somewhat undesirable – you can make the shell refuse to overwrite a file that exists, and instead return an error, using the set shell builtin command as follows:

```
set -o noclobber
```

or, equivalently:

set -C

Using redirection

```
#!/bin/bash
# Remove left over running file
rm -f running
# Run iterator with passed arguments
./iterator "${@}" > "stdout-${4}"
# Remove left over running file
rm -f running
# Rename output file
mv output.dat "output-${4}.dat"
```

Modify the file run-once.sh in the scripts directory as shown above (remember to save it when you've finished). Now it captures what the iterator program outputs to the screen (standard output) as well (hurrah!). Change to your home directory and try this:

scripts/run-once.sh 100 100 1000 0.05

Do another ${\tt ls}$ of your home directory and see what it has produced.



The >> operator redirects the output from a command to a file, *appending* it to that file. You place this operator at the end of the command, after all of its arguments. If the file does not exist, it will be created.



Modify the file run-once.sh in the scripts directory as shown above (remember to save it when you've finished). Now every time it runs it stores a record of what it is doing in the file logfile in the current directory. Making your shell scripts keep a record of what they are doing is an extremely good idea, especially if they are going to run for a long time or on a remote machine or when you are not around.

Notice that we have something written to the logfile *before* we start running the iterator program <u>and</u> something *after* it is finished. This means that if the shell script crashes or is stopped before it is finished there is a very good chance we'll be able to tell from the log file as it will not have the "Output file:" or "Standard output:" lines in it. There are better, more sophisticated ways of checking whether things have gone wrong, but this is a nice simple one that is well worth remembering.

Now change to your home directory and try this:

```
scripts/run-once.sh 100 100 1000 0.05
cat logfile
```



We can repeat a set of commands using a for loop. A for loop repeats a set of commands once for each element in a collection of values it has been given. We use a for loop like this:

where <collection of values> is a set of one or more values (strings of characters). Each time the for loop is executed the shell variable VARIABLE is set to the next value in <collection of values>. The two most common ways of specifying this set of values is by putting them in a another shell variable and then using the \${} construct to get its value (note that this should not be in quotation marks), or by using a wildcard (e.g. *) to specify a collection of file names (pathname expansion). <some commands> is a list of one or more commands to be executed.

There are some examples of how to use it in the for.sh in the $\tt examples$ directory of your home directory.

```
Multiple runs
#!/bin/bash
# Parameters that stay the same each run
myFIXED PARAMS="100 100 1000"
# Run iterator program once for each argument
# Note: *no* guotes around ${mvFIXED PARAMS}
#
         or they'll be interpreted as one argument!
for zzARGS in "${@}" ; do
    ~/scripts/run-once.sh ${myFIXED_PARAMS} ${zzARGS}
done
> cđ
> rm -f *.dat stdout-* logfile
> scripts/multi-run.sh 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45 0.5
escience-support@ucs.cam.ac.uk
                             Unix Systems: Shell Scripting (I)
                                                                  50
```

The file multi-run.sh in the scripts directory (shown above) takes one or more command line arguments and then runs the run-once.sh script (which in turn runs the iterator program) with 4 arguments - 3 that are always the same and that are hard-coded into the script, and one of its command line arguments. It does this repeatedly until there are no more of its command line arguments. This script is much more versatile than the script we wrote for the earlier exercise. Modifying that script for each different set of values we might want to run would have rapidly become extremely tedious, whereas we don't need to modify this script at all - we just run it with different arguments.

Note that when we use the value of the shell variable myFIXED_PARAMS we **don't** surround it with quotes – if we did then it would be treated as a single value instead of as 3 separate values (when the shell treats spaces in this way – as a separator between values – it is called *word splitting*).

Give it a try – change to your home directory and type the following commands (the rm command is to remove the files produced by our previous runs of earlier scripts):

```
rm -f *.dat stdout-* logfile
scripts/multi-run.sh 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45 0.5
more logfile
```

And finally do a ls of your home directory and see what files have been produced.



We are specifically using the gnuplot program and the output of the iterator program we've met before. (gnuplot is a program that creates graphs, histograms, etc from numeric data.) Think of this task as basically: I have some data sets and I want to process them all in the same way. My processing might produce graphical output, as here, or it might produce more data in some other format.

If you haven't met gnuplot before, you may wish to look at its WWW page:

http://www.gnuplot.info/



Note that the output of "ls output.png" may look slightly different – in particular, the colours may be slightly different shades.





Your task is to create a shell script that does the above task. Basically, for each of the .dat files we've just produced, you want to run gnuplot on it to create a graph (which will be stored as a .png file). The iterator.gplt file you've been given will only work if the .dat file is called output.dat and is in the current directory. Also, you don't want gnuplot to overwrite each .png file, so you'll need to rename it after gnuplot's created it.

We have gone through everything you need to do this exercise. You should comment your shell script, preferably as you are writing it.

Hint: the best way to do this is with a for loop over all the .dat files in the directory - we haven't used that kind of for loop much yet, but you've seen the syntax for it, and there is an example of that sort of for loop in the for.sh file in the examples directory.