

Similarities and Differences

	Linux/Biocluster	R
Command prompt	\$	>
Where are you1?	Head node/worker node?	If on biocluster, better be worker node!
Where are you2?	Folder in directory structure	Same, but called "working directory"
Spaces	Very important, separate commands/options/arguments	Rarely important, rarely used to separate input
Math symbols	Some have specific meanings, others treated as character	Used as math symbols (don't use dash in names!!)
Commands/functions	First word of new line	Can be anywhere; indicated by ()
Options	Indicated by - or -- right after command name; order doesn't matter	Both are inside () separated by commas; order matters if unnamed
Arguments	After options, order does matter	
#lines per command/function	Must be one; can use \ at end of line to continue on the next	Can be more than one line; no special character needed if function has not been "finished" on previous line
Command 1 output to Command 2 input	Pipe symbol: <code>command1 command2</code>	<code>funct2(funct1())</code> or <code>*funct1() %>% funct2()</code>
Assign results to something instead of printing to screen	<code>command > outfile.txt</code> [written in current folder]	<code>objectName <- function()</code> [written in memory workspace only]
Using scripts	Best for commands that take many minutes/hours/days to run	Can be used, but most functions very quick so interactive working is best
Getting help on commands/functions	<code>man commandName</code> or <code>commandName -h</code>	<code>?functionName</code> or <code>help(functionName)</code>
Loading program/package	<code>module load programName</code>	<code>library(packageName)</code>
How to exit/quit	<code>exit</code>	<code>q()</code>
		* need to load magrittr or tidyverse package first to use <code>%>%</code>

Jenny Drnevich, University of Illinois

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