

Introduction to Bash Scripting

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Computational Molecular Evolution Course
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Overview

- Variables
- Command Line Arguments
- Loops
- Conditions
- Exercises!

Scripts

- Begin with: `#!/bin/bash`
- Make executable via `chmod 775 script.sh`
- Execute via `./script.sh`
- Task: Create a script that prints “Hello World”

Variables

- Store some information
- Assign via `foo="Hello CoME"`
- Read via `$foo` or `${foo}`
- Task: Change the script so that it uses a variable with the text

Command Line Arguments

- Access to how the script was called, e.g.
`./script.sh some arguments`
- Use `$#` for number of arguments
- Use `$@` for all argument contents
- Use `$1` (etc) for single argument content
- Task: Print the number of arguments and the content of the first argument, and on the next line, the full content of the command line arguments

Loops

- Use to repeat a certain thing

- Syntax:

```
for variable in list
do
    ...
done
```

- Task: Loop over all words in the argument content and print them

Loops

- To repeat a certain number of times:
- `for variable in `seq 10`
do
...
done`
- Task: Print all numbers that are divisible by 10, counting from 100 to 0, i.e.,

`100 90 .. 0`

Conditions

- Only execute certain parts of the script
- Use for control flow

- Syntax:

```
if [ "foo" = "foo" ]; then
    echo "it's foo!"
fi
```

- Task: Print `"it's foo!"` if the first command line argument is `"foo"`

Conditions

- Use `else` for the other case

- Syntax:

```
if [ "@1" = "foo" ]; then
    echo "it's foo!"
else
    echo "oohh no"
fi
```

Conditions

- Use special if statements to check file stuff
- File exists: `[-e file]`
- Directory exists: `[-d file]`
- File exists and not empty: `[-s file]`
- `file1` newer than `file2`:
`[file1 -nt file2]`
- Negate expression: `[! -e file]`

Google

Search

Google is |

google is **god**

google is **gold**

google is **your friend**

google is

Task: Write a script

Download “day_2” from
`github.com/lczech/come2017_linux`

- Loop over all `.fasta` files: `for file in ...`
- Get the base name: `name=${file%%.fasta}`
- Move the file to a directory of that name
- Call `mafft` to get `file.aln`
- Call `FastTree` to get `tree.newick`

Task: Write a script

- Take a number as input
- Create that many directories, named like this:
`dir_ + a random number`

(optional: make sure the directory does not yet exists)

- Create a script in each directory that outputs the random number
- Call these scripts from within your main script

IT TOOK A LOT OF WORK, BUT THIS
LATEST LINUX PATCH ENABLES SUPPORT
FOR MACHINES WITH 4,096 CPUs,
UP FROM THE OLD LIMIT OF 1,024.

DO YOU HAVE SUPPORT FOR SMOOTH
FULL-SCREEN FLASH VIDEO YET?

NO, BUT WHO USES *THAT*?

