Advanced Linux and Command Line Tools

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2025-09-20

Advanced text processing, scripting, and system administration

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Learn a lot from Harvard Chan Bioinformatics Core

1 Prerequisites

Before diving into this advanced material, you should be comfortable with:

- Basic Linux commands: ls, cd, pwd, mkdir, cp, mv, rm, cat, head, tail
- File permissions: Understanding chmod and chown
- Text editors: Basic usage of nano or vim
- File system navigation: Understanding directory structure and paths
- Basic shell concepts: Environment variables, command history, tab completion

If you're not familiar with these concepts, please complete the Linux Basics tutorial first.

2 Advanced Text Processing Tools

2.1 grep - Advanced Pattern Matching

grep is one of the most powerful text search tools. Let's explore its advanced features.

2.1.1 Basic grep Usage

```
# Search for a pattern in a file
grep "pattern" file.txt

# Search case-insensitive
grep -i "pattern" file.txt

# Search in multiple files
grep "pattern" *.txt

# Search recursively in directories
grep -r "pattern" directory/
```

2.1.2 Advanced grep Options

```
# Show line numbers
grep -n "pattern" file.txt

# Show context (2 lines before and after)
grep -C 2 "pattern" file.txt

# Show only filenames with matches
grep -l "pattern" *.txt

# Show only lines that DON'T match (invert)
grep -v "pattern" file.txt

# Use regular expressions
grep -E "^[0-9]+" file.txt # Lines starting with numbers

# Count matches
grep -c "pattern" file.txt

# Show only the matching part
grep -o "pattern" file.txt
```

2.1.3 Regular Expressions with grep

```
# Lines starting with specific text
grep "^start" file.txt

# Lines ending with specific text
grep "end$" file.txt

# Lines containing either pattern1 OR pattern2
grep -E "pattern1|pattern2" file.txt

# Lines with exactly 3 digits
grep -E "^[0-9]{3}$" file.txt

# Lines containing word boundaries
grep -w "word" file.txt
```

2.2 awk - Pattern Scanning and Processing

awk is a powerful programming language for text processing. It processes files line by line.

2.2.1 Basic awk Syntax

```
# Print entire lines
awk '{print}' file.txt

# Print specific fields (space-separated by default)
awk '{print $1}' file.txt # First field
awk '{print $2}' file.txt # Second field
awk '{print $1, $3}' file.txt # First and third fields

# Print last field
awk '{print $NF}' file.txt

# Print number of fields in each line
awk '{print NF}' file.txt
```

2.2.2 Advanced awk Examples

```
# Print lines with more than 3 fields
awk 'NF > 3' file.txt

# Print lines where first field equals "name"
awk '$1 == "name"' file.txt

# Print lines where second field is greater than 100
awk '$2 > 100' file.txt

# Add line numbers
awk '{print NR, $0}' file.txt

# Print specific lines (e.g., lines 5-10)
awk 'NR >= 5 && NR <= 10' file.txt

# Calculate sum of second column
awk '{sum += $2} END {print sum}' file.txt

# Print average of second column
awk '{sum += $2; count++} END {print sum/count}' file.txt</pre>
```

2.2.3 awk with Field Separators

```
# Use comma as field separator
awk -F',' '{print $1, $2}' file.csv

# Use multiple separators
awk -F'[,;]' '{print $1, $2}' file.txt

# Use tab as separator
awk -F'\t' '{print $1, $2}' file.tsv
```

2.3 cut - Extract Columns from Files

cut is simpler than awk for basic column extraction.

2.3.1 Basic cut Usage

```
# Extract first column (space-separated)
cut -d' ' -f1 file.txt

# Extract first and third columns
cut -d' ' -f1,3 file.txt

# Extract columns 1-3
cut -d' ' -f1-3 file.txt

# Use comma as delimiter
cut -d',' -f1,2 file.csv

# Use tab as delimiter
cut -d$'\t' -f1,2 file.tsv

# Extract by character positions
cut -c1-10 file.txt # Characters 1-10
cut -c1,5,10 file.txt # Characters 1, 5, and 10
```

2.4 sed - Stream Editor

sed is used for text substitution and editing.

2.4.1 Basic sed Usage

```
# Replace first occurrence of "old" with "new"
sed 's/old/new/' file.txt

# Replace all occurrences of "old" with "new"
sed 's/old/new/g' file.txt

# Replace only on specific lines (e.g., line 5)
sed '5s/old/new/' file.txt

# Delete lines containing "pattern"
sed '/pattern/d' file.txt
```

```
# Delete empty lines
sed '/^$/d' file.txt

# Print only lines 5-10
sed -n '5,10p' file.txt
```

2.4.2 Advanced sed Examples

```
# Replace multiple patterns
sed -e 's/old1/new1/g' -e 's/old2/new2/g' file.txt

# Use different delimiter (useful for paths)
sed 's|/old/path|/new/path|g' file.txt

# Case-insensitive replacement
sed 's/old/new/gi' file.txt

# In-place editing (modify file directly)
sed -i 's/old/new/g' file.txt

# Backup original file
sed -i.bak 's/old/new/g' file.txt
```

2.5 sort - Sort Lines

```
# Sort alphabetically
sort file.txt

# Sort numerically
sort -n file.txt

# Sort in reverse order
sort -r file.txt

# Sort by specific field
sort -k2 file.txt # Sort by second field

# Sort by multiple fields
sort -k1,1 -k2,2n file.txt # Sort by field 1, then by field 2 numerically
```

```
# Remove duplicates while sorting
sort -u file.txt

# Sort ignoring case
sort -f file.txt
```

2.6 uniq - Remove Duplicate Lines

```
# Remove consecutive duplicate lines
uniq file.txt

# Count occurrences of each line
uniq -c file.txt

# Show only unique lines
uniq -u file.txt

# Show only duplicate lines
uniq -d file.txt

# Ignore case when comparing
uniq -i file.txt
```

3 Advanced File Operations

3.1 find - Find Files and Directories

```
# Find files by name
find . -name "*.txt"

# Find files by type
find . -type f # Files only
find . -type d # Directories only

# Find files by size
find . -size +100M # Files larger than 100MB
find . -size -1k # Files smaller than 1KB
```

```
# Find files by modification time
find . -mtime -7  # Modified in last 7 days
find . -mtime +30  # Modified more than 30 days ago

# Find files by permissions
find . -perm 644  # Files with 644 permissions
find . -perm -u+x  # Files executable by owner

# Execute commands on found files
find . -name "*.txt" -exec rm {} \;  # Delete all .txt files
find . -name "*.log" -exec mv {} logs/ \;  # Move .log files to logs directory
```

3.2 xargs - Execute Commands on Multiple Arguments

```
# Find and delete files
find . -name "*.tmp" | xargs rm

# Find and copy files
find . -name "*.txt" | xargs cp -t backup/

# Count lines in multiple files
find . -name "*.txt" | xargs wc -l

# Search in multiple files
find . -name "*.py" | xargs grep "import"
```

4 Shell Scripting Basics

4.1 Creating and Running Scripts

```
# Create a script file
nano my_script.sh

# Make it executable
chmod +x my_script.sh

# Run the script
./my_script.sh
```

4.2 Basic Script Structure

```
#!/bin/bash
# This is a comment

# Set variables
NAME="Linux User"
COUNT=10

# Use variables
echo "Hello, $NAME!"
echo "Count is: $COUNT"

# Use command substitution
CURRENT_DIR=$(pwd)
echo "Current directory: $CURRENT_DIR"

# Use arithmetic
RESULT=$((COUNT * 2))
echo "Double count: $RESULT"
```

4.3 Control Structures

4.3.1 If-Else Statements

```
#!/bin/bash

if [ -f "file.txt" ]; then
    echo "File exists"
else
```

```
echo "File does not exist"
fi

# String comparison
if [ "$1" = "hello" ]; then
    echo "You said hello"
elif [ "$1" = "goodbye" ]; then
    echo "You said goodbye"
else
    echo "You said something else"
fi
```

4.3.2 Loops

```
#!/bin/bash

# For loop
for i in {1..5}; do
    echo "Number: $i"
done

# For loop with files
for file in *.txt; do
    echo "Processing: $file"
done

# While loop
count=1
while [ $count -le 5 ]; do
    echo "Count: $count"
    count=$((count + 1))
done
```

4.4 File Manipulation Scripts

4.4.1 Q1: How to move files to subfolders

I have many files inside a folder. I want to move them into two sub-folders named f1 and f2 (I made them using mkdir -p f1 f2). How to do that?

This is the way:

```
#!/bin/bash
# move_files.sh
# Create subdirectories if they don't exist
mkdir -p f1 f2
# Counter for files
i = 0
# Loop through all .fastq.gz files (sorted by version)
for file in $(ls *.fastq.gz | sort -V); do
    if [ $i -le 400 ]; then
        mv "$file" f1/
        echo "Moved $file to f1/"
    else
        mv "$file" f2/
        echo "Moved $file to f2/"
    fi
    i=\$((i + 1))
done
echo "File moving completed!"
echo "Files in f1: $(ls f1/ | wc -1)"
echo "Files in f2: $(ls f2/ | wc -1)"
```

Here, I am sending fastq.gz files having 0-400 in their name to f1 folder and remaining ones to f2. You just need to use your file naming pattern in the code block, and you are all set. For example, if you have many .fasta files, use .fasta instead of .fastq.gz. You got the idea, right?

How to execute/run this file now? Run these:

```
chmod +x move_files.sh
./move_files.sh
```

chmod +x is making the file named move_files.sh executable. Then we are running it using
./move_files.sh.

5 High Performance Computing (HPC) Basics

5.1 SSH Connection to HPC Clusters

I am going to connect to Uni-Greifswald's Brain cluster.

```
ssh username@brain.uni-greifswald.de
```

You have to use your real username and password. Now, let's get an interactive session to the gpu compute node (it is named "vision" for uni-greifswald's gpu node, check for yours).

```
srun --pty --gres=gpu:1 --partition=vision --mem=16g -t 12:00:00 bash -i
```

So, I am taking the session for 12 hours.

5.2 Environment Management on HPC

5.2.1 Installing Conda on HPC

Let's install conda for our environment management (if you don't have already).

```
# Download the Miniconda installer for Linux
wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh
# Run the installer, specifying the installation path
bash Miniconda3-latest-Linux-x86_64.sh -b -p ~/miniconda_install/
```

Now, let's initialize conda:

```
# Source the conda shell script to make the 'conda' command available
source ~/miniconda_install/bin/activate

# Initialize conda for the current shell session.
conda init bash
```

Since we're using an interactive session, we won't need to manually source anything after this. The conda init command makes it so we can use conda and conda activate as we normally would.

N.B. We could make some aliases for conda commands to write conda codes in shorter format, but we can do/see it later. Get used to the normal ones.

5.3 Advanced Environment Setup

Let's make an environment and install our required tools there. Well, our goal is to make a system where we will use some images/characters and make short videos using them to teach Italian. We need to process photos, images, text, and sync lips (video) with audio/speech. We need MuseTalk for this. Let's configure our environment accordingly.

Step 1 – Create conda environment

```
# Create new environment for MuseTalk
conda create -n musetalk python=3.10
conda activate musetalk
```

Step 2 – Install Dependencies

```
# Install PyTorch (adapt cuda version to your cluster, here CUDA 11.8 example)
pip install torch==2.1.0 torchvision==0.16.0 torchaudio==2.1.0 --extra-index-url https://d
# HuggingFace core libs
pip install transformers accelerate diffusers safetensors

# MuseTalk repo (clone)
git clone https://github.com/TMElyralab/MuseTalk.git
cd MuseTalk

# Install requirements
pip install -r requirements.txt

# Install whisper encoder
pip install --editable ./musetalk/whisper

# Extra: ffmpeg for video processing
conda install -c conda-forge ffmpeg -y
```

Step 3 – Download MuseTalk Models

MuseTalk Hugging Face repo: https://huggingface.co/TMElyralab/MuseTalk We need: -musetalk.pth (main model) - gfpgan (optional face enhancer)

Run inside MuseTalk:

```
mkdir checkpoints cd checkpoints
```

```
# Download core model
wget https://huggingface.co/TMElyralab/MuseTalk/resolve/main/musetalk.pth
# Optional face enhancer
git clone https://github.com/TencentARC/GFPGAN.git
cd ..
```

5.4 CUDA Environment Configuration

5.4.1 Better way:

```
export CUDA_HOME=/usr/local/cuda-11.7
export PATH=$CUDA_HOME/bin:$PATH
export LD_LIBRARY_PATH=$CUDA_HOME/lib64:$LD_LIBRARY_PATH
```

In my HPC Cluster, it is cuda 11.7. I am configuring for that. We could add these lines in my ~/.bashrc file as well. We might see it later.

Let's load our cuda module first to get things done smoothly.

```
module load cuda/11.7
```

Now, make the yml file to make the environment with all the tools required.

```
name: musetalk3
channels:
  - pytorch
  - nvidia
  - defaults
dependencies:
  - python=3.10
  - pip
  - ffmpeg
  - pip:
      # PyTorch + CUDA 11.8 compatible with 11.7 system
      - torch==2.1.0+cu118
      - torchvision==0.16.0+cu118
      - torchaudio==2.1.0+cu118
      - --extra-index-url https://download.pytorch.org/whl/cu118
      # OpenMMLab dependencies
```

```
- mmcv==2.0.1 -f https://download.openmmlab.com/mmcv/dist/cu118/torch2.1.0/index.htm
- mmdet==3.1.0
- gradio
- opencv-python
- numpy
- scipy
- matplotlib
- tqdm
- pyyaml
- pillow
- soundfile
- librosa
- moviepy
- imageio
```

Save this as musetalk3.yml and run:

```
conda env create -f musetalk3.yml
conda activate musetalk3
```

Now, we have our environment ready to use. Let's use it.

```
conda activate musetalk3
```

Now, install museetalk repo dependencies.

```
git clone https://github.com/TMElyralab/MuseTalk.git
cd MuseTalk
pip install -r requirements.txt
```

Let's get the faces I want to use. I uploaded them to my Google Drive.

```
pip install gdown

# Get shareable link from Google Drive and copy file id
gdown https://drive.google.com/uc?id=FILE_ID -0 data/faces/alice.jpg
gdown https://drive.google.com/uc?id=FILE_ID -0 data/faces/bob.jpg
```

Modify the google drive links for the images and their destination name as you like it.

5.4.2 Real work

Now, let's follow the author's guideline.

```
pip install --no-cache-dir -U openmim
mim install mmengine
mim install "mmcv==2.0.1"
mim install "mmdet==3.1.0"
mim install "mmpose==1.1.0"
```

Let's download the model's weight.

```
sh ./download_weights.sh

# Check ffmpeg installation
ffmpeg -version
```

The conversation