Setting Up and Understanding Linux & WSL for Bioinformatics

1. Introduction to Linux & WSL

Linux is an open-source Unix-like operating system widely used in bioinformatics due to its efficiency, modularity, and compatibility with most bioinformatics tools. For Windows users, Windows Subsystem for Linux (WSL) allows running a full Linux environment without leaving Windows.

2. How to Set Up WSL (Windows Subsystem for Linux) Follow

these steps to install Linux on your Windows machine using WSL:

1. Enable WSL via 'Turn Windows Features On or Off'. Check 'Windows Subsystem Linux' Also check ' Hypervisor Platform', 'Virtual Machine Platform'
2. Restart your computer.
3. Install Ubuntu (e.g., Ubuntu 22.04 LTS or Ubuntu 20.04 LTS) from the Microsoft Store. OR Open Windows Powershell and type the command `wsl --install`
4. Open Ubuntu from the Start menu. Run as administrator.
5. Set default version using: wsl --set-default-version
6. Visit https://aka.ms/wsl2kernel to update your WSL kernel if

3. Linux Environment Overview

Linux is known for its directory structure starting from the root directory (/), support for multiple shells (Bash, Zsh), permission management, and command-line interface. You interact with Linux using a terminal.

4. Key Linux Terms to Understand

Terminal: A text-based interface to interact with the operating

system. Shell: A command-line interpreter that executes user

commands. Bash: The most commonly used shell in Linux systems.

File System: Linux uses a hierarchical structure starting from '/'

Command Line Interface (CLI): Allows you to control the system using text

commands. Home Directory: Default directory for a user's files.

sudo: Command to perform tasks requiring administrator (root)

chmod: Changes file or directory permissions.

chown: Changes file ownership.

cd: Change directory.

ls: List contents of a directory.

cp: Copy files or directories.

mv: Move or rename files or directories.

rm: Remove files or directories.

pwd: Print current working directory.

5. Typical Linux Workflow in Bioinformatics Projects

- **Install Linux via WSL or**
- **Use terminal to navigate directories and manage**
- **Install tools (e.g., bedtools, samtools) using package managers like conda, apt, pip.**
- **Use Bash scripting to automate preprocessing, alignment, and variant calling.**
- **Interact with bioinformatics files (.fastq, .bam, .vcf) using command-line tools.**
- **Version control your scripts with Git and manage environments using Conda.**
- **Run analyses and visualize outputs using Python, R, or tools like FastQC and IGV.**