

Unix Shell - Introduction

About the Instructor







About the Instructor

- Researcher at the <u>Advanced Institute for Artificial</u> <u>Intelligence</u>;
- Associate Researcher at the <u>São Paulo State University UNESP</u>;
- Member of the <u>SPRACE project</u> (a <u>CMS LHC collaboration</u>);
- Chair of the CODATA-RDA Data School groups since 2018;
- RDA Technical Advisory Board since 2022;
- Background on Artificial Intelligence and High Performance Computing;



Background

- Human Computer Interaction
- Graphical User Interface GUI
 - (Personal Computers);
 - Heavy use of the Mouse;
 - "Menu-driven interactions";
 - Very intuitive to learn;
 - Scales very poorly;



Background (continued)

Imagine the following task:

For a literature search, you have to:

- 1. copy the third line
- 2. of one thousand text files
- 3. in one thousand different directories and
- 4. paste it into a single file



Background (continued)

One thing we know for sure:





The Shell

- Both a command-line interface (CLI) and a scripting language;
- Allowing repetitive tasks to be done automatically... and fast;
- Bourne Again SHell BASH
 - Default shell on most modern implementations of Unix;
- Maybe not as easy as the GUI \(\sigma\);
- Easiest way to interact with supercomputers



The Shell (continued)

- Essential to use a variety of specialized tools and resources including high-performance computing systems;
 - Clusters, clouds, etc.
- Need to learn a few commands;
 - Like a vocabulary of a new language;
 - A small number of "words" gets you a long way;
- Let's get started!



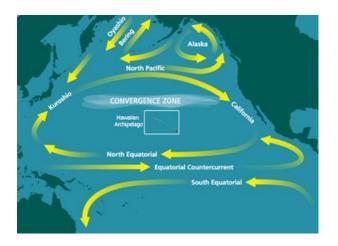
SW Carpentry Materials on Bash

- Setup
- Working with Files and Directories
- Working with Pipes and Filters
- For Loops
- Shell Scripts
- File Permissions
- Job Control

Nelle's Pipeline: A Typical Problem



- Example that we will use throughout the lessons;
- Six-month survey data containing samples of gelatinous marine life in the <u>Great Pacific Garbage Patch</u>;



Nelle's Pipeline: A Typical Problem (continued)



- ▶ 1520 samples;
- Measure the relative abundance of 300 proteins;
- Perform the analysis using imaginary program called goostats.sh (GUI);
 - Select and open a file 1520 times;
 - 30 seconds to run each file;
 - More than 12 hours of Nelle's attention
- Assign a computer this task while she focuses on writing a paper about this results;