## Research Computing at Mines Workshop Serial and Parallel Computing

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# **Recap of Day 1**

- Overview of the world of Cyberinfrastructure & Research Computing
- HPC options for Mines Researchers
- Overview of skills needed to be a successful researcher on HPC
  - Linux/Bash
  - Slurm/Job Scheduler
  - Parallel Computing
  - Computational Notebook Practices
- Intro to Linux/Bash Lab
- Overview of Job Schedulers, SLURM and Python
- Intro to Slurm & Python Lab

# **Goals for Day 2**

- Overview of Serial vs Parallel Computing
- A case study using a Python serial code (Lab)
- Parallel Programming Overview
  - Shared vs Distributed Memory
  - MPI
  - OpenMP
- Lab on using parallelized software: GROMACS

# **HPC Resource Usage**

- How do I use them?
  - Most programs spawn 1 process ("task" in Slurm) and use one thread ("cpu" in Slurm)
    - On a desktop, some programs can see how many CPU cores you have and request that many threads for the process and use them
      - Examples: Some MATLAB functions, Games using DX12, Chrome/Firefox
  - Slurm does not know how your program will use the resources you give it
    - If you give it 12 cores ("cpus") but program only works with 1 core, those 11 cores will idle and do nothing
  - To think about how to utilize HPC resources, we need to learn how **parallel programming/processing** is implemented.

# **Serial vs Parallel Computing**

- When a program uses a single process ("task") with 1 core ("cpu"), we say it is a **serial computing** program.
- When a program uses multiple cores, we say it is a **parallel computing** program.
- Before thinking about parallel computing, we need to focus on how well the program performs with serial computing.

## **Note: Optimization before Parallelization!**

- "Premature optimization is the root of all evil" Donald Knuth
- Often, writing your code to run as fast as possible (*within reason*) with a single core is necessary before thinking about parallelization.
- We will explore optimization with a simple Python code for a single core next!

# How to profile Python code

### cProfile

- Gives you a breakdown of all functions' runtime in a code
- Multiple ways to use it:
  - Call it in the command line:
    - \$ python -m cProfile myscript.py
  - Call it in another script:

import cProfile

cProfile.run("mycode.main()")

• Other options: lineprofiler, timeit, pstats

References: <u>https://towardsdatascience.com/how-to-profile-your-code-in-python-e70c834fad89</u> <u>https://github.com/pyutils/line\_profiler</u>

# A starting point for optimization: Writing an ODE solver

Consider the initial value problem of the form:

$$y'(t) = f(t, y)$$
$$y(t_0) = y_0$$

which can numerically solved using Heun's Method:

$$\hat{y}^{[i+1]} = y^{[i]} + h f(t^{[i]}, y^{[i]})$$
$$y^{[i+1]} = y^{[i]} + \frac{h}{2} \left( f(t^{[i]}, y^{[i]}) + f(t^{[i+1]}, \hat{y}^{[i+1]}) \right)$$

Where *h* is the time step size, *i* is the time step index, and  $\hat{y}$  denotes the intermediate solution. Let's use this problem to see how to optimize writing scientific code for Python!

# Lab #1: Serial Python Optimization

Copy the workshop materials using the following command:

cp /sw/BUILD/src/workshop/Workshop\_Fall2024\_day2.tar.gz ~/scratch And go to that directory and untar it:

cd ~/scratch && tar -xf Workshop\_Fall2024\_day2.tar.gz

cd Workshop\_Fall2024/rk2\_python && ls

Using Open OnDemand Interface

Go To: <u>https://wendian-ondemand.mines.edu</u>

# Lab #1 Summary: Profiling multiple versions of our ODE code

- Pure Python
  - Surprisingly Performant!
- NumPy only
  - Performs poorly due to lack of vectorization
- NumPy + Cython
  - <u>https://cython.org/</u>
  - Cython effectively allows one to write static-typed code in Python/"Cython", which is parsed into C and compiled into a Python module.

#### Shared Memory Parallelism: 1 task, 4 threads

## **Parallel Programming**

- Shared vs Distributed Memory Programming
  - Shared (e.g. OpenMP)
    - All CPU cores have access to the same pool of memory
    - Typically, all CPU cores are on the same CPU node
    - Ideal for multi-threaded loops
  - Distributed-memory program (e.g. MPI)
    - Éach CPU core is given access to a specific pool of memory, which may or may not be shared
    - A "communicator" designates how each CPU core can talk to another CPU core
    - CPU cores do not have to live on the same CPU node



#### Distributed Memory Parallelism: 4 tasks, 1 thread per task



## **Shared Memory Parallelism: OpenMP**

- OpenMP is a portable, high-level API that is used to write multithreaded applications
  - It provides a set of directives that can be used to parallelize loops, regions of code, and entire functions.
  - Supported by a wide range of compilers and hardware platforms (e.g. C/C++, Fortran, Python, etc)
  - For loops typically a compiler directive is added before a loop to tell the compiler that OpenMP is being used:
    - *#pragma omp parallel*
  - The environment variable OMP\_NUM\_TASKS will tell the operating system how many OpenMP threads to use in the program.

# A note on Python and the GIL: A constraint on shared memory programming

- Python Global Interpreter Lock (GIL)
  - A mechanism with Python which allows only one CPU thread to use the Python interpreter
  - The GIL addressed the problem of memory management for Python programs.
  - Releasing the GIL can cause memory leaks if not managed correctly.
- Solutions:
  - Use multiprocessing instead of multithreading
    - Each process gets its own Python interpreter and memory space
    - Module options: mpi4py, multiprocessing
  - Use a different interpreter
  - Use Cython to release the GIL to allow multithreading within subroutines

Reference: <u>https://realpython.com/python-gil/</u>

## **Distributed Memory Parallelism: MPI**

- MPI stands for **m**essage-**p**assing **i**nterface, standard provided as a library for exchanging data (called messages) between objects.
- Different libraries have implemented the MPI standard:
  - OpenMPI
  - MPICH
  - Intel MPI
- Objects that can be used to send messages are separated by memory
  - Can be entire CPU nodes, or CPU cores, called *ranks*.
  - By breaking up by memory of each tasks, a rank can send messages theoretically anywhere as long as there is another layer of network communication
    - MPI most commonly uses Infiniband for node-to-node communication
    - Intra-node communication uses CPU architecture

## **Distributed Memory Parallelism: MPI**

- It provides a set of functions for sending and receiving messages, as well as for synchronizing the execution of different processes. Common functions:
  - Send a message from one rank to another: MPI\_SEND
  - Receive a message from a rank: MPI\_RECV
  - Broadcast the same message to all ranks from a particular rank: MPI\_BCAST
  - Take a message from multiple ranks to a single rank: MPI\_GATHER
  - Block messages from continuing until all ranks have finished: MPI\_BARRIER

## **Choosing between Shared vs Distributed Memory Parallelism**

- Shared Memory Parallel is ideal for:
  - Single computer/node workloads
  - Speeding up for-loops
    - By splitting up the work across loop iterations
- Distributed Memory Parallel works best for
  - Large memory workloads that require multiple compute nodes
- Shared and distributed memory parallel programming can sometimes be combined
  - Called hybrid parallel programming
    - Combining MPI and OpenMP

## Summary of useful Slurm commands

- sbatch <job\_script\_filename> submit job
- salloc -n1 submit an interactive job with 1 task
- squeue View job queue
- squeue --me View job queue for your jobs
- sacct –j <jobid> Get info on a particular job ID
- sinfo Show info on nodes
- scontrol show node <name> show info on a particular node
- scancel \$JOBID Cancel a specific job
- scancel --me Cancel all your current jobs

## **GPU: Further Accelerate computational workloads**

- Use graphical processing units (GPUs)
  - NVIDIA
    - The CUDA library is by far the most popular GPU computing language
      - Provides an API to use NVIDIA CUDA codes
    - Popular CUDA uses:
      - AI/ML: PyTorch, Tensorflow
      - Molecular Dynamics: LAMMPS, GROMACS
      - Scientific Visualization: Paraview
  - OpenCL
    - Open source alternative to CUDA
    - Works on AMD, NVIDIA, and Intel GPUs
  - HIP (Heterogeneous-Compute Interface)
    - GPU acceleration library developed by AMD

## **Limitations to GPUs**

- Hardware is more expensive and less widely available
  Also true if paying for time on cloud compute (e.g. AWS)
- Programming for GPUs requires more setup
  - Programs like GROMACS support this for some physical solvers
- Not all workloads can be easily ported to GPUs

## **Final Takeaways**

- When developing your own scientific programs, get the serial case working as efficiently as possible (within time constraints)
  - Try different libraries, compiler options, etc.
  - Run benchmarks to compare setups
- When jumping to parallel programming
  - Understand the differences between shared and distributed memory parallel programming
  - Leverage established libraries to implement parallel programming methods
  - Use software with these libraries already in use (e.g. GROMACS)

## Lab #2: Running Parallel Code: GROMACS

And exploration of SLURM commands

## **Further Resources**

Python Parallel Processing: <u>https://wiki.python.org/moin/ParallelProcessing</u>

Parallel Programming with MPI for Python:

<u>https://rabernat.github.io/research\_computing/parallel-programming-</u> with-mpi-for-python.html

Intro to F2Py:

<u>https://www2.atmos.umd.edu/~dkleist/docs/pythonTraining/Slides/F2</u> <u>Py\_SSSO.pdf</u>

OpenMPI: <u>Open MPI: Open Source High Performance Computing</u> (open-mpi.org)

OpenMP: <u>Specifications – OpenMP</u>

NVIDIA CUDA Toolkit: <u>CUDA Toolkit - Free Tools and Training | NVIDIA</u> <u>Developer</u>