Final Exam (part 3) - Computational Physics 2

Deadline: Friday 6 June 2025 (by 23h59) 10/10

Credits: 10 points Good work.

Please keep the structure provided below and submit an organised notebook with clear answers to each item.

3. MPI Parallelisation of Molecular Dynamics Simulations

In this problem, you will use **Message Passing Interface (MPI)** library to parallelise the execution of molecular dynamics simulations for different temperatures. The goal is to distribute the simulation of various temperatures across multiple MPI processes, significantly reducing the overall computational time.

Code:

The reference (serial) script can be found here:

https://github.com/wbandabarragan/computational-physics-2/blob/main/exams/thermostat.py

You should only modify the code below the indicated line:

Your MPI parallelization code should start here. Do not modify the code above.

The core simulation logic within the run function should remain untouched.

Tasks:

Use the provided script (thermostat.py) to create a new version of the script (thermostat_mpi.py) that uses the mpi4py library to parallelise the simulation execution. Here are the specific requirements for your MPI implementation:

- (a) Set up a world communicator to distribute tasks among processes. Determine the rank of each process and the total number of processes.
- **(b)** Distribute a range of temperatures among the available MPI processes. Each process should be responsible for running the simulation at one or more unique temperatures.

- **(c)** Ensure proper initialization and finalization of the MPI environment. Cores should also send completion signals.
- (d) The root/master process (rank 0) should handle workload communications and collect the simulation results from all other processes.
- **(e)** For each simulated temperature, generate the temperature—N_atoms.png plot and the traj-hydrogen-3D-N_atoms.dump file. In addition the root/master process should:
 - Collect and present the combined results (i.e., a single plot with all the temperature curves).
 - Save the total execution time and the number of CPU cores used to a CSV file (mpi_scaling.csv).
- (f) Run the script with mpirun and different number of processors in an HPC facility.

Scaling and analysis:

Report the simulation results (temperature plots and scaling) in this notebook:

- (g) After running the MPI code for various numbers of CPU cores (e.g., 1, 2, 4, 8, 16, etc.), use the data accumulated in the CSV file (mpi_scaling.csv) from multiple runs to:
 - Plot the observed speedup (e.g., $S_p=T_1/T_p$, where T_1 is the execution time on 1 CPU and T_p is the execution time on p CPUs) as a function of the number of CPU cores.
 - Compare your observed speedup to Amdahl's Law and discuss any discrepancies between the observed and theoretical speedup.

```
In []: # !/usr/bin/python
"""

A molecular dynamics solver that simulates the motion of non-interacting par
in the canonical ensemble using a Langevin thermostat.
Reference: https://github.com/Comp-science-engineering/Tutorials/tree/master
"""
import time
import numpy as np
import matplotlib.pyplot as plt

# Define global physical constants
from scipy.constants import Avogadro, Boltzmann

def wallHitCheck(pos, vels, box):
    """ This function enforces reflective boundary conditions.
```

```
All particles that hit a wall have their velocity updated
    in the opposite direction.
   @pos: atomic positions (ndarray)
   @vels: atomic velocity (ndarray, updated if collisions detected)
   @box: simulation box size (tuple)
   ndims = len(box)
   for i in range(ndims):
       vels[((pos[:,i] \le box[i][0]) | (pos[:,i] \ge box[i][1])),i] *= -1
def integrate(pos, vels, forces, mass, dt):
   """ A simple forward Euler integrator that moves the system in time
   @pos: atomic positions (ndarray, updated)
   @vels: atomic velocity (ndarray, updated)
   pos += vels * dt
   vels += forces * dt / mass[np.newaxis].T
def computeForce(mass, vels, temp, relax, dt):
   """ Computes the Langevin force for all particles
   @mass: particle mass (ndarray)
   @vels: particle velocities (ndarray)
   @temp: temperature (float)
   @relax: thermostat constant (float)
   @dt: simulation timestep (float)
   returns forces (ndarray)
   1111111
   natoms, ndims = vels.shape
   sigma = np.sgrt(2.0 * mass * temp * Boltzmann / (relax * dt))
   noise = np.random.randn(natoms, ndims) * sigma[np.newaxis].T
   force = - (vels * mass[np.newaxis].T) / relax + noise
    return force
def run(**args):
   """ This is the main function that solves Langevin's equations for
   a system of natoms usinga forward Euler scheme, and returns an output
   list that stores the time and the temperture.
   @natoms (int): number of particles
   @temp (float): temperature (in Kelvin)
   @mass (float): particle mass (in Kg)
   @relax (float): relaxation constant (in seconds)
   @dt (float): simulation timestep (s)
   @nsteps (int): total number of steps the solver performs
   @box (tuple): simulation box size (in meters) of size dimensions x 2
   e.g. box = ((-1e-9, 1e-9), (-1e-9, 1e-9)) defines a 2D square
   @ofname (string): filename to write output to
   @freq (int): write output every 'freq' steps
   @[radius]: particle radius (for visualization)
   Returns a list (of size nsteps x 2) containing the time and temperature.
    .....
```

```
natoms, box, dt, temp = args['natoms'], args['box'], args['dt'], args['t
   mass, relax, nsteps = args['mass'], args['relax'], args['steps']
   ofname, freq, radius = args['ofname'], args['freq'], args['radius']
   dim = len(box)
   pos = np.random.rand(natoms,dim)
   for i in range(dim):
       pos[:,i] = box[i][0] + (box[i][1] - box[i][0]) * pos[:,i]
   vels = np.random.rand(natoms,dim)
   mass = np.ones(natoms) * mass / Avogadro
   radius = np.ones(natoms) * radius
   step = 0
   output = []
   while step <= nsteps:</pre>
       step += 1
       # Compute all forces
       forces = computeForce(mass, vels, temp, relax, dt)
       # Move the system in time
       integrate(pos, vels, forces, mass, dt)
       # Check if any particle has collided with the wall
       wallHitCheck(pos, vels, box)
       # Compute output (temperature)
       output.append([step * dt, ins_temp])
       if not step%freq:
           #dump.writeOutput(ofname, natoms, step, box, radius=radius, pos=
           writeOutput(ofname, natoms, step, box, radius=radius, pos=pos, v
   return np.array(output)
def writeOutput(filename, natoms, timestep, box, **data):
   """ Writes the output (in dump format) """
   axis = ('x', 'y', 'z')
   with open(filename, 'a') as fp:
       fp.write('ITEM: TIMESTEP\n')
       fp.write('{}\n'.format(timestep))
       fp.write('ITEM: NUMBER OF ATOMS\n')
       fp.write('{}\n'.format(natoms))
       fp.write('ITEM: BOX BOUNDS' + ' f' * len(box) + '\n')
       for box bounds in box:
           fp.write('{} {}\n'.format(*box_bounds))
```

```
for i in range(len(axis) - len(box)):
                fp.write('0 0\n')
            keys = list(data.keys())
            for key in keys:
                isMatrix = len(data[key].shape) > 1
                if isMatrix:
                    _, nCols = data[key].shape
                    for i in range(nCols):
                        if key == 'pos':
                            data['{}'.format(axis[i])] = data[key][:,i]
                        else:
                            data['{}_{}'.format(key,axis[i])] = data[key][:,i]
                    del data[key]
            keys = data.keys()
            fp.write('ITEM: ATOMS' + (' {}' * len(data)).format(*data) + '\n')
            output = []
            for key in keys:
                output = np.hstack((output, data[key]))
            if len(output):
                np.savetxt(fp, output.reshape((natoms, len(data)), order='F'))
    # Your MPI parallelization code should start here. Do not modify the code at
    import time
    import numpy as np
    import matplotlib.pyplot as plt
    from scipy.constants import Avogadro, Boltzmann
    import os
    import csv
    from mpi4py import MPI
    from thermostat import run
    # MPI setup
   comm = MPI.COMM_WORLD
    rank = comm.Get_rank()
    size = comm.Get_size()
temperatures = [250, 275, 300, 325, 350, 375, 400, 425, 450, 475]
    N_atoms = 1000
    # Base simulation parameters
    base_params = {
        'natoms': N atoms,
```

```
'mass': 0.001,
    'radius': 120e-12,
    'relax': 1e-13,
    'dt': 1e-15,
    'steps': 10000,
    'freq': 100,
    'box': ((0, 1e-8), (0, 1e-8), (0, 1e-8)),
def write_scaling_csv(filename, cores, exec_time):
    header = ['n_cores', 'execution_time']
    file_exists = os.path.isfile(filename)
    with open(filename, 'a', newline='') as f:
        writer = csv.writer(f)
        if not file exists:
            writer.writerow(header)
        writer.writerow([cores, exec_time])
if __name__ == "__main__":
    # Start timing
    start_time = time.time()
    # Distribute temperatures evenly among processes
    local_temps = [temp for i, temp in enumerate(temperatures) if i % size =
    local_results = []
    for temp in local_temps:
        print(f"Process {rank}: Simulating temperature {temp}K")
        params = base_params.copy()
        params['temp'] = temp
        params['ofname'] = f'traj-hydrogen-3D-{N_atoms}-{temp}K.dump'
        output = run(**params)
        # Save individual plot
        plt.figure(figsize=(6, 5))
        plt.plot(output[:, 0] * 1e12, output[:, 1])
        plt.xlabel('Time (ps)')
        plt.ylabel('Temperature (K)')
        plt.title(f'Temperature Evolution at {temp}K')
        plt.tight_layout()
        plt.savefig(f'temperature-{N_atoms}-{temp}K.png')
        plt.close()
        local_results.append((temp, output))
    # Gather results at root
    all_results = comm.gather(local_results, root=0)
    # Root process handles aggregation
    if rank == 0:
        combined_results = []
        for proc_data in all_results:
            combined_results.extend(proc_data)
```

```
# Sort by temperature
    combined_results.sort(key=lambda x: x[0])
    # Plot all temperature curves
    plt.figure(figsize=(10, 7))
    for temp, output in combined results:
        plt.plot(output[:, 0] * 1e12, output[:, 1], label=f'{temp}K')
    plt.xlabel('Time (ps)')
    plt.ylabel('Temperature (K)')
    plt.title(f'Temperature Evolution for All Simulations ({N_atoms} atd
    plt.legend()
    plt.grid(True, alpha=0.3)
    plt.tight layout()
    plt.savefig(f'combined-temperature-{N atoms}.png', dpi=300)
    plt.close()
    # Compute and store total execution time
    exec time = time.time() - start time
    print(f"Total execution time using {size} cores: {exec_time:.2f} sed
    write_scaling_csv('mpi_scaling.csv', size, exec_time)
# Finalize MPI (optional, usually implicit)
MPI.Finalize()
```

```
Process 0: Simulating temperature 250K
Process 0: Simulating temperature 275K
Process 0: Simulating temperature 300K
Process 0: Simulating temperature 325K
Process 0: Simulating temperature 350K
Process 0: Simulating temperature 375K
Process 0: Simulating temperature 400K
Process 0: Simulating temperature 425K
Process 0: Simulating temperature 450K
Process 0: Simulating temperature 475K
Total execution time using 1 cores: 21.63 seconds
```

This Next code is for running a mpi paralelization work in my own pc

```
In []: %%bash
    mpirun -n 8 python -c "
    import time
    import numpy as np
    import matplotlib.pyplot as plt
    from scipy.constants import Avogadro, Boltzmann
    import os
    import csv
    from mpi4py import MPI

    # !/usr/bin/python
    """
    A molecular dynamics solver that simulates the motion of non-interacting par
    in the canonical ensemble using a Langevin thermostat.
    Reference: https://github.com/Comp-science-engineering/Tutorials/tree/master"""
```

```
import time
import numpy as np
import matplotlib.pyplot as plt
# Define global physical constants
from scipy.constants import Avogadro, Boltzmann
def wallHitCheck(pos, vels, box):
   """ This function enforces reflective boundary conditions.
   All particles that hit a wall have their velocity updated
   in the opposite direction.
   @pos: atomic positions (ndarray)
   @vels: atomic velocity (ndarray, updated if collisions detected)
   @box: simulation box size (tuple)
   ndims = len(box)
   for i in range(ndims):
        vels[((pos[:,i] \le box[i][0]) | (pos[:,i] \ge box[i][1])),i] *= -1
def integrate(pos, vels, forces, mass, dt):
   """ A simple forward Euler integrator that moves the system in time
   @pos: atomic positions (ndarray, updated)
   @vels: atomic velocity (ndarray, updated)
   pos += vels * dt
   vels += forces * dt / mass[np.newaxis].T
def computeForce(mass, vels, temp, relax, dt):
   """ Computes the Langevin force for all particles
   @mass: particle mass (ndarray)
   @vels: particle velocities (ndarray)
   @temp: temperature (float)
   @relax: thermostat constant (float)
   @dt: simulation timestep (float)
   returns forces (ndarray)
   natoms, ndims = vels.shape
   sigma = np.sqrt(2.0 * mass * temp * Boltzmann / (relax * dt))
   noise = np.random.randn(natoms, ndims) * sigma[np.newaxis].T
   force = - (vels * mass[np.newaxis].T) / relax + noise
    return force
def run(**args):
   """ This is the main function that solves Langevin's equations for
   a system of natoms usinga forward Euler scheme, and returns an output
   list that stores the time and the temperture.
   @natoms (int): number of particles
   @temp (float): temperature (in Kelvin)
   @mass (float): particle mass (in Kg)
   @relax (float): relaxation constant (in seconds)
   @dt (float): simulation timestep (s)
   @nsteps (int): total number of steps the solver performs
```

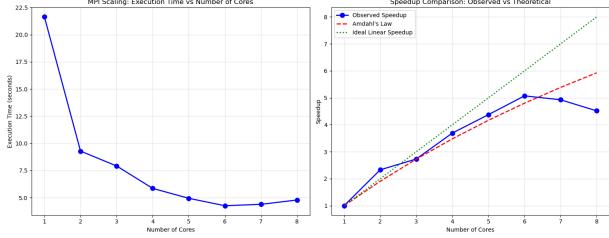
```
@box (tuple): simulation box size (in meters) of size dimensions x 2
   e.g. box = ((-1e-9, 1e-9), (-1e-9, 1e-9)) defines a 2D square
   @ofname (string): filename to write output to
   @freq (int): write output every 'freq' steps
   @[radius]: particle radius (for visualization)
   Returns a list (of size nsteps x 2) containing the time and temperature.
   0.000
   natoms, box, dt, temp = args['natoms'], args['box'], args['dt'], args['t
   mass, relax, nsteps = args['mass'], args['relax'], args['steps']
   ofname, freq, radius = args['ofname'], args['freq'], args['radius']
   dim = len(box)
   pos = np.random.rand(natoms,dim)
   for i in range(dim):
        pos[:,i] = box[i][0] + (box[i][1] - box[i][0]) * pos[:,i]
   vels = np.random.rand(natoms,dim)
   mass = np.ones(natoms) * mass / Avogadro
   radius = np.ones(natoms) * radius
   step = 0
   output = []
   while step <= nsteps:</pre>
       step += 1
       # Compute all forces
       forces = computeForce(mass, vels, temp, relax, dt)
       # Move the system in time
       integrate(pos, vels, forces, mass, dt)
       # Check if any particle has collided with the wall
       wallHitCheck(pos,vels,box)
       # Compute output (temperature)
        ins_temp = np.sum(np.dot(mass, (vels - vels.mean(axis=0))**2)) / (Bd
       output.append([step * dt, ins_temp])
        if not step%freq:
           #dump.writeOutput(ofname, natoms, step, box, radius=radius, pos=
            writeOutput(ofname, natoms, step, box, radius=radius, pos=pos, v
    return np.array(output)
def writeOutput(filename, natoms, timestep, box, **data):
   """ Writes the output (in dump format) """
   axis = ('x', 'y', 'z')
   with open(filename, 'a') as fp:
```

```
fp.write('ITEM: TIMESTEP\n')
        fp.write('{}\n'.format(timestep))
        fp.write('ITEM: NUMBER OF ATOMS\n')
        fp.write('{}\n'.format(natoms))
        fp.write('ITEM: BOX BOUNDS' + ' f' * len(box) + '\n')
        for box_bounds in box:
            fp.write('{} {}\n'.format(*box_bounds))
        for i in range(len(axis) - len(box)):
            fp.write('0 0\n')
        keys = list(data.keys())
        for key in keys:
            isMatrix = len(data[key].shape) > 1
            if isMatrix:
                _, nCols = data[key].shape
                for i in range(nCols):
                    if key == 'pos':
                        data['{}'.format(axis[i])] = data[key][:,i]
                    else:
                        data['{}_{{}}'.format(key,axis[i])] = data[key][:,i]
                del data[key]
        keys = data.keys()
        fp.write('ITEM: ATOMS' + (' {}' * len(data)).format(*data) + '\n')
        output = []
        for key in keys:
            output = np.hstack((output, data[key]))
        if len(output):
            np.savetxt(fp, output.reshape((natoms, len(data)), order='F'))
# MPI setup
comm = MPI.COMM WORLD
rank = comm.Get_rank()
size = comm.Get_size()
# Your main simulation code
temperatures = [250, 275, 300, 325, 350, 375, 400, 425, 450, 475]
N_atoms = 1000
base params = {
    'natoms': N_atoms,
    'mass': 0.001,
    'radius': 120e-12,
    'relax': 1e-13,
    'dt': 1e-15,
    'steps': 10000,
```

```
'box': ((0, 1e-8), (0, 1e-8), (0, 1e-8)),
         }
         start_time = time.time()
         local temps = [temp for i, temp in enumerate(temperatures) if i % size == ra
         local results = []
         for temp in local temps:
             print(f'Process {rank}: Simulating temperature {temp}K')
             params = base_params.copy()
             params['temp'] = temp
             params['ofname'] = f'traj-hydrogen-3D-{N atoms}-{temp}K.dump'
             output = run(**params)
             local results.append((temp, output))
         all_results = comm.gather(local_results, root=0)
         if rank == 0:
             combined results = []
             for proc_data in all_results:
                 combined results.extend(proc data)
             combined_results.sort(key=lambda x: x[0])
             exec_time = time.time() - start_time
             print(f'Total execution time using {size} cores: {exec_time:.2f} seconds
             write_scaling_csv('mpi_scaling.csv', size, exec_time)
         MPI.Finalize()
        Process 1: Simulating temperature 275K
        Process 5: Simulating temperature 375K
        Process 6: Simulating temperature 400K
        Process 2: Simulating temperature 300K
        Process 0: Simulating temperature 250K
        Process 3: Simulating temperature 325K
   ✓ Process 7: Simulating temperature 425K
        Process 4: Simulating temperature 350K
        Process 1: Simulating temperature 475K
        Process 0: Simulating temperature 450K
        Total execution time using 8 cores: 4.79 seconds
In [24]: import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         # Read the scaling data
         my pc = pd.read csv('mpi scaling.csv')
         # Calculate speedup from the data (S_p = T_1 / T_p)
         speedup = my_pc['execution_time'].iloc[0] / my_pc['execution_time']
         my pc['speedup'] = speedup
         # Calculate theoretical Amdahl's Law speedup
```

'freg': 100,

```
p = 0.95
amdahl_speedup_data = 1 / ((1 - p) + p / my_pc['n_cores'])
# Create two subplots
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(15, 6))
# Plot 1: Execution Time vs Number of Cores
ax1.plot(my_pc['n_cores'], my_pc['execution_time'], marker='o', linestyle='-
ax1.set title('MPI Scaling: Execution Time vs Number of Cores')
ax1.set xlabel('Number of Cores')
ax1.set_ylabel('Execution Time (seconds)')
ax1.grid(True, alpha=0.3)
ax1.set xticks(my pc['n cores'])
# Plot 2: Speedup Comparison
ax2.plot(my_pc['n_cores'], my_pc['speedup'], marker='o', linestyle='-', cold
ax2.plot(my_pc['n_cores'], amdahl_speedup_data, linestyle='--', color='r', l
ax2.plot(my_pc['n_cores'], my_pc['n_cores'], linestyle=':', color='g', linew
ax2.set title('Speedup Comparison: Observed vs Theoretical')
ax2.set xlabel('Number of Cores')
ax2.set_ylabel('Speedup')
ax2.grid(True, alpha=0.3)
ax2.legend()
ax2.set_xticks(my_pc['n_cores'])
plt.tight layout()
plt.show()
# Print detailed analysis
print("Scaling Analysis:")
print(f"Maximum observed speedup: {my pc['speedup'].max():.2f}x with {my pc.
print(f"Efficiency at maximum cores ({my pc['n cores'].iloc[-1]}): {(my pc['n cores'].iloc[-1]}): {(my pc['n cores'].iloc[-1])}
# Calculate efficiency for each core count
my_pc['efficiency'] = my_pc['speedup'] / my_pc['n_cores'] * 100
print(f"\nEfficiency by core count:")
for _, row in my_pc.iterrows():
    print(f" {int(row['n cores'])} cores: {row['efficiency']:.1f}%")
         MPI Scaling: Execution Time vs Number of Cores
                                                   Speedup Comparison: Observed vs Theoretical
```



```
Scaling Analysis:
Maximum observed speedup: 5.07x with 6 cores
Efficiency at maximum cores (8): 56.4%

Efficiency by core count:
   1 cores: 100.0%
   2 cores: 116.4%
   3 cores: 91.0%
   4 cores: 92.3%
   5 cores: 87.5%
   6 cores: 84.5%
   7 cores: 70.4%
   8 cores: 56.4%
```

Then i used the same script to run in hpc Cedia

```
In [26]: # Read the HPC scaling data
             hpc = pd.read_csv('mpi_scaling_hpc.csv')
      \checkmark # Calculate speedup from the HPC data (S p = T 1 / T p)
             speedup_hpc = hpc['execution_time'].iloc[0] / hpc['execution_time']
             hpc['speedup'] = speedup_hpc
             # Calculate theoretical Amdahl's Law speedup for HPC data
             amdahl speedup hpc = 1 / ((1 - p) + p / hpc['n cores'])
             # Create two subplots for HPC data
             fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(15, 6))
             # Plot 1: Execution Time vs Number of Cores (HPC)
             ax1.plot(hpc['n cores'], hpc['execution time'], marker='s', linestyle='-', d
             ax1.set title('HPC MPI Scaling: Execution Time vs Number of Cores')
            ax1.set xlabel('Number of Cores')
             ax1.set_ylabel('Execution Time (seconds)')
             ax1.grid(True, alpha=0.3)
             ax1.set_xticks(hpc['n_cores'])
             # Plot 2: Speedup Comparison (HPC)
             ax2.plot(hpc['n_cores'], hpc['speedup'], marker='s', linestyle='-', color='r
             ax2.plot(hpc['n_cores'], hpc['n_cores'], linestyle=':', color='g', linewidth
             ax2.plot(hpc['n cores'], amdahl speedup hpc, linestyle='--', color='b', line
             ax2.set_title('HPC Speedup Comparison: Observed vs Theoretical')
             ax2.set xlabel('Number of Cores')
             ax2.set ylabel('Speedup')
             ax2.grid(True, alpha=0.3)
             ax2.legend()
             ax2.set xticks(hpc['n cores'])
             plt.tight_layout()
             plt.show()
             # Print detailed analysis for HPC
             print("HPC Scaling Analysis:")
             print(f"Maximum observed speedup: {hpc['speedup'].max():.2f}x with {hpc.loc|
             print(f"Efficiency at maximum cores ({hpc['n_cores'].iloc[-1]}): {(hpc['spector')].iloc[-1]}): {(hpc['spector')].iloc[-1]}.
```

```
# Calculate efficiency for each core count (HPC)
    hpc['efficiency'] = hpc['speedup'] / hpc['n_cores'] * 100
✓ print(f"\nHPC Efficiency by core count:")
    for _, row in hpc.iterrows():
         print(f" {int(row['n_cores'])} cores: {row['efficiency']:.1f}%")
              HPC MPI Scaling: Execution Time vs Number of Cores
                                                              HPC Speedup Comparison: Observed vs Theoretical
                                                       HPC Observed Speedup
HPC Ideal Linear Speedup
                                                       -- HPC Amdahl's Law
   1200
   1000
                                                    20
    800
    600
                                                    10
    400
    200
                                                                        16
Number of Cores
   HPC Scaling Analysis:
   Maximum observed speedup: 31.76x with 32 cores
   Efficiency at maximum cores (32): 99.3%
   HPC Efficiency by core count:
     1 cores: 100.0%
     2 cores: 100.0%
     4 cores: 100.0%
     8 cores: 99.3%
     16 cores: 99.3%
```

In []:

32 cores: 99.3%