

```
####!/usr/local/bin/env python
```

```
# I made the following changes to this test case:
```

```
#
```

```
# 1) Changed the test system from harmonic oscillators to the alanine dipeptide
```

```
# 2) Changed the number of MC iterations
```

```
# 3) Changed select (internal) function names
```

```
# =====
```

```
# GLOBAL IMPORTS
```

```
# =====
```

```
# Non-scientific python packages needed for this protocol
```

```
import os
import sys
import timeit
from io import StringIO
import openmmtools as mmttools
from openmmtools import testsystems
from simtk import unit
```

```
# This is where replica exchange utilities are imported from Yank
```

```
from yank import mpi
from yank.multistate import MultiStateReporter, MultiStateSampler, ReplicaExchangeSampler,
ParallelTemperingSampler, SAMSSampler
from yank.multistate import ReplicaExchangeAnalyzer, SAMSAnalyzer
from yank.multistate.multistatereporter import _DictYamlLoader
from yank.utils import config_root_logger
from yank.commands import analyze
```

```
# quiet down some citation spam
```

```
MultiStateSampler._global_citation_silence = True
```

```
# =====
```

```
# RUN REPLICA EXCHANGE
```

```
# =====
```

```
def run_replica_exchange(verbose=False, verbose_simulation=False):
```

```
    sampler_states = list()
    thermodynamic_states = list()
```

```
    # Define thermodynamic states.
```

```
    temperatures = [250.0, 300.0, 350.0, 400.0, 450.0] * unit.kelvin # Temperatures.
```

```
    for temperature in temperatures:
```

```
        testsystem = testsystems.AlanineDipeptideVacuum()
```

```
        # Create thermodynamic state and save positions.
```

```
        system, positions = [testsystem.system, testsystem.positions]
```

```
        sampler_states.append(mmttools.states.SamplerState(positions))
```

```
        thermodynamic_states.append(mmttools.states.ThermodynamicState(system=system,
                                temperature=temperature))
```

```
    # Create and configure simulation object.
```

```
    move = mmttools.mcmc.LangevinDynamicsMove(timestep=2.0*unit.femtoseconds,
                                              collision_rate=20.0/unit.picosecond,
                                              n_steps=100, reassign_velocities=True)
```

```
    simulation = ReplicaExchangeSampler(mcmc_moves=move, number_of_iterations=20)
```

```
    # Define file for temporary storage.
```

```
    if os.getcwd() == os.getcwd():
```

```
        storage = os.path.join(os.getcwd(), 'test_storage.nc')
```

```
        if os.path.exists(storage): os.remove(storage)
```

```

reporter = MultiStateReporter(storage, checkpoint_interval=1)
simulation.create(thermodynamic_states, sampler_states, reporter)

config_root_logger(verbose_simulation)
simulation.run()

# Clean up.
del simulation

if verbose:
    print("PASSED.")

# =====
# MAIN
# =====

if __name__ == "__main__":
    # Configure logger.
    config_root_logger(False)

    start_time = timeit.default_timer()
    run_replica_exchange()
    stop_time = timeit.default_timer()
    print("Calculation time was: "+str(stop_time-start_time)+" seconds.")

    analyze.dispatch_extract_trajectory({'--checkpoint':
'test_storage_checkpoint.nc', '--fulltraj': True, '--netcdf': 'test_storage.nc',
'--output': 'traj1', '--replica': 1, '--trajectory': 1, '--state': 1, 'extract-trajectory':
True, '--discardequil': False, '--distcutoff': None,
'--end': None, '--energycutoff': None, '--format': None, '--serial': None, '--skip':
None, '--skipunbiasing': True, '--start': None,
'--imagemol': None, '--nosolvent': None, '--verbose': False})

```