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MONTE CARLO CODE PARALLELIZATION

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DAY 1: OPTIMIZATION AND PROFILING

Optimization:

- O2, -O3, -fast, -unroll
- No significant improvement

Profiling:

- gprof, valgrind
- conclusion: code should be parallelized

DAY 2: OpenMP IMPLEMENTATION

1.

- Several Monte Carlo steps at the same time on different threads
- Chosen molecules should be independent
- Trivial problem
- **#pragma omp parallel private(tid,...)**

2.

- Energy calculation function parallelization
- Trivial problem
- **#pragma omp parallel for private(rx_i, ry_i, rz_i, rx_{ij}, ry_{ij}, rz_{ij}, v_{ij}, w_{ij}) reduction(+ : vv, ww)**

DAY 2: OpenMP IMPLEMENTATION

```
-icc -openmp -fstatic napthalene2.cpp -o napthalene.ex
```

```
#!/bin/bash
#PBS -q hpsee
#PBS -l nodes=1:ppn=8
#PBS -l walltime=00:10:00
#PBS -e ${PBS_JOBID}.err
#PBS -o ${PBS_JOBID}.out
```

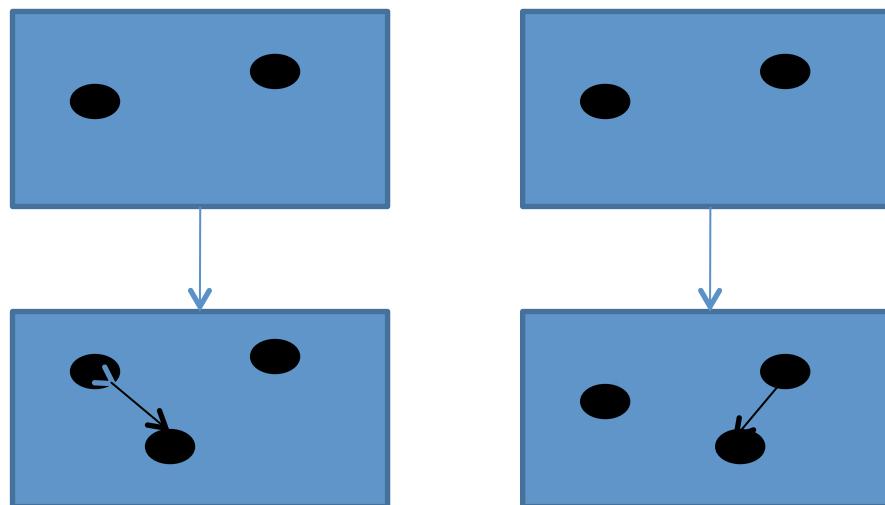
```
cd $PBS_O_WORKDIR
```

```
export OMP_NUM_THREADS=8
chmod +x napthalene.ex
./napthalene.ex > tmp
```

DAY 3: MPI IMPLEMENTATION

1.

- Several Monte Carlo steps at the same time on different processors
- Chosen molecules should be independent
- Non-trivial problem



```
MPI_Allreduce(change, change_all, 1 , MPI_DOUBLE, MPI_SUM, MPI_COMM_WORLD);
```

DAY 3: MPI IMPLEMENTATION

```
mpic++ naphtalene2.cpp -o naphtalene.ex -lm
```

```
#!/bin/bash
#PBS -q hpsee
#PBS -l nodes=2:ppn=1
#PBS -l walltime=12:00:00
#PBS -e ${PBS_JOBID}.err
#PBS -o ${PBS_JOBID}.out
```

```
cd $PBS_O_WORKDIR
cat $PBS_NODEFILE
```

```
 ${MPI_MPICH2_MPIEXEC} --comm=pmi ./naphtalene.ex > tmp
```

DAY 4: TESTING

- correct results
- parallel Monte Carlo will reach equilibrium configuration faster than serial (less steps needed)
- OpenMP implementation is faster than MPI (due to additional variables and MPI_Allreduce routine used in MPI implementation)
- energy calculation routine speed-up: $7/2 = 3.5$, 8 threads (can be increased)