Split Molecular Dynamics

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Goal: Learn MPI communicator concept using in situ data analysis of molecular dynamics simulation
• `MPI_Comm_split()` subdivides a communicator, `mothercomm`, into a set of daughter communicators, where processes of the same color belong to the same daughter communicator. Processes within each color are ranked according to `key`, or if `key` is the same, according to the rank in `mothercomm`. It returns a pointer to a daughter communicator, `daughtercomm`, to which the process belongs.

• `MPI_Comm_split()` is a simpler, more high-level function to construct communicators, instead of using `MPI_Comm_create()` combined with `MPI_Group_excl()` or `MPI_Group_incl()`.
• Split MPI_COMM_WORLD into two communicators; one performs molecular dynamics (MD) simulation, whereas the other analyzes simulation data on the fly in background.

```c
int gid, sid, md;
MPI_Comm workers;
MPI_Comm_rank(MPI_COMM_WORLD,&gid);  // Global rank
md = gid%2;  // = 1 (MD workers) or 0 (analysis workers)
MPI_Comm_split(MPI_COMM_WORLD,md,0,&workers);
MPI_Comm_rank(workers,&sid);  // Rank in workers
```

Run as mpirun –np 2×nproc

# of processors needed for MD (specified in pmd.h)
### Analysis: Velocity Probability Density

\[ P(v) : \text{Probability density function of atom velocity } v \]

```c
#define VMAX 5.0  // Maximum velocity value to construct a velocity histogram
#define NBIN 100  // # of bins in the histogram

void calc_pv() {
    double lpv[NBIN], pv[NBIN], dv, v;
    int i;

    dv = VMAX/NBIN;  // Bin size
    for (i=0; i<NBIN; i++) lpv[i] = 0.0;  // Reset local histogram
    for (i=0; i<n; i++) {
        v = sqrt(pow(rv[i][0],2)+pow(rv[i][1],2)+pow(rv[i][2],2));
        lpv[v/dv < NBIN ? (int)(v/dv) : NBIN-1] += 1.0;
    }
    MPI_Allreduce(lpv, pv, NBIN, MPI_DOUBLE, MPI_SUM, workers);
    MPI_Allreduce(&n, &nglob, 1, MPI_INT, MPI_SUM, workers);
    for (i=0; i<NBIN; i++) pv[i] /= (dv*nglob);  // Normalization
    if (sid == 0) {
        for (i=0; i<NBIN; i++) fprintf(fpv,"%le %le\n",i*dv,pv[i]);
        fprintf(fpv,"
");
    }
}
```

\[ v = |\vec{v}| = \sqrt{v_x^2 + v_y^2 + v_z^2} \]

\[ \int dv p(v) = 1 \]
Main Program: Initialization

```c
init_params();
if (md) {
    set_topology();
    init_conf();
    atom_copy();
    compute_accel();
}
else
    if (sid == 0) fpv = fopen("pv.dat","w");
```

- All processes read input parameters, `init_params()`. The `nproc` processes of MD workers (`md == 1`) perform MD initialization tasks, whereas only rank 0 among the other `nproc` analysis workers (`md == 0`) opens a file to output the calculated velocity probability density function.
Main Program: Main MD Loop

for (stepCount=1; stepCount<=StepLimit; stepCount++) {
    if (md) single_step();
    if (stepCount%StepAvg == 0) {
        if (md) {
            Send # of atoms, n, to rank gid-1 in MPI_COMM_WORLD
            Send velocities of n atoms to rank gid-1 in MPI_COMM_WORLD
            eval_props();
        }
        else {
            Receive # of atoms, n, from rank gid+1 in MPI_COMM_WORLD
            Receive velocities of n atoms from rank gid+1 in MPI_COMM_WORLD
            calc_pv();
        }
    }
}

• MD workers perform MD simulation. Every stepAvg steps, MD workers send their atom velocities to corresponding analysis workers (i.e., those with the same ranks in respective daughter communicators). Upon receiving the velocities, analysis workers calculate the velocity probability density function.
if (md && sid == 0)
    printf("CPU & COMT = %le %le\n", cpu, comt);
if (!md && sid == 0)
    fclose(fpv);

- Rank 0 of MD workers reports the computing & communication times, whereas rank 0 of analysis workers closes the probability density output file.

- **Finally:** Change all MPI_COMM_WORLD’s in the original MD functions to workers ~ it’s only a matter in the small MD world!
Results

pmd.in
5 5 5 // InitUcell[0|1|2]
0.8 // Density
1.0 // InitTemp
0.005 // DeltaT
30 // StepLimit
10 // StepAvg
Maxwell-Boltzmann Distribution

\[ P_{\text{Maxwell-Boltzmann}}(v) = \frac{4}{\sqrt{\pi}} \left( \frac{m}{2k_B T} \right)^{3/2} v^2 \exp \left( -\frac{mv^2}{2k_B T} \right) \]
**In Situ Data Analysis**

Use communicators to add data analytics & extra logic to parallel simulations

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**FIGURE 2.** DCR in time. (a) Molecular dynamics (MD) simulations have sequential time dependence. (b) Parallel replica dynamics (PRD) predicts long-time behavior through statistical analysis of multiple parallel MD trajectories. (c) Conventional file-based and (d) new in situ PRD simulations. ML represents machine-learning tasks.

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