



Example — Molecular Dynamics

- Goal is to simulate what happens to large molecule.
- Approach is to treat molecule as a collection of balls (atoms) connected by springs (chemical bonds). Then do "standard time-stepping" — divide time into discrete steps, and at each step use classical mechanics to figure out new positions for atoms based on current positions and forces among them.

Slide 3

Molecular Dynamics Pseudocode
<pre>Int const N // number of atoms Array of Real :: atoms (3,N) //3D coordinates Array of Real :: velocities (3,N) //velocity vector Array of Real :: forces (3,N) //force in each dimension</pre>
Array of List :: neighbors(N) //atoms in cutoff volume
loop over time steps
vibrational_forces (N, atoms, forces)
rotational_forces (N, atoms, forces)
<pre>neighbor_list (N, atoms, neighbors)</pre>
<pre>non_bonded_forces (N, atoms, neighbors, forces)</pre>
update_atom_positions_and_velocities
(N, atoms, velocities, forces)
physical_properties (\dots Lots of stuff \dots)
end loop





	Heat Diffusion Code
double *uk = m	<pre>hlloc(sizeof(double) * NX);</pre>
<pre>double *ukpl = double *temp;</pre>	<pre>malloc(sizeof(double) * NX);</pre>
double dx = 1. double maxdiff	<pre>//NX; double dt = 0.5*dx*dx; . diff;</pre>
initialize(uk,	ukpl);
for (int $k = 0$: (k < NSTEPS) && (maxdiff >= threshold); ++k) {
/* compute n	w values */
for (int i =	l; i < NX-l; ++i) {
ukpl[i]=uk }	i]+ (dt/(dx*dx))*(uk[i+1]-2*uk[i]+uk[i-1]);
/* check for	convergence */
maxdiff = 0.);
for (int i =	1; i < NX-1; ++i) {
dlII = IAD	S(UK[1] - UKDI[1]);
}	maxuili, maxuili - uili,
/* "copy" uk	ol to uk by swapping pointers */
temp = ukpl;	ukpl = uk; uk = temp;
printValues(ık, k);
}	

Starting point in our grand strategy for developing parallel applications. Overall idea — capture how experienced parallel programmers think about initial design of parallel applications. Might not be necessary if clear match between application and an *Algorithm Structure* pattern.
Idea is to work through three groups of patterns in sequence (possibly with backtracking):
Decomposition patterns (*Task Decomposition, Data Decomposition*): Break problem into tasks that maybe can execute concurrently.
Dependency analysis patterns (*Group Tasks, Order Tasks, Data Sharing*): Organize tasks into groups, analyze dependencies among them. *Design Evaluation*: Review what you have so far, possibly backtrack.
Keep in mind — best to focus attention on computationally intensive parts of problem.



Slide 10 Flack Decomposition Goal here is to break up (some of) computation into "tasks" — logical elements of overall computation that might be independent enough to do concurrently. At this stage, try to stay abstract and portable; also try to identify lots of tasks (can always recombine them later if too many), as independent of each other as possible. Places to look for tasks include groups of function calls (e.g., in divide-and-conquer strategy), loop iterations (e.g., many examples we've discussed). Simple example — matrix multiplication. Once you have this, consider data related to each task (*Data Decomposition*).



Molecular Dynamics Example — Task Decomposition

- Tasks that find the vibrational forces on an atom.
- Tasks that find the rotational forces on an atom.

(Together, these are tasks to compute "bonded forces" — those due to chemical bonds.)

- Tasks that find the non-bonded forces on an atom (the ones due to electrical charges).
- Tasks that update the position and velocity of an atom.
- Tasks that update the neighbor list for an atom. (Or we could consider updating all the neighbor lists as one task, as in the book, if we think it won't be done very often and therefore is not worthwhile to parallelize.)







Group Tasks
Once you've broken down problem into tasks / data chunks, need to put it back together as design for parallel algorithm.
First step — look for "groups of tasks" — logically related, or interdependent, or all with same constraints, etc. Often just one group.







