# A Parallel-Object Programming Model for PetaFLOPS Machines and BlueGene/Cyclops

Gengbin Zheng, Arun Singla,

Joshua Unger, Laxmikant Kalé

Parallel Programming Laboratory

Department of Computer Science

University of Illinois at Urbana-Champaign

http://charm.cs.uiuc.edu

# Massive Parallel Processors-In-Memory

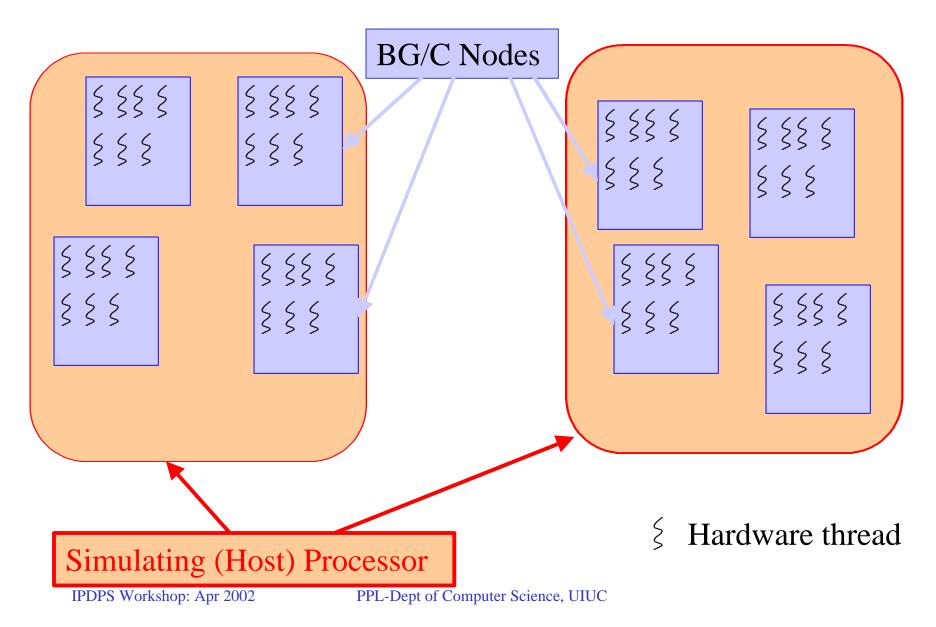
#### MPPIM

- Large number of identical chips
- Each contains multiple processors and memory
- Blue Gene/C
  - $-34 \times 34 \times 36$  cube
  - Multi-million hardware threads
- Challenges
  - How to program?
  - Software challenges: cost-effective

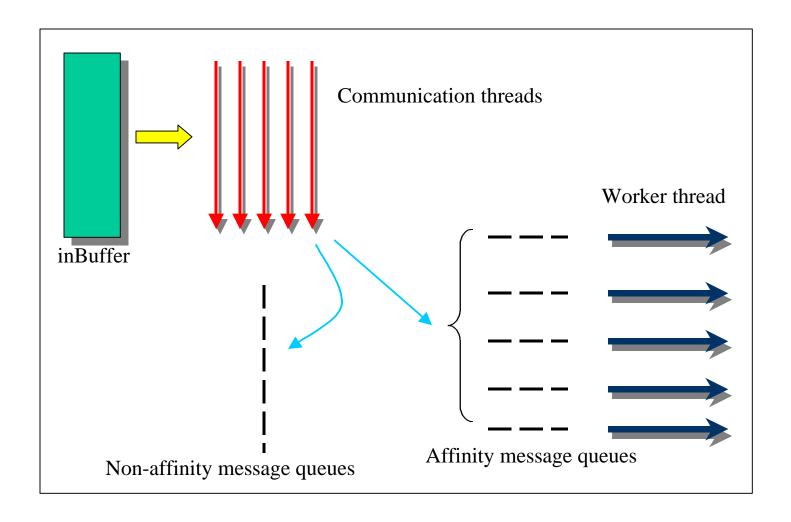
### Need for Emulator

- Emulate BG/C machine API on conventional supercomputers and clusters.
  - Emulator enables programmer to develop, compile, and run software using programming interface that will be used in actual machine
- Performance estimation (with proper time stamping)
- Allow further research on high level parallel languages like Charm++
- Low memory-to-processor ratio make it possible
  - Half terabyte memory require 1000 processors 512MB

# Emulation on a Parallel Machine

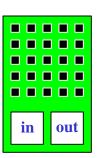


# Bluegene Emulator one BG/C Node



# Blue Gene Programming API

- Low-level
  - Machine initialization
    - Get node ID: (x, y, z)
    - Get Blue Gene size
  - Register handler functions on node
  - Send packets to other nodes (x,y,z)
    - With handler ID



#### Blue Gene application example - Ring

```
typedef struct {
 char core[CmiBlueGeneMsgHeaderSizeBytes];
 int data;
} RingMsg;
void BgNodeStart(int argc, char **argv) {
  int x,y,z, nx, ny, nz;
  RingMsg msg;
                                msg.data = 888;
  BgGetXYZ(&x, &y, &z);
                                nextxyz(x, y, z, &nx, &ny, &nz);
  if (x == 0 \&\& y == 0 \&\& z == 0)
     BgSendPacket(nx, ny, nz, passRingID, LARGE_WORK, sizeof(int), (char *)&msg);
void passRing(char *msg) {
  int x, y, z, nx, ny, nz;
  BgGetXYZ(&x, &y, &z); nextxyz(x, y, z, &nx, &ny, &nz);
  if (x==0 \&\& y==0 \&\& z==0) if (++iter== MAXITER) BgShutdown();
  BgSendPacket(nx, ny, nz, passRingID, LARGE_WORK, sizeof(int), msg);
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```

#### **Emulator Status**

- Implemented on Charm++/Converse
  - 8 Million processors being emulated on 100 ASCI-Red processors
- How much time does it take to run an emulation v.s. how much time does it take to run on real BG/C?
  - Timestamp module
- Emulation efficiency
  - On a Linux cluster:
    - Emulation shows good speedup(later slides)

# Programming issues for MPPIM

- Need higher level of programming language
- Data locality
- Parallelism
- Load balancing
- Charm++ is a good programming model candidate for MPPIMs

#### Charm++

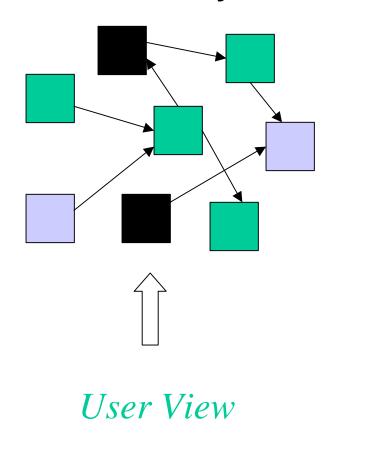
- Parallel C++ with *Data Driven* Objects
- Object Arrays/ Object Collections
- Object Groups:
  - Global object with a "representative" on each PE
- Asynchronous method invocation
- Built-in load balancing(runtime)
- Mature, robust, portable
- http://charm.cs.uiuc.edu

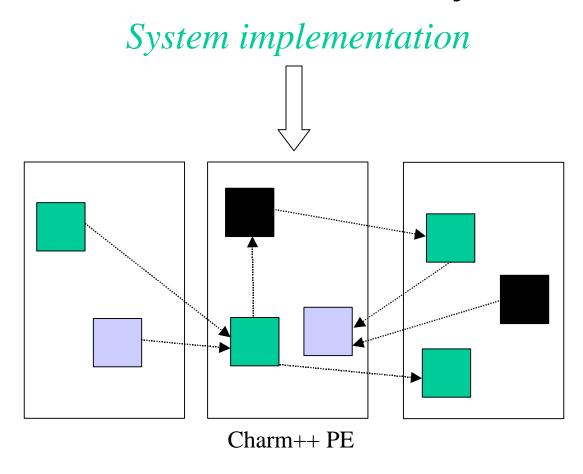
# Multi-partition Decomposition

- Idea: divide the computation into a large number of pieces(parallel objects)
  - Independent of number of processors
  - Typically larger than number of processors
  - Let the system map entities to processors
- Optimal division of labor between "system" and programmer:
  - Decomposition done by programmer,
  - Everything else automated

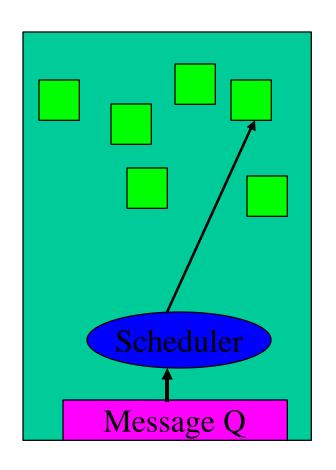
# Object-based Parallelization

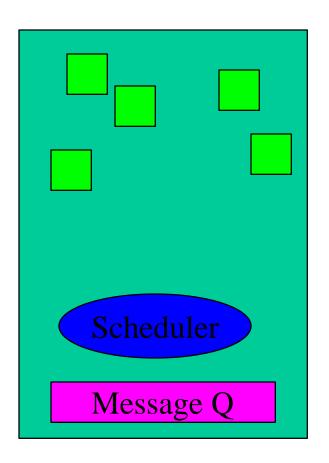
#### User is only concerned with interaction between objects





# Data driven execution





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# Load Balancing Framework

- Based on object migration
  - Partitions implemented as objects (or threads) are mapped to available processors by LB framework
- Measurement based load balancers:
  - Principle of persistence
    - Computational loads and communication patterns
  - Runtime system measures actual computation times of every partition, as well as communication patterns
- Variety of "plug-in" LB strategies available
  - Scalable to a few thousand processors
  - Including those for situations when principle of persistence does not apply

### Charm++ is a Good Match for MPPIM

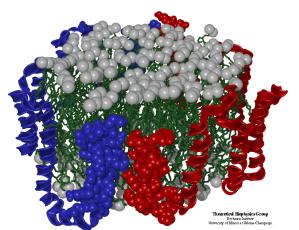
- Message driven/Data driven
- Encapsulation : objects
- Explicit cost model:
  - Object data, read-only data, remote data
  - Aware of the cost of accessing remote data
- Migration and resource management: automatic
- One sided communication
- Asynchronous global operations (reductions, ..)

# Charm++ Applications

- Charm++ developed in the context of real applications
- Current applications we are involved with:
  - Molecular dynamics(NAMD)
  - Crack propagation
  - Rocket simulation: fluid dynamics + structures +
  - QM/MM: Material properties via quantum mech
  - Cosmology simulations: parallel analysis+viz
  - Cosmology: gravitational with multiple timestepping

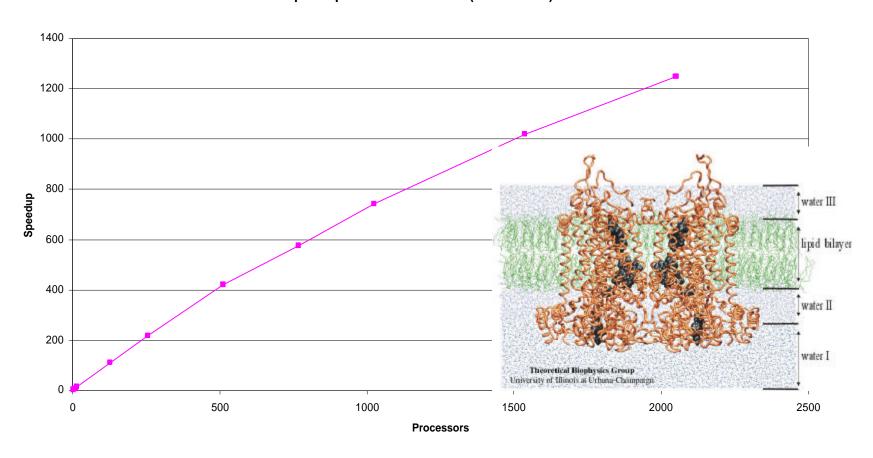
# Molecular Dynamics

- Collection of [charged] atoms, with bonds
- Newtonian mechanics
- At each time-step
  - Calculate forces on each atom
    - Bonds:
    - Non-bonded: electrostatic and van der Waal's
  - Calculate velocities and advance positions
- 1 femtosecond time-step, millions needed!
- Thousands of atoms (1,000 100,000)



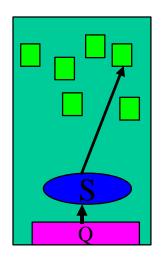
# Performance Data: SC2000

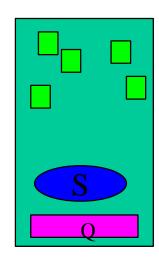
#### Speedup on ASCI Red: BC1 (200k atoms)



#### Further Match With MPPIM

- Ability to predict:
  - Which data is going to be needed and which code will execute
  - Based on the ready queue of object method invocations
  - So, we can:
    - Prefetch data accurately
    - Prefetch code if needed

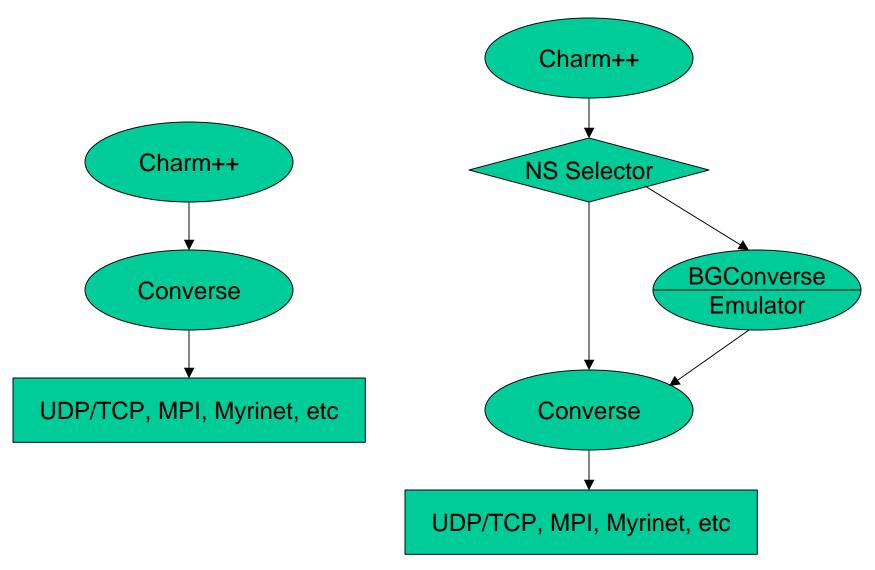




#### Blue Gene/C Charm++

- Implemented Charm++ on Blue Gene/C Emulator
  - Almost all existing Charm++ applications can run w/o change on emulator
- Case study on some real applications
  - leanMD: Fully functional MD with only cutoff (PME later)
  - AMR
- Time stamping(ongoing work)
  - Log generation and correction

# Parallel Object Programming Model



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#### BG/C Charm++

Object affinity

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- Object mapped to a BG node
  - A message can be executed by any thread
  - Load balancing at node level
  - Locking needed
- Object mapped to a BG thread
  - An object is created on a particular thread
  - All messages to the object will go to that thread
  - No locking needed.
  - Load balancing at thread level

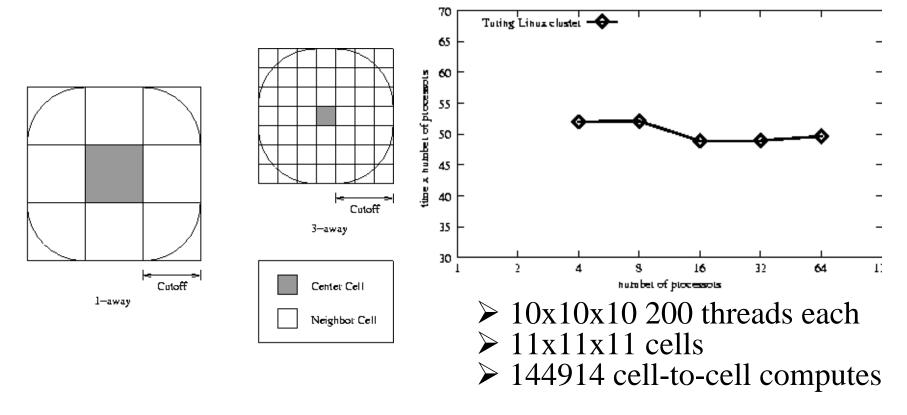
# Applications on the current system

#### • LeanMD:

- Research quality Molecular Dynamics
- Version 0: only electrostatics + van der Vaal
- Simple AMR kernel
  - Adaptive tree to generate millions of objects
    - Each holding a 3D array
  - Communication with "neighbors"
    - Tree makes it harder to find nbrs, but Charm makes it easy

#### LeanMD

- K-array molecular dynamics simulation
- Using Charm++ Chare arrays

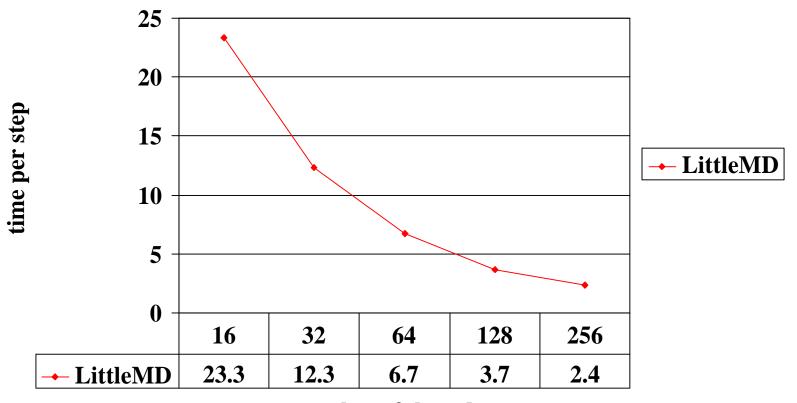


# Correction of Time stamps at runtime

- Timestamp
  - Per thread timer
  - Message arrive time
    - Calculate at time of sending
      - Based on hop and corner
    - Update thread timer when arrive
- Correction needed for out-of-order messages
  - Correction messages send out



#### **LittleMD Blue Gene Time**



number of threads

- > 200,000 atoms
- ➤ Use 4 simulating processors

# Summary

- Emulation of BG/C with millions of threads
  - On conventional supercomputers and clusters
- Charm++ on BG Emulator
  - Legacy Charm++ applications
  - Load balancing(need more research)
- We have Implemented multi-million object applications using Charm++
  - And tested on emulated Blue Gene/C
- Getting accurate simulating timing data
- More info: http://charm.cs.uiuc.edu
  - Both Emulator and BG Charm++ are available for download