More Data Parallelism: Domain Maps
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Data Parallelism Implementation Qs

**Q1: How are arrays laid out in memory?**
- Are regular arrays laid out in row- or column-major order? Or…?
- How are sparse arrays stored? (COO, CSR, CSC, block-structured, …?)

**Q2: How are arrays stored by the locales?**
- Completely local to one locale? Or distributed?
- If distributed… In a blocked manner? cyclically? block-cyclically? recursively bisected? dynamically rebalanced? …?
Q1: How are arrays laid out in memory?
- Are regular arrays laid out in row- or column-major order? Or…?
- How are sparse arrays stored? (COO, CSR, CSC, block-structured, …?)

Q2: How are arrays stored by the locales?
- Completely local to one locale? Or distributed?
- If distributed… In a blocked manner? cyclically? block-cyclically? recursively bisected? dynamically rebalanced? …?

A: Chapel’s *domain maps* are designed to give the user full control over such decisions.
Jacobi Iteration in Chapel

```chapel
config const n = 6,
    epsilon = 1.0e-5;

const BigD = {0..n+1, 0..n+1},
    D = BigD[1..n, 1..n],
    LastRow = D.exterior(1,0);

var A, Temp : [BigD] real;

A[LastRow] = 1.0;

do {
    forall (i,j) in D do

    const delta = max reduce abs(A[D] - Temp[D]);
    A[D] = Temp[D];
} while (delta > epsilon);

writeln(A);
```

By default, domains and their arrays are mapped to a single locale. Any data parallelism over such domains/arrays will be executed by the cores on that locale. Thus, this is a shared-memory parallel program.
Jacobi Iteration in Chapel

```chapel
config const n = 6,
    epsilon = 1.0e-5;

const BigD = {0..n+1, 0..n+1} dmapped Block({1..n, 1..n}),
    D = BigD[1..n, 1..n],
    LastRow = D.exterior(1,0);

var A, Temp : [BigD] real;
```

With this simple change, we specify a mapping from the domains and arrays to locales. Domain maps describe the mapping of domain indices and array elements to locales. Specifies how array data is distributed across locales. Specifies how iterations over domains/arrays are mapped to locales.
Jacobi Iteration in Chapel

```chapel
config const n = 6,
    epsilon = 1.0e-5;

const BigD = {0..n+1, 0..n+1} dmapped Block({1..n, 1..n}),
    D = BigD[1..n, 1..n],
    LastRow = D.exterior(1,0);

var A, Temp : [BigD] real;
A[LastRow] = 1.0;

do {
    forall (i,j) in D do

    const delta = max reduce abs(A[D] - Temp[D]);
    A[D] = Temp[D];
} while (delta > epsilon);

writeln(A);

use BlockDist;
```
STREAM Triad: Chapel

Chapel

config const m = 1000,
    alpha = 3.0;

const ProblemSpace = {1..m} dmapped ...

var A, B, C: [ProblemSpace] real;

B = 2.0;
C = 1.0;
A = B + alpha * C;

Philosophy: Good, top-down language design can tease system-specific implementation details away from an algorithm, permitting the compiler, runtime, applied scientist, and HPC expert to each focus on their strengths.
STREAM Triad in Chapel

\`const ProblemSpace = \{1..m\};\`

\`var A, B, C: [ProblemSpace] real;\`

\`A = B + alpha * C;\`
STREAM Triad in Chapel (multicore)

```
const ProblemSpace = {1..m};

var A, B, C: [ProblemSpace] real;

A = B + alpha * C;
```

No domain map specified ⇒ use default layout
- current locale owns all domain indices and array values
- computation will execute using local processors only
STREAM Triad in Chapel (multilocation, cyclic)

\[
\text{const ProblemSpace} = \{1..m\}
\]
\[
\text{dmapped Cyclic(startIdx=1);}
\]

\[
\text{var A, B, C: [ProblemSpace] real;}
\]

\[
\alpha \cdot \begin{align*}
A &= B + \alpha \cdot C;
\end{align*}
\]
STREAM Triad in Chapel (multilocale, blocked)

\[ \text{const ProblemSpace} = \{1..m\} \]
\[ \text{dmapped} \quad \text{Block(boundingBox}={1..m}) ; \]

\[ \text{var A, B, C: [ProblemSpace]} \text{ real;} \]

\[ A = B + \alpha \cdot C; \]
Domain Maps

Domain maps are “recipes” that instruct the compiler how to map the global view of a computation...

\[ A = B + \alpha \cdot C; \]

...to the target locales’ memory and processors:
Chapel’s Domain Map Philosophy

1. Chapel provides a library of standard domain maps
   ● to support common array implementations effortlessly

2. Expert users can write their own domain maps in Chapel
   ● to cope with any shortcomings in our standard library

3. Chapel’s standard domain maps are written using the same end-user framework
   ● to avoid a performance cliff between “built-in” and user-defined cases
Domain Map Roles

They define data storage:
● Mapping of domain indices and array elements to locales
● Layout of arrays and index sets in each locale’s memory

…as well as operations:
● random access, iteration, slicing, reindexing, rank change, …
● the Chapel compiler generates calls to these methods to implement the user’s array operations
Layouts and Distributions

Domain Maps fall into two major categories:

**layouts:**
- e.g., a desktop machine or multicore node
- **examples:** row- and column-major order, tilings, compressed sparse row, space-filling curves

**distributions:**
- e.g., a distributed memory cluster or supercomputer
- **examples:** Block, Cyclic, Block-Cyclic, Recursive Bisection, …
Sample Distributions: Block and Cyclic

```plaintext
var Dom = {1..4, 1..8} dmapped Block( {1..4, 1..8} );
```

```
var Dom = {1..4, 1..8} dmapped Cyclic( startIdx=(1,1) );
```
All Domain Types Support Domain Maps

- **dense**
- **strided**
- **sparse**

- **associative**
  - “steve”
  - “lee”
  - “sung”
  - “david”
  - “jacob”
  - “albert”
  - “brad”

- **unstructured**
**Goal:** Solve one octant of the spherical Sedov problem (blast wave) using Lagrangian hydrodynamics for a single material

pictures courtesy of Rob Neely, Bert Still, Jeff Keasler, LLNL
LULESH in Chapel
LULESH in Chapel

1288 lines of source code

plus 266 lines of comments

487 blank lines

(the corresponding C+MPI+OpenMP version is nearly 4x bigger)

This can be found in the Chapel release under examples/benchmarks/lulesh/*.chpl
LULESH in Chapel

This is all of the representation dependent code. It specifies:

• data structure choices
  • structured vs. unstructured mesh
  • local vs. distributed data
  • sparse vs. dense materials arrays
• a few supporting iterators
For More Information on Domain Maps

HotPAR’10: *User-Defined Distributions and Layouts in Chapel: Philosophy and Framework*
Chamberlain, Deitz, Iten, Choi; June 2010

CUG 2011: *Authoring User-Defined Domain Maps in Chapel*
Chamberlain, Choi, Deitz, Iten, Litvinov; May 2011

Chapel release:
Two Other Thematically Similar Features

1) **parallel iterators**: Permit users to specify the parallelism and work decomposition used by forall loops
   - including zippered forall loops

2) **locale models**: Permit users to model the target architecture and how Chapel should be implemented on it
   - e.g., how to manage memory, create tasks, communicate, …

Like domain maps, these are…
   …written in Chapel by expert users using lower-level features
   - e.g., task parallelism, on-clauses, base language features, …
   …available to the end-user via higher-level abstractions
   - e.g., forall loops, on-clauses, lexically scoped PGAS memory, …
Summary of this Section

● Chapel avoids locking crucial implementation decisions into the language specification
  ● local and distributed parallel array implementations
  ● parallel loop scheduling policies
  ● target architecture models

● Instead, these can be…
  …specified in the language by an advanced user
  …swapped between with minimal code changes

● The result cleanly separates the roles of domain scientist, parallel programmer, and compiler/runtime
Any Questions about Domain Maps?
Overarching Example: Smith-Waterman Algorithm for Sequence Alignment
Smith-Waterman

Goal: Determine the similarities/differences between two protein sequences/nucleotides.
- e.g., ACACACTA and AGCACACA

Basis of Computation: Defined via a recursive formula:

\[ H(i, 0) = 0 \]
\[ H(0, j) = 0 \]
\[ H(i, j) = f(H(i-1, j-1), H(i-1, j), H(i, j-1)) \]

Caveat: This is a classic, rather than cutting-edge sequence alignment algorithm, but it illustrates an important parallel paradigm: wavefront computation

Naïve Task-Parallel Approach:

```plaintext
proc computeH(i, j) {
    if (i == 0 || j == 0) then
        return 0;
    else
        var h_NW, h_N, h_W: int;

        cobegin {
            h_NW = computeH(i-1, j-1);
            h_N  = computeH(i-1, j);
            h_W  = computeH(i, j-1);
        }

        return f(h_NW, h_N, h_W);
    }
}
```

Note: Recomputes most subexpressions redundantly

This is a case for dynamic programming!
## Smith-Waterman

### Dynamic Programming Approach:

**Step 1: Initialize boundaries to 0**

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Smith-Waterman

Dynamic Programming Approach:

Step 2: Compute cells when we’re able to
Smith-Waterman

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Step 3: Follow trail of breadcrumbs back
### Dynamic Programming Approach:

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Step 3: Follow trail of breadcrumbs back
Dynamic Programming Approach:

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Step 4: Interpret the path against the original sequences

AGCACAC - A
A - CACACTA
Dynamic Programming Approach:

Step 2: Compute cells when we’re able to

How could we do this in parallel?
Smith-Waterman

Data-Parallel Approach:

```plaintext
proc computeH(H: [0..n, 0..n] int) {
  for upperDiag in 1..n do
    forall diagPos in 0..#upperDiag {
      const (i,j) = (diagPos+1, upperDiag-diagPos);
      H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
    }
  for lowerDiag in 1..n-1 do
    forall diagPos in lowerDiag..n-1 by -1 {
      const (i,j) = (diagPos+1, lowerDiag+diagPos);
      H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
    }
}
```

**Advantages:**
- Reasonably clean (if I got my indexing correct)

**Disadvantages:**
- Not so great in terms of cache use
- A bit fine-grained
  - small number of iterations per task

Loop over upper diagonals serially
Process each diagonal in parallel
Repeat for lower diagonals
Smith-Waterman

Naïve Data-Driven Task-Parallel Approach:

```cpp
proc computeH(H: [0..n, 0..n] int) {
    const ProbSpace = H.domain.translate(1,1);
    var NeighborsDone: [ProbSpace] atomic int;
    var Ready$: [ProbSpace] sync int;

    NeighborsDone[1, ..].add(1);
    NeighborsDone[.., 1].add(1);
    NeighborsDone[1, 1].add(1);
    Ready$[1,1] = 1;

    coforall (i, j) in ProbSpace {
        const goNow = Ready$[i,j];
        H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
        const eastReady = NeighborsDone[i, j+1].fetchAdd(1);
        const seReady = NeighborsDone[i+1,j+1].fetchAdd(1);
        const southReady = NeighborsDone[i+1,j].fetchAdd(1);
        if (eastReady == 2) then Ready$[i, j+1] = 1;
        if (seReady == 2) then Ready$[i+1,j+1] = 1;
        if (southReady == 2) then Ready$[i+1,j ] = 1;
    }
}
```

Create a domain describing shifted version of H’s domain

Arrays to count how many of our 3 neighbors are done; and to signal when we can compute

Set up boundaries: north and west elements have a neighbor done; top-left is ready

Create a task per matrix element and have it block until ready

Compute our element

Increment our neighbors’ counts

Signal our neighbors as ready if we’re the third
Naïve Data-Driven Task-Parallel Approach:

```plaintext
proc computeH(H : [0..n, 0..n] int) {
    const ProbSpace = H.domain.translate(1,1);
    var NeighborsDone: [ProbSpace] atomic int;
    var Ready$: [ProbSpace] sync int;
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    Ready$[1,1] = 1;
    coforall (i,j) in ProbSpace {
        const goNow = Ready$[i,j];
        H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
        const eastReady = NeighborsDone[i, j+1].fetchAdd(1);
        const seReady = NeighborsDone[i+1,j+1].fetchAdd(1);
        const southReady = NeighborsDone[i+1,j].fetchAdd(1);
        if (eastReady == 2) then Ready$[i, j+1] = 1;
        if (seReady == 2) then Ready$[i+1,j+1] = 1;
        if (southReady == 2) then Ready$[i+1,j] = 1;
    }
}
```

Disadvantages:
- Still not great in cache use
- Uses $n^2$ tasks
- Most spend most of their time blocking
Slightly Less Naïve Data-Driven Task-Parallel Approach:

```plaintext
proc computeH(H: [0..n, 0..n] int) {
    const ProbSpace = H.domain.translate(1,1);
    var NeighborsDone: [ProbSpace] atomic int;

    NeighborsDone[1, ..].add(1);
    NeighborsDone[.., 1].add(1);
    NeighborsDone[1, 1].add(1);
    sync { computeHHelp(1,1); }

    proc computeHHelp(i, j) {
        H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
        const eastReady = NeighborsDone[i, j+1].fetchAdd(1);
        const seReady = NeighborsDone[i+1,j+1].fetchAdd(1);
        const southReady = NeighborsDone[i+1,j ].fetchAdd(1);
        if (eastReady == 2) then begin computeHHelp(i, j+1);
        if (seReady == 2) then begin computeHHelp(i+1,j+1);
        if (southReady == 2) then begin computeHHelp(i+1,j  );
    }
}
```

Rather than create the tasks a priori, fire them off once we know they’re ready to compute.

Sync to ensure they’re all done before we go on.
Smith-Waterman

Slightly Less Naïve Data-Driven Task-Parallel Approach:

```plaintext
proc computeH(H: [0..n, 0..n] int) {
    const ProbSpace = H.domain.translate(1,1);
    var NeighborsDone: [ProbSpace] atomic int;

    NeighborsDone[1, ..].add(1);
    NeighborsDone[.., 1].add(1);
    NeighborsDone[1, 1].add(1);
    sync { computeHHelp(1,1); }

    proc computeHHelp(i,j) {
        H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
        const eastReady = NeighborsDone[i, j+1].fetchAdd(1);
        const seReady = NeighborsDone[i+1,j+1].fetchAdd(1);
        const southReady = NeighborsDone[i+1,j].fetchAdd(1);
        if (eastReady == 2) then begin computeHHelp(i, j+1);
        if (seReady == 2) then begin computeHHelp(i+1,j+1);
        if (southReady == 2) then begin computeHHelp(i+1,j );
    }
}
```

Disadvantages:
- Still uses a lot of tasks
- Each task is very fine-grained
### Coarsening the Parallelism into Chunks:

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Smith-Waterman
Chunked Data-Driven Task-Parallel Approach:

```plaintext
proc computeH(H: [0..n, 0..n] int) {
  const ProbSpace = H.domain.translate(1,1);
  const StrProbSpace = ProbSpace by (rowsPerChunk, colsPerChunk);
  var NeighborsDone: [StrProbSpace] atomic int;

  NeighborsDone[1, ..].add(1);
  NeighborsDone[.., 1].add(1);
  NeighborsDone[1, 1].add(1);
  sync { computeHHelp(1,1); }

  proc computeHHelp(x,y) {
    for (i,j) in ProbSpace[x..#rowsPerChunk, y..#colsPerChunk] do
      H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
    const eastReady = NeighborsDone[x, y+colsPerChunk].fetchAdd(1);
    const seReady = NeighborsDone[x+rowsPerChunk, y+colsPerChunk].fetchAdd(1);
    const southReady = NeighborsDone[x+rowsPerChunk, y].fetchAdd(1);
    if (eastReady == 2) then begin computeHHelp(x, y+colsPerChunk);
    if (seReady == 2) then begin computeHHelp(x+rowsPerChunk, y+colsPerChunk);
    if (southReady == 2) then begin computeHHelp(x+rowsPer Chunk, y);
    }
}
```

Use strided array for atomics
Change helper to iterate over a chunk serially
Stride indices to get to next chunk’s origin

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Distributed Smith-Waterman
Distributed Smith-Waterman

Now, what about distributed memory?

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   0 1 2 3 4 5 6 7 8
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 1 0 0 0 0 0 0 0 0 0
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```
### Distributed Smith-Waterman

Now, what about distributed memory?

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</table>

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Distributed Smith-Waterman

Now, what about distributed memory?

Advantages:
• Good cache behavior: Nice fat blocks of data touchable in memory order
• Pipeline parallelism: Good utilization once pipeline is filled
Distributed Chunked Data-Driven Task-Parallel Approach:

```cpp
const Hspace = {0..n, 0..n};
const LocaleGrid = Locales.reshape({0..#numLocales, 0..0});
const DistHSpace = Hspace mapped Block(Hspace, LocaleGrid);
var H: [DistHSpace] int;

proc computeH(H: [ ] int) {
    const ProbSpace = H.domain.translate(1,1);
    const StrProbSpace = ProbSpace by (rowsPerChunk, colsPerChunk);
    var NeighborsDone: [StrProbSpace] atomic int;

    ... etc...
    proc computeHHelp(x,y) {
        on H[x,y] {
            for (i,j) in ProbSpace[x..#rowsPerChunk, y..#colsPerChunk] do
                H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
            const eastReady = NeighborsDone[x, y+colsPerChunk].fetchAdd(1);
            ... etc...
            if (eastReady == 2) then begin computeHHelp(x, y+colsPerChunk);
            ... etc...
        }
    }
}
```
Any Questions about Smith-Waterman?
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