



# Task Parallelism By Example



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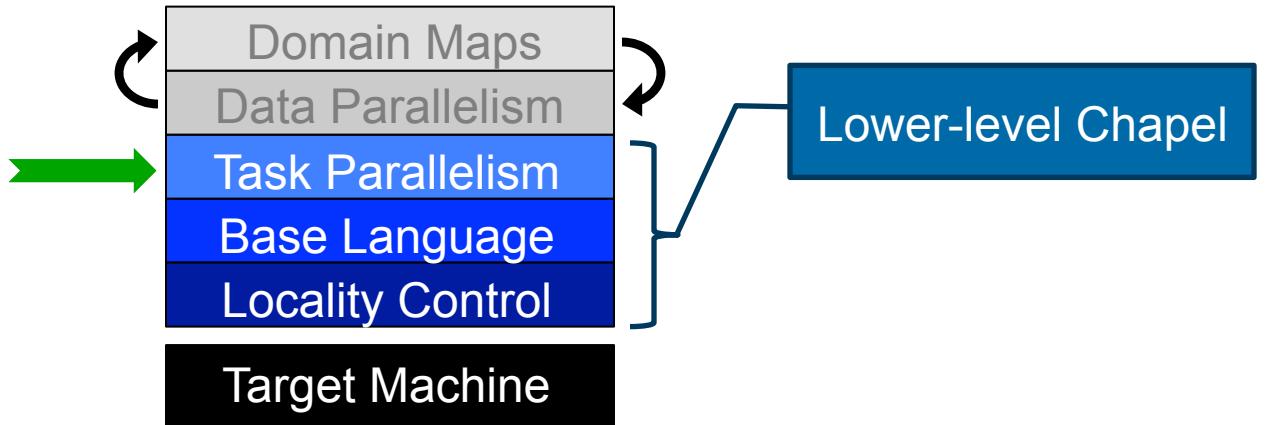
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# Task Parallel Features



# Task Parallel “Hello, world!”

- Multicore Hello World

```
config const numTasks = here.maxTaskPar;  
  
coforall tid in 0..#numTasks do  
    writeln("Hello, world! ",  
           "from task ", tid, " of ", numTasks);
```

```
Hello, world! from task 2 of 4  
Hello, world! from task 0 of 4  
Hello, world! from task 3 of 4  
Hello, world! from task 1 of 4
```

# Defining our Terms

**Task:** a unit of computation that can/should execute in parallel with other tasks

**Thread:** a system resource that executes tasks

- not exposed in the language
- occasionally exposed in the implementation

**Task Parallelism:** a style of parallel programming in which parallelism is driven by programmer-specified tasks

(in contrast with):

**Data Parallelism:** a style of parallel programming in which parallelism is driven by computations over collections of data elements or their indices

# Task Parallelism: Begin Statements

```
// create a fire-and-forget task for a statement
begin writeln("hello world");
writeln("goodbye");
```

## Possible outputs:

hello world  
goodbye

goodbye  
hello world

# Cobegin/Serial by Example: QuickSort

```
proc quickSort(arr: [?D],  
              thresh = log2(here.maxTaskPar),  
              depth = 0,  
              low: int = D.low,  
              high: int = D.high) {  
  
    if high - low < 8 {  
        bubbleSort(arr, low, high);  
    } else {  
        const pivotVal = findPivot(arr, low, high);  
        const pivotLoc = partition(arr, low, high, pivotVal);  
        serial (depth >= thresh) do cobegin {  
            quickSort(arr, thresh, depth+1, low, pivotLoc-1);  
            quickSort(arr, thresh, depth+1, pivotLoc+1, high);  
        }  
    }  
}
```

# Cobegin/Serial by Example: QuickSort

```
proc quickSort(arr: [?D],  
              depth = 0,  
              low: int = D.low,  
              high: int = D.high) {  
    if high - low < 8 {  
        bubbleSort(arr, low, high);  
    } else {  
        const pivotVal = findPivot(arr, low, high);  
        const pivotLoc = partition(arr, low, high, pivotVal);  
        serial (here.runningTasks > here.maxTaskPar) do  
            cobegin {  
                quickSort(arr, depth+1, low, pivotLoc-1);  
                quickSort(arr, depth+1, pivotLoc+1, high);  
            }  
        }  
    }  
}
```

# Task Parallelism: Cobegin Statements

```
// create a task per child statement
cobegin {
    producer(1);
    producer(2);
    consumer(1);
} // implicit join of the three tasks here
```

# Task Parallelism: Coforall Loops

```
// create a task per iteration
coforall t in 0..#numTasks {
    writeln("Hello from task ", t, " of ", numTasks);
} // implicit join of the numTasks tasks here

writeln("All tasks done");
```

## Sample output:

```
Hello from task 2 of 4
Hello from task 0 of 4
Hello from task 3 of 4
Hello from task 1 of 4
All tasks done
```

# What's worrisome about this loop?

```
var A: [1..1000000] real;  
coforall a in A do  
    a = 1.0;
```

# Comparison of Loops: For, Forall, and Coforall

## For loops: executed using one task

- use when a loop must be executed serially
- or when one task is sufficient for performance

## Forall loops: typically executed using $1 < \#tasks << \#iters$

- use when a loop *should* be executed in parallel...
- ...but *can* legally be executed serially
- use when desired # tasks  $<<$  # of iterations

## Coforall loops: executed using a task per iteration

- use when the loop iterations *must* be executed in parallel
- use when you want # tasks == # of iterations
- use when each iteration has substantial work

# Comparison of Begin, Cobegin, and Coforall

## begin:

- Use to create a dynamic task with an unstructured lifetime
- “fire and forget”

## cobegin:

- Use to create a related set of heterogeneous tasks
- ...or a small, finite set of homogenous tasks
- The parent task depends on the completion of the tasks

## coforall:

- Use to create a fixed or dynamic # of homogenous tasks
- The parent task depends on the completion of the tasks

**Note: All these concepts can be composed arbitrarily**

# Task Parallelism: Data-Driven Synchronization

1) ***atomic variables***: support atomic operations (as in C++)

- e.g., compare-and-swap; atomic sum, mult, etc.

2) ***single-assignment variables***: reads block until assigned

3) ***synchronization variables***: store full/empty state

- by default, reads/writes block until the state is full/empty

# Bounded Buffer Producer/Consumer Example

```

cobegin { producer(); consumer(); }

// 'sync' types store full/empty state along with value
var buff$: [0..#buffersize] sync real;

proc producer() {
    var i = 0;
    for ... {
        i = (i+1) % buffersize;
        buff$[i] = ...; // writes block until empty, leave full
    } }

proc consumer() {
    var i = 0;
    while ... {
        i= (i+1) % buffersize;
        ...buff$[i]...; // reads block until full, leave empty
    } }

```

# Synchronization Variables

- **Syntax**

```
sync-type:  
  sync type
```

- **Semantics**

- Stores *full/empty* state along with normal value
- Defaults to *full* if initialized, *empty* otherwise
- Default read blocks until *full*, leaves *empty*
- Default write blocks until *empty*, leaves *full*

- **Examples: Critical sections and futures**

```
var future$: sync real;  
  
begin future$ = compute();  
res = computeSomethingElse();  
useComputedResults(future$, res);
```

```
var lock$: sync bool;  
  
lock$ = true;  
critical();  
var lockval = lock$;
```

# Atomic Variables

- **Syntax**

```
sync-type:  
    atomic type
```

- **Semantics**

- Supports operations on variable atomically w.r.t. other tasks
- Based on C/C++ atomic operations

- **Example: Trivial barrier**

```
var count: atomic int, done: atomic bool;  
  
proc barrier(numTasks) {  
    const myCount = count.fetchAdd(1);  
    if (myCount < numTasks) then  
        done.waitFor(true);  
    else  
        done.testAndSet();  
}
```

# Atomic Methods

- **read() :t**                          return current value
- **write(v:t)**                          store v as current value
- **exchange(v:t) :t**                          store v, returning previous value
- **compareExchange(old:t, new:t) :bool**  
    store new iff previous value was *old*; returns true on success
- **waitFor(v:t)**                          wait until the stored value is v
- **add(v:t)**                                  add v to the value atomically
- **fetchAdd(v:t)**  
*(sub, or, and, xor also supported similarly)*                          same, returning pre-sum value
  
- **testAndSet()**  
    bool    like *exchange(true)* for atomic
- **clear()**    like *write(false)* for atomic bool

# Comparison of Synchronization Types

## sync/single:

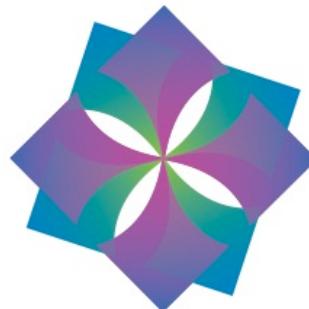
- Best for producer/consumer style synchronization
  - “this task should block until something happens”
- Use single for write-once values

## atomic:

- Best for uncoordinated accesses to shared state



# Smith-Waterman Algorithm for Sequence Alignment



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# Smith-Waterman

**Goal:** Determine the similarities/differences between two protein sequences/nucleotides.

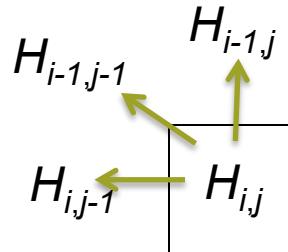
- e.g., ACACACTA and AGCACACA\*

**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*

\*Source of running example: Wikipedia

# Smith-Waterman

## Naïve Task-Parallel Approach:

```

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);
}

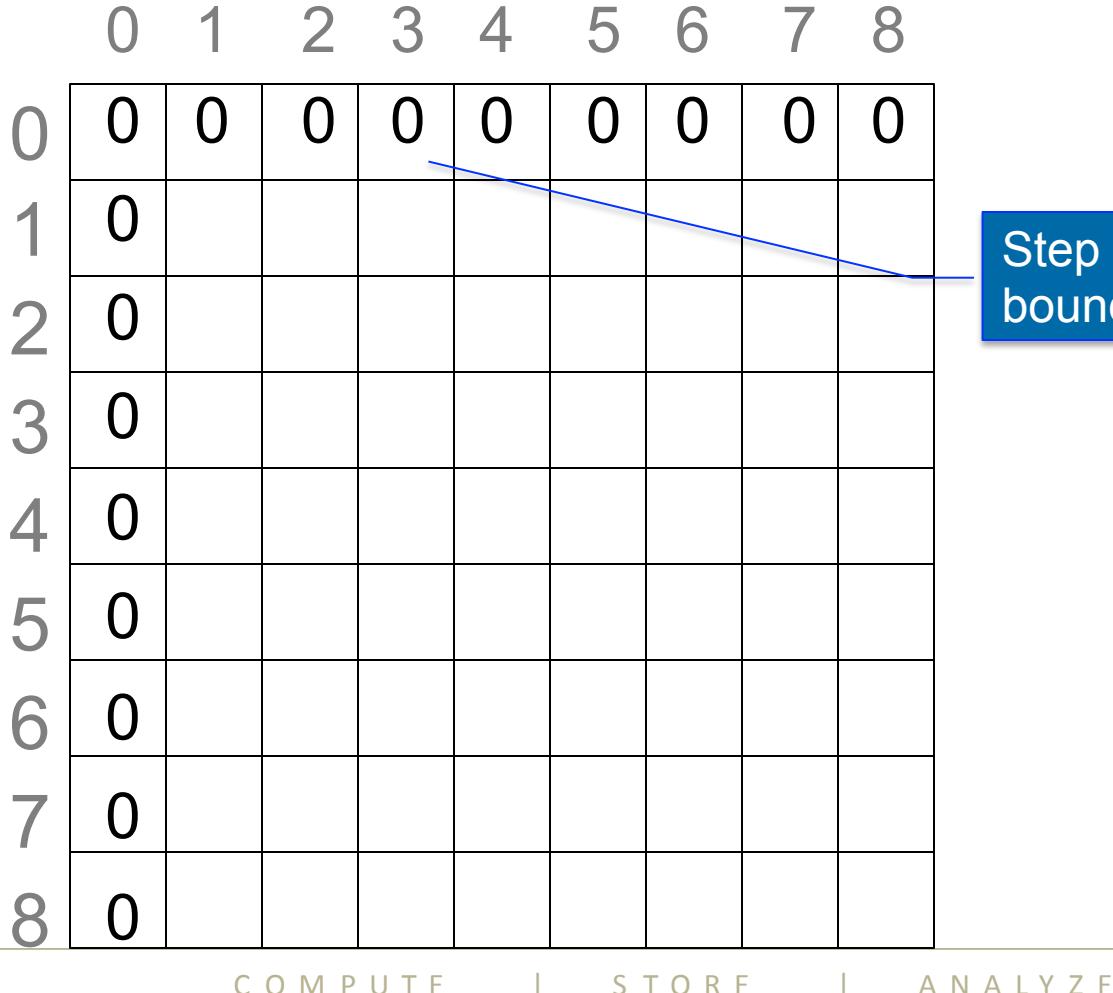
```

Note: Recomputes most subexpressions redundantly

This is a case for dynamic programming!

# Smith-Waterman

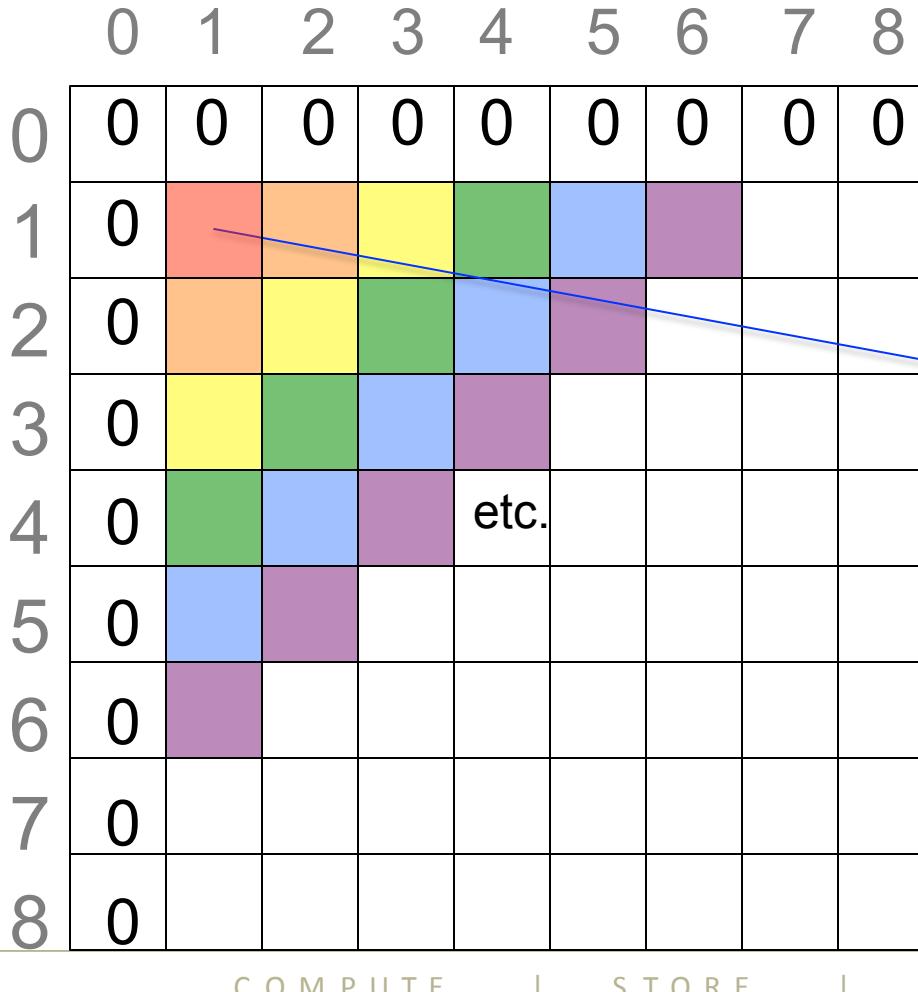
## Dynamic Programming Approach:



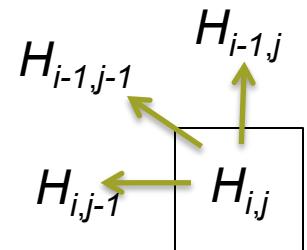
Step 1: Initialize boundaries to 0

# Smith-Waterman

## Dynamic Programming Approach:



Step 2: Compute cells when we're able to



# Smith-Waterman

## Dynamic Programming Approach:

	0	1	2	3	4	5	6	7	8
0	0	0	0	0	0	0	0	0	0
1	0	2	1	2	1	2	1	0	2
2	0	1	1	1	1	1	1	0	1
3	0	0	3	2	3	2	3	2	1
4	0	2	2	5	4	5	4	3	4
5	0	1	4	4	7	6	7	6	5
6	0	2	3	6	6	9	8	7	8
7	0	1	4	5	8	8	11	10	9
8	0	2	3	6	7	10	10	10	12

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Step 3: Follow trail of breadcrumbs back

# Smith-Waterman

## Dynamic Programming Approach:

	0	1	2	3	4	5	6	7	8
0	0	0	0	0	0	0	0	0	0
1	0	2	1	2	1	2	1	0	2
2	0	1	1	1	1	1	1	0	1
3	0	0	3	2	3	2	3	2	1
4	0	2	2	5	4	5	4	3	4
5	0	1	4	4	7	6	7	6	5
6	0	2	3	6	6	9	8	7	8
7	0	1	4	5	8	8	11	10	9
8	0	2	3	6	7	10	10	10	12

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Step 3: Follow trail of breadcrumbs back

# Smith-Waterman

## Dynamic Programming Approach:

	A	C	A	C	A	C	T	A
0	0	0	0	0	0	0	0	0
A	0	2	1	2	1	2	1	0
G	0	1	1	1	1	1	1	0
C	0	0	3	2	3	2	3	2
A	0	2	2	5	4	5	4	3
C	0	1	4	4	7	6	7	6
A	0	2	3	6	6	9	8	7
C	0	1	4	5	8	8	11	10
A	0	2	3	6	7	10	10	10

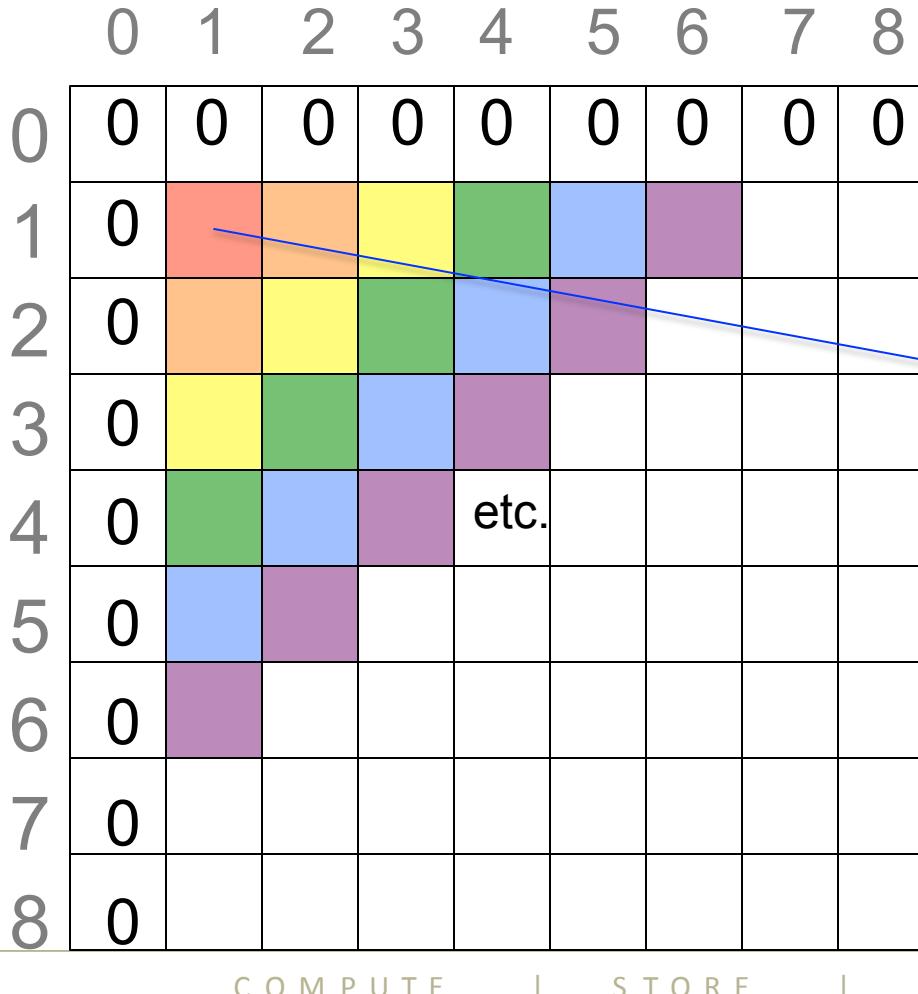
Step 4: Interpret the path against the original sequences

AGCACAC-A  
A-CACACTA

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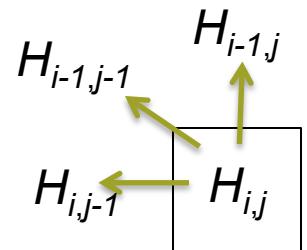
# Smith-Waterman

## Dynamic Programming Approach:



Step 2: Compute cells when we're able to

How could we do this in parallel?



# Smith-Waterman

## Data-Parallel Approach:

```

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]);
        }
}

```

Loop over upper diagonals serially

Process each diagonal in parallel

Repeat for lower diagonals

### 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

# Smith-Waterman

## Naïve Data-Driven Task-Parallel Approach:

```

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;
}

```

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

```

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 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

# Smith-Waterman

## Naïve Data-Driven Task-Parallel Approach:

```

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;
    }
}

```

### Disadvantages:

- Still not great in cache use
- Uses  $n^2$  tasks
- Most spend most of their time blocking

# Smith-Waterman

## Slightly Less Naïve Data-Driven Task-Parallel Approach:

```

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); }

```

sync to ensure they're all done before we go on

```

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

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# Smith-Waterman

## Slightly Less Naïve Data-Driven Task-Parallel Approach:

```
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); }
```

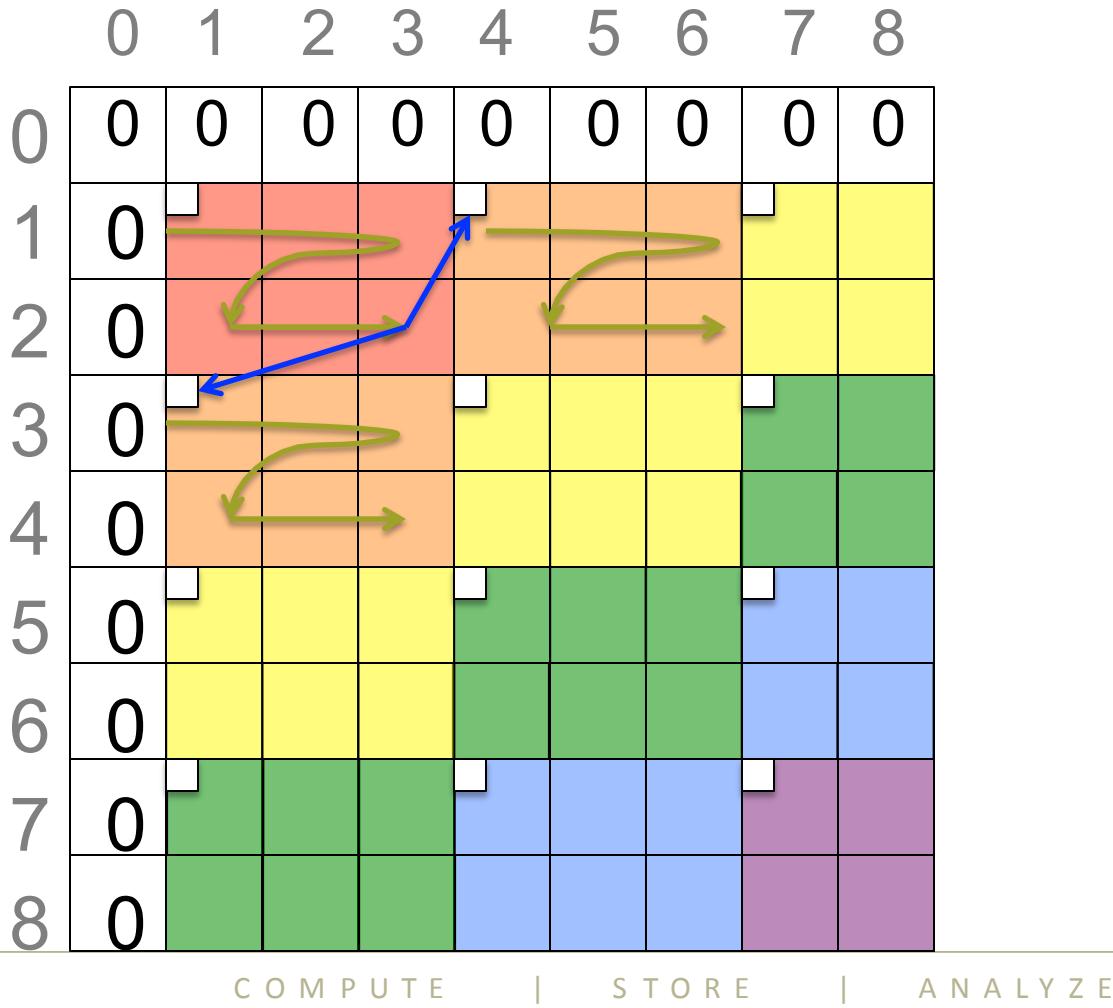
```
proc computeHHelp(i,j) {
    H[i,j] = f(H[i-1,j-1], H[i-1,j], H[i,j-1]);
    const eastReady = NeighborsDone[i, j+1].fetchAdd(1);
    const seReady = NeighborsDone[i+1,j+1].fetchAdd(1);
    const southReady = NeighborsDone[i+1,j ].fetchAdd(1);
    if (eastReady == 2) then begin computeHHelp(i, j+1);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

# Smith-Waterman

## Coarsening the Parallelism into Chunks:



# Smith-Waterman

## Chunked Data-Driven Task-Parallel Approach:

```
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;
```

Use strided array for atomics

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

Change helper to iterate over a chunk serially

```
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+rowsPerChunk, y);
}
```

Stride indices to get to next chunk's origin

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# Questions about Task Parallelism in Chapel?



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