
CS481: Bioinformatics Algorithms

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APPROXIMATE STRING MATCHING: BANDED ALIGNMENT

Limiting indels

- We know how to calculate global and local alignments in $O(mn)$ time
 - What if the problem definition limits the indels to w , where $w \ll n$ and $w \ll m$?
 - Can we improve run time?
-

Limiting indels

		A	C	C	A	C	A	C	A
	0								
A		1							
C			2						
A				1					
C					0				
C						1			
A							2		
T								1	
A									2

Example: Limit indels to $w=2$

Banded global alignment

		A	C	C	A	C	A	C	A
	0	-2	-4	-6					
A	-2	1	-1	-3	-5				
C	-4	-1	2	0	-2	-4			
A	-6	-3	0	1	1	-1	-3		
C		-5	-2	1	0	2	0	-2	
C			-4	-1	0	1	1	1	-1
A				-3	0	-1	2	0	2
T					-2	-1	0	1	0
A						-1	0	-1	2

- Example
 - $w=2$
- What's the running time?

DP IN LINEAR SPACE & DIVIDE AND CONQUER ALGORITHMS

Divide and Conquer Algorithms

- ❑ **Divide** problem into sub-problems
 - ❑ **Conquer** by solving sub-problems recursively. If the sub-problems are small enough, solve them in brute force fashion
 - ❑ **Combine** the solutions of sub-problems into a solution of the original problem (tricky part)
-

Sorting Problem

- Given: an unsorted array

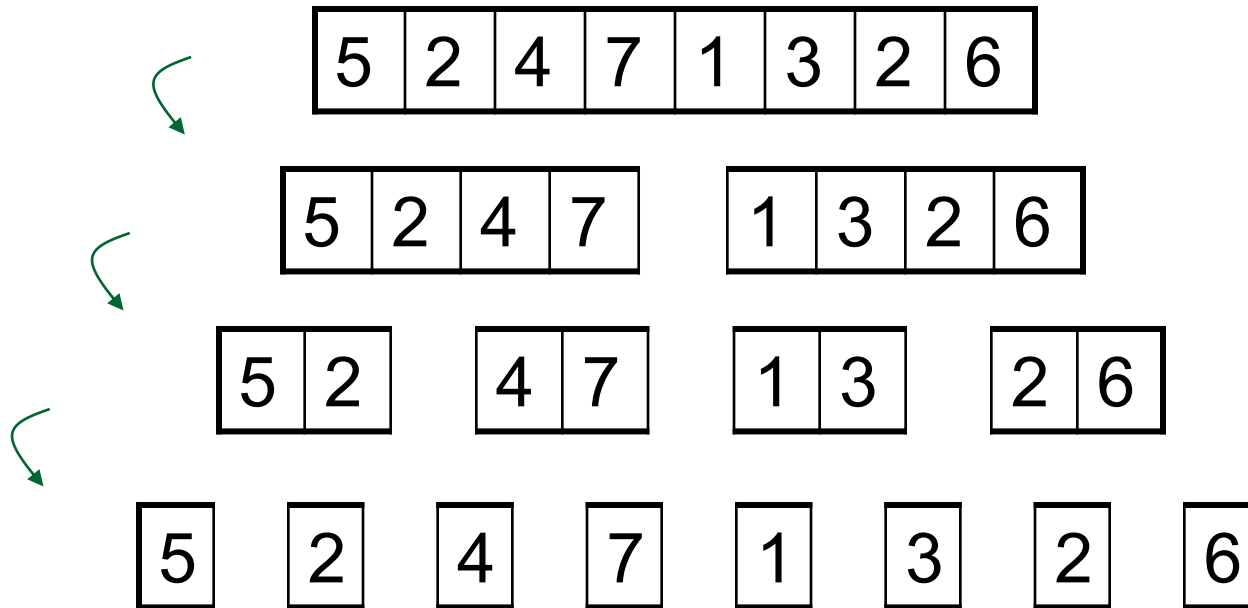
5	2	4	7	1	3	2	6
---	---	---	---	---	---	---	---

- Goal: sort it

1	2	2	3	4	5	6	7
---	---	---	---	---	---	---	---

Mergesort: Divide Step

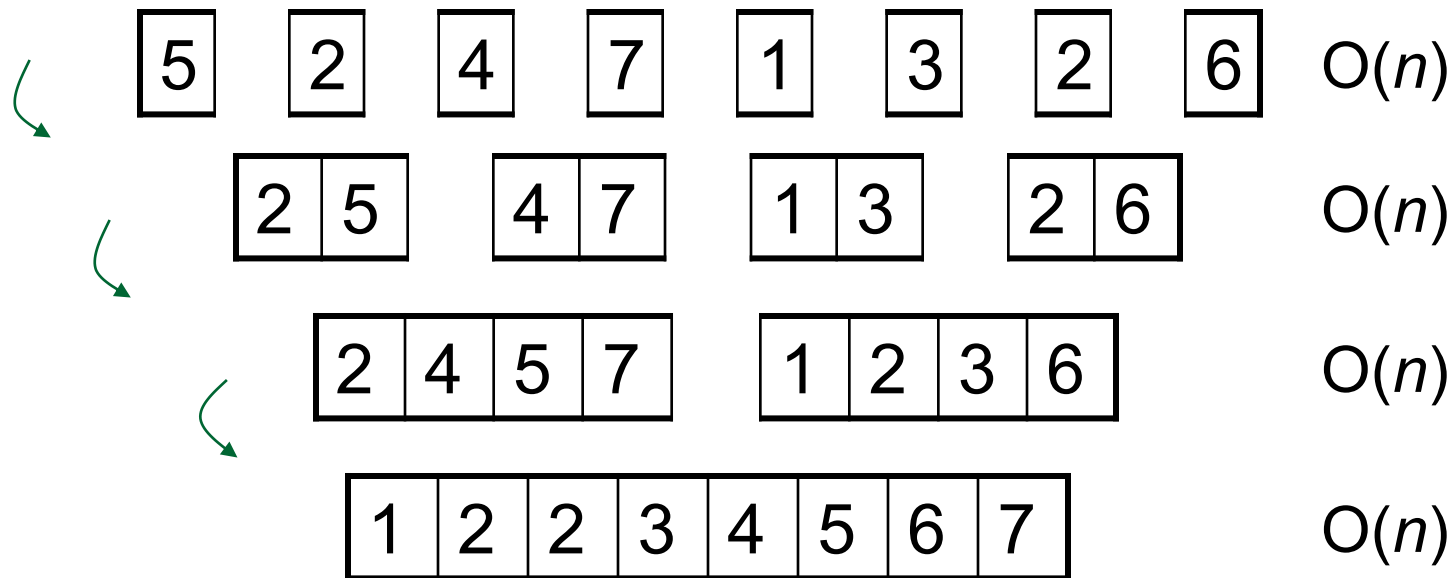
Step 1 – Divide



$\log(n)$ divisions to split an array of size n into single elements

Mergesort: Conquer Step

Step 2 – Conquer



$\log n$ iterations, each iteration takes $O(n)$ time. Total Time: $O(n \log n)$

Mergesort: Combine Step

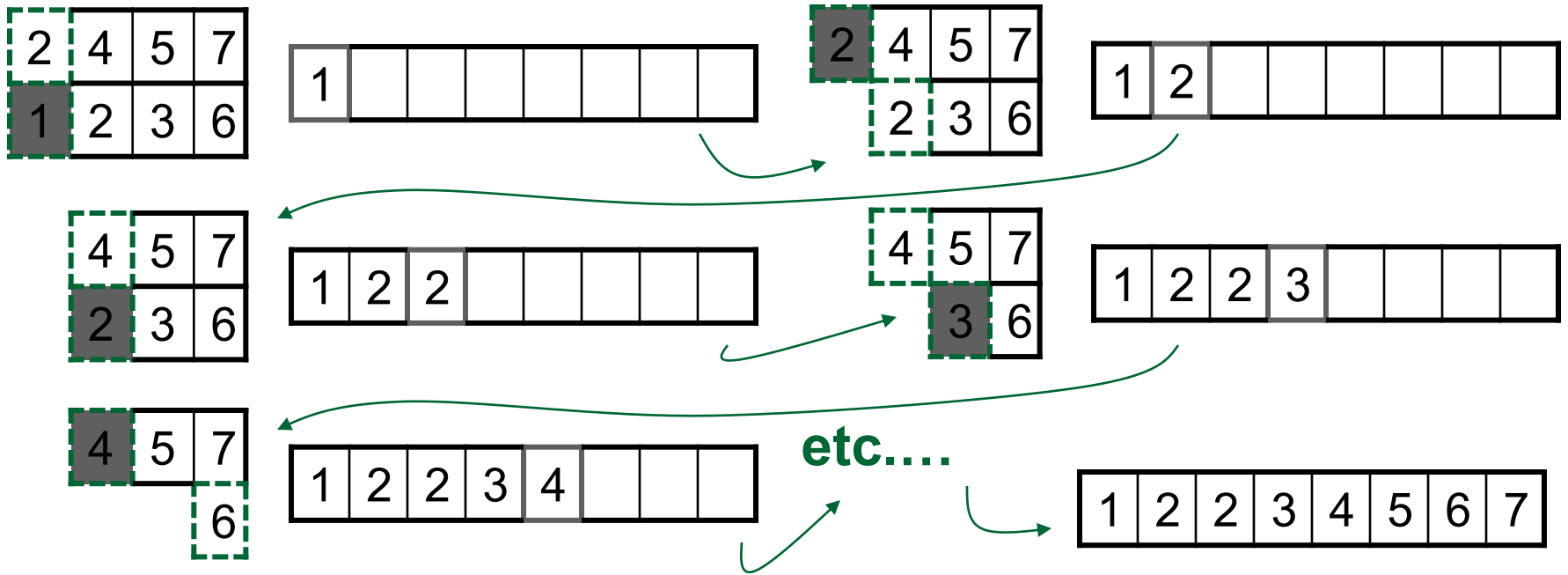
Step 3 – Combine



- 2 arrays of size 1 can be easily merged to form a sorted array of size 2
- 2 sorted arrays of size n and m can be merged in $O(n+m)$ time to form a sorted array of size $n+m$

Mergesort: Combine Step

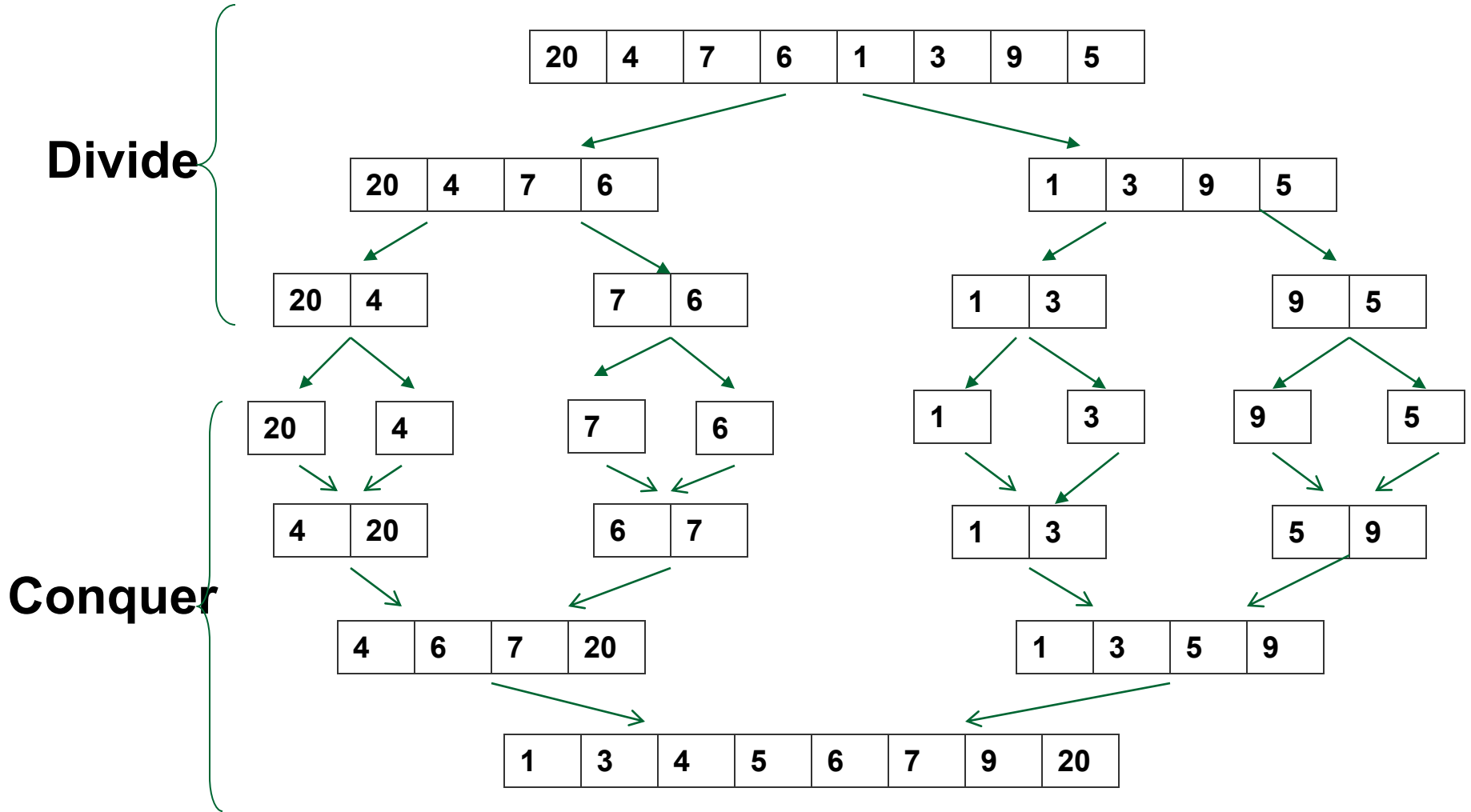
Combining 2 arrays of size 4



Merge Algorithm

1. Merge(a, b)
2. $n1 \leftarrow$ size of array a
3. $n2 \leftarrow$ size of array b
4. $a_{n1+1} \leftarrow \infty$
5. $a_{n2+1} \leftarrow \infty$
6. $i \leftarrow 1$
7. $j \leftarrow 1$
8. **for** $k \leftarrow 1$ to $n1 + n2$
9. **if** $a_i < b_j$
10. $c_k \leftarrow a_i$
11. $i \leftarrow i + 1$
12. **else**
13. $c_k \leftarrow b_j$
14. $j \leftarrow j + 1$
15. **return** c

Mergesort: Example



MergeSort Algorithm

1. MergeSort(c)
2. $n \leftarrow$ size of array c
3. *if* $n = 1$
4. *return* c
5. $left \leftarrow$ list of first $n/2$ elements of c
6. $right \leftarrow$ list of last $n - n/2$ elements of c
7. $sortedLeft \leftarrow$ MergeSort($left$)
8. $sortedRight \leftarrow$ MergeSort($right$)
9. $sortedList \leftarrow$ Merge($sortedLeft, sortedRight$)
10. *return* $sortedList$

MergeSort: Running Time

- The problem is simplified to smaller steps
 - for the i 'th merging iteration, the complexity of the problem is $O(n)$
 - number of iterations is $O(\log n)$
 - running time: $O(n \log n)$
-

Divide and Conquer Approach to LCS

Path(*source*, *sink*)

- if(*source* & *sink* are in consecutive columns)
 - output the longest path from *source* to *sink*
 - else
 - *middle* ← middle vertex between *source* & *sink*
 - Path(*source*, *middle*)
 - Path(*middle*, *sink*)
-

Divide and Conquer Approach to LCS

Path(*source*, *sink*)

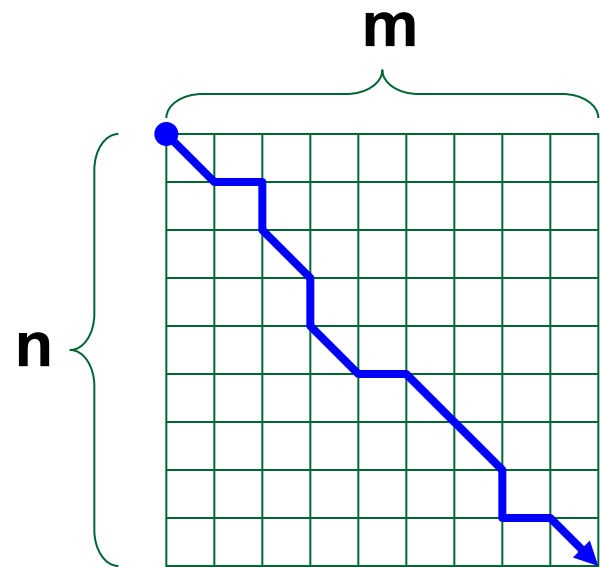
- if(*source* & *sink* are in consecutive columns)
- output the longest path from *source* to *sink*
- else
- *middle* ← middle vertex between *source* & *sink*
- Path(*source*, *middle*)
- Path(*middle*, *sink*)

The only problem left is how to find this “middle vertex”!

Computing Alignment Path Requires Quadratic Memory

Alignment Path

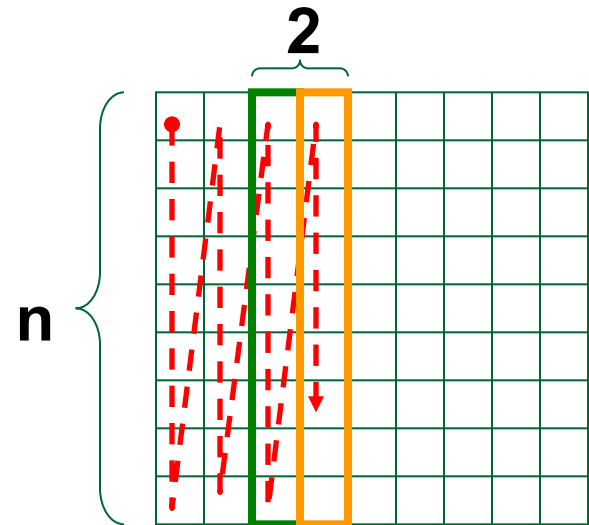
- Space complexity for computing alignment path for sequences of length n and m is $O(nm)$
- We need to keep all backtracking references in memory to reconstruct the path (backtracking)



Computing Alignment Score with Linear Memory

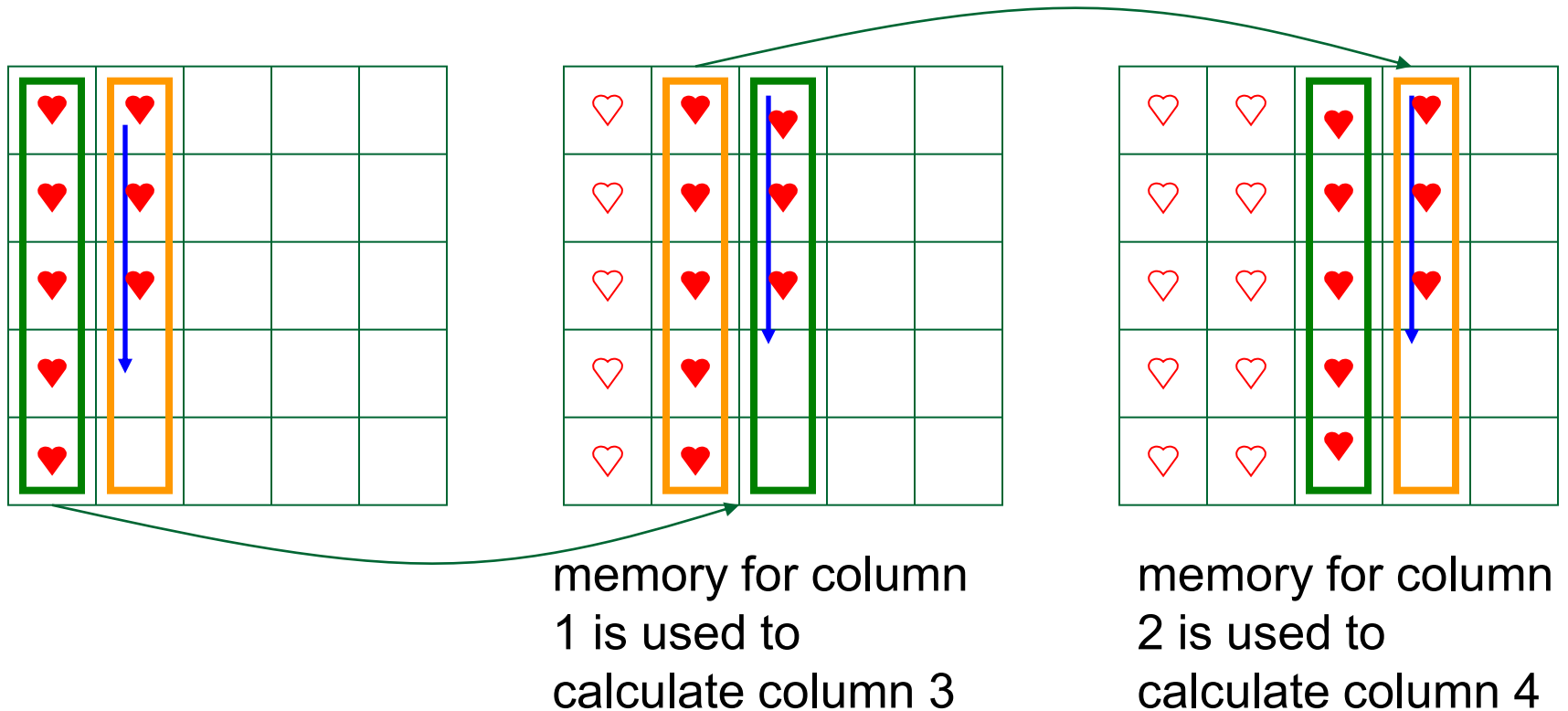
Alignment Score

- Space complexity of computing just the score itself is $O(n)$
- We only need the previous column to calculate the current column, and we can then throw away that previous column once we're done using it

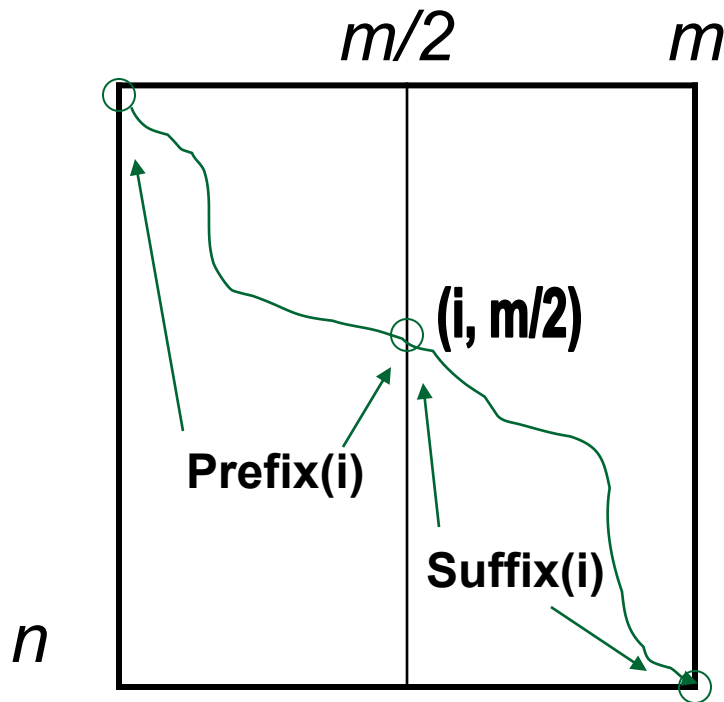


Computing Alignment Score: Recycling Columns

Only two columns of scores are saved at any given time



Crossing the Middle Line



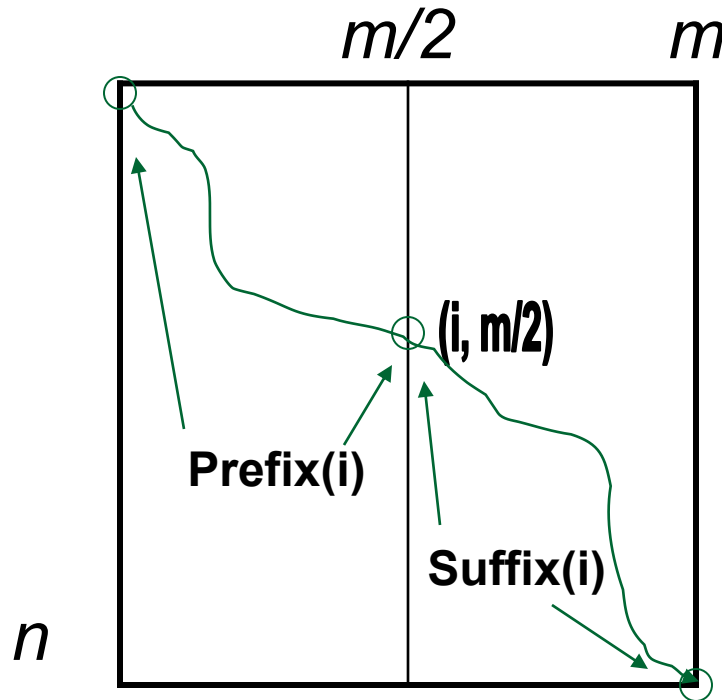
We want to calculate the longest path from $(0,0)$ to (n,m) that passes through $(i, m/2)$ where i ranges from 0 to n and represents the i -th row

Define

$length(i)$

as the length of the longest path from $(0,0)$ to (n,m) that passes through vertex $(i, m/2)$

Crossing the Middle Line

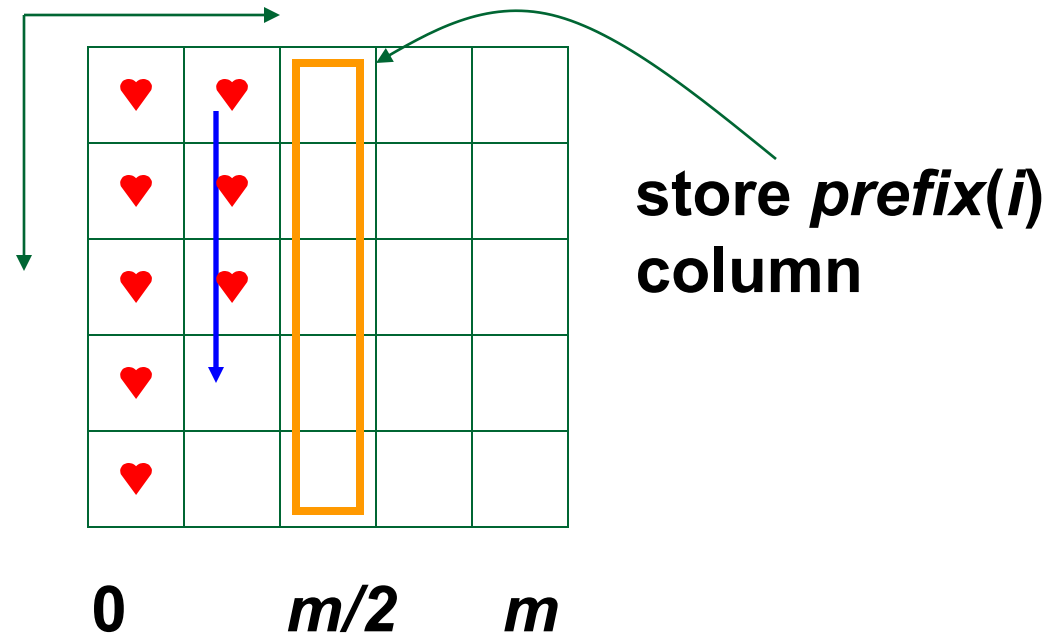


Define $(mid, m/2)$ as the vertex where the longest path crosses the middle column.

$$length(mid) = \text{optimal length} = \max_{0 \leq i \leq n} length(i)$$

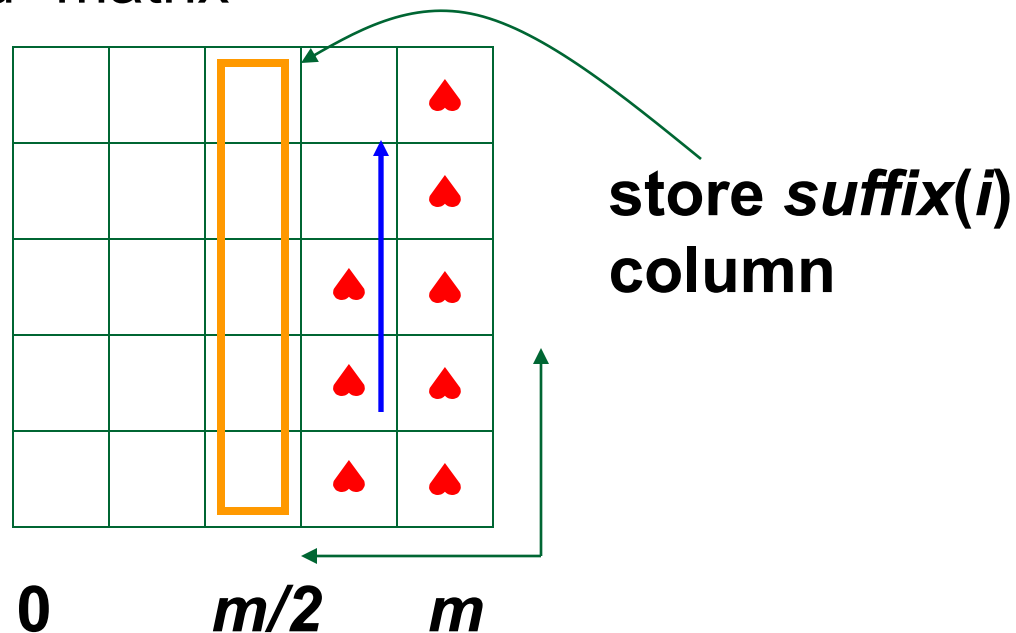
Computing Prefix(i)

- $prefix(i)$ is the length of the longest path from $(0,0)$ to $(i, m/2)$
- Compute $prefix(i)$ by dynamic programming in the left half of the matrix



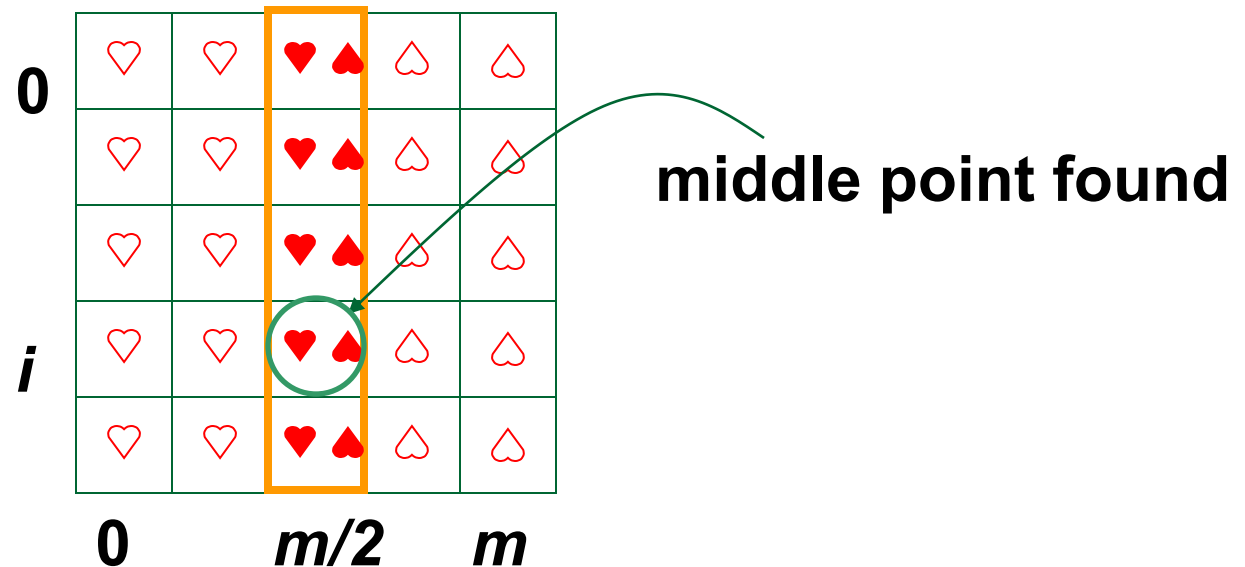
Computing $\text{Suffix}(i)$

- $\text{suffix}(i)$ is the length of the longest path from $(i, m/2)$ to (n, m)
- $\text{suffix}(i)$ is the length of the longest path from (n, m) to $(i, m/2)$ with all edges reversed
- Compute $\text{suffix}(i)$ by dynamic programming in the right half of the “reversed” matrix

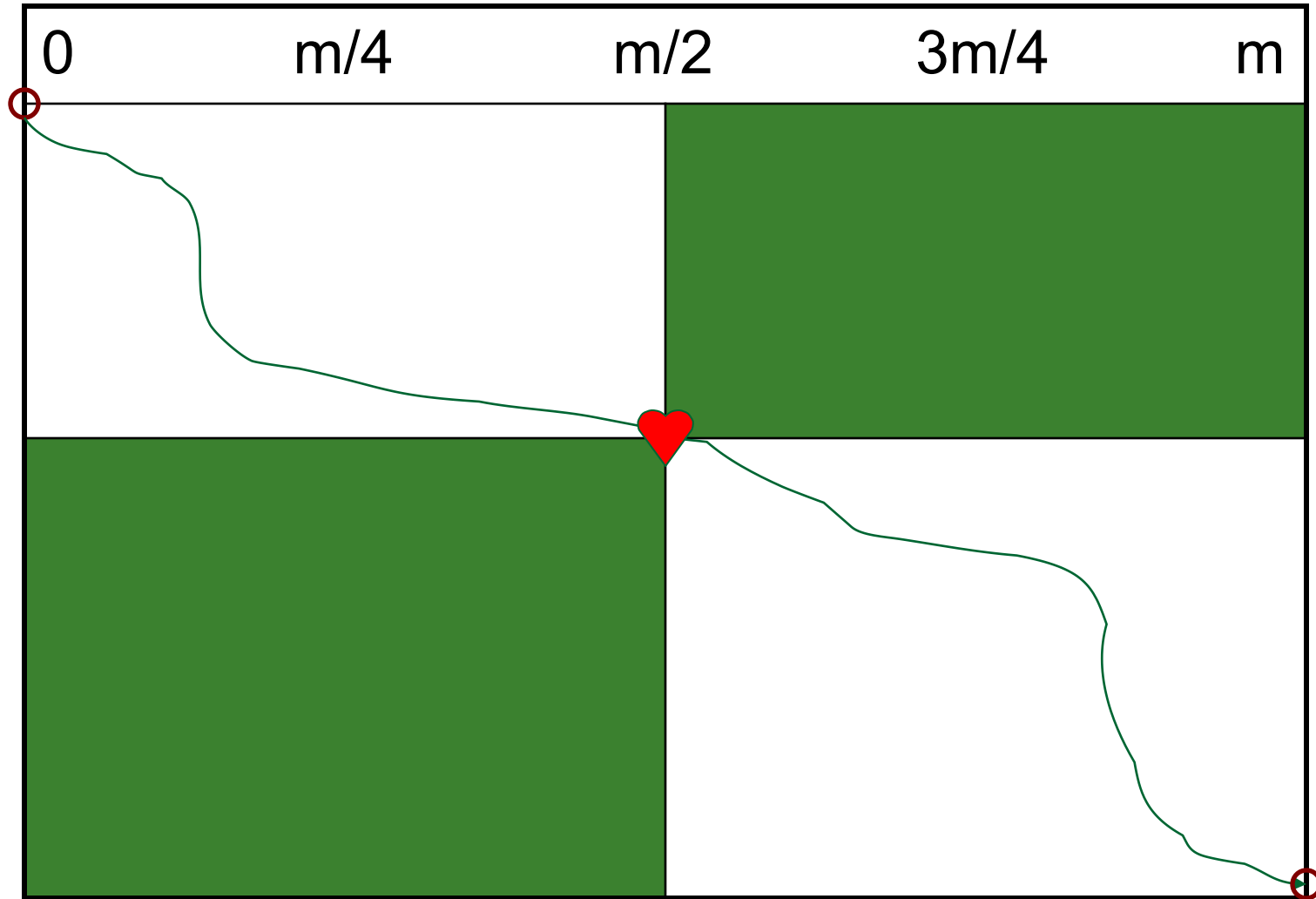


$$Length(i) = Prefix(i) + Suffix(i)$$

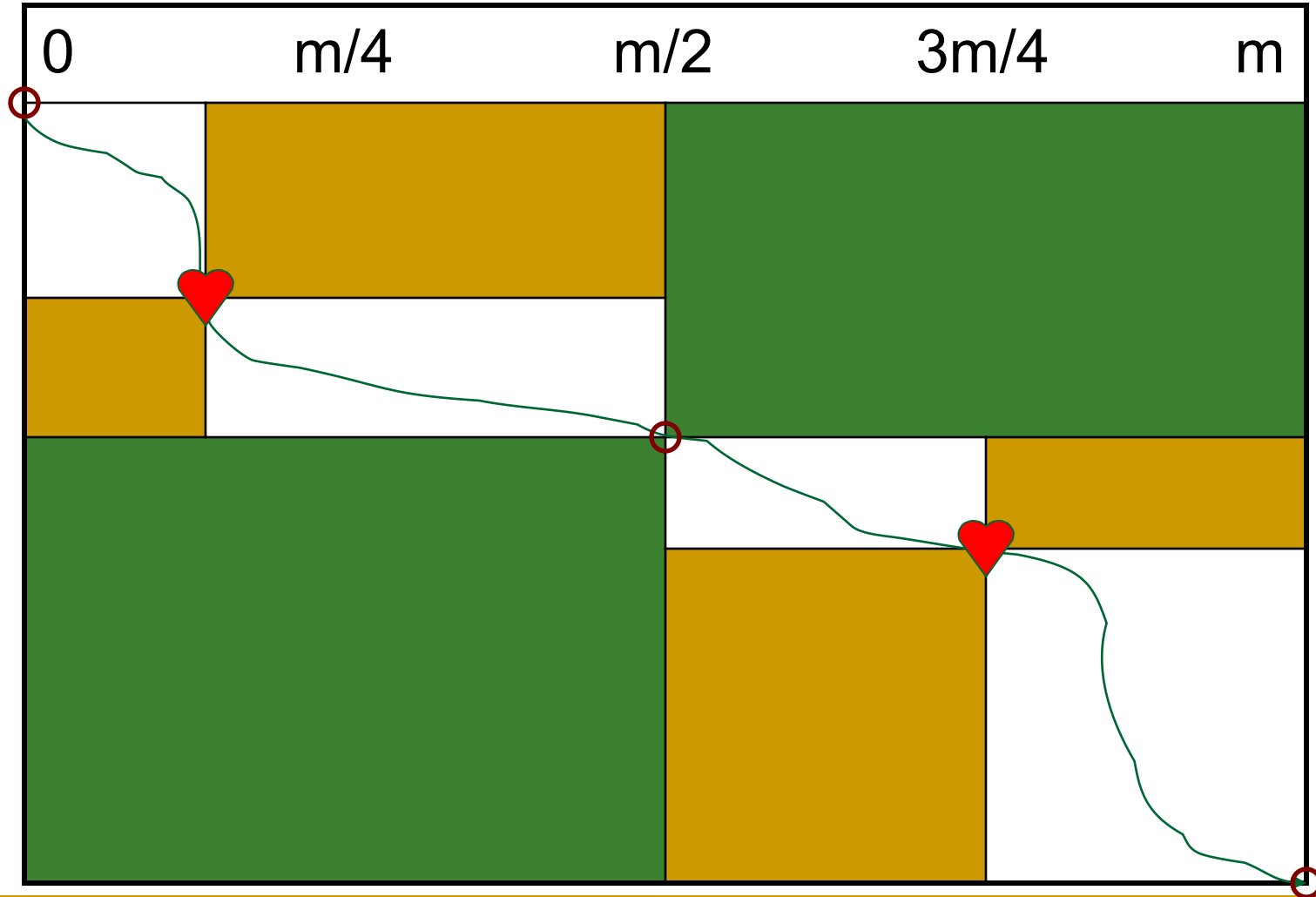
- Add $prefix(i)$ and $suffix(i)$ to compute $length(i)$:
 - $length(i) = prefix(i) + suffix(i)$
- You now have a middle vertex of the maximum path $(i, m/2)$ as maximum of $length(i)$



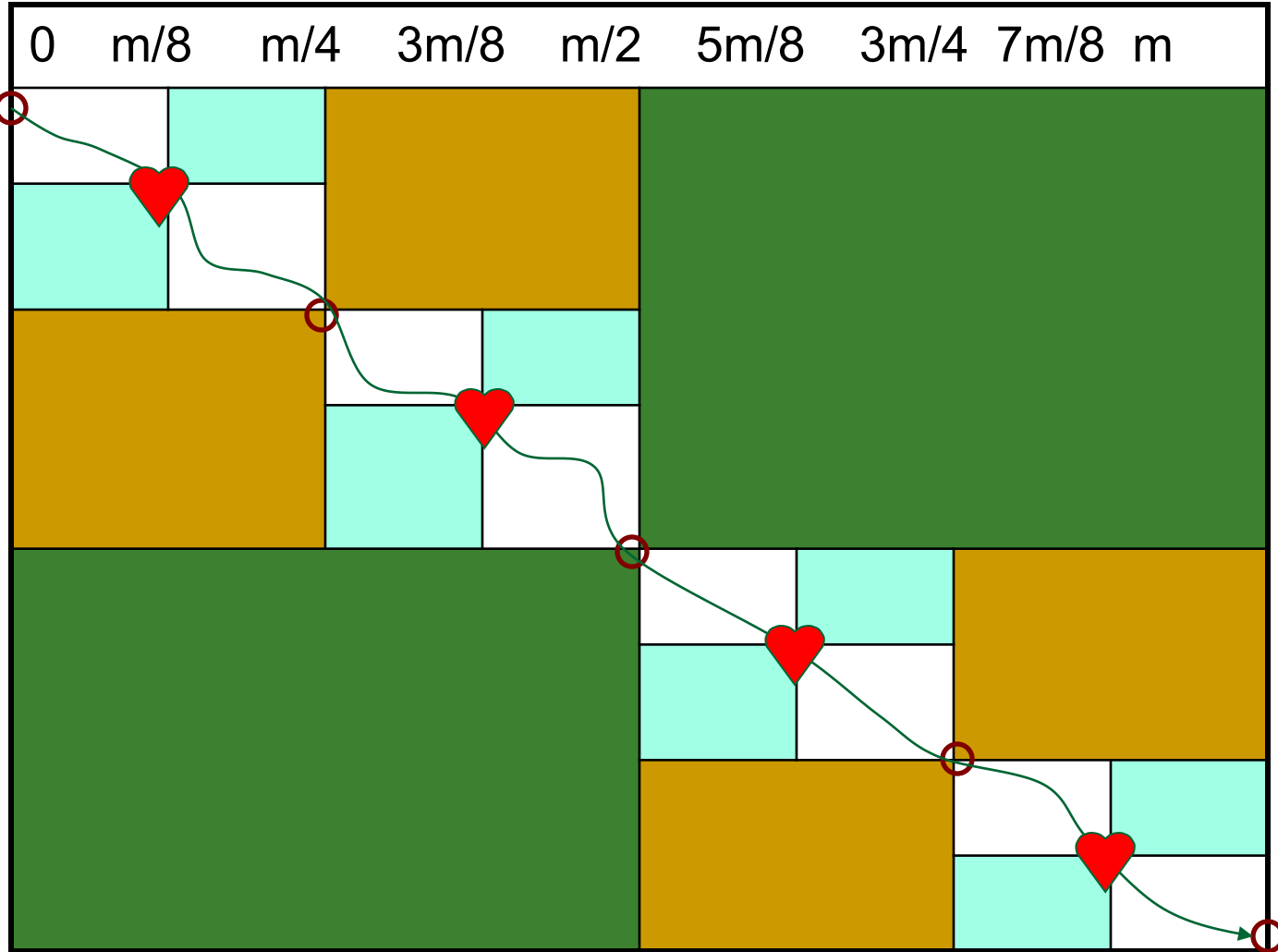
Finding the Middle Point



Finding the Middle Point again



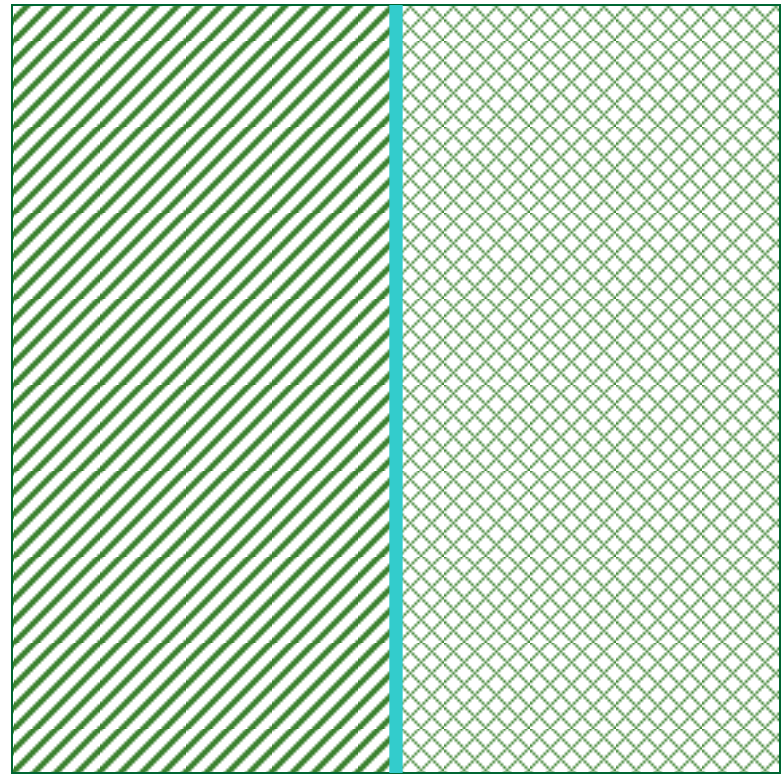
And Again



Time = Area: First Pass

- On first pass, the algorithm covers the entire area

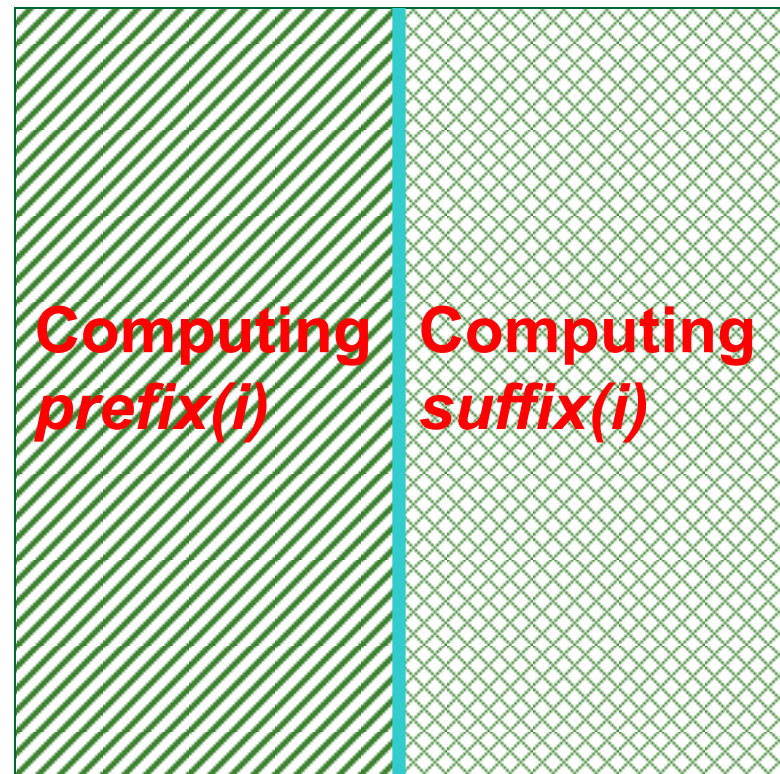
$$\text{Area} = n \cdot m$$



Time = Area: First Pass

- On first pass, the algorithm covers the entire area

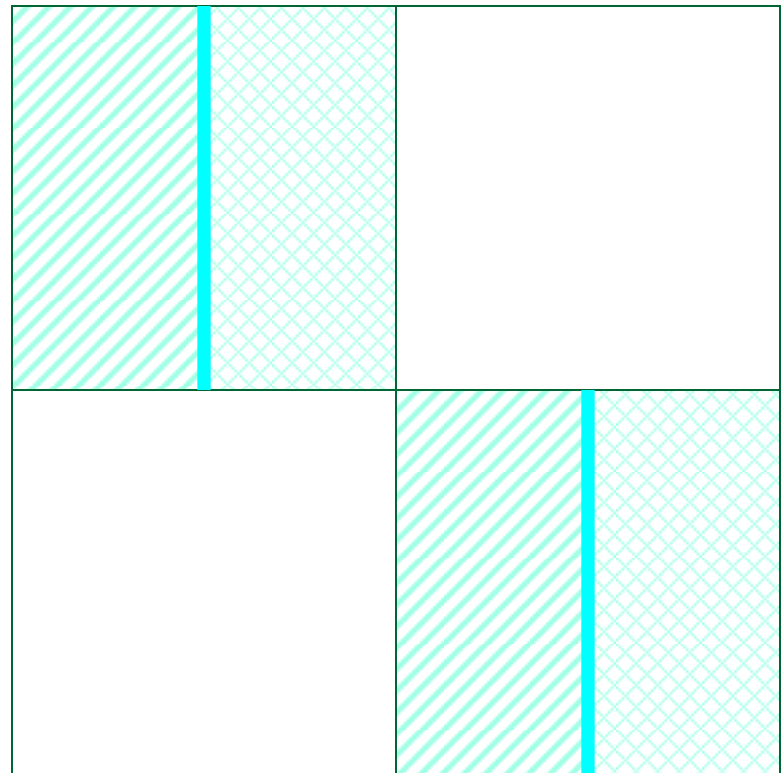
$$\text{Area} = n \cdot m$$



Time = Area: Second Pass

- On second pass, the algorithm covers only $1/2$ of the area

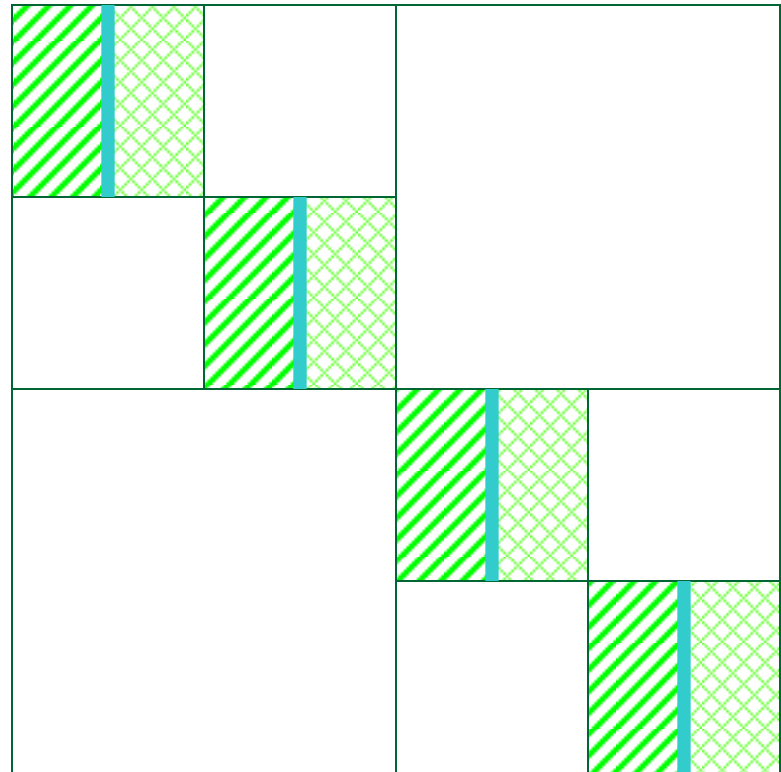
Area/2



Time = Area: Third Pass

- On third pass, only 1/4th is covered.

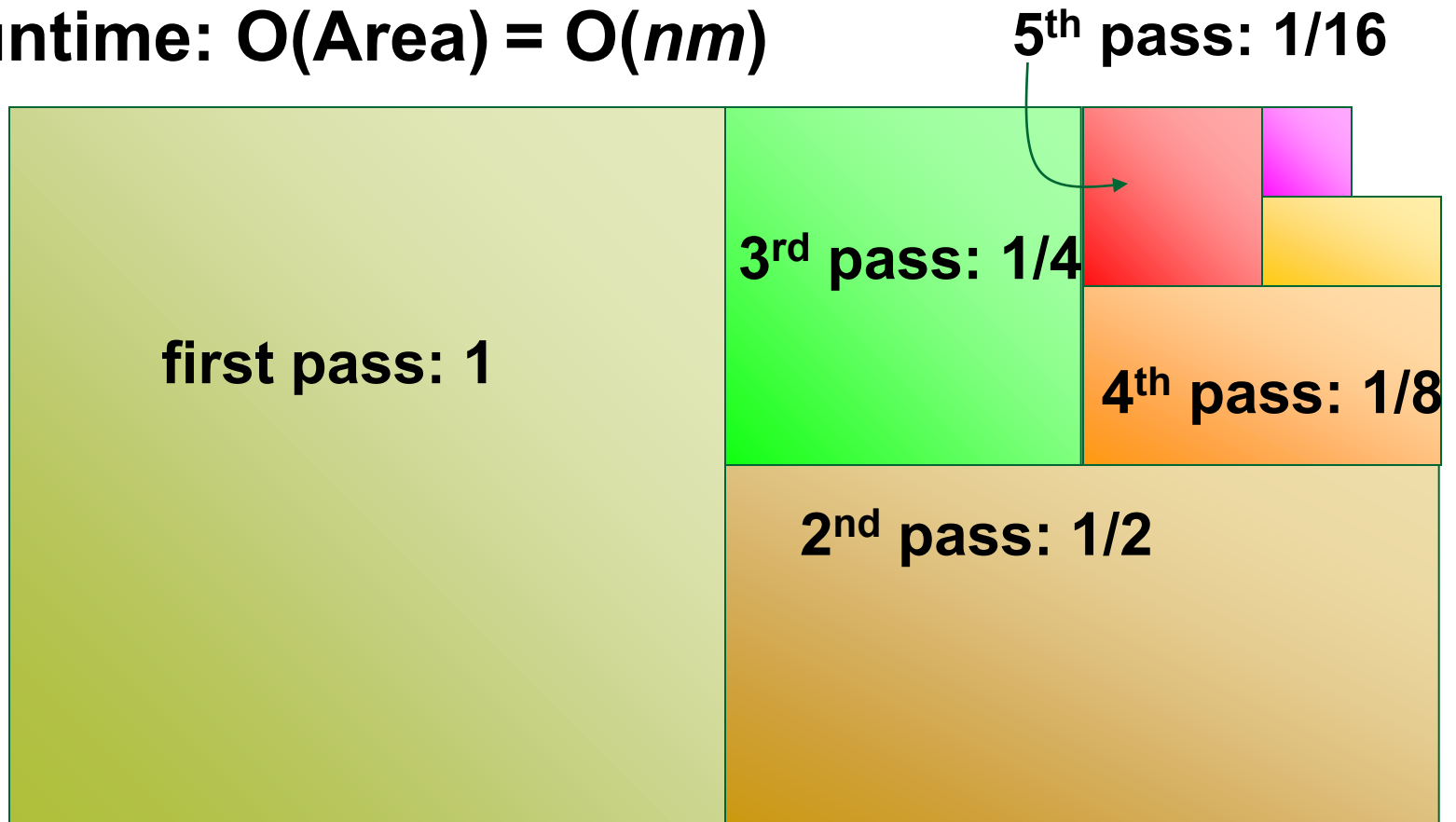
Area/4



Geometric Reduction At Each Iteration

$$1 + \frac{1}{2} + \frac{1}{4} + \dots + \left(\frac{1}{2}\right)^k \leq 2$$

- **Runtime: $O(\text{Area}) = O(nm)$**



Is It Possible to Align Sequences in Subquadratic Time?

- Dynamic Programming takes $O(n^2)$ for global alignment
 - Can we do better?
 - Yes, use *Four-Russians Speedup*
-

Partitioning Sequences into Blocks

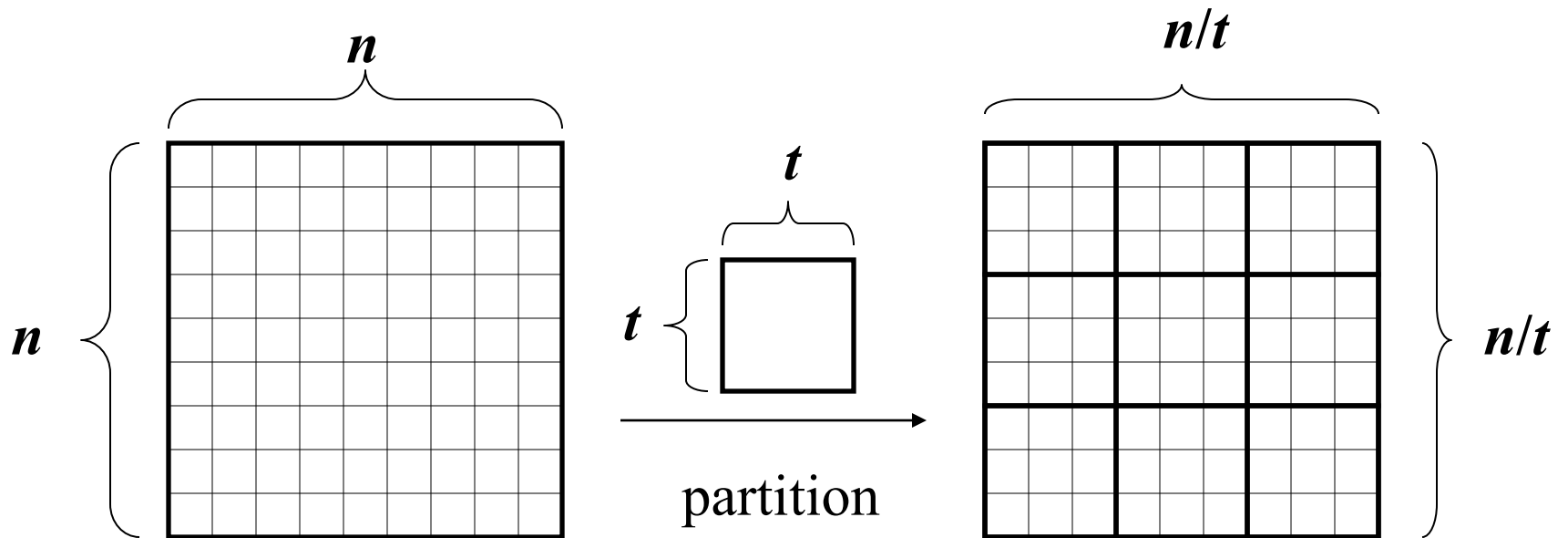
- Partition the $n \times n$ grid into blocks of size $t \times t$
- We are comparing two sequences, each of size n , and each sequence is sectioned off into chunks, each of length t
- Sequence $\mathbf{u} = u_1 \dots u_n$ becomes

$$|u_1 \dots u_t| |u_{t+1} \dots u_{2t}| \dots |u_{n-t+1} \dots u_n|$$

and sequence $\mathbf{v} = v_1 \dots v_n$ becomes

$$|v_1 \dots v_t| |v_{t+1} \dots v_{2t}| \dots |v_{n-t+1} \dots v_n|$$

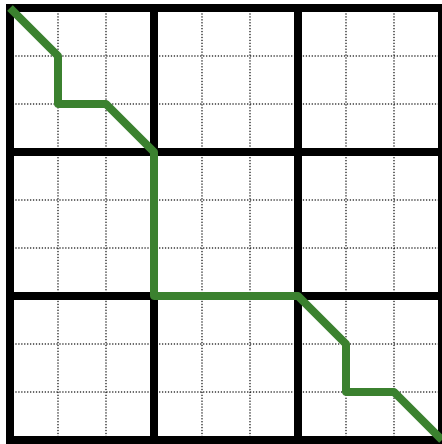
Partitioning Alignment Grid into Blocks



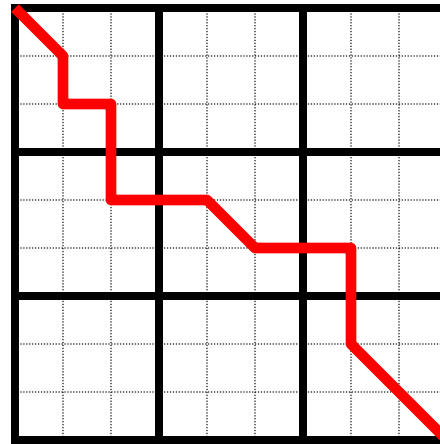
Block Alignment

- **Block alignment** of sequences u and v :
 1. An entire block in u is aligned with an entire block in v
 2. An entire block is inserted
 3. An entire block is deleted
 - **Block path**: a path that traverses every $t \times t$ square through its corners
-

Block Alignment: Examples



valid



invalid

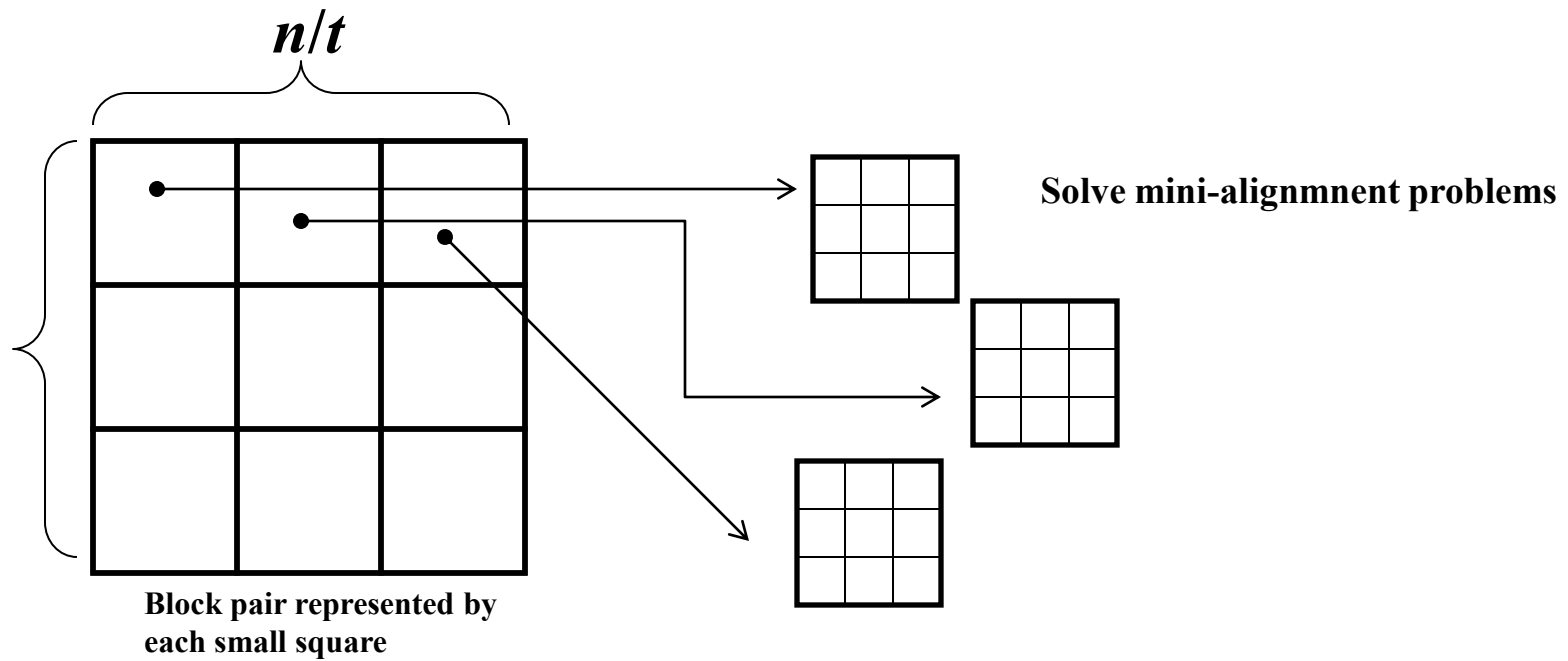
Block Alignment Problem

- Goal: Find the longest block path through an edit graph
 - Input: Two sequences, u and v partitioned into blocks of size t . This is equivalent to an $n \times n$ edit graph partitioned into $t \times t$ subgrids
 - Output: The block alignment of u and v with the maximum score (longest block path through the edit graph)
-

Constructing Alignments within Blocks

- To solve: compute alignment score $\beta_{i,j}$ for each pair of blocks $|u_{(i-1)*t+1} \dots u_{i*t}|$ and $|v_{(j-1)*t+1} \dots v_{j*t}|$
 - How many blocks are there per sequence?
 (n/t) blocks of size t
 - How many pairs of blocks for aligning the two sequences?
 $(n/t) \times (n/t)$
 - For each block pair, solve a mini-alignment problem of size $t \times t$
-

Constructing Alignments within Blocks



Block Alignment: Dynamic Programming

- Let $s_{i,j}$ denote the optimal block alignment score between the first i blocks of u and first j blocks of v

$$s_{i,j} = \max \left\{ \begin{array}{l} s_{i-1,j} - \sigma_{\text{block}} \\ s_{i,j-1} - \sigma_{\text{block}} \\ s_{i-1,j-1} - \beta_{i,j} \end{array} \right.$$

σ_{block} is the penalty for inserting or deleting an entire block

$\beta_{i,j}$ is score of pair of blocks in row i and column j .

Block Alignment Runtime

- Indices i, j range from 0 to n/t

- Running time of algorithm is

$$O([n/t] * [n/t]) = O(n^2/t^2)$$

if we don't count the time to compute each $\beta_{i,j}$

Block Alignment Runtime (cont'd)

- Computing all $\beta_{i,j}$ requires solving $(n/t)^*(n/t)$ mini block alignments, each of size $(t*t)$
- So computing all $\beta_{i,j}$ takes time
$$O([n/t]^*[n/t]^*t*t) = O(n^2)$$
- This is the same as dynamic programming
- How do we speed this up?

Four Russians Technique

- Let $t = \log(n)$, where t is block size, n is sequence size.
 - Instead of having $(n/t)^*(n/t)$ mini-alignments, construct $4^t \times 4^t$ mini-alignments for all pairs of strings of t nucleotides (huge size), and put in a lookup table.
 - However, size of lookup table is not really that huge if t is small. Let $t = (\log n)/4$. Then $4^t \times 4^t = n$
-

Look-up Table for Four Russians Technique

each sequence
has t
nucleotides

	AAAAA	AAAAAC	AAAAAG	AAAAAT	AAAACA	..
AAAAAA						
AAAAAC						
AAAAAG						
AAAAAT						
AAAACA						
...						

Lookup table “*Score*”

size is only n ,
instead of
 $(n/t) * (n/t)$

New Recurrence

- The new lookup table *Score* is indexed by a pair of *t*-nucleotide strings, so

$$s_{i,j} = \max \left\{ \begin{array}{l} s_{i-1,j} - \sigma_{\text{block}} \\ s_{i,j-1} - \sigma_{\text{block}} \\ s_{i-1,j-1} - \text{Score}(i^{\text{th}} \text{ block of } v, j^{\text{th}} \text{ block of } u) \end{array} \right.$$

Four Russians Speedup Runtime

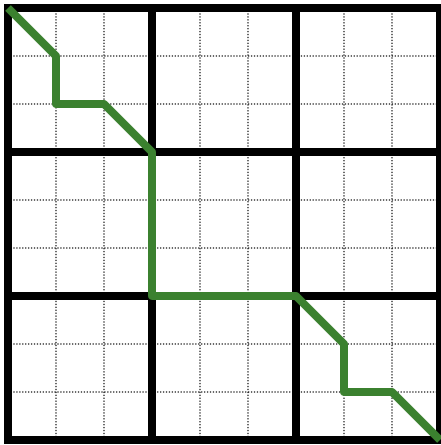
- Since computing the lookup table *Score* of size n takes $O(n)$ time, the running time is mainly limited by the $(n/t)^*(n/t)$ accesses to the lookup table
 - Each access takes $O(\log n)$ time
 - Overall running time: $O([n^2/t^2]*\log n)$
 - Since $t = \log n$, substitute in:
 - $O([n^2/\{\log n\}^2]*\log n) \geq O(n^2/\log n)$
-

So Far...

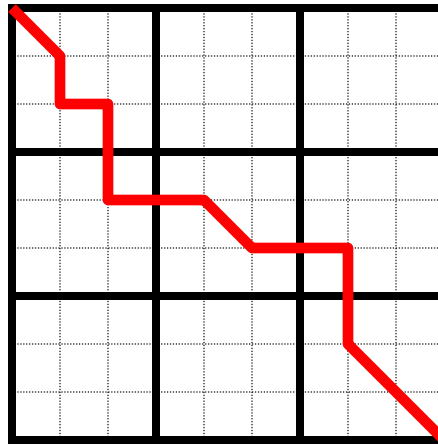
- We can divide up the grid into blocks and run dynamic programming only on the corners of these blocks
 - In order to speed up the mini-alignment calculations to under n^2 , we create a lookup table of size n , which consists of all scores for all t -nucleotide pairs
 - Running time goes from quadratic, $O(n^2)$, to subquadratic: $O(n^2/\log n)$
-

Four Russians Speedup for LCS

- Unlike the block partitioned graph, the LCS path does not have to pass through the vertices of the blocks.



**block
alignment**

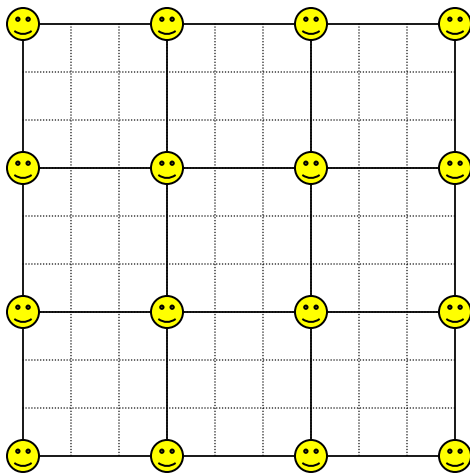


**longest common
subsequence**

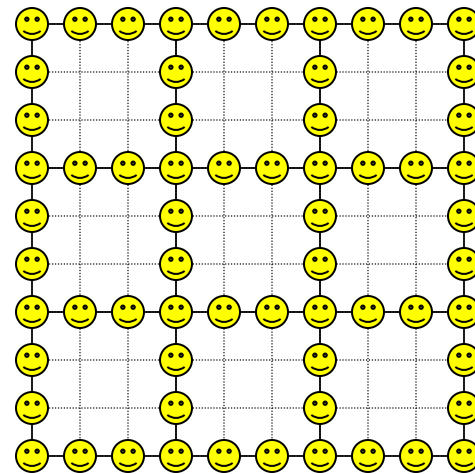
Block Alignment vs. LCS

- In block alignment, we only care about the corners of the blocks.
 - In LCS, we care about all points on the edges of the blocks, because those are points that the path can traverse.
 - Recall, each sequence is of length n , each block is of size t , so each sequence has (n/t) blocks.
-

Block Alignment vs. LCS: Points Of Interest



block alignment
has $(n/t) * (n/t) =$
 (n^2/t^2) points of
interest



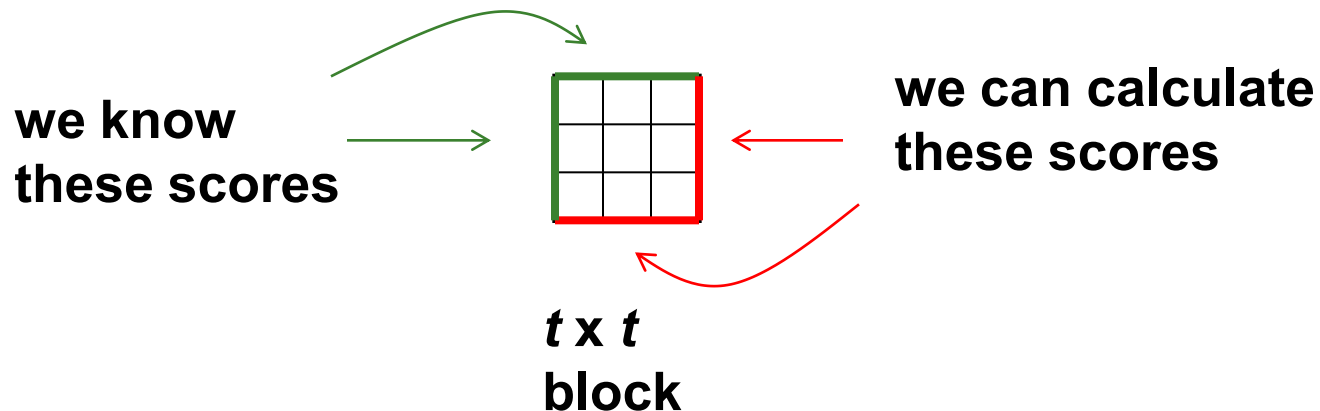
LCS alignment
has $O(n^2/t)$
points of
interest

Traversing Blocks for LCS

- Given alignment scores $s_{i,*}$ in the first row and scores $s_{*,j}$ in the first column of a $t \times t$ mini square, compute alignment scores in the last row and column of the minisquare.
- To compute the last row and the last column score, we use these 4 variables:
 1. alignment scores $s_{i,*}$ in the first row
 2. alignment scores $s_{*,j}$ in the first column
 3. substring of sequence u in this block (4^t possibilities)
 4. substring of sequence v in this block (4^t possibilities)

Traversing Blocks for LCS (cont'd)

- If we used this to compute the grid, it would take quadratic, $O(n^2)$ time, but we want to do better.



Four Russians Speedup

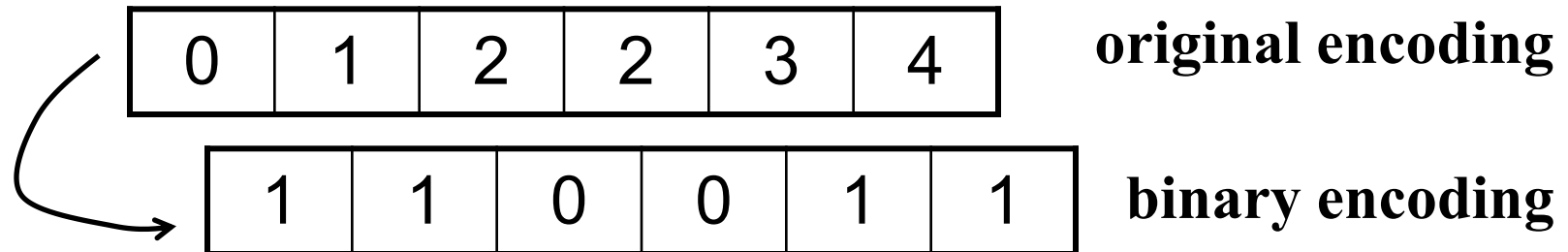
- Build a lookup table for all possible values of the four variables:
 1. all possible scores for the first row $S_{*,j}$
 2. all possible scores for the first column $S_{*,j}$
 3. substring of sequence u in this block (4^t possibilities)
 4. substring of sequence v in this block (4^t possibilities)
- For each quadruple we store the value of the score for the last row and last column.
- This will be a huge table, but we can eliminate alignments scores that don't make sense

Reducing Table Size

- Alignment scores in LCS are monotonically increasing, and adjacent elements can't differ by more than 1
 - Example: 0, 1, 2, 2, 3, 4 is ok; 0, 1, **2, 4**, 5, 8, is not because 2 and 4 differ by more than 1 (and so do 5 and 8)
 - Therefore, we only need to store quadruples whose scores are monotonically increasing and differ by at most 1
-

Efficient Encoding of Alignment Scores

- Instead of recording numbers that correspond to the index in the sequences u and v , we can use binary to encode the differences between the alignment scores



Reducing Lookup Table Size

- 2^t possible scores ($t =$ size of blocks)
- 4^t possible strings
 - Lookup table size is $(2^t * 2^t) * (4^t * 4^t) = 2^{6t}$
- Let $t = (\log n)/4$;
 - Table size is: $2^{6((\log n)/4)} = n^{(6/4)} = n^{(3/2)}$
- Time = $O([n^2/t^2] * \log n)$
- $O([n^2/\{\log n\}^2] * \log n) \geq O(n^2/\log n)$

Main Observation

Within a rectangle of the DP matrix,
values of D depend only
on the values of A, B, C,
and substrings $x_{l\dots l'}$, $y_{r\dots r'}$

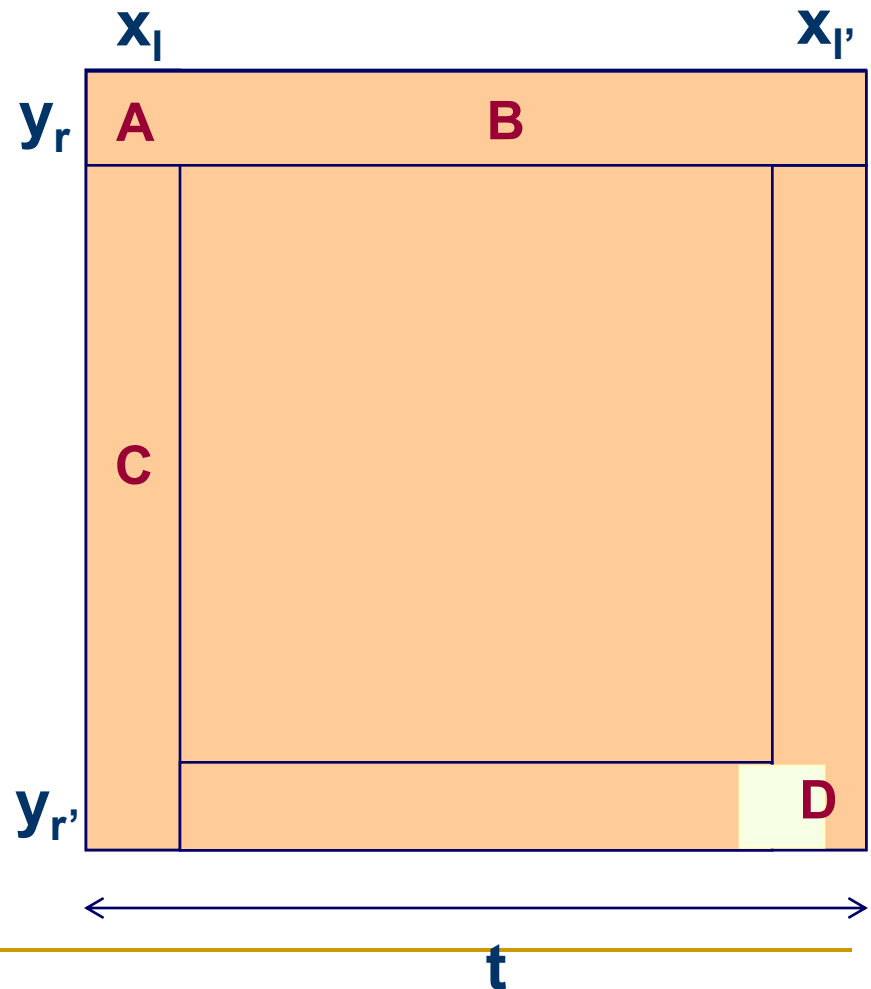
Definition:

A t-block is a $t \times t$ square of the
DP matrix

Idea:

Divide matrix in t-blocks,
Precompute t-blocks

Speedup: $O(t)$

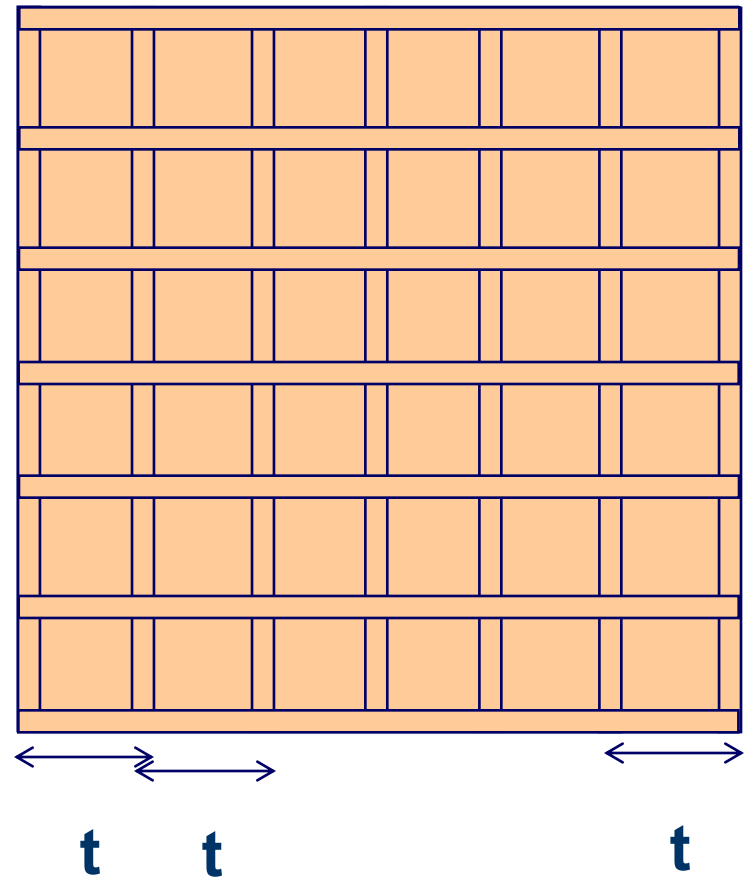


The Four-Russian Algorithm

Main structure of the algorithm:

- Divide $N \times N$ DP matrix into $K \times K \log_2 N$ -blocks that overlap by 1 column & 1 row
- For $i = 1 \dots K$
- For $j = 1 \dots K$
- Compute $D_{i,j}$ as a function of $A_{i,j}$, $B_{i,j}$, $C_{i,j}$, $x[l_i \dots l'_i]$, $y[r_j \dots r'_j]$

Time: $O(N^2 / \log^2 N)$



Precomputation

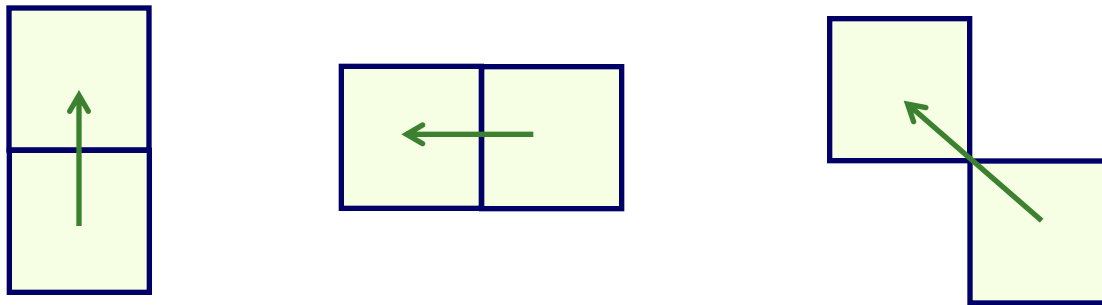
- By definition every cell has a value in $[0, \dots, n]$
- There are $(n+1)^t$ possible values for any t -length row or column
- If $\sigma = |\Sigma|$, then there are σ^t possible substrings of length t
- Number of distinct computations is $(n+1)^{2t} \sigma^{2t}$
- t^2 computations required to evaluate a t -block
- Overall: $\Theta((n+1)^{2t} \sigma^{2t} t^2) = \Omega(n^2)$

The Four-Russian Algorithm

Another observation:

(Assume $m = 0$, $s = 1$, $d = 1$)

Lemma. Two adjacent cells of $F(.,.)$ differ by at most 1



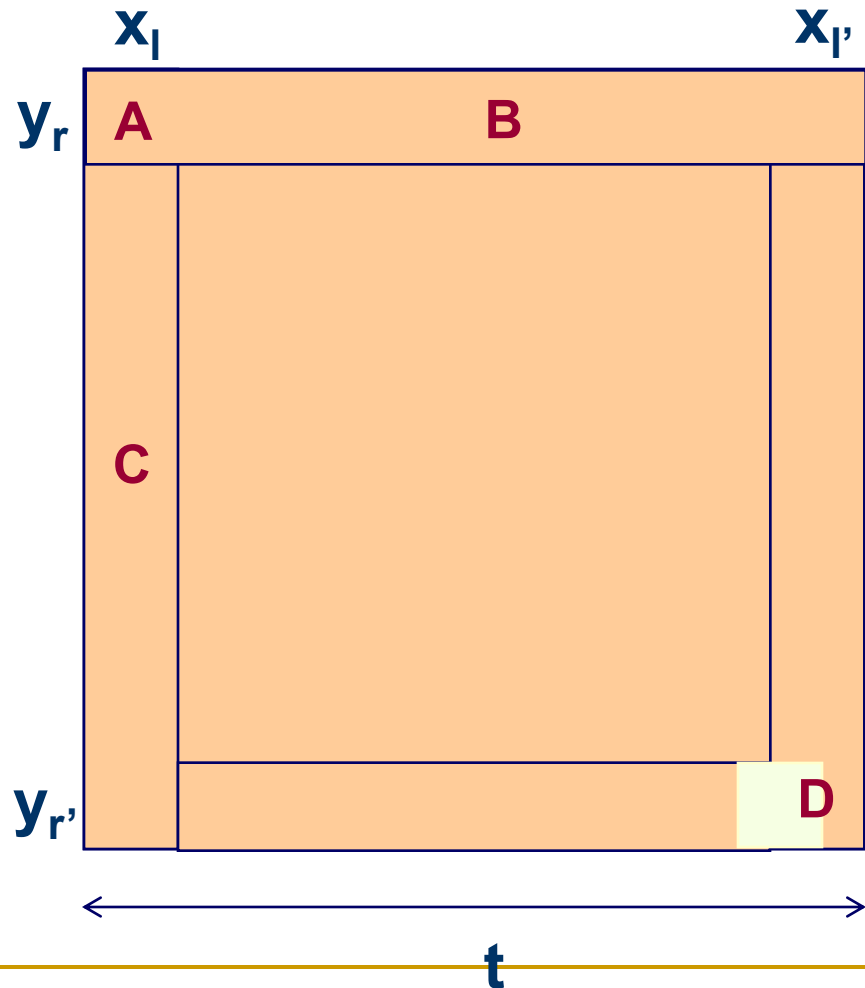
The Four-Russian Algorithm

Definition:

The offset vector is a t -long vector of values from $\{-1, 0, 1\}$, where the first entry is 0

If we know the value at A, and the top row, left column offset vectors, and $x_1, \dots, x_{l'}$, $y_r, \dots, y_{r'}$,

Then we can find D



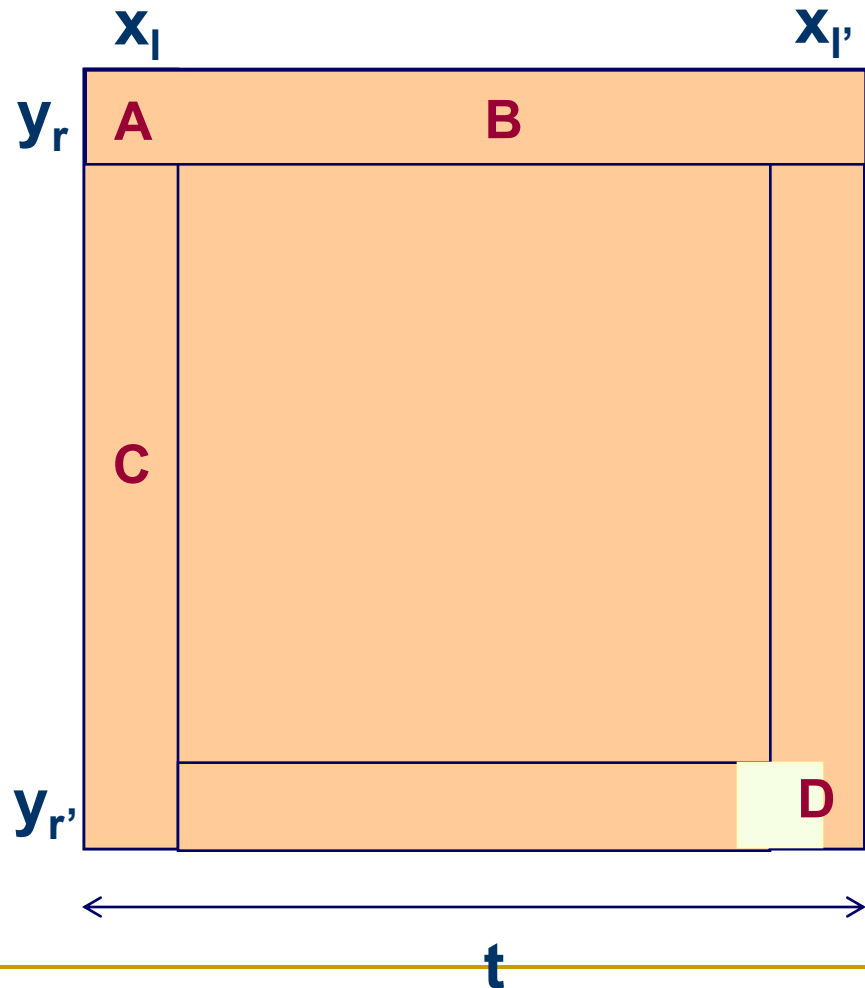
The Four-Russian Algorithm

Definition:

The offset function of a t-block is a function that for any given offset vectors of top row, left column,

and $x_l \dots x_{l'}$, $y_r \dots y_{r'}$,

produces offset vectors of bottom row, right column



An Example

	----	C	T	T	C	G	A	T	G	A
----	0	0	0	0	0	0	0	0	0	0
T	0	<i>0</i>	<i>1</i>	<i>1</i>	<i>1</i>	<i>1</i>	<i>1</i>	<i>1</i>	<i>1</i>	<i>1</i>
T	0	<i>0</i>	1	2	2	<i>2</i>	2	2	2	<i>2</i>
A	0	<i>0</i>	1	2	2	<i>2</i>	3	3	3	<i>3</i>
C	0	<i>1</i>	1	2	3	<i>3</i>	3	3	3	<i>3</i>
G	0	<i>1</i>	<i>1</i>	<i>2</i>	<i>3</i>	<i>4</i>	<i>4</i>	<i>4</i>	<i>4</i>	<i>4</i>
T	0	<i>1</i>	2	2	3	<i>4</i>	4	5	5	<i>5</i>
G	0	<i>1</i>	2	2	3	<i>4</i>	4	5	6	<i>6</i>
C	0	<i>1</i>	2	2	3	<i>4</i>	4	5	6	<i>6</i>
A	0	<i>1</i>	<i>2</i>	<i>2</i>	<i>3</i>	<i>4</i>	<i>5</i>	<i>5</i>	<i>6</i>	<i>7</i>

An Example

	---	C	T	T	C	G	A	T	G	A

T		<i>0/0</i>	<i>1</i>	<i>0</i>	<i>0</i>	<i>1/0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>1/0</i>
T		<i>0</i>				<i>1</i>				<i>1</i>
A		<i>0</i>				<i>0</i>				<i>1</i>
C		<i>1</i>				<i>1</i>				<i>0</i>
G		<i>0/1</i>	<i>0</i>	<i>1</i>	<i>1</i>	<i>1/1</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>1/0</i>
T		<i>0</i>				<i>0</i>				<i>1</i>
G		<i>0</i>				<i>0</i>				<i>1</i>
C		<i>0</i>				<i>0</i>				<i>0</i>
A		<i>0/1</i>	<i>1</i>	<i>0</i>	<i>1</i>	<i>0/1</i>	<i>1</i>	<i>0</i>	<i>1</i>	<i>1/1</i>

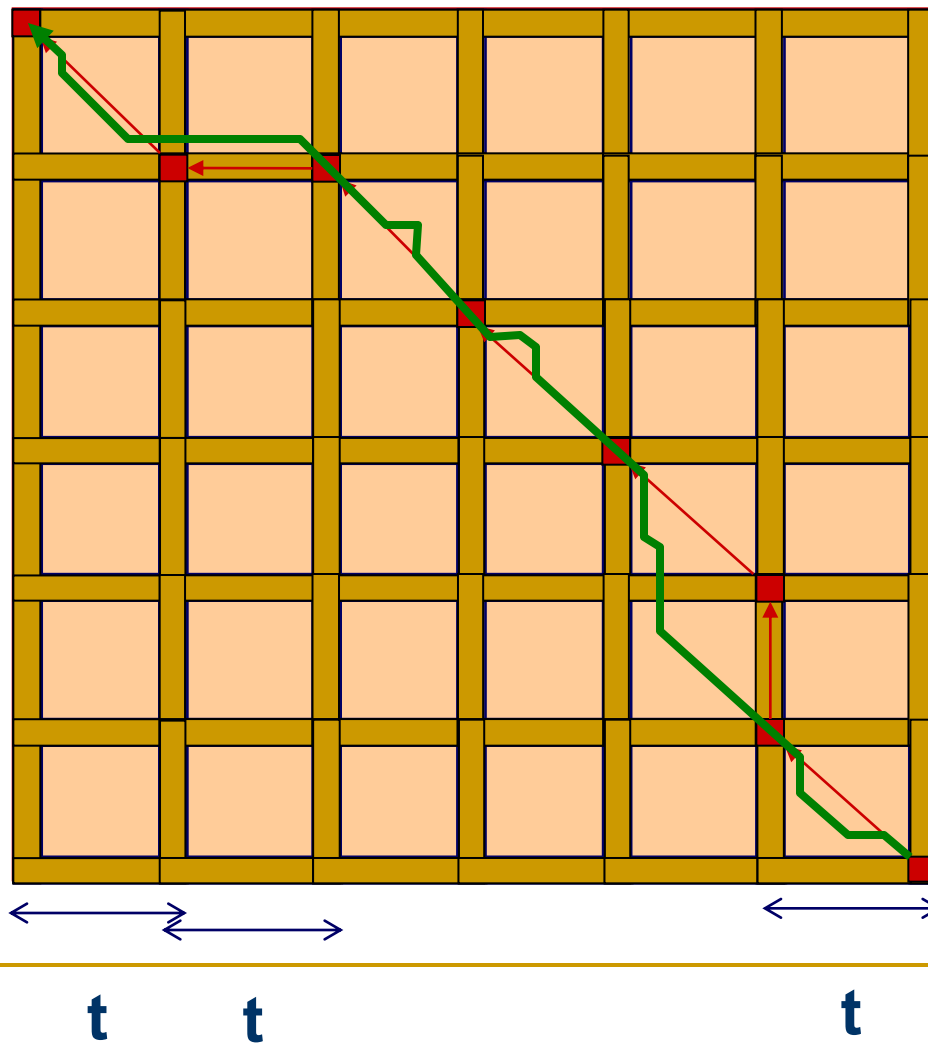
The Four-Russian Algorithm

Four-Russians Algorithm: (Arlazarov, Dinic, Kronrod, Faradzev)

1. Cover the DP table with t -blocks
2. Initialize values $F(.,.)$ in first row & column
3. Row-by-row, use offset values at leftmost column and top row of each block, to find offset values at rightmost column and bottom row
4. Let Q = total of offsets at row n ; $F(n, n) = Q + F(n, 0) = Q + n$

Runtime: $O(n^2 / \log n)$

The Four-Russian Algorithm



Summary

- We take advantage of the fact that for each block of $t = \log(n)$, we can pre-compute all possible scores and store them in a lookup table of size $n^{(3/2)}$
 - We used the Four Russian speedup to go from a quadratic running time for LCS to subquadratic running time: $O(n^2/\log n)$
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