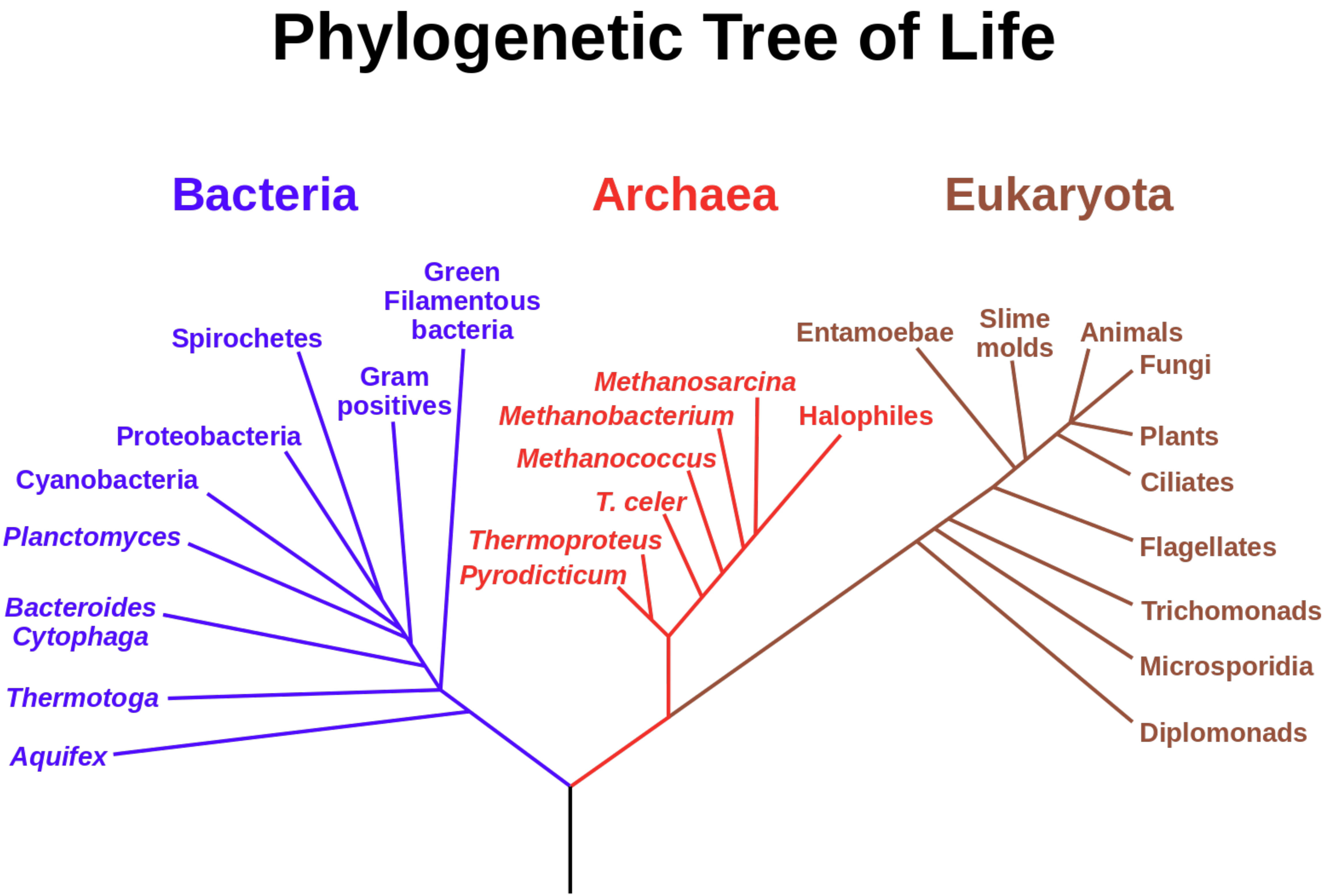
CSE 549 Lecture 3: Sequence Similarity & Alignment

Stony Brook University

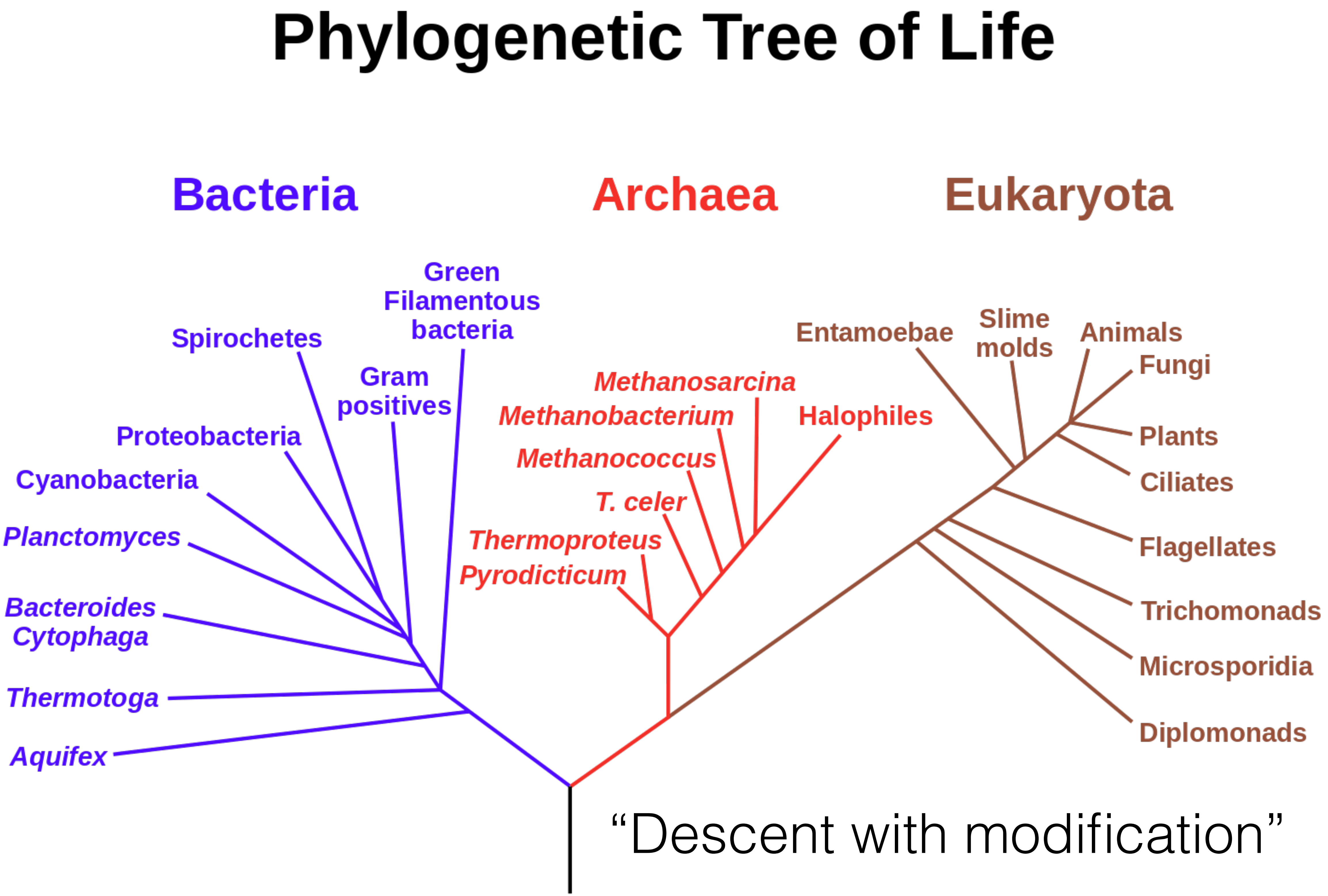
slides (w/*) courtesy of Carl Kingsford

Relatedness of Biological Sequence



https://en.wikipedia.org/wiki/Phylogenetic_tree

Relatedness of Biological Sequence

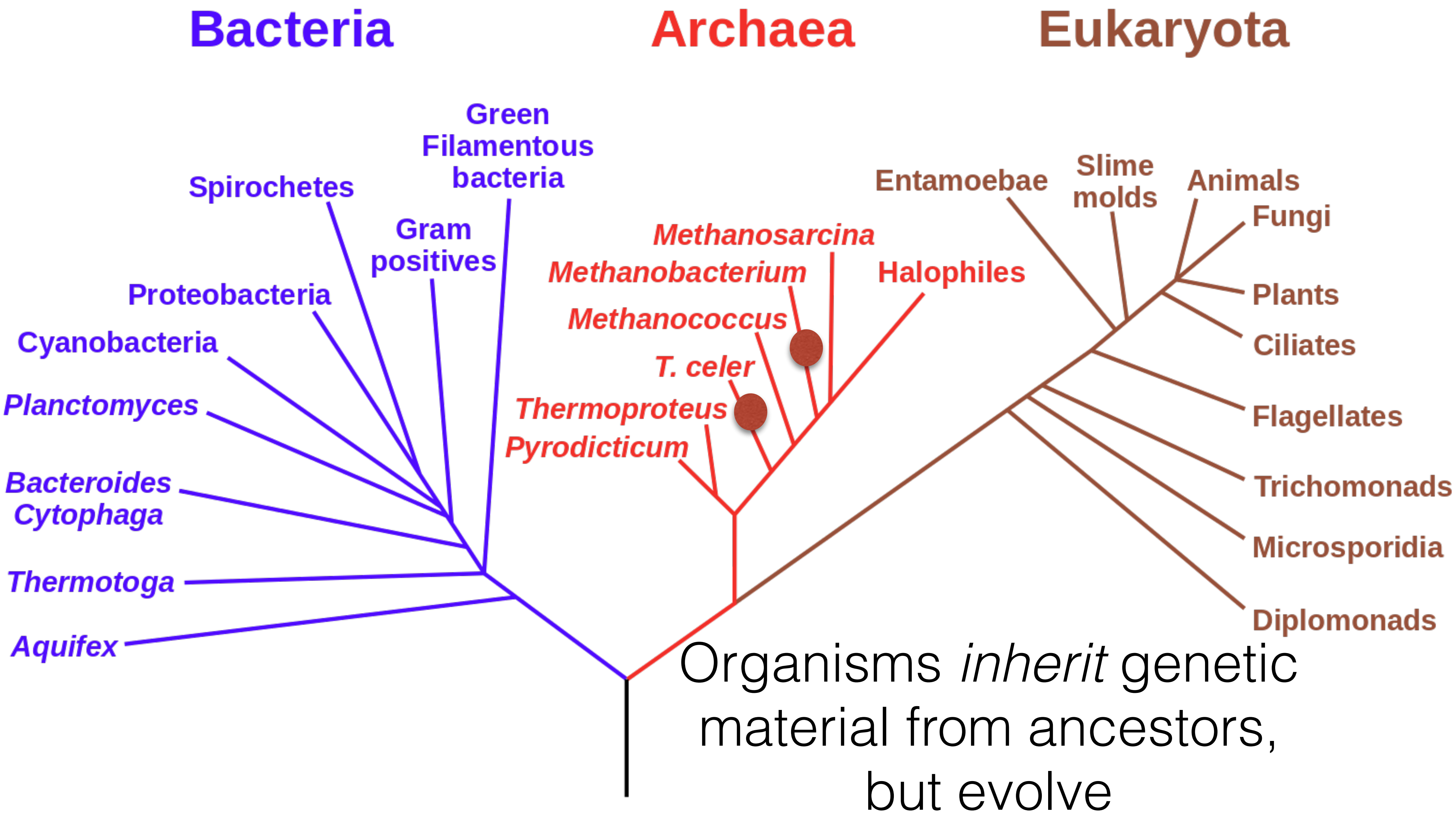


"Descent with modification"

https://en.wikipedia.org/wiki/Phylogenetic_tree

Relatedness of Biological Sequence

Phylogenetic Tree of Life



Organisms *inherit* genetic material from ancestors, but evolve "independently"

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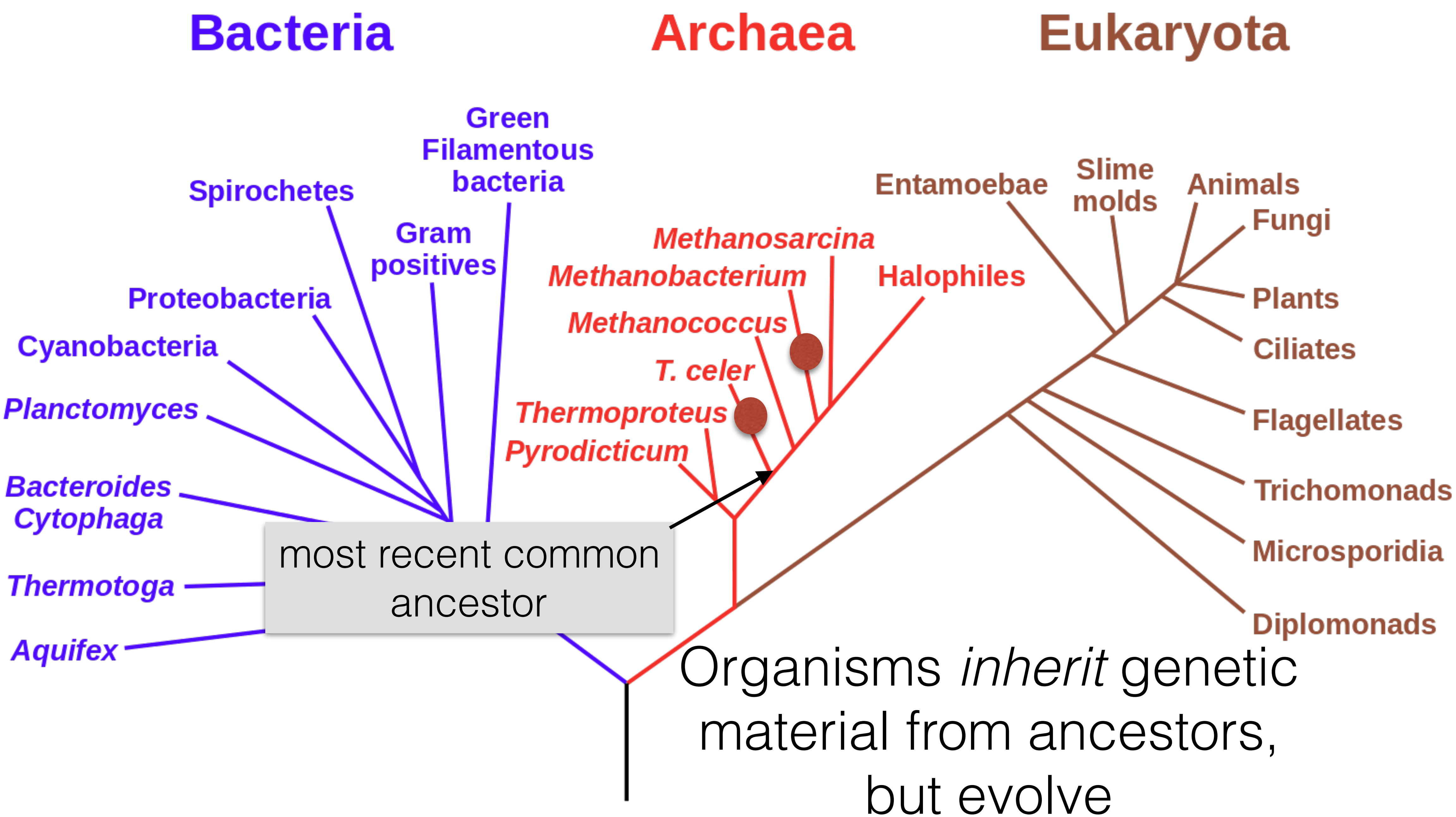
Relatedness of Biological Sequence

Phylogenetic Tree of Life

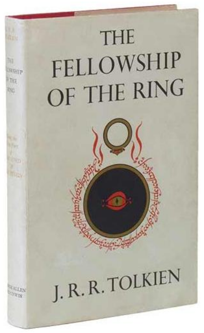


most recent common ancestor

Organisms *inherit* genetic material from ancestors, but evolve "independently"

https://en.wikipedia.org/wiki/Phylogenetic_tree

Consider an analogy



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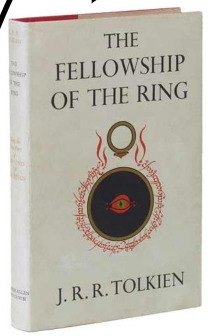
"When Mr. Bilbo Baggins of Bag End announced that he would shortly be celebrating his eleventy-first birthday with a party of special magnificence, there was much talk and excitement in Hobbiton"



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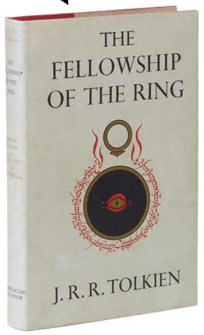

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+:https://en.wikipedia.org/wiki/The_Fellowship_of_the_Ring

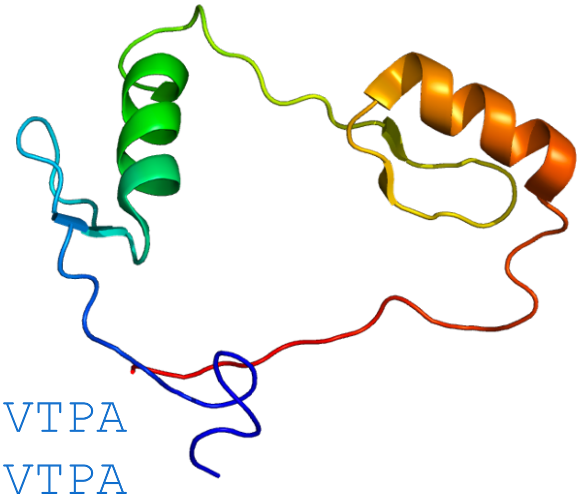
Sequence tells a story

- If two sequences are *similar*, this provides evidence of descent from a common ancestor

- Sequences are *conserved* at different rates

- Very similar sequence can indicate a very *recent common ancestor*, or a *highly conserved function*

Why compare DNA or protein sequences?



Partial CTCF protein sequence in 8 organisms:

```
H. sapiens      -EDSSDS-ENAEPDLDDNEDEEEPAVEIEPEPE----------PQPVTPA
P. troglodytes  -EDSSDS-ENAEPDLDDNEDEEEPAVEIEPEPE----------PQPVTPA
C. lupus        -EDSSDS-ENAEPDLDDNEDEEEPAVEIEPEPE----------PQPVTPA
B. taurus       -EDSSDS-ENAEPDLDDNEDEEEPAVEIEPEPE----------PQPVTPA
M. musculus     -EDSSDSEENAEPDLDDNEEEEEPAVEIEPEPE--PQPQPPPPPQPVAPA
R. norvegicus   -EDSSDS-ENAEPDLDDNEEEEEPAVEIEPEPEPQPQPQPQPQPQPVAPA
G. gallus       -EDSSDSEENAEPDLDDNEDEEETAVEIEAEPE----------VSAEAPA
D. rerio        DDDDDDSDEHGEPDLDDIDEEDEDDL-LDEDQMGLLDQAPPSVPIP-APA
```

- Identify important sequences by finding conserved regions.
- Find genes similar to known genes.
- Understand evolutionary relationships and distances (D. rerio aka zebrafish is farther from humans than G. gallus aka chicken).
- Interface to databases of genetic sequences.
- As a step in genome assembly, and other sequence analysis tasks.
- Provide hints about protein structure and function (next slides).

en.wikipedia.org CC3

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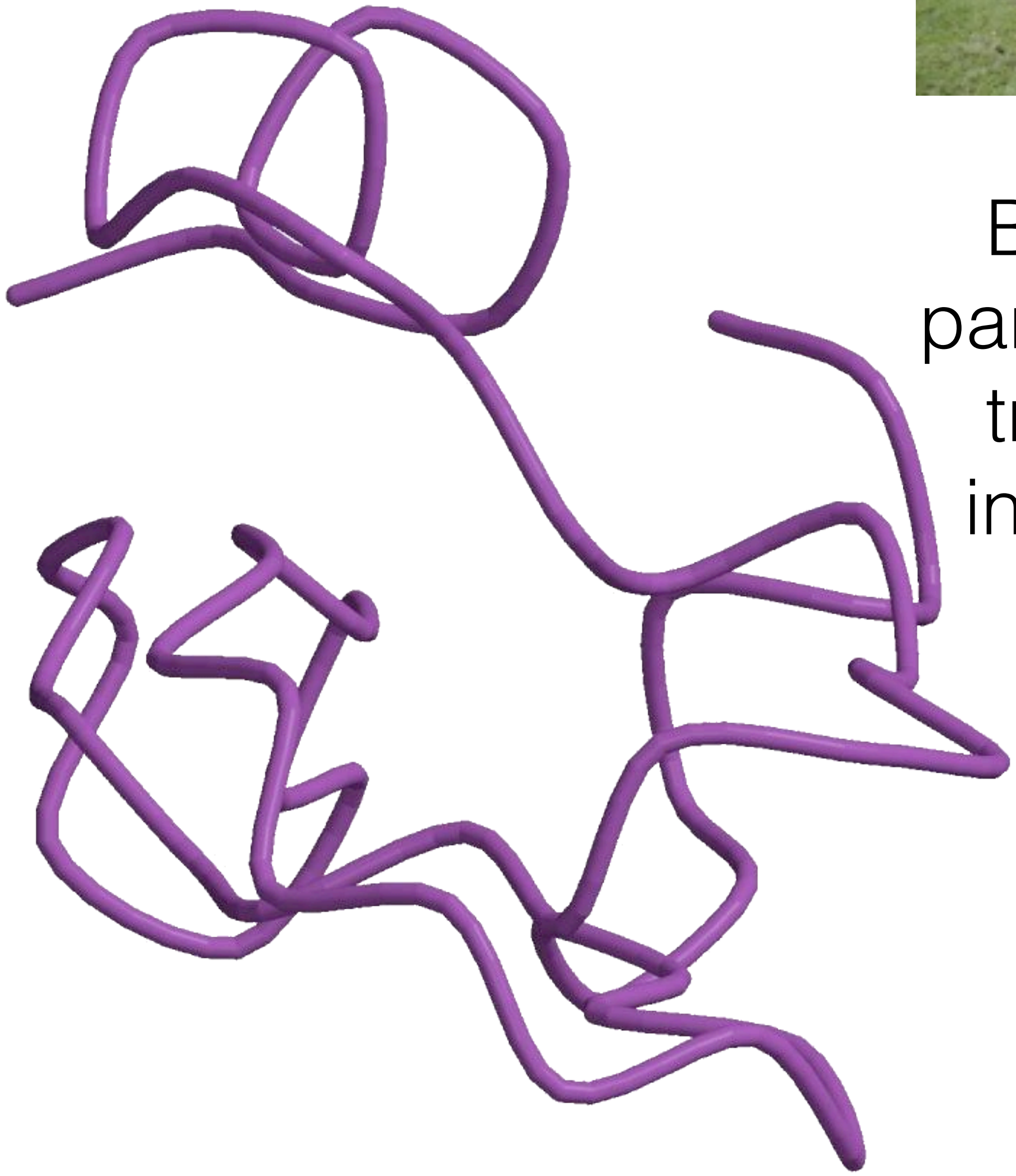
Sequence can reveal structure

dendrotoxin K

(a) 1dtk



(b) 5pti

Bovine
pancreatic
trypsin
inhibitor

1dtk XAKY**C**KL**P**LRI**GPCK**RK**I**PSFY**Y**KW**KA**KQ**C**LP**F**D**Y**S**GC**GGNA**N**R**FK**TI**E**E**C**R**RTC**V**G**-
5pti RPDF**C**LE**P**PYT**GPCK**AR**I**IRYF**Y**NA**KA**GL**C**QT**F**V**Y**G**GC**RAKR**N**N**FK**SA**E**D**C**M**RTC**G**G**A

*

Why Not Exact Matching?

Suffix tree / array and BWT / FM-index are powerful tools for finding exact patterns in a large text, but exact matching is insufficient. Reads have **errors** and there is **true genomic variation** between a reference and a sample.

Typical strategy (many variants):

- Find all places where a substring of the query matches the reference exactly (seeds)

Requires efficient exact search

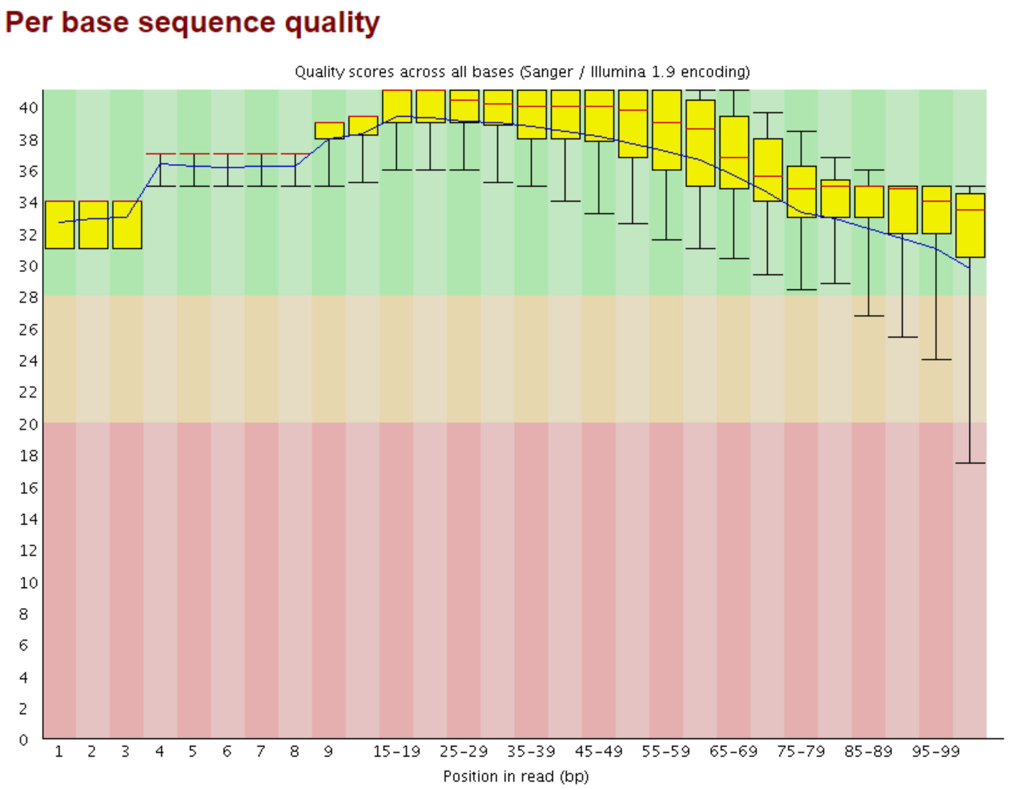
- Filter out regions with insufficient exact matches to warrant further investigation
- Perform a “constrained” alignment that includes these exact matching “seeds”

Here is where we use our alignment DPs

Why Is This Possible?

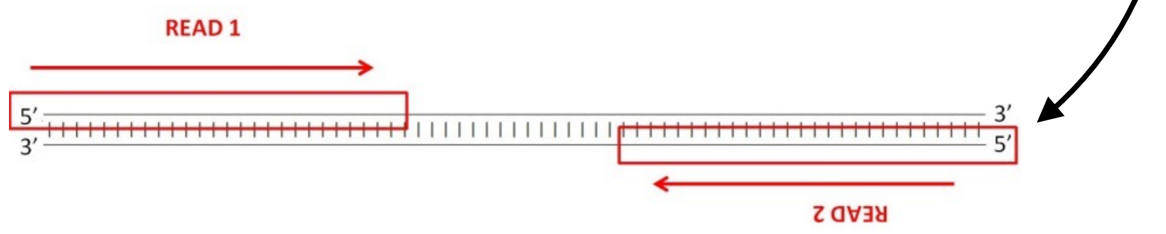
This is (*usually*) a **heuristic** (doesn't guarantee you find all alignment locations within the budget for a read).

But, due to the error profiles of reads, this often works well.



Per base sequence quality

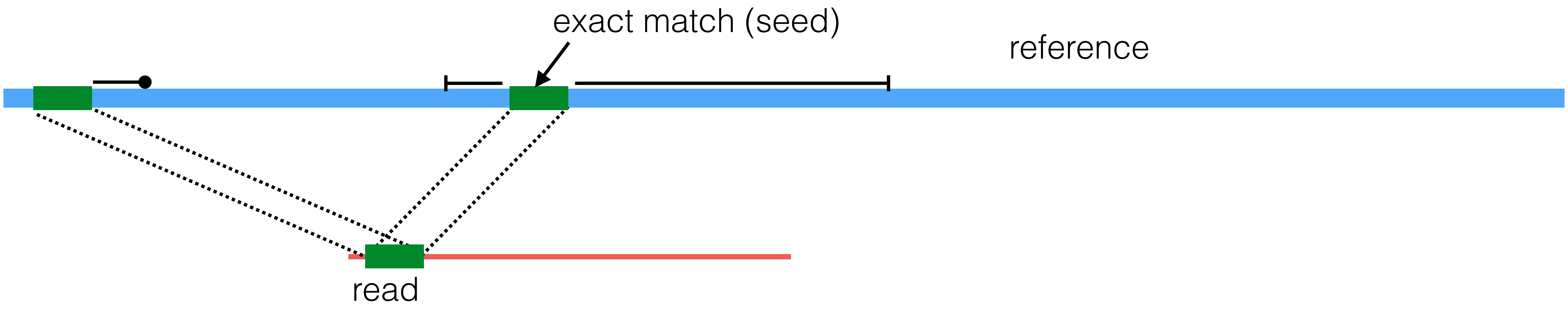
	error type	error rate	read length
Illumina	subst.	~0.1%	50-300
Nanopore	indel	10-30%	5-10kb
Pac Bio	indel	10-15%	10-15kb



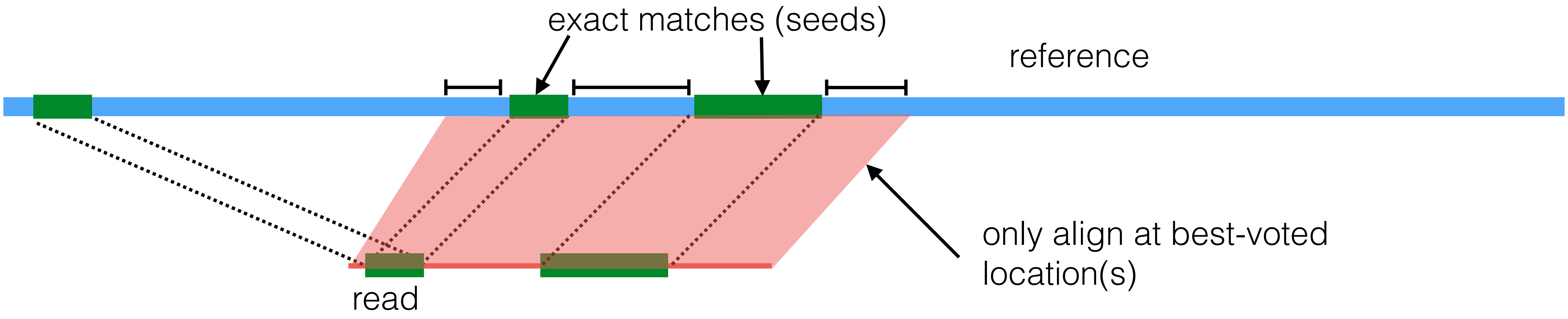
2nd generation reads are often "paired-end"

Typical Strategies

Seed & Extend:



Seed & Vote:



only align at best-voted location(s)

The Language of Strings

A string **s** is a finite sequence of characters

|**s**| denotes the length of the string — the number of characters in the sequence.

A string is defined *over* an alphabet, Σ

Σ_{DNA} = {A,T,C,G}
Σ_{RNA} = {A,U,C,G}
$\Sigma_{AminoAcid}$ = {A, R, N, D, C, E, Q, G, H, I, L, K, M, F, P, S, T, W, Y, V}

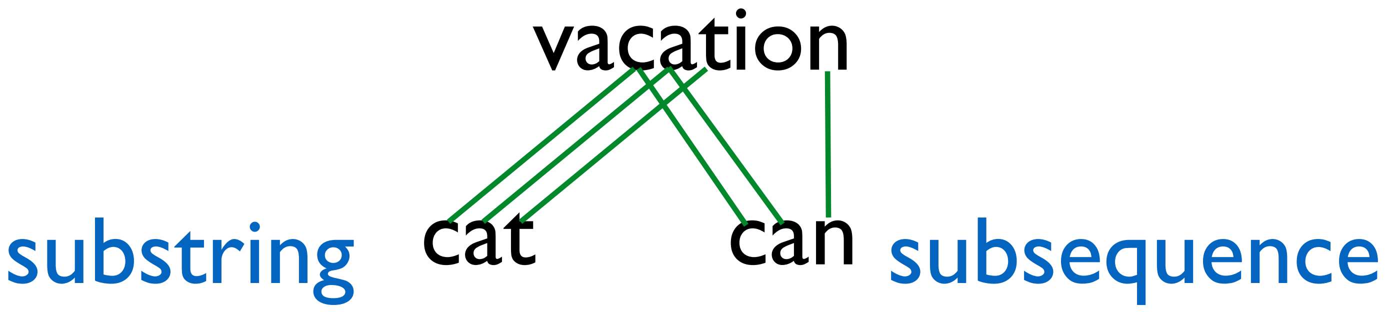
The empty string is denoted ϵ — $|\epsilon| = 0$

The Language of Strings

Given two strings **s,t** over the same alphabet Σ, we denote the concatenation as **st** — this is the sequence of **s** followed by the sequence of **t**

String **s** is a substring of **t** if there exist two (potentially empty) strings **u** and **v** such that **t = usv**

String **s** is a subsequence of **t** if the characters of **s** appear in order (but not necessarily consecutively) in **t**



vacation

substring cat

can subsequence

String **s** is a prefix/suffix of **t** if **t** = **su/us** — if neither **s** nor **u** are ϵ, then **s** is a proper prefix/suffix of **t**

The Simplest String Comparison Problem

Given: Two strings

$$a = a_1a_2a_3a_4 \ldots a_m$$
$$b = b_1b_2b_3b_4 \ldots b_n$$

where a_i, b_i are letters from some alphabet, Σ, like {A,C,G,T}.

Compute how similar the two strings are.

What do we mean by “similar”?

Edit distance between strings *a* and *b* = the smallest number of the following operations that are needed to transform *a* into *b*:

- mutate (replace) a character
- delete a character
- insert a character

$$\text{riddle} \xrightarrow{\text{delete}} \text{ridle} \xrightarrow{\text{mutate}} \text{riple} \xrightarrow{\text{insert}} \text{triple}$$

*

The String Alignment Problem

Parameters:

- "*gap*" is the cost of inserting a "-" character, representing an insertion or deletion (insertion/deletion are dual operations depending on the string)
- *cost*(x,y) is the cost of aligning character x with character y. In the simplest case, *cost*(x,x) = 0 and *cost*(x,y) = mismatch penalty.

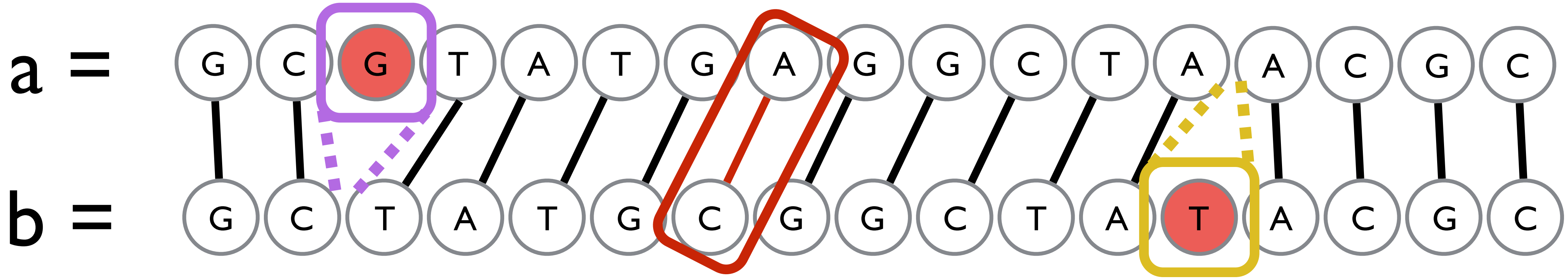
Goal:

- Can compute the edit distance by finding the **lowest cost alignment**. (often phrased as finding **highest scoring alignment**.)
- Cost of an alignment is: sum of the *cost*(x,y) for the pairs of characters that are aligned + *gap* × number of - characters inserted.

Another View: Alignment as a Matching

Each string is a set of nodes, one for each character.

Looking for a low-cost matching (pairing) between the sequences.



The operations at our disposal

Insertion (into **a** ~ deletion from **b**)

Mutation

Deletion (from **a** ~ insertion into **b**)

When we "delete a" character in **a** this is the same as inserting the character "-" in **b**. Conceptually, you can think of this as aligning the deleted character with "-". Under this model cost(x,'-') = cost('-',x) = gap for any x ∈ Σ

Another View: Alignment as a Matching

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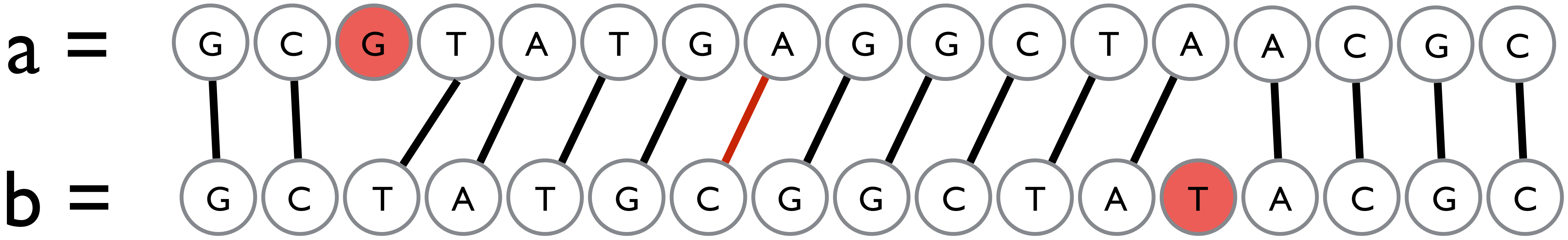
Looking for a low-cost matching (pairing) between the sequences.



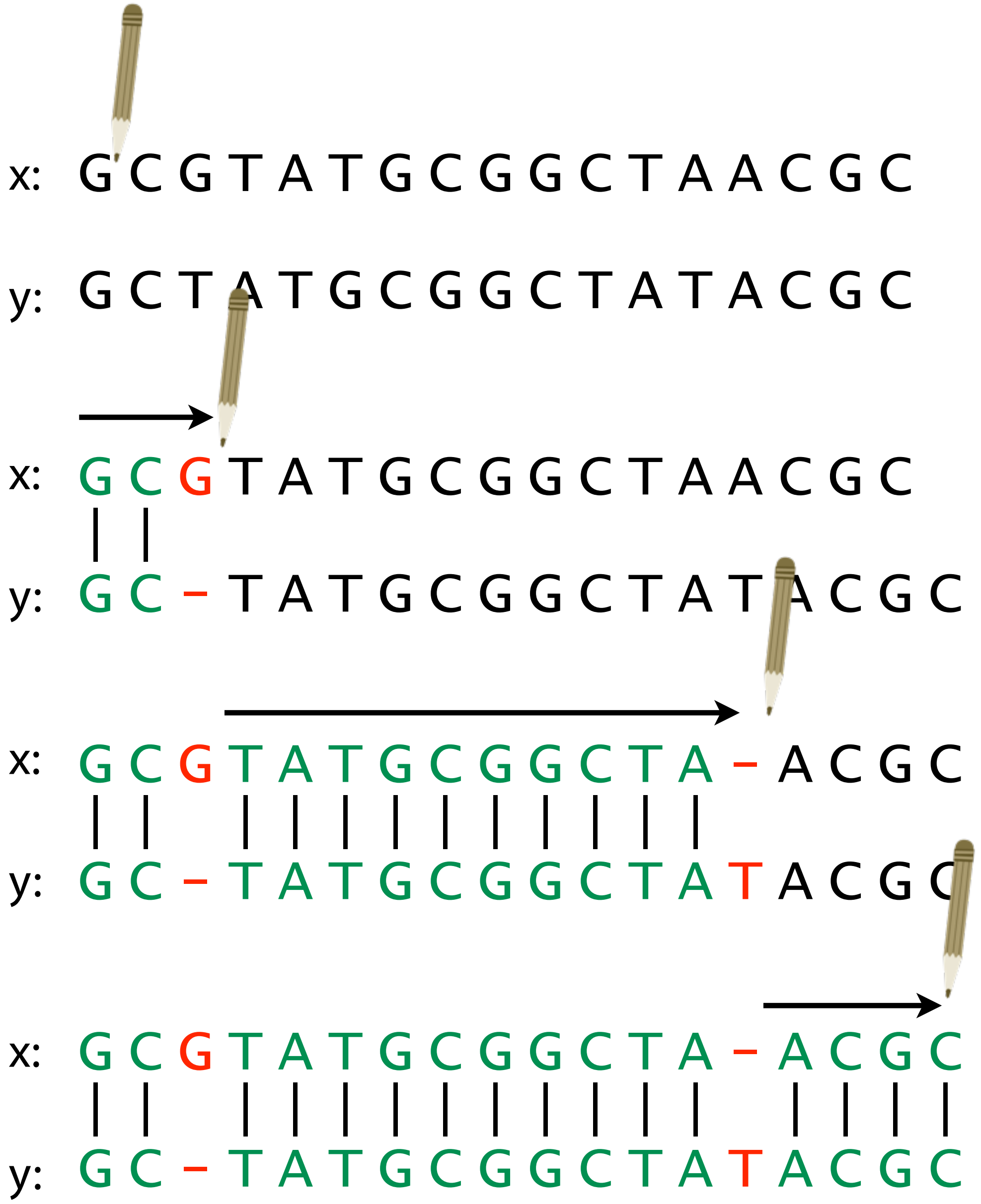
Cost of a matching is:

$$\text{gap} \times \#\mathit{unmatched} + \sum_{(a_i,b_j)} \mathit{cost}(a_i, b_j)$$

Edges are not allowed to cross!

Representing alignments as edit transcripts

Can think of edits as being introduced by an *optimal editor* working left-to-right. *Edit transcript* describes how editor turns *x* into *y.*



```
x:  G C G T A T G C G G C T A A C G C

y:  G C T A T G C G G C T A T A C G C
```

```
x:  G C G T A T G C G G C T A A C G C
    | |
y:  G C - T A T G C G G C T A T A C G C
```

```
x:  G C G T A T G C G G C T A - A C G C
    | |   | | | | | | | | | |
y:  G C - T A T G C G G C T A T A C G C
```

```
x:  G C G T A T G C G G C T A - A C G C
    | |   | | | | | | | | | |   | | | |
y:  G C - T A T G C G G C T A T A C G C
```

Operations:

M = match, **R** = replace,

I = insert into *x*, **D** = delete from *x*

MMD

MMDMMMMMMMMMMI

MMDMMMMMMMMMMIMMMM

Slide courtesy of Ben Langmead

Representing edits as alignments

```
prin-ciple
|||| |||xx
prinncipal
(1 gap, 2 mm)
MMMMIMMMRR
```

```
misspell
||| ||||
mis-pell
(1 gap)
MMMIMMMM
```

```
aa-bb-ccaabb
|x || | | |
ababbbc-a-b-
(5 gaps, 1 mm)
MRIMMIMDMDMD
```

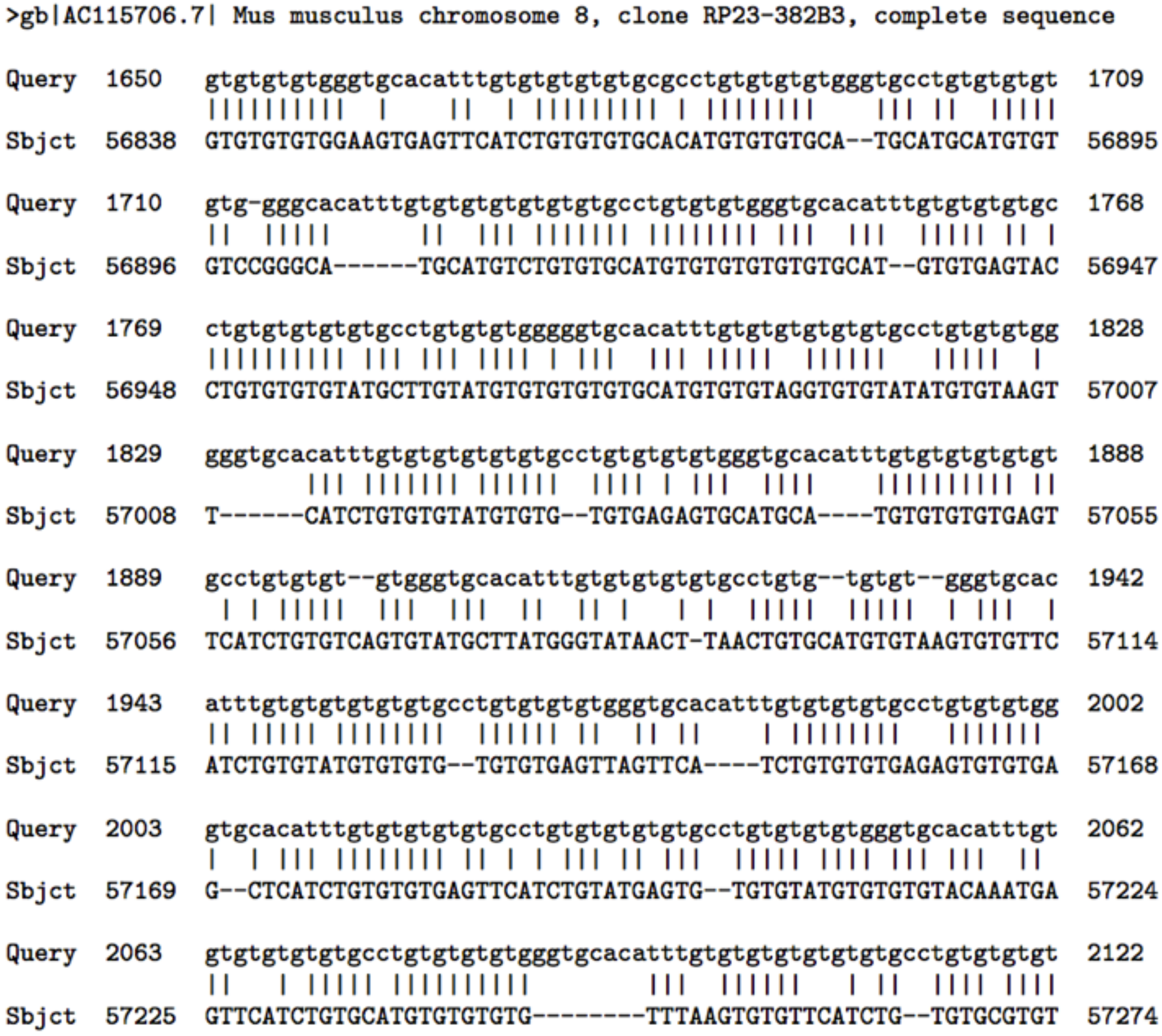
```
prin-cip-le
|||| |||  |
prinncipal-
(3 gaps, 0 mm)
MMMMIMMMIMD
```

```
prehistoric
   ||||||||
---historic
(3 gaps)
DDDMMMMMMMM
```

```
al-go-rithm-
|| xx ||x |
alKhwariz-mi
(4 gaps, 3 mm)
MMIRRIMMRDMI
```

*

NCBI BLAST DNA Alignment



```
>gb|AC115706.7| Mus musculus chromosome 8, clone RP23-382B3, complete sequence

Query  1650   gtgtgtgtgggtgcacatttgtgtgtgtgtgcgcctgtgtgtgtgggtgcctgtgtgtgt  1709
              ||||||||||  |    ||  | ||||||||| | ||||||||    ||| ||  |||||
Sbjct  56838  GTGTGTGTGGAAGTGAGTTCATCTGTGTGTGCACATGTGTGTGCA--TGCATGCATGTGT  56895

Query  1710   gtg-gggcacatttgtgtgtgtgtgtgtgcctgtgtgtgggtgcacatttgtgtgtgtgc  1768
              ||  |||||      ||  ||| ||||||| |||||||| |||  |||  ||||| || |
Sbjct  56896  GTCCGGGCA------TGCATGTCTGTGTGCATGTGTGTGTGTGTGCAT--GTGTGAGTAC  56947

Query  1769   ctgtgtgtgtgtgcctgtgtgtgggggtgcacatttgtgtgtgtgtgtgcctgtgtgtgg  1828
              |||||||||| ||| ||| |||| | |||  ||| |||||  ||||||   |||||  |
Sbjct  56948  CTGTGTGTGTATGCTTGTATGTGTGTGTGTGCATGTGTGTAGGTGTGTATATGTGTAAGT  57007

Query  1829   gggtgcacatttgtgtgtgtgtgtgcctgtgtgtgtgggtgcacatttgtgtgtgtgtgt  1888
                     ||| ||||||| ||||||  |||| | |||  ||||    |||||||||| ||
Sbjct  57008  T------CATCTGTGTGTATGTGTG--TGTGAGAGTGCATGCA----TGTGTGTGTGAGT  57055

Query  1889   gcctgtgtgt--gtgggtgcacatttgtgtgtgtgtgcctgtg--tgtgt--gggtgcac  1942
               | | |||||  |||  |||  ||  || |   | |  |||||  |||||  | |||  |
Sbjct  57056  TCATCTGTGTCAGTGTATGCTTATGGGTATAACT-TAACTGTGCATGTGTAAGTGTGTTC  57114

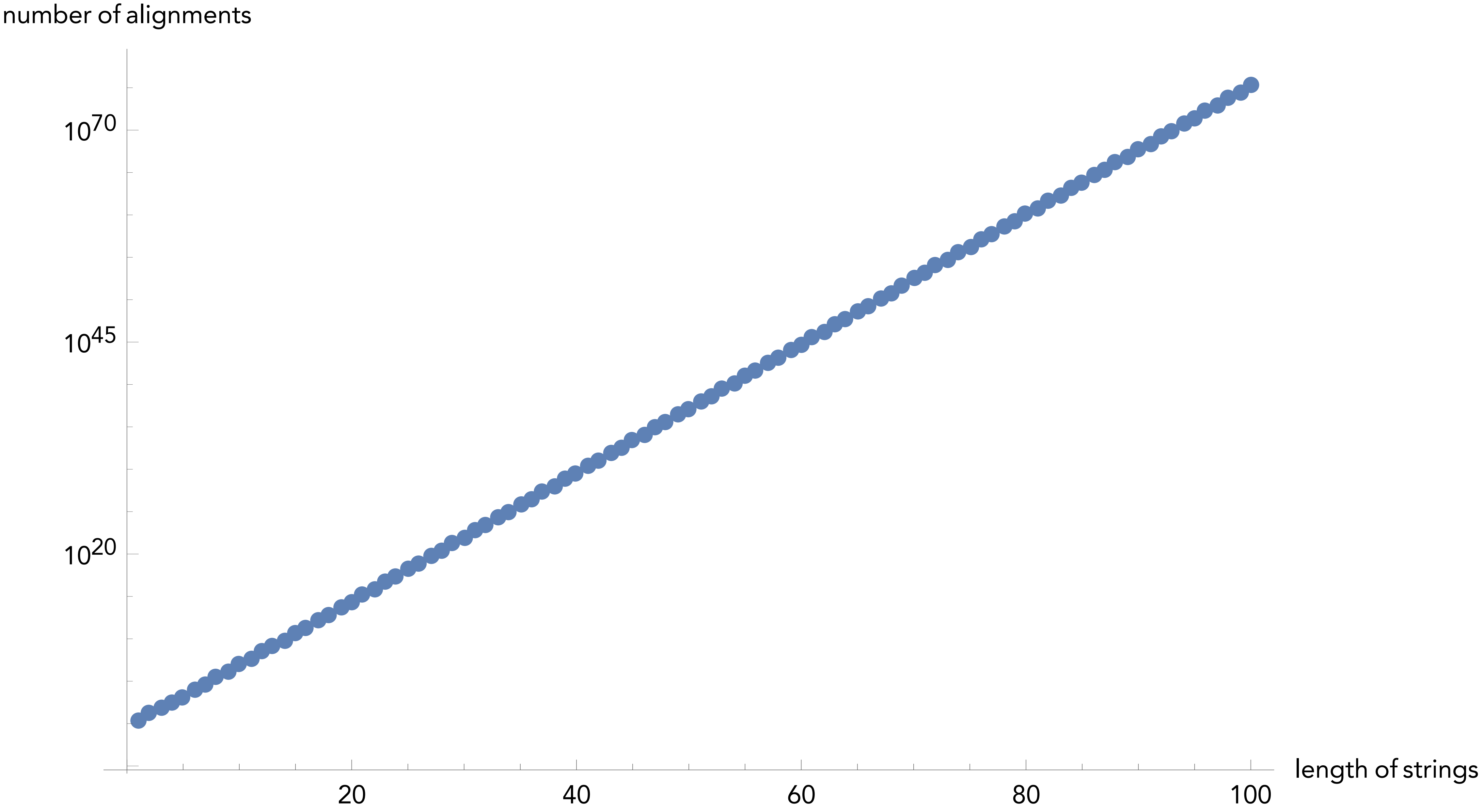
Query  1943   atttgtgtgtgtgtgtgcctgtgtgtgtgggtgcacatttgtgtgtgtgcctgtgtgtgg  2002
              || ||||| ||||||||  |||||| ||  || ||    | ||||||||   |||||||
Sbjct  57115  ATCTGTGTATGTGTGTG--TGTGTGAGTTAGTTCA----TCTGTGTGTGAGAGTGTGTGA  57168

Query  2003   gtgcacatttgtgtgtgtgtgcctgtgtgtgtgtgcctgtgtgtgtgggtgcacatttgt  2062
              |  | ||| |||||||| || | | ||| || |||  ||||| |||| ||| |||  ||
Sbjct  57169  G--CTCATCTGTGTGTGAGTTCATCTGTATGAGTG--TGTGTATGTGTGTGTACAAATGA  57224

Query  2063   gtgtgtgtgtgcctgtgtgtgtgggtgcacatttgtgtgtgtgtgtgtgcctgtgtgtgt  2122
              ||   | ||||| ||||||||||        |||  ||||||   | ||  |||| ||||
Sbjct  57225  GTTCATCTGTGCATGTGTGTGTG--------TTTAAGTGTGTTCATCTG--TGTGCGTGT  57274
```

*

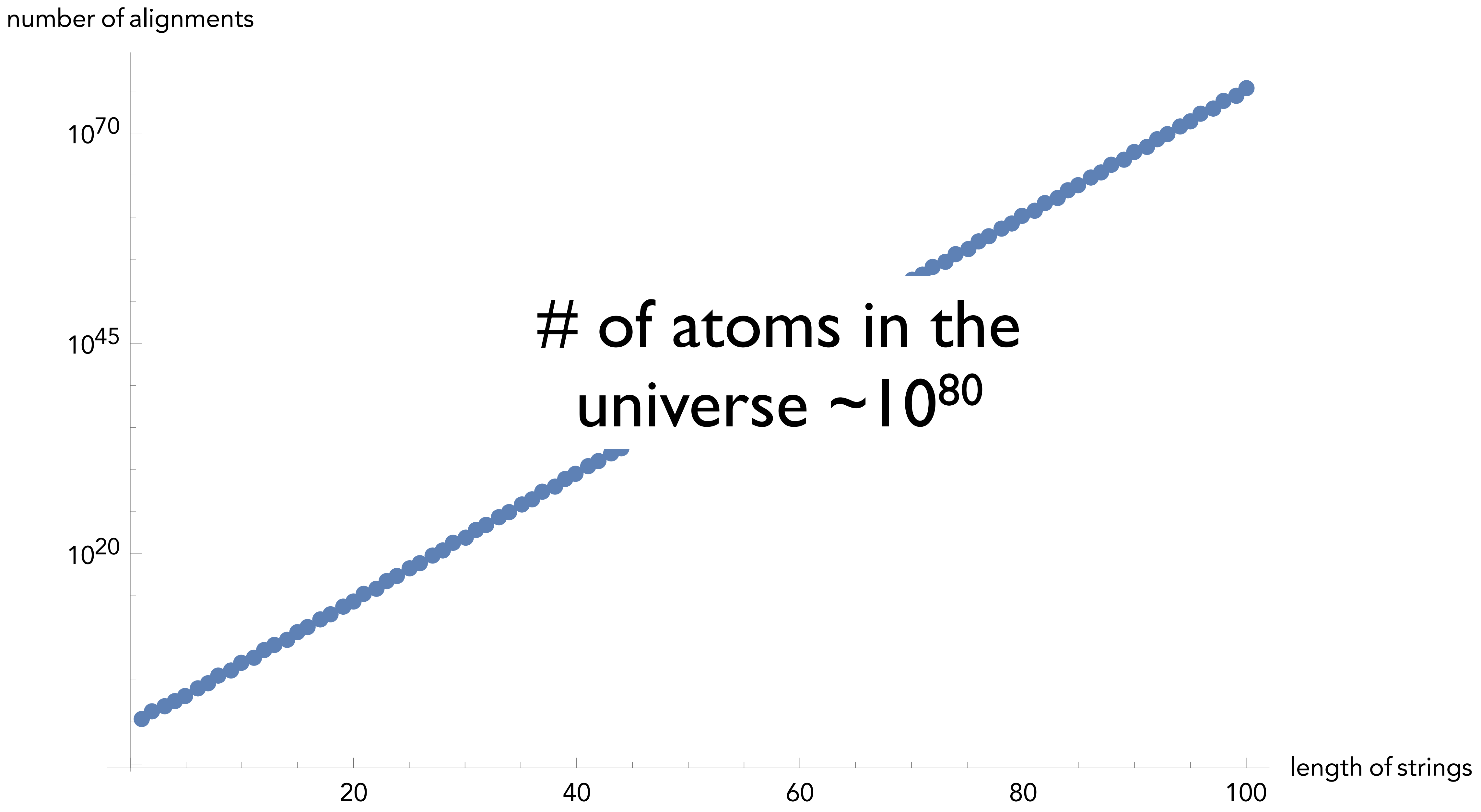
How many alignments are there?



$$f(n,m) = \sum_{k=0}^{\min(m,n)} 2^k \binom{m}{k} \binom{n}{k}$$

Andrade, Helena, et al. "The number of reduced alignments between two DNA sequences." BMC bioinformatics 15.1 (2014): 94.

How many alignments are there?



# of atoms in the universe ~10^{80}

$$f(n,m) = \sum_{k=0}^{\min(m,n)} 2^k \binom{m}{k} \binom{n}{k}$$

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Interlude: Dynamic Programming

General and powerful *algorithm design* technique

“Programming” in the mathematical sense — nothing to do with e.g. code

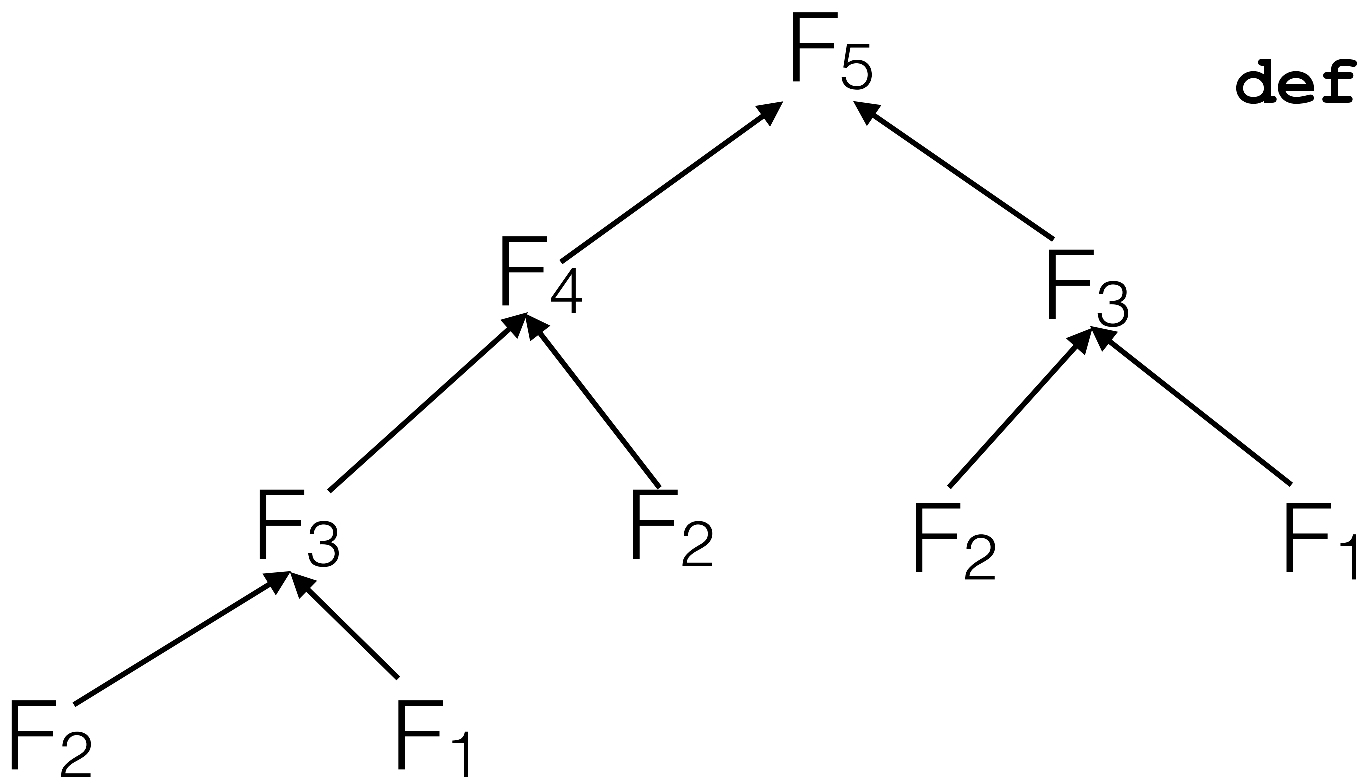
To apply DP, we need optimal substructure and overlapping subproblems

optimal substructure — can combine solutions to “smaller” problems to generate solutions to “larger” problems.

overlapping subproblems — solutions to subproblems can be “re-used” in multiple contexts (to solve multiple) larger problems

Example 1: Fibonacci Sequence

$F_n = F_{n-1} + F_{n-2}$ with $F_1 = F_2 = 1$



```
def fib(n):
    if n == 1 or n == 2:
        return 1
    else:
        return fib(n-1) + fib(n-2)
```

This recursive way of computing fib(n) is **very** inefficient!

What is the runtime of this approach (i.e. fib(n) = O(?))

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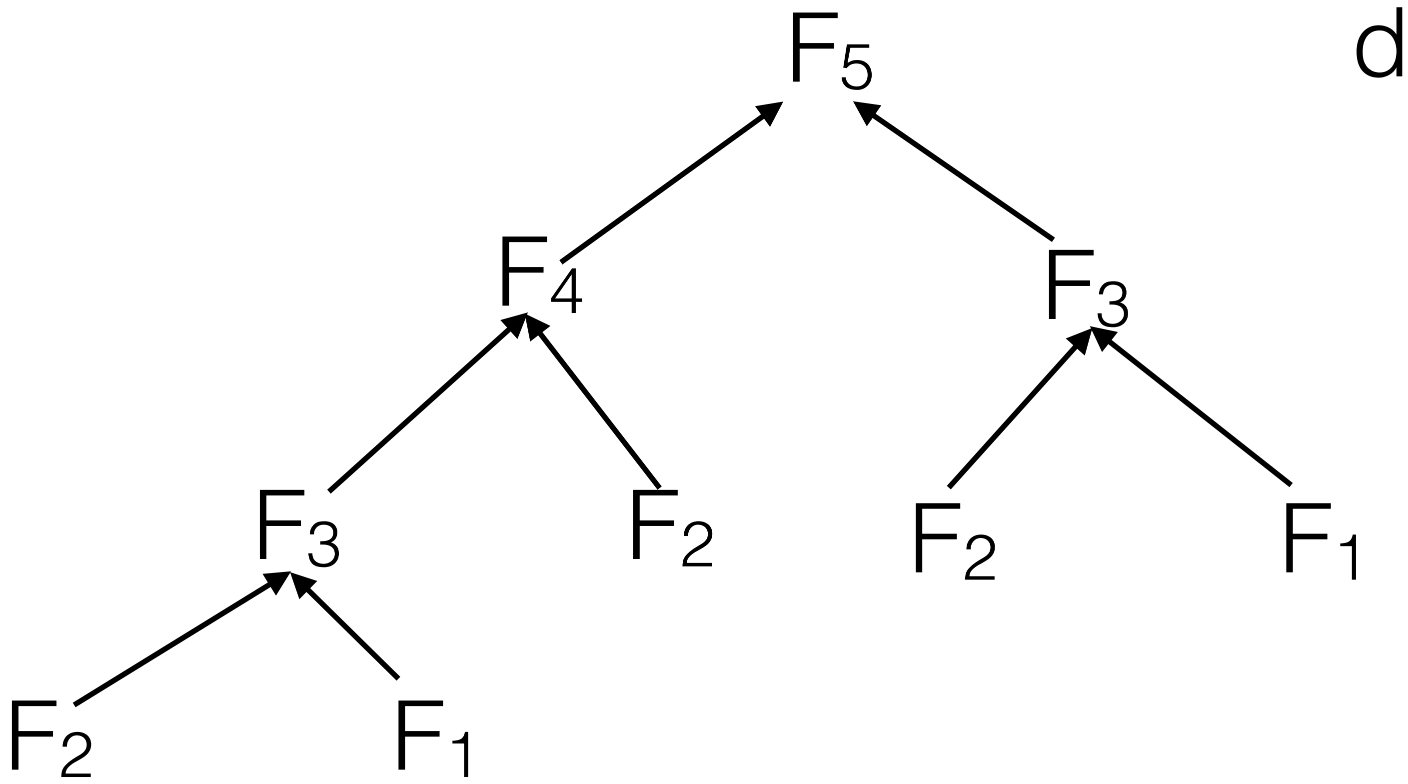

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```

This recursive way of computing fib(n) is **very** inefficient!

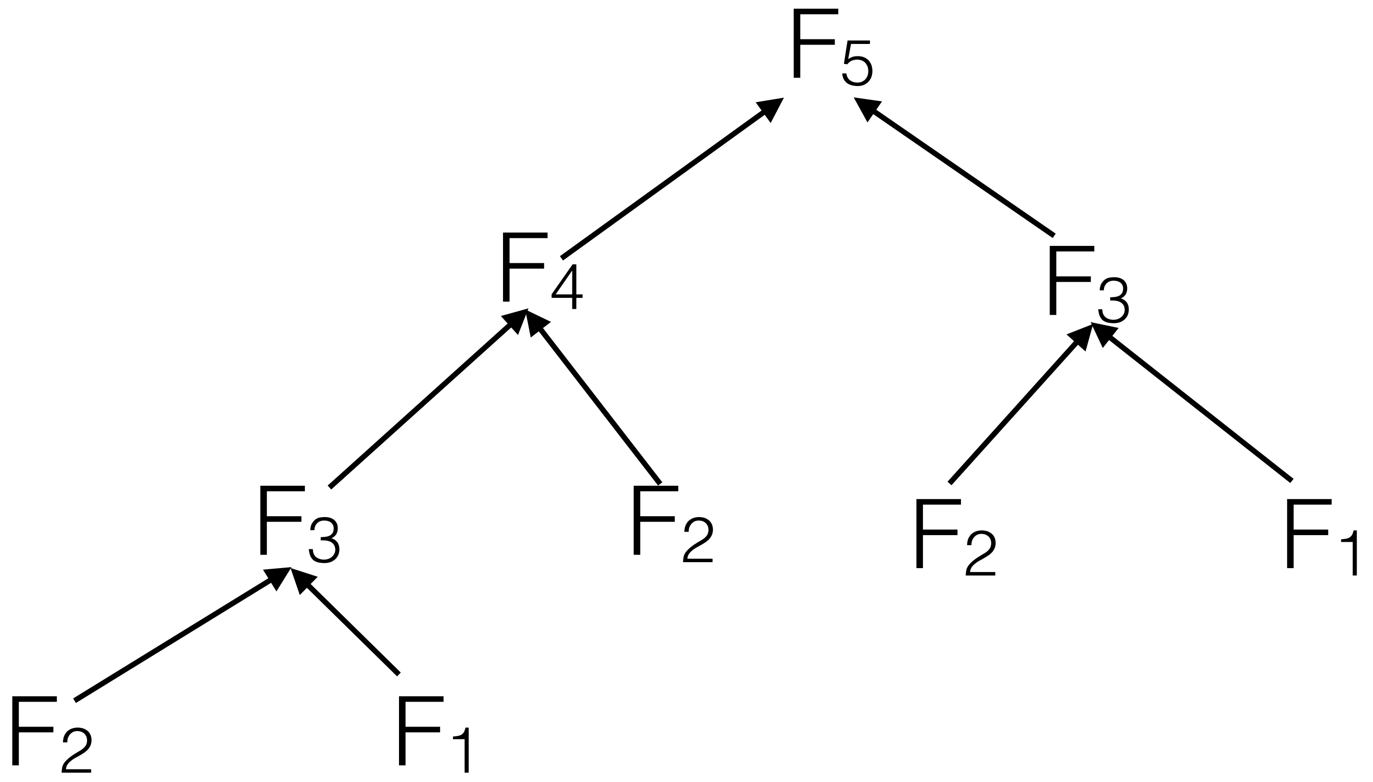
Runtime of this approach is fib(n) = $O(\phi^n) = O(2^n)$

golden ratio

Example 1: Fibonacci Sequence

$F_n = F_{n-1} + F_{n-2}$ with $F_1 = F_2 = 1$

How do we do better than $O(\phi^n)$?



Example 1: Fibonacci Sequence

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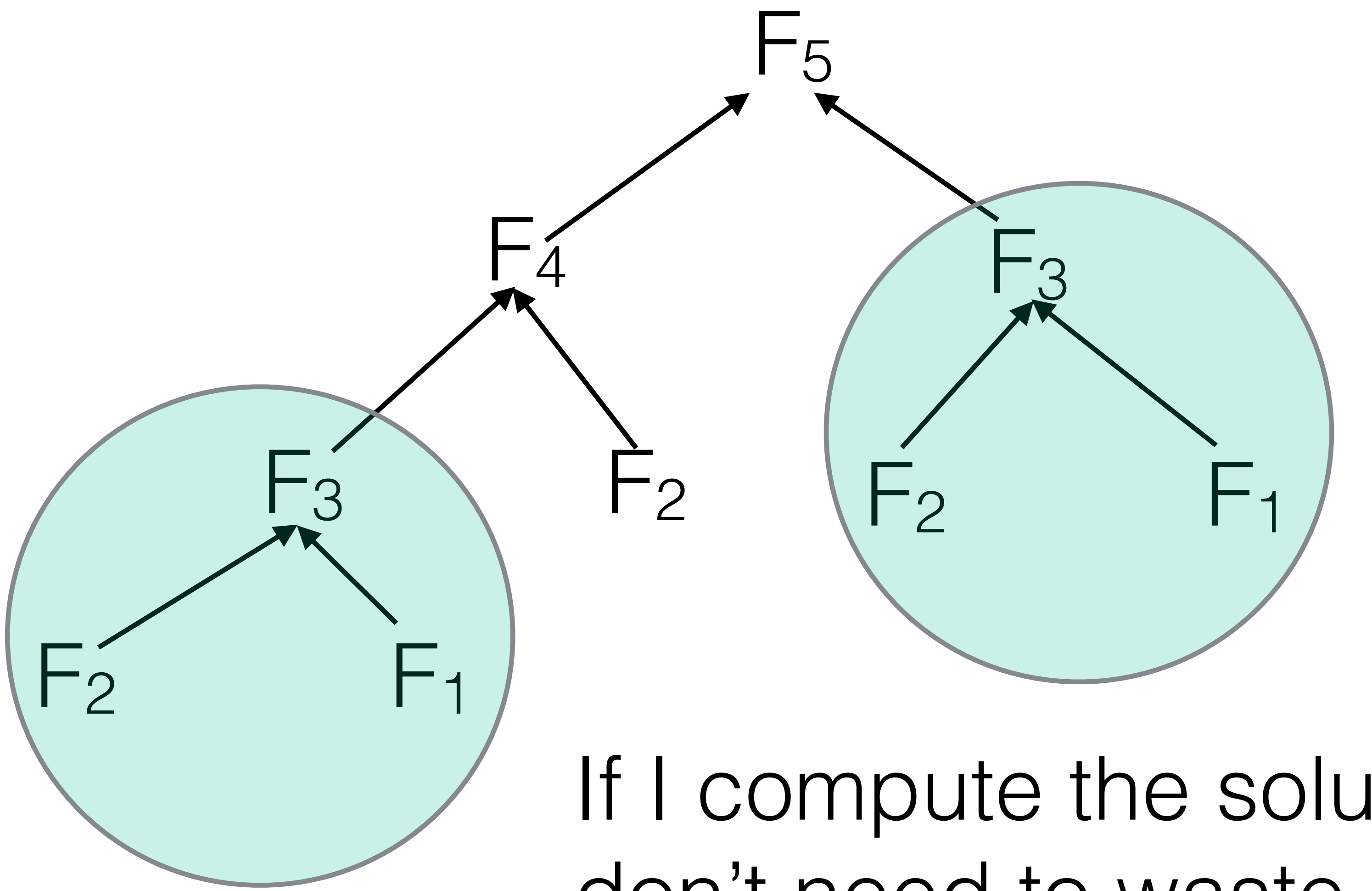

If I compute the solutions in the “right order”, I don’t need to waste time re-computing the same values.

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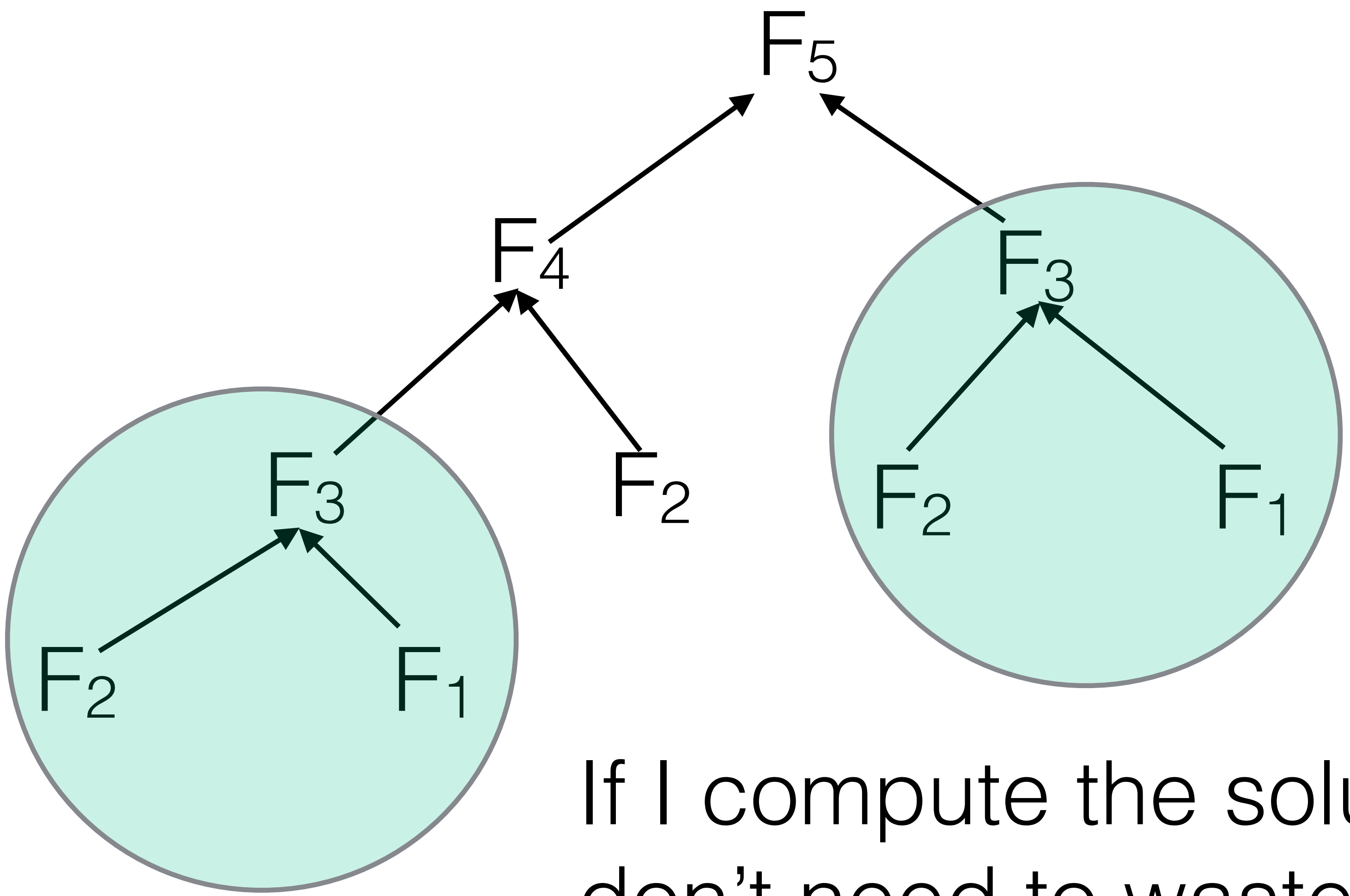

What is the “right order”?

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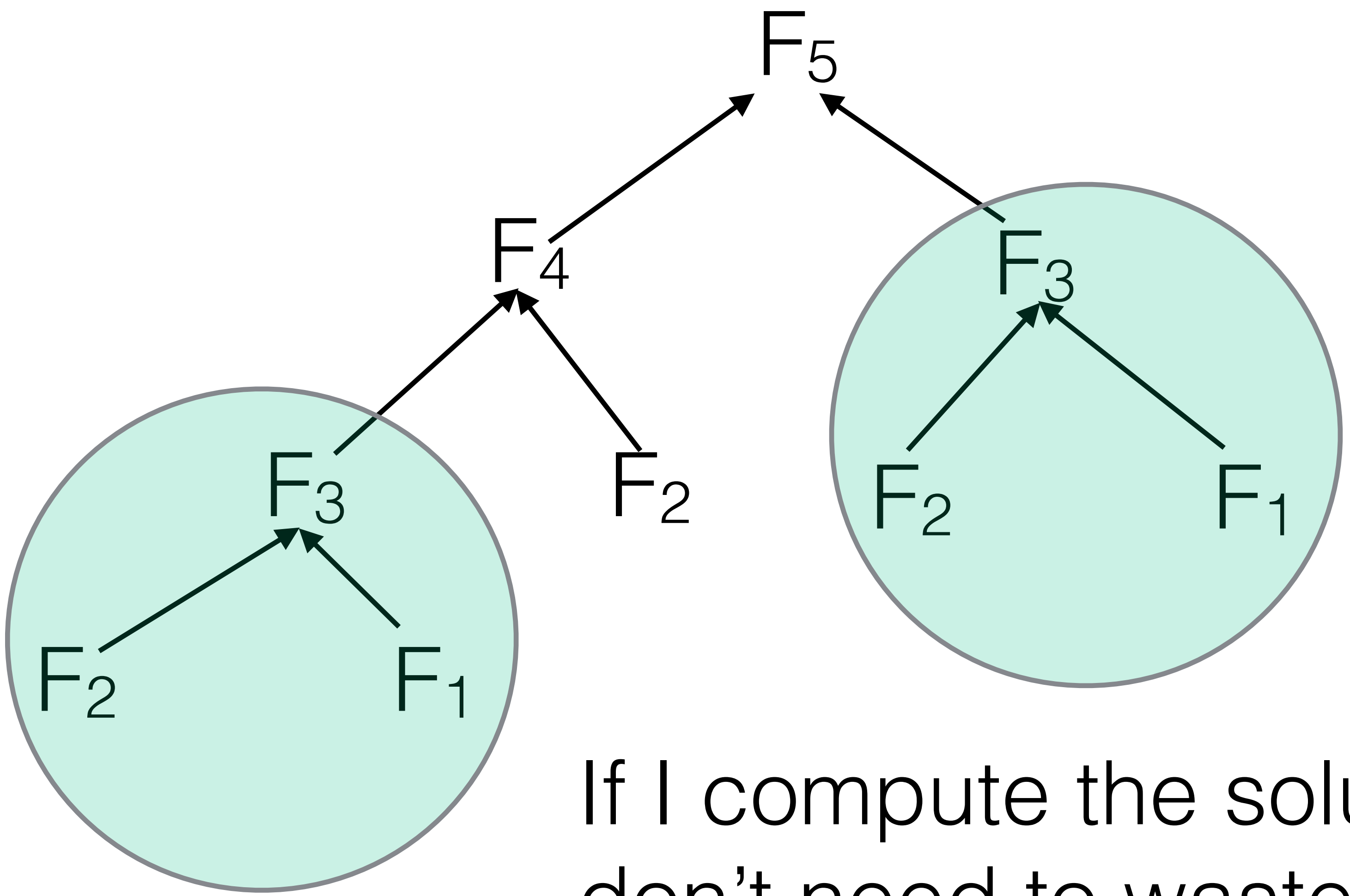


What is the “right order”?

$F_1 \rightarrow F_2 \rightarrow F_3 \rightarrow F_4 \rightarrow F_5 \ldots$

If I compute the solutions in the “right order”, I don’t need to waste time re-computing the same values.

Example 1: Fibonacci Sequence

$F_n = F_{n-1} + F_{n-2}$ with $F_1 = F_2 = 1$

How do we do better than $O(\phi^n)$?

Take 2:

```
def fib(n):
  if n == 1 or n == 2:
    return 1
  fm2, fm1 = 1, 1
  for i in xrange(2, n):
      fm2, fm1 = fm1, fm2 + fm1
  return fm1
```

We loop up to n, and perform an addition in each iteration —> O(n); **much better!** Note: O(n) assumes addition is constant, not true for large enough n.

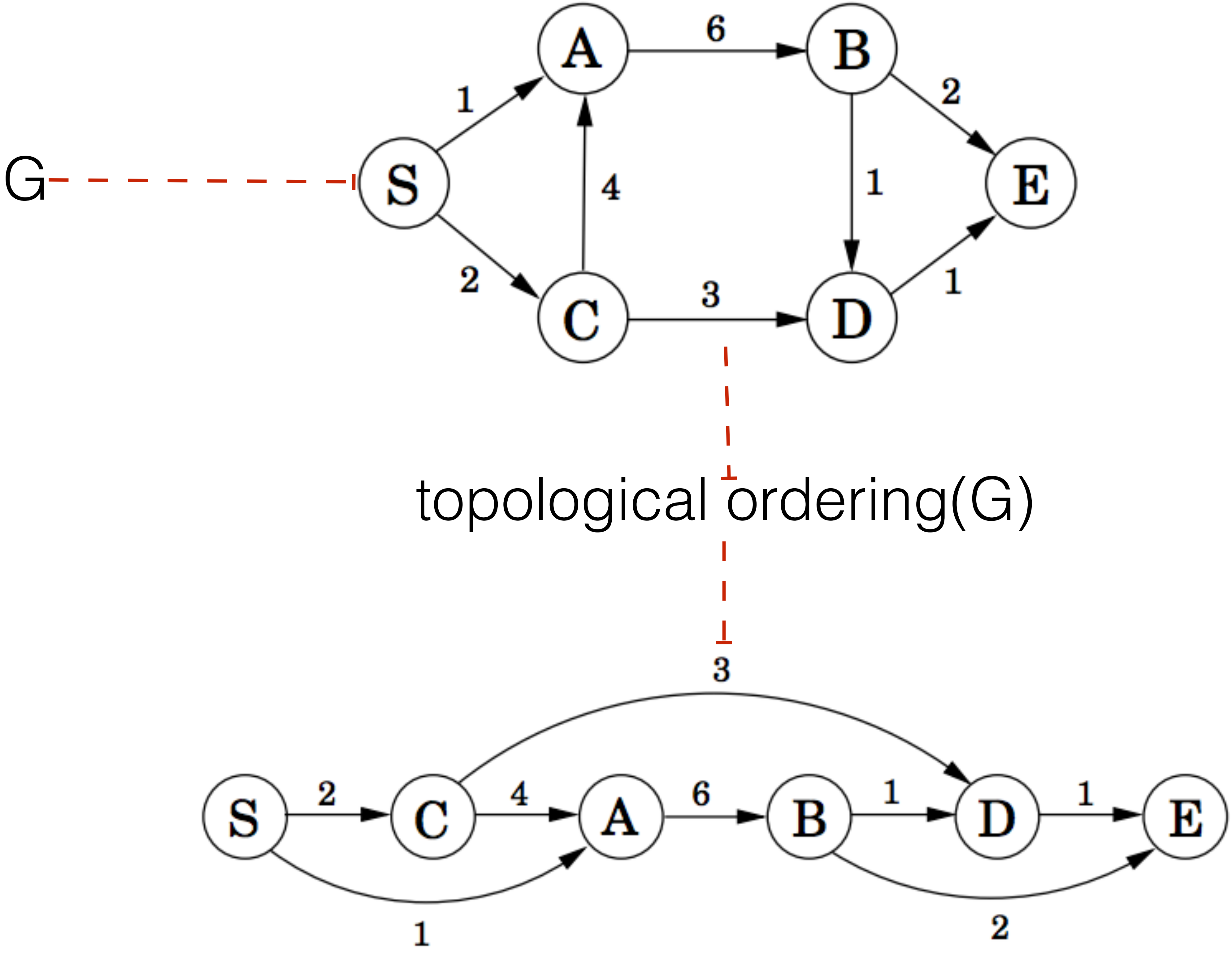
Example 2: Shortest Path in a DAG

Let G = (V,E) be a **d**irected **a**cyclic **g**raph (DAG) with vertex set V and edge set E.

Since G directed and free of cycles, there exists a (at least one) **topological order** of G — an ordering $p(v_1)$, $p(v_2)$, …, $p(v_n)$ such that for all $e = (v_i, v_j)$ in E, $p(v_i) < p(v_j)$

In other words, we can label the nodes of G such that all edges point from a vertex with a smaller label to a vertex with a larger label.

Example 2: Shortest Path in a DAG



G

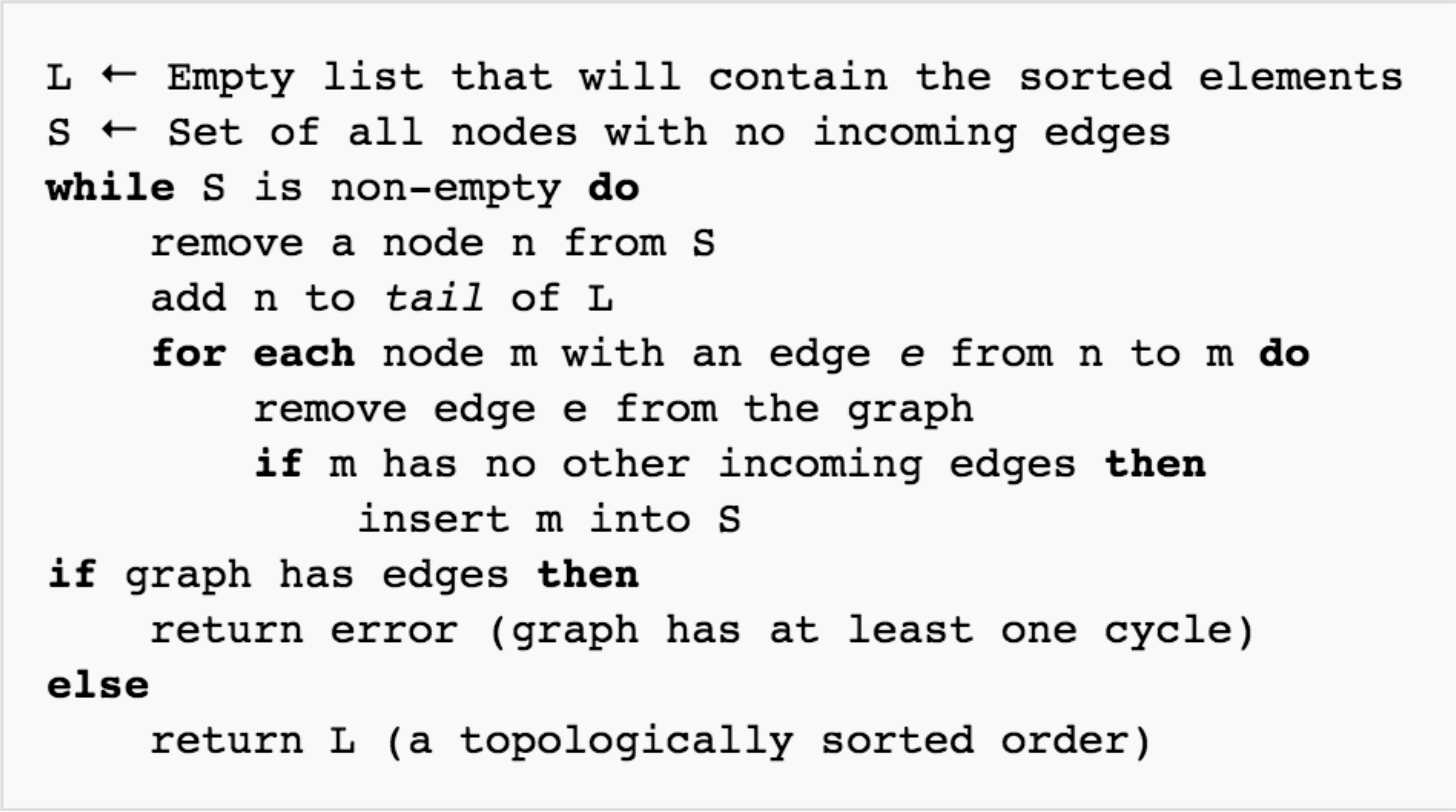
topological ordering(G)

Dasgupta, Sanjoy, Christos H. Papadimitriou, and Umesh Vazirani. Algorithms. McGraw-Hill, Inc., 2006.

Obtaining a topological ordering

Kahn's algorithm

Builds up a valid topo order node-by-node

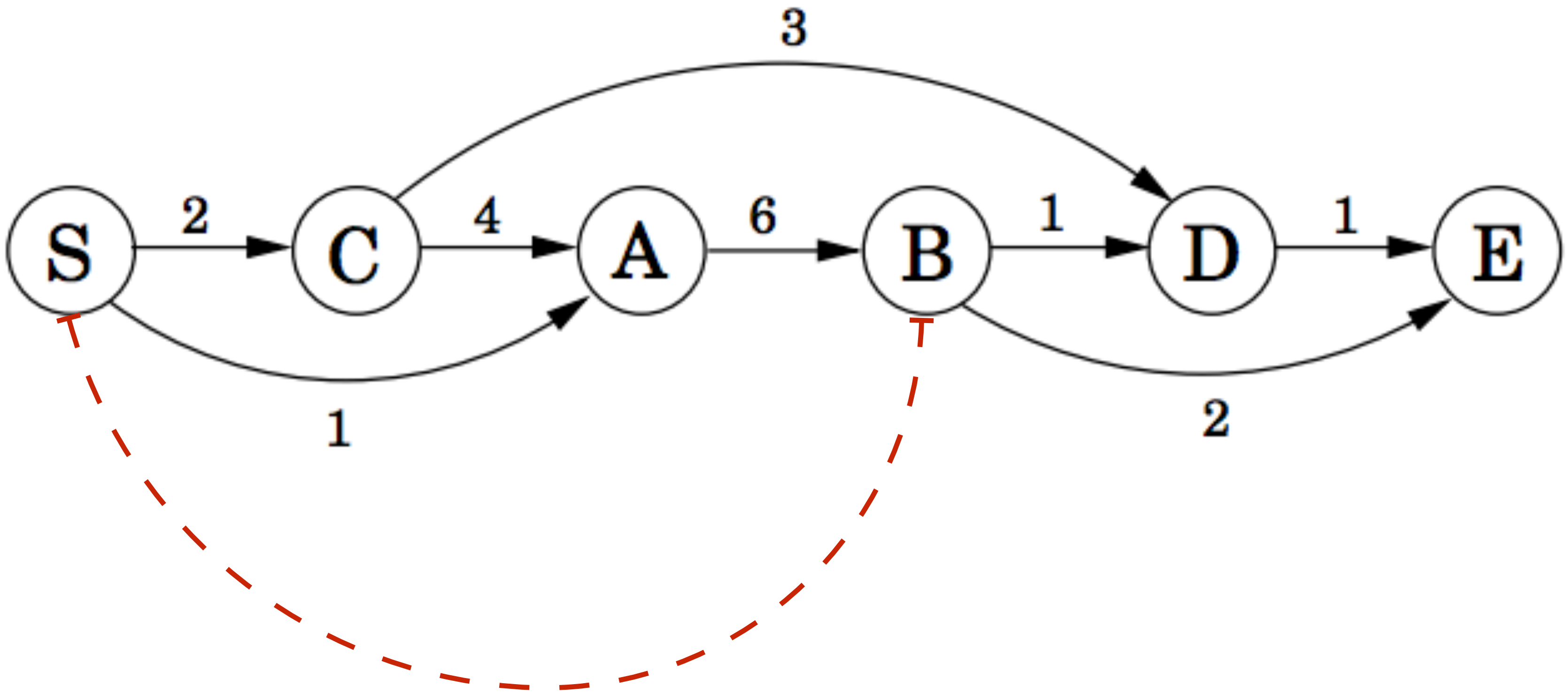


```
L ← Empty list that will contain the sorted elements
S ← Set of all nodes with no incoming edges
while S is non-empty do
    remove a node n from S
    add n to tail of L
    for each node m with an edge e from n to m do
        remove edge e from the graph
        if m has no other incoming edges then
            insert m into S
if graph has edges then
    return error (graph has at least one cycle)
else
    return L (a topologically sorted order)
```

O(|V| + |E|); why?

https://en.wikipedia.org/wiki/Topological_sorting

Example 2: Shortest Path in a DAG

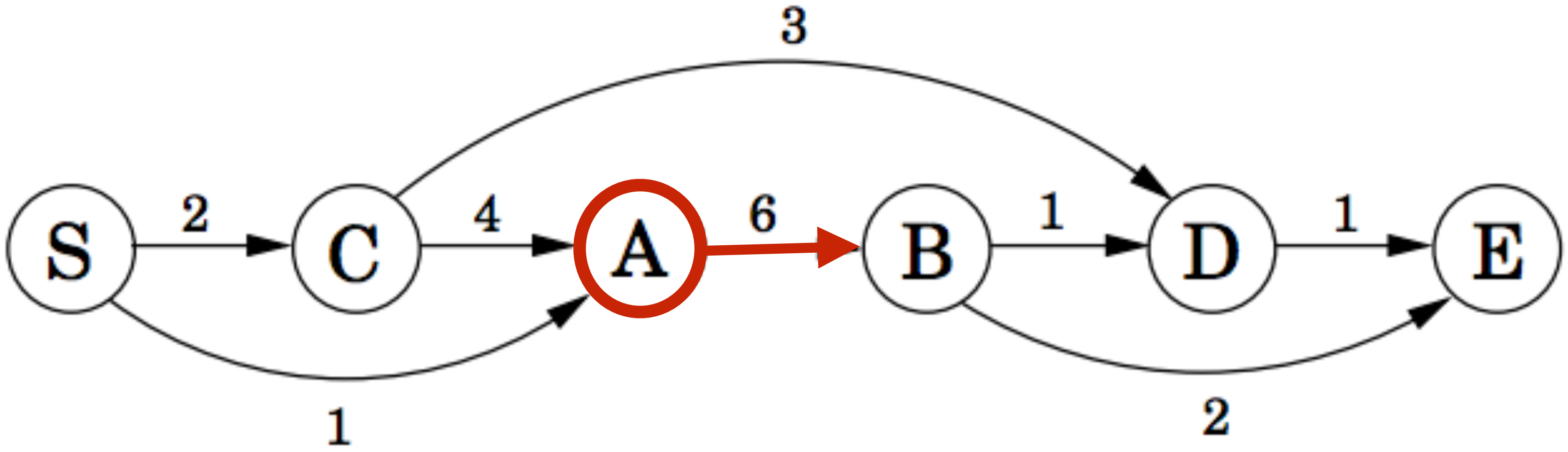


What's the distance from S to B — d(S,B) ?

Dasgupta, Sanjoy, Christos H. Papadimitriou, and Umesh Vazirani. Algorithms. McGraw-Hill, Inc., 2006.

Example 2: Shortest Path in a DAG

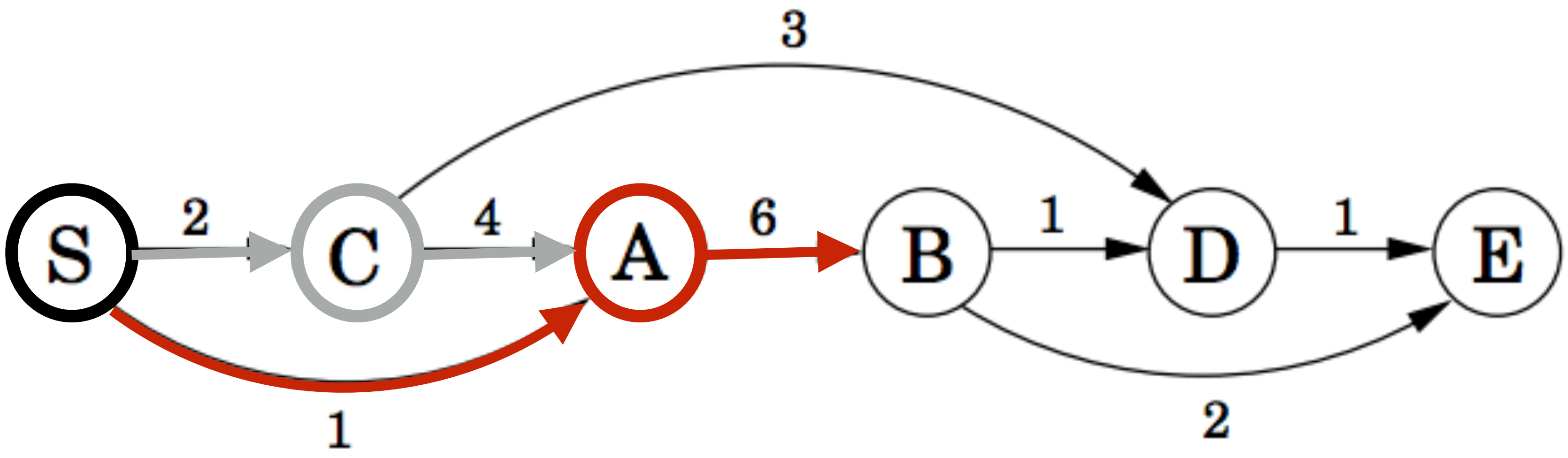
First, I **must** go through A, so it's at least d(S,A) + 6



Dasgupta, Sanjoy, Christos H. Papadimitriou, and Umesh Vazirani. Algorithms. McGraw-Hill, Inc., 2006.

Example 2: Shortest Path in a DAG

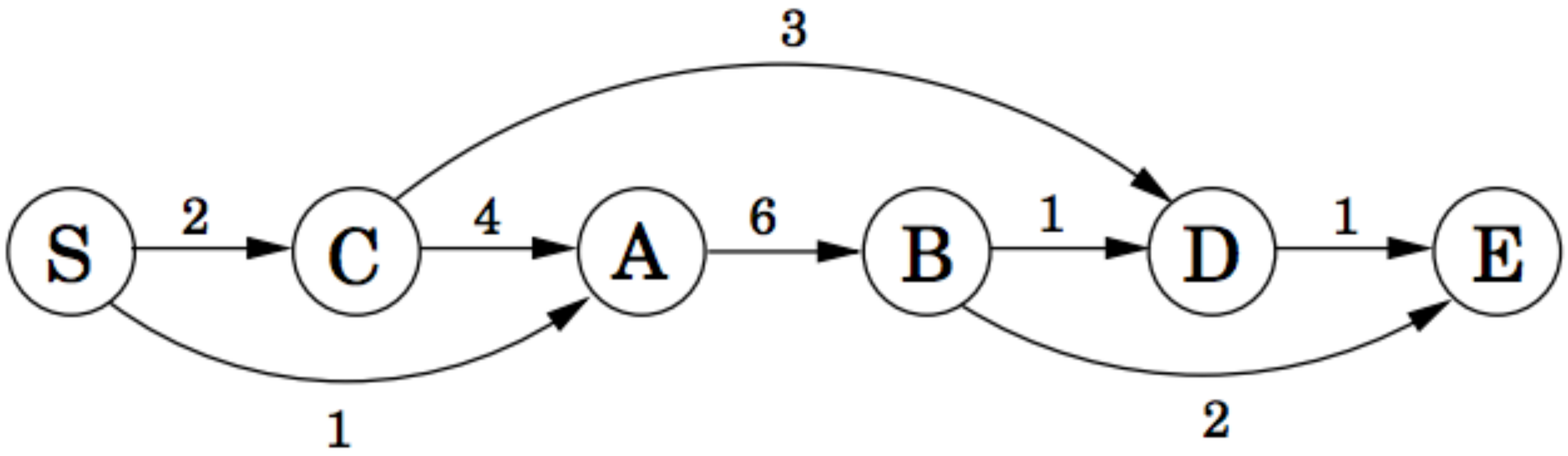
Then, there are 2 ways of getting to A — we choose the shortest.



Dasgupta, Sanjoy, Christos H. Papadimitriou, and Umesh Vazirani. Algorithms. McGraw-Hill, Inc., 2006.

Example 2: Shortest Path in a DAG

In general, d(S,X) is the
minimum value of d(S,Y) + d(Y,X) for all Y that precede X
and are connected by an edge



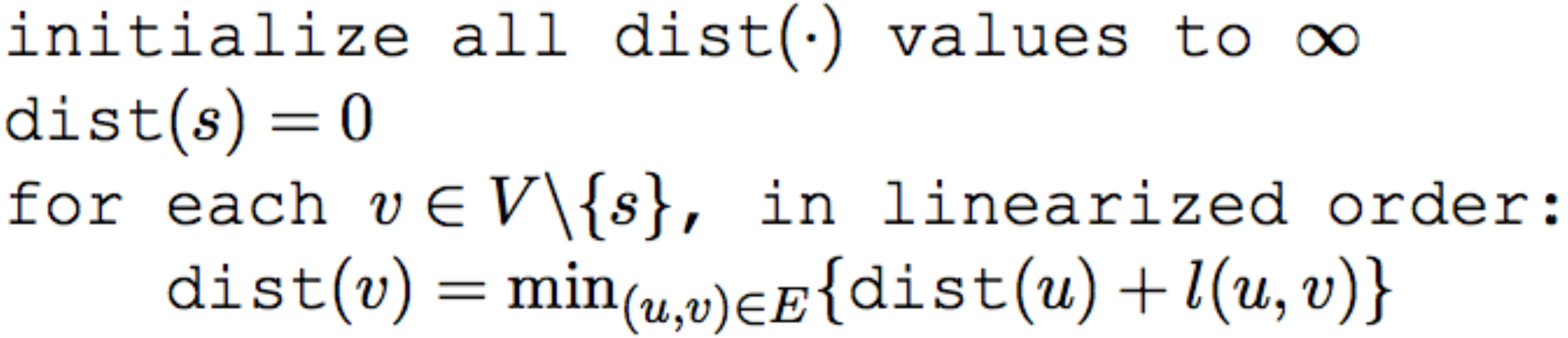
$$d(S,X) = \min_{Y \mid (Y,X) \in E} \{d(S,Y) + d(Y,X)\}$$

This becomes the DP recurrence for our problem

Dasgupta, Sanjoy, Christos H. Papadimitriou, and Umesh Vazirani. Algorithms. McGraw-Hill, Inc., 2006.

Example 2: Shortest Path in a DAG

The problem is solved efficiently by the following algorithm



```
initialize all dist(·) values to $\infty$
dist($s$) $= 0$
for each $v \in V \backslash \{s\}$, in linearized order:
    dist($v$) $= \min_{(u,v) \in E}\{$dist($u$) $+ l(u,v)\}$
```

Dasgupta, Sanjoy, Christos H. Papadimitriou, and Umesh Vazirani. Algorithms. McGraw-Hill, Inc., 2006.

Algorithm for Computing Edit Distance

Consider the last characters of each string:

$$a = a_1a_2a_3a_4\ldots a_m$$
$$b = b_1b_2b_3b_4\ldots b_n$$

One of these possibilities must hold:

1. (a_m,b_n) are matched to each other
2. a_m is not matched at all
3. b_n is not matched at all
4. a_m is matched to some b_j $(j \neq n)$ and b_n is matched to some a_k $(k \neq m)$.

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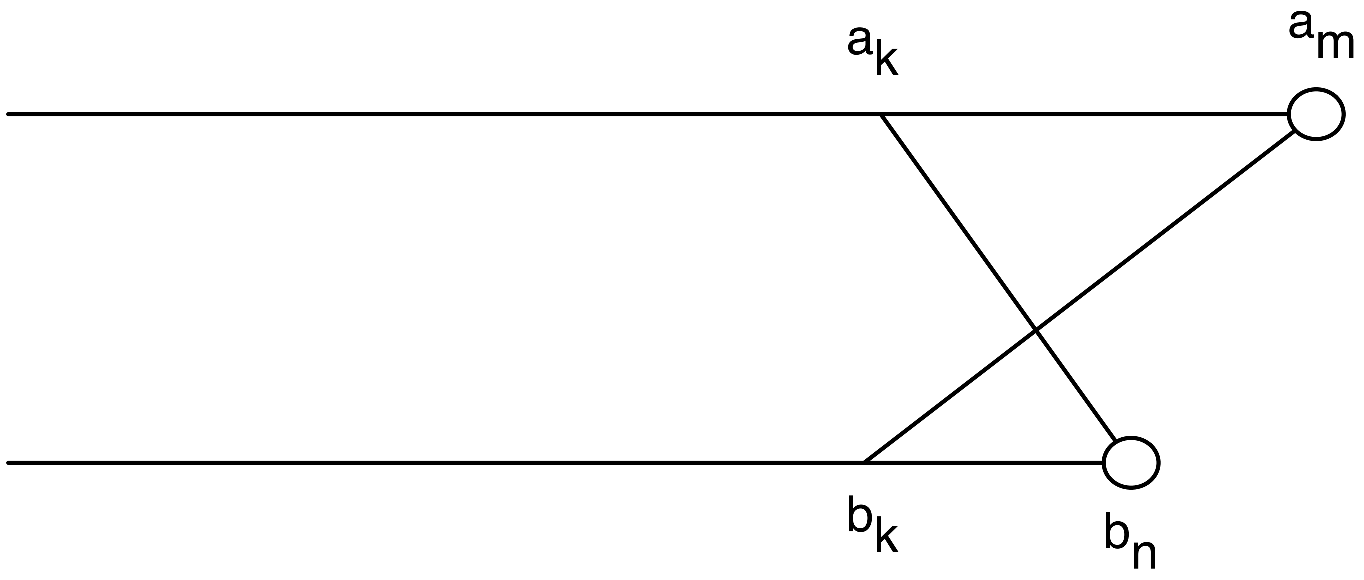
↑

#4 can’t happen! Why?

*

No Crossing Rule Forbids #4

4. a_m is matched to some b_j ($j \neq n$) and b_n is matched to some a_k ($k \neq$m).



So, the only possibilities for what happens to the last characters are:

1. (a_m, b_n) are matched to each other
2. a_m is not matched at all
3. b_n is not matched at all

Recursive Solution

Turn the 3 possibilities into 3 cases of a recurrence:

$$OPT(i,j) = \min \begin{cases} \text{cost}(a_i, b_j) + OPT(i-1, j-1) & \text{match } a_i, b_j \\ \text{gap} + OPT(i-1, j) & a_i \text{ is not matched} \\ \text{gap} + OPT(i, j-1) & b_j \text{ is not matched} \end{cases}$$

↑ Cost of the optimal alignment between $a_1 \ldots a_i$ and $b_1 \ldots b_j$

↑ Written in terms of the costs of smaller problems

Key: we don't know which of the 3 possibilities is the right one, so we try them all.

<u>Base case:</u> $OPT(i, 0) = i \times \text{gap}$ and $OPT(0, j) = j \times \text{gap}$.

(Aligning *i* characters to 0 characters must use *i* gaps.)

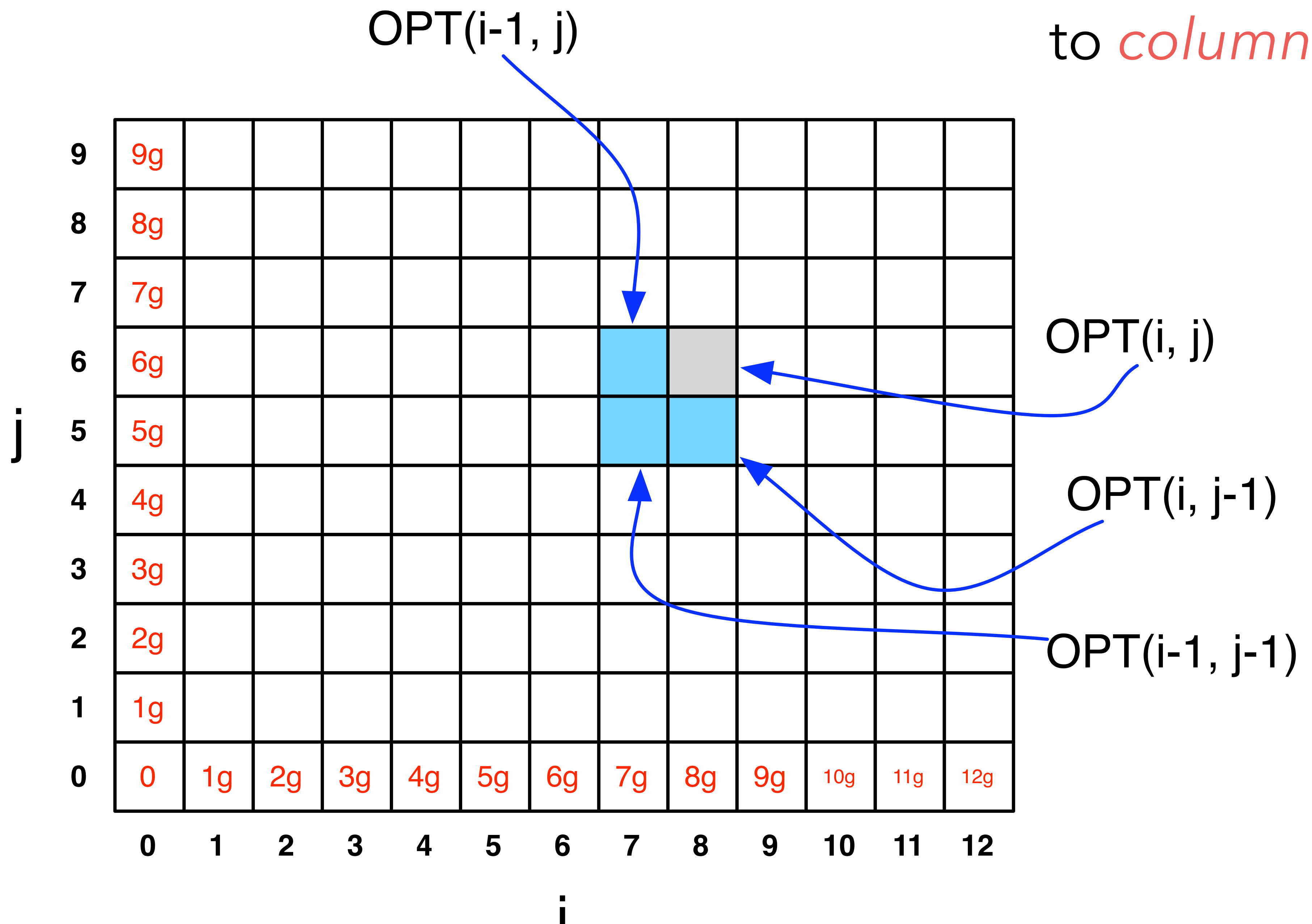
*

Computing OPT(i,j) Efficiently

We're ultimately interested in $OPT(n,m)$, but we will compute all other $OPT(i,j)$ ($i \leq n, j \leq m$) on the way to computing $OPT(n,m)$.

Store those values in a 2D array:

NOTE: observe the non-standard notation here; OPT(**i**,**j**) is referring to *column* i, *row* j of the matrix.



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

OPT(i-1, j)

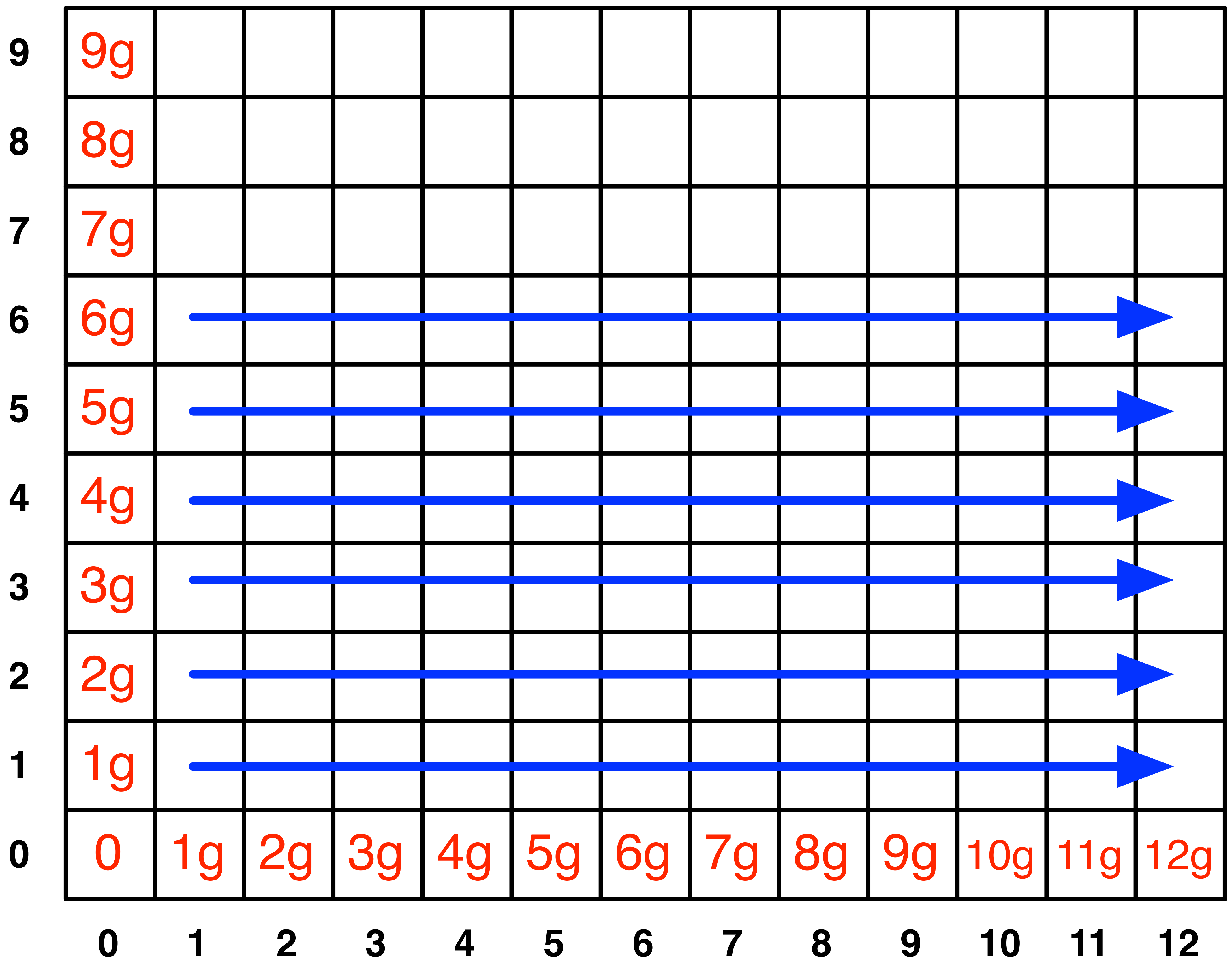
OPT(i, j)

OPT(i, j-1)

OPT(i-1, j-1)

*

Filling in the 2D Array



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

*

Edit Distance Computation

```
EditDistance(X,Y):
   For i = 1,...,m: A[i,0] = i*gap
   For j = 1,...,n: A[0,j] = j*gap

   For i = 1,...,m:
      For j = 1,...,n:
         A[i,j] = min(
            cost(a[i],b[j]) + A[i-1,j-1],
            gap + A[i-1,j],
            gap + A[i,j-1]
         )
      EndFor
   EndFor
   Return A[m,n]
```

Where's the answer?

OPT(n,m) contains the edit distance between the two strings.

Why? By induction: EVERY cell contains the optimal edit distance between some prefix of string 1 with some prefix of string 2.

Running Time

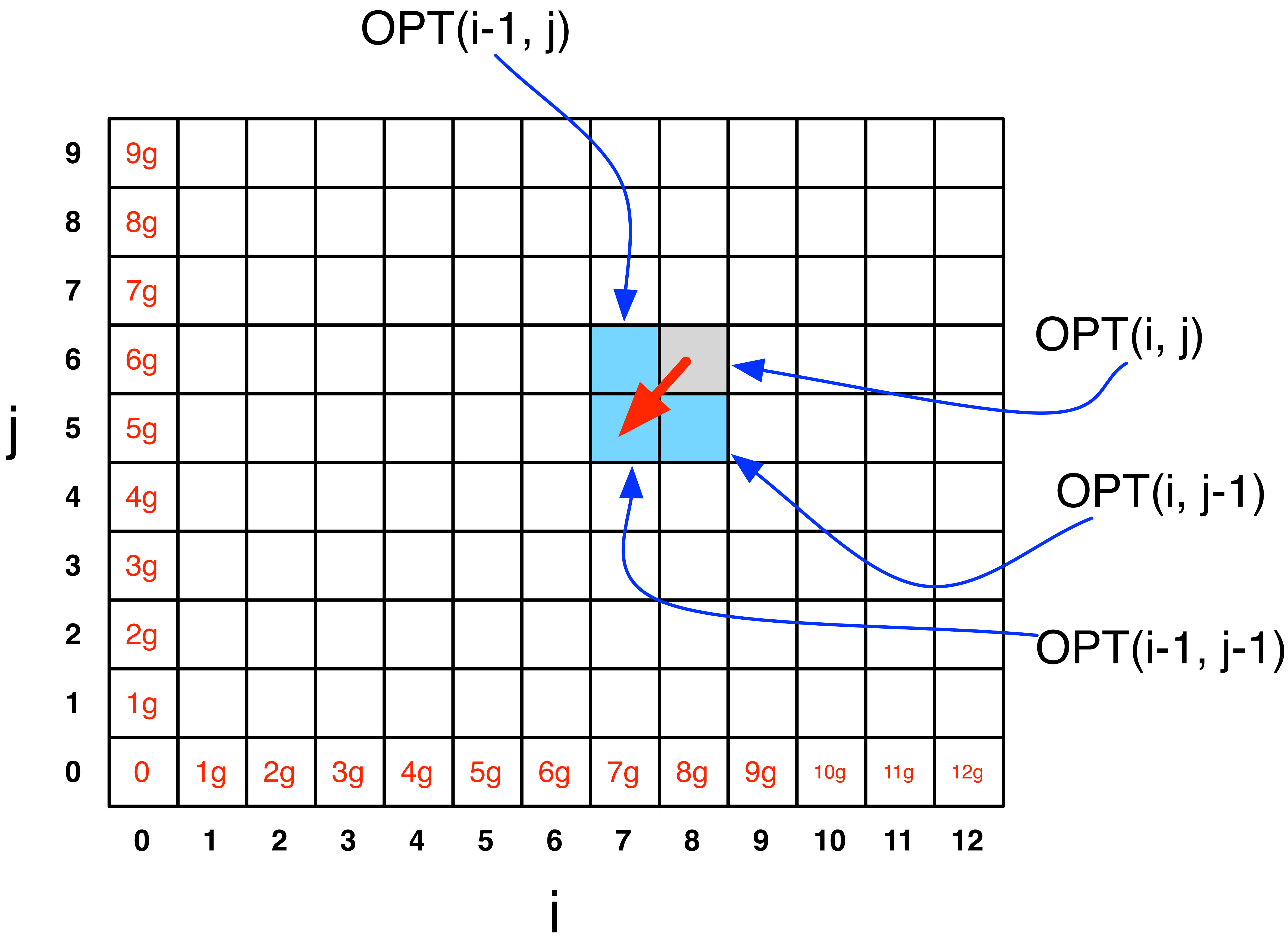
Number of entries in array = O($m \times n$), where m and n are the lengths of the 2 strings.

Filling in each entry takes constant O(1) time.

Total running time is O(mn).

*

Finding the actual alignment

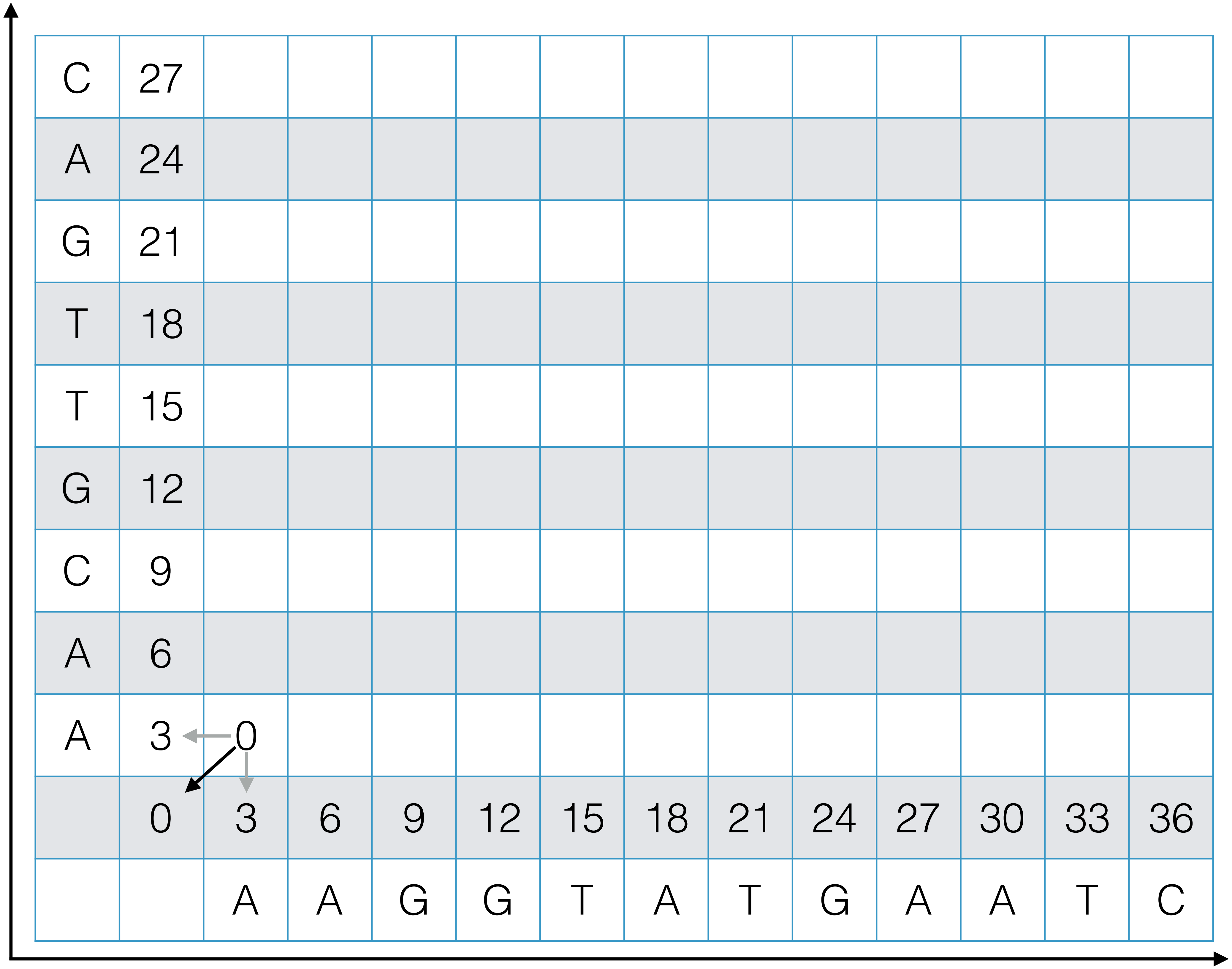


j													
9	9g												
8	8g												
7	7g												
6	6g												
5	5g												
4	4g												
3	3g												
2	2g												
1	1g												
0	0	1g	2g	3g	4g	5g	6g	7g	8g	9g	10g	11g	12g
i	0	1	2	3	4	5	6	7	8	9	10	11	12

*

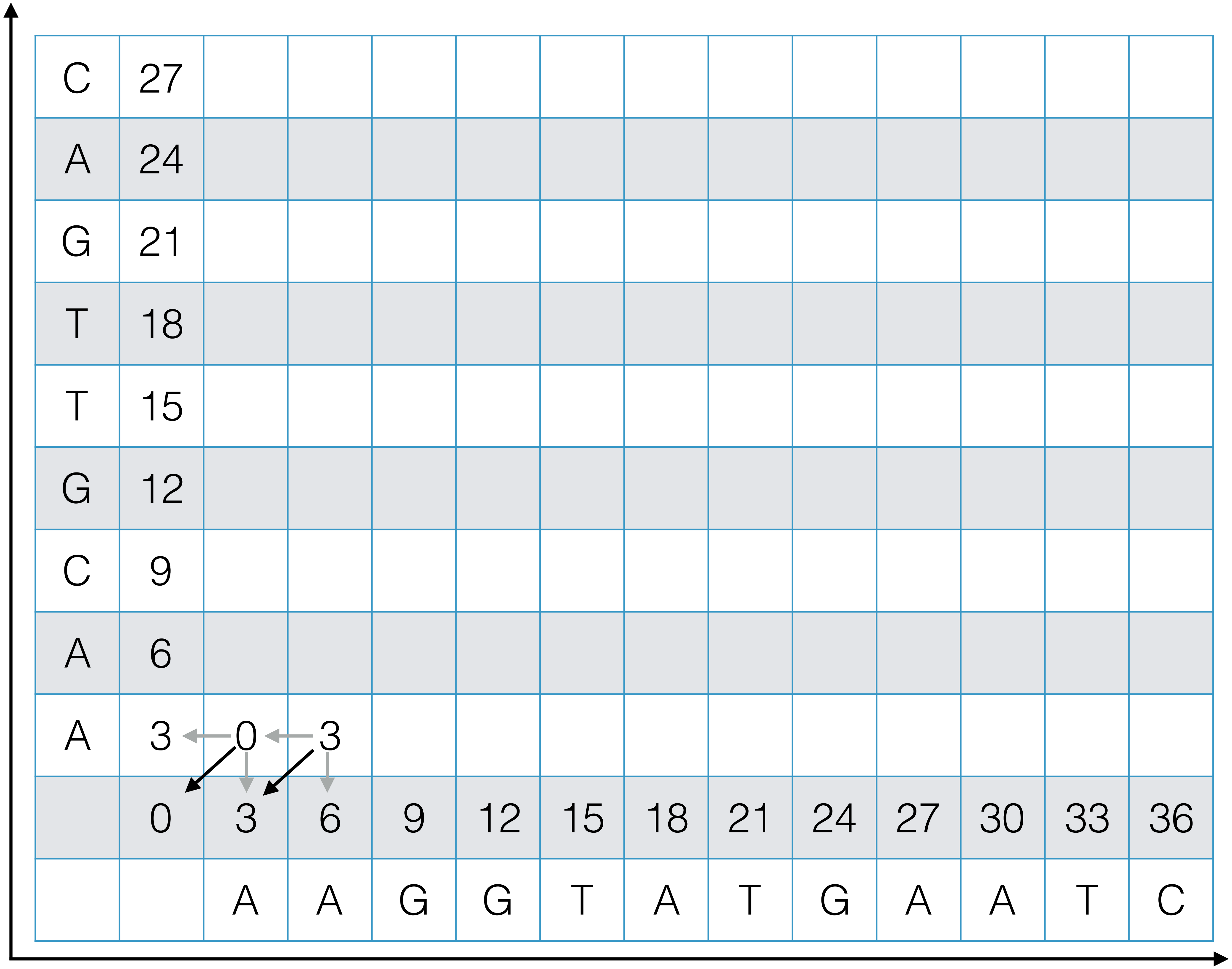
gap cost = 3
mismatch cost = 1

Example



C	27												
A	24												
G	21												
T	18												
T	15												
G	12												
C	9												
A	6												
A	3	0											
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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T	15												
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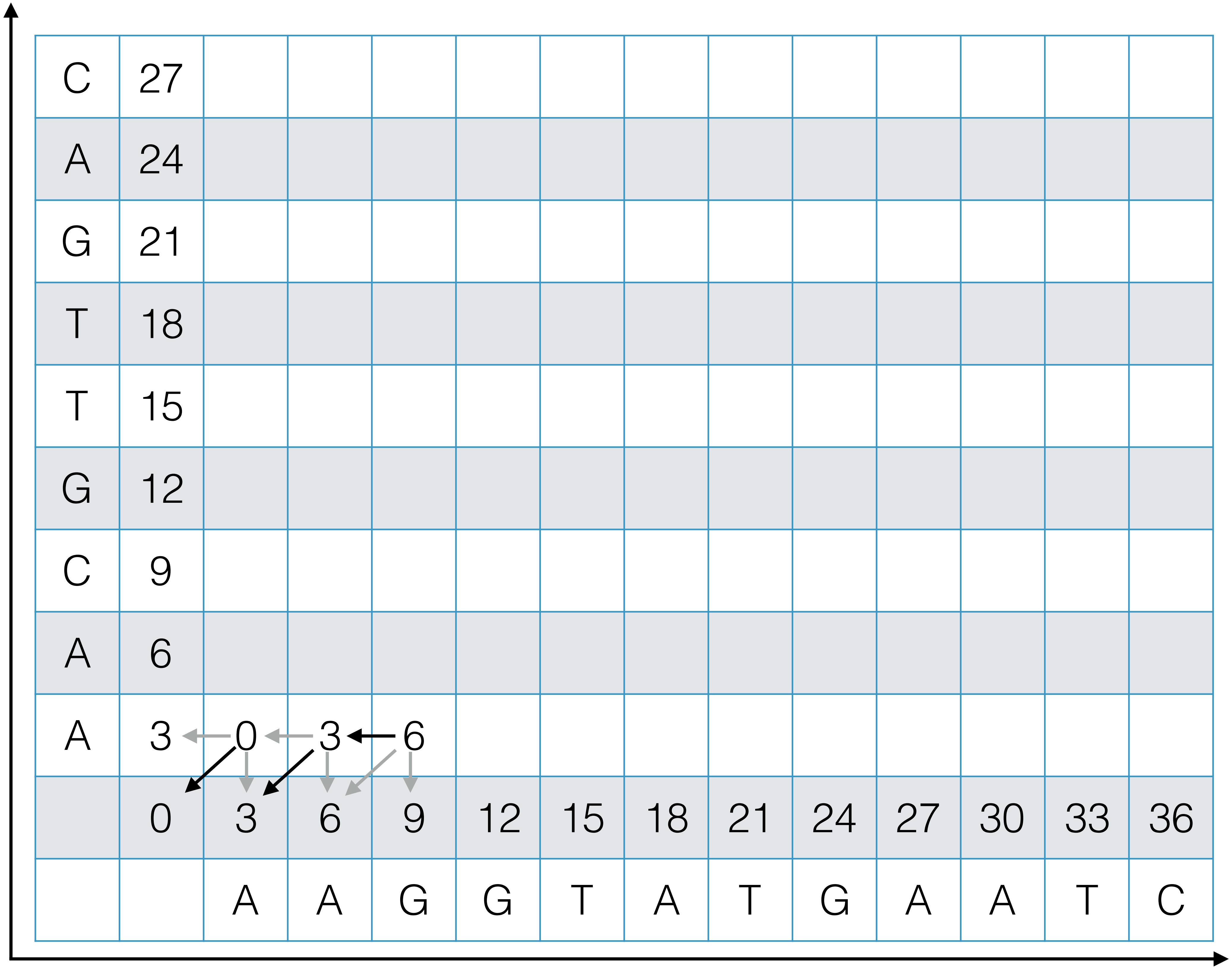
A	3	0	3										
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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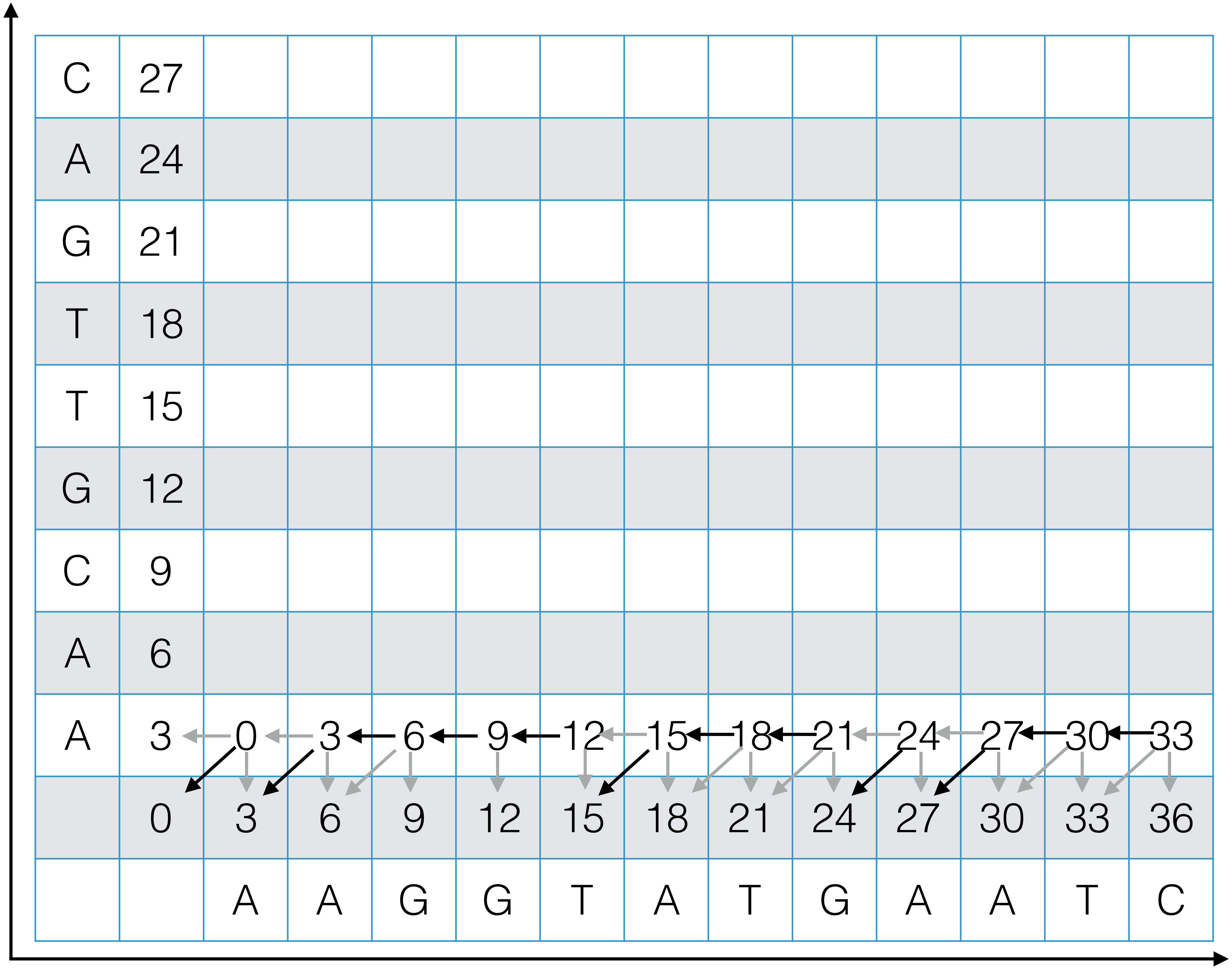
G	12												
C	9												
A	6												
A	3	0	3	6									
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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A	24												
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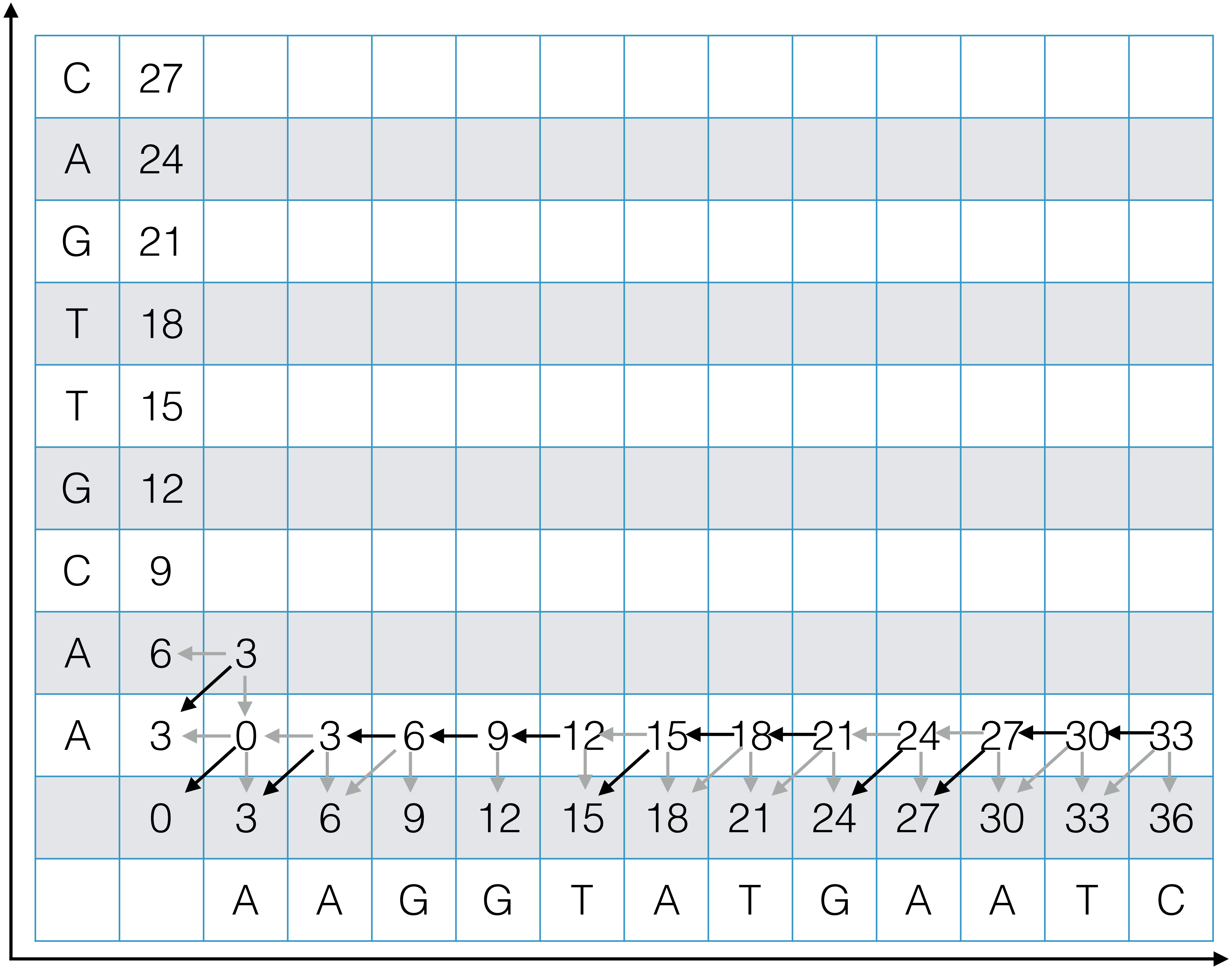
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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

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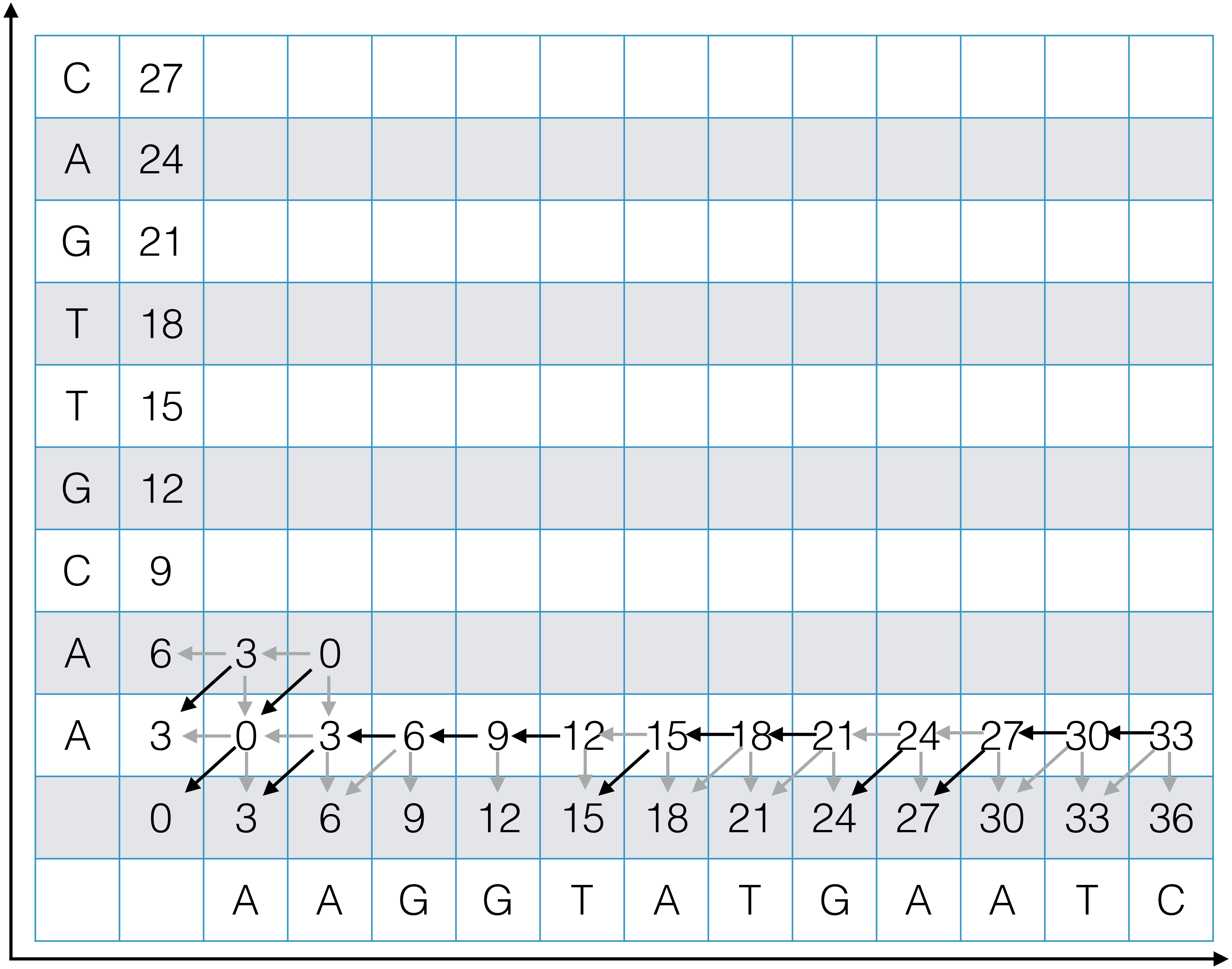
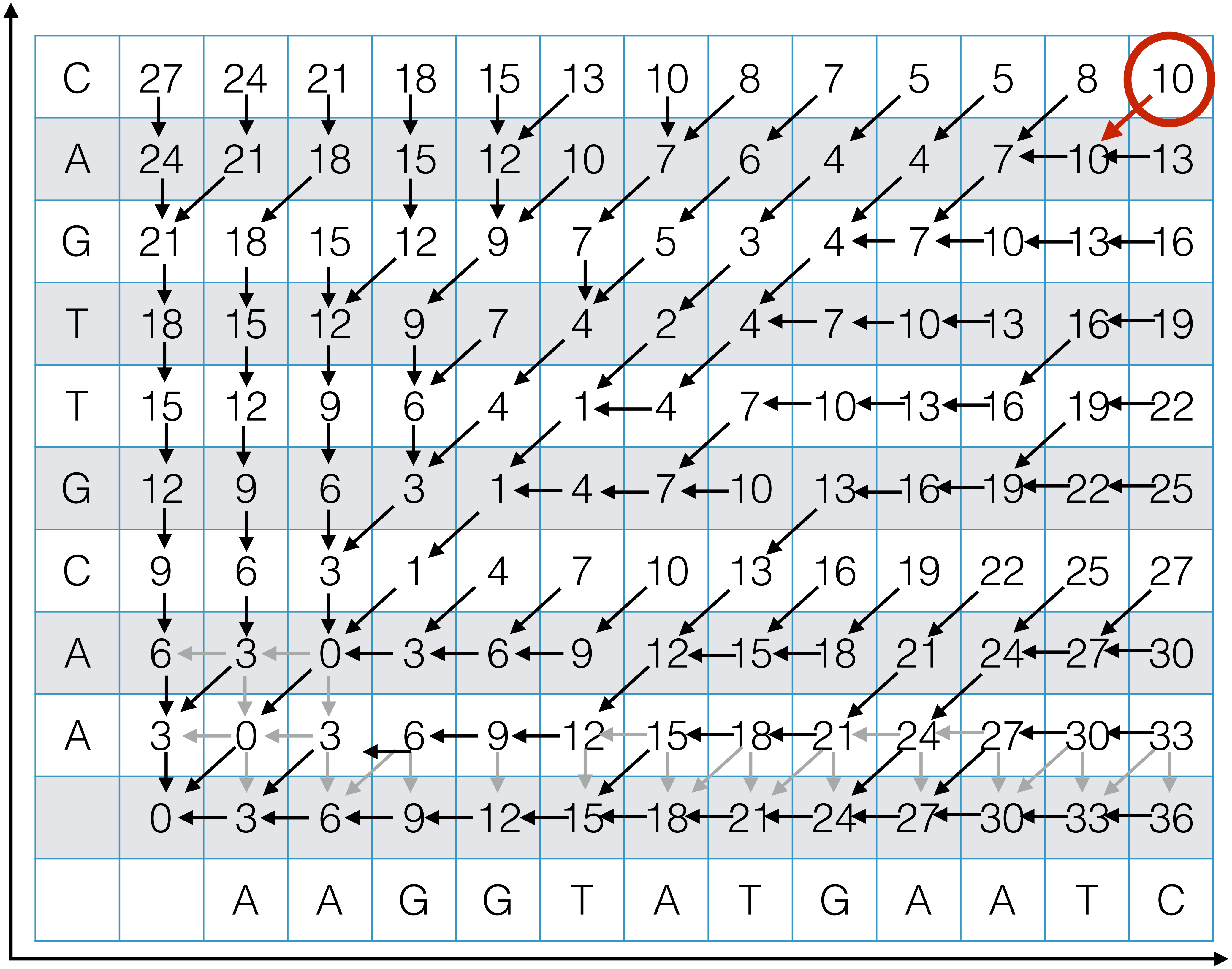


C	27												
A	24												
G	21												
T	18												
T	15												
G	12												
C	9												
A	6	3	0										
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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A	24	21	18	15	12	10	7	6	4	4	7	10	13
G	21	18	15	12	9	7	5	3	4	7	10	13	16
T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
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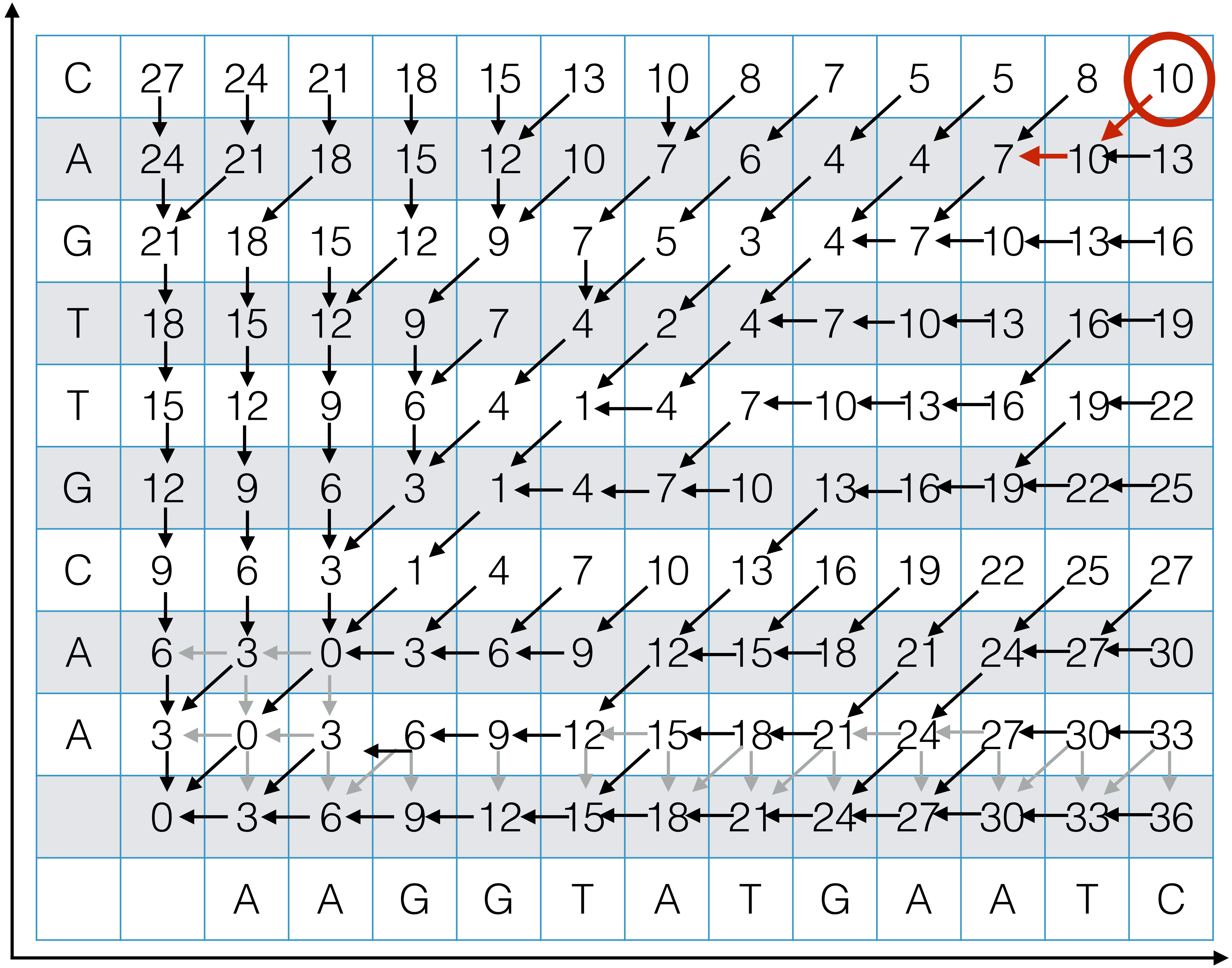
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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T	18	15	12	9	7	4	2	4	7	10	13	16	19
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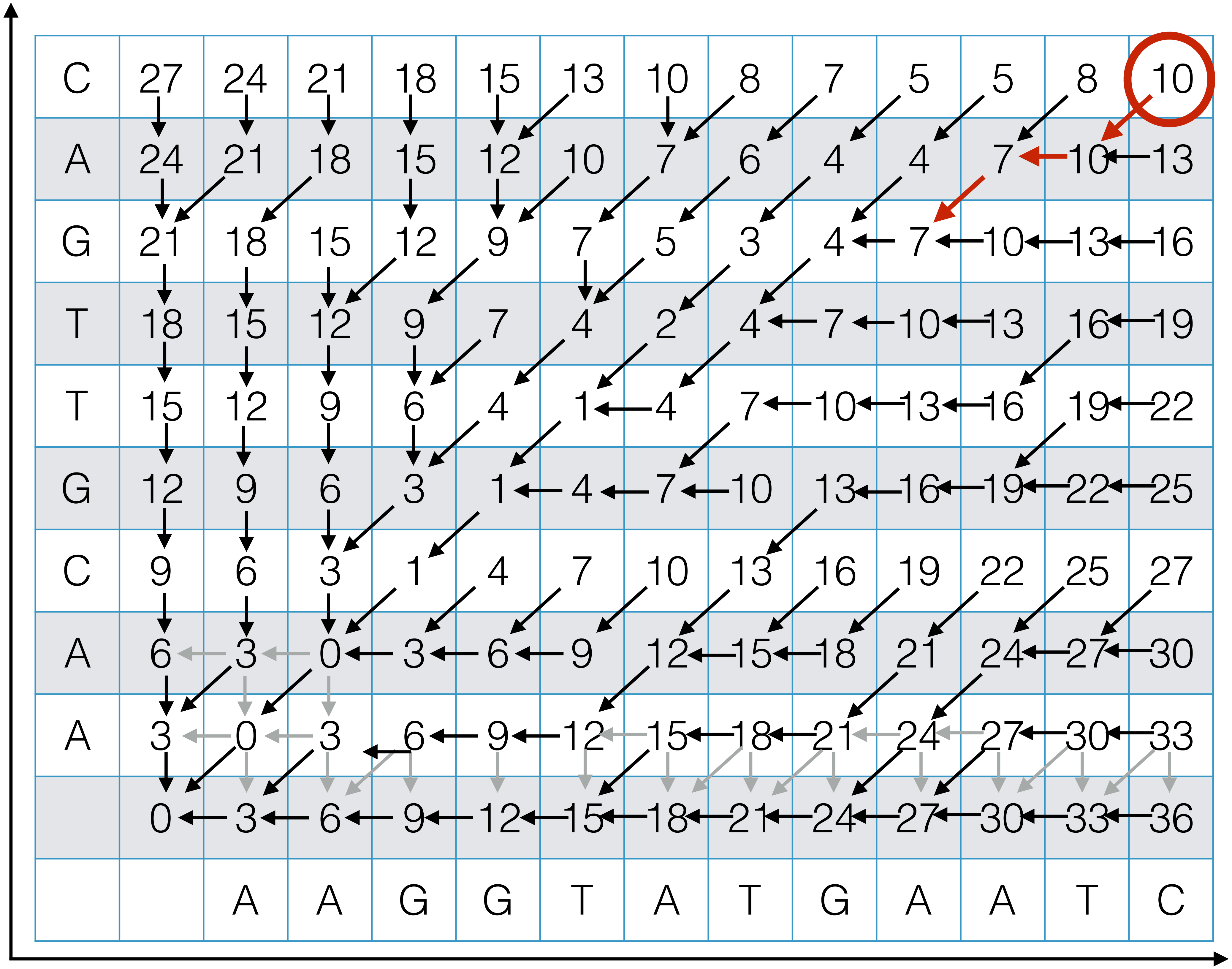
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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A	24	21	18	15	12	10	7	6	4	4	7	10	13
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T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
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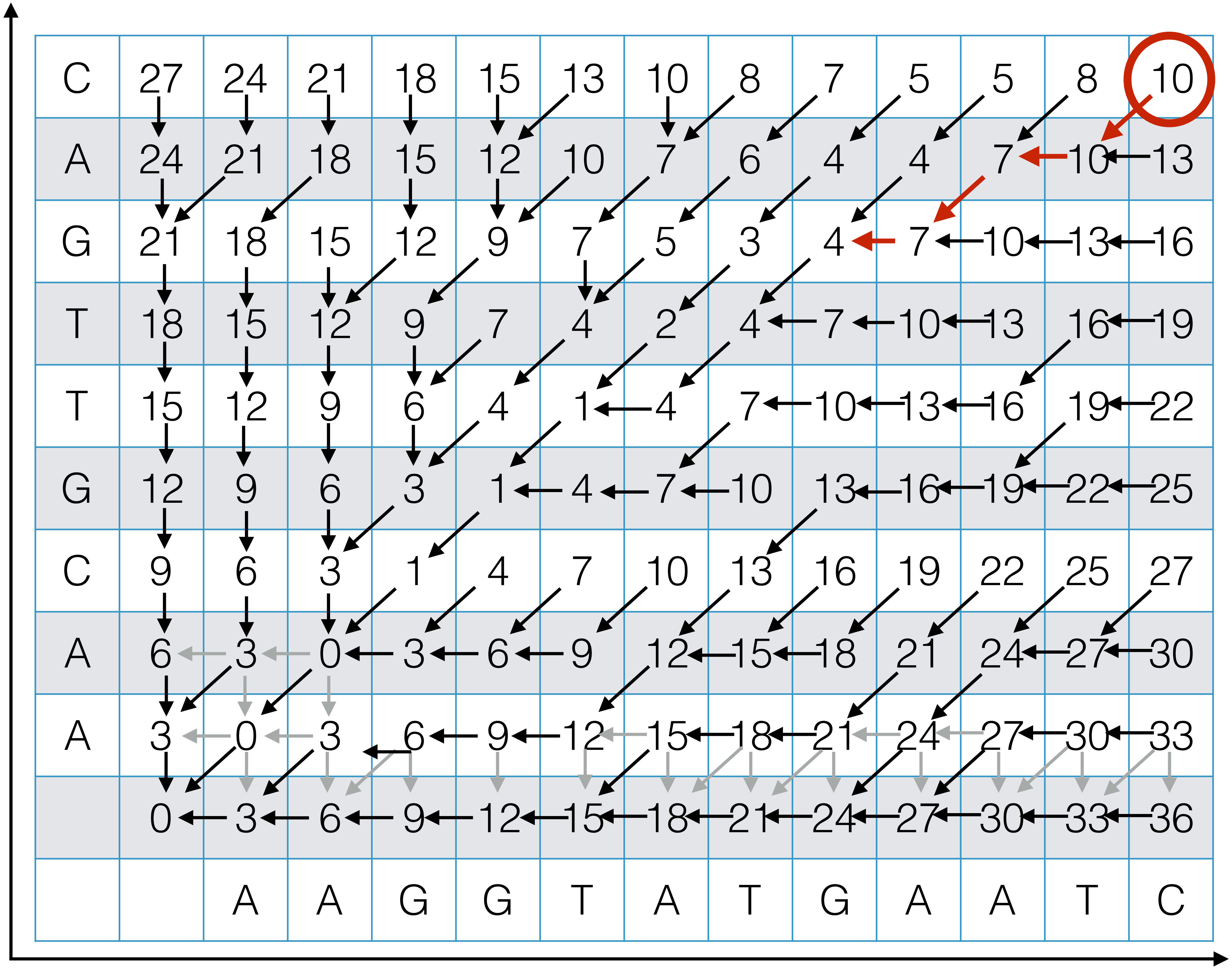
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
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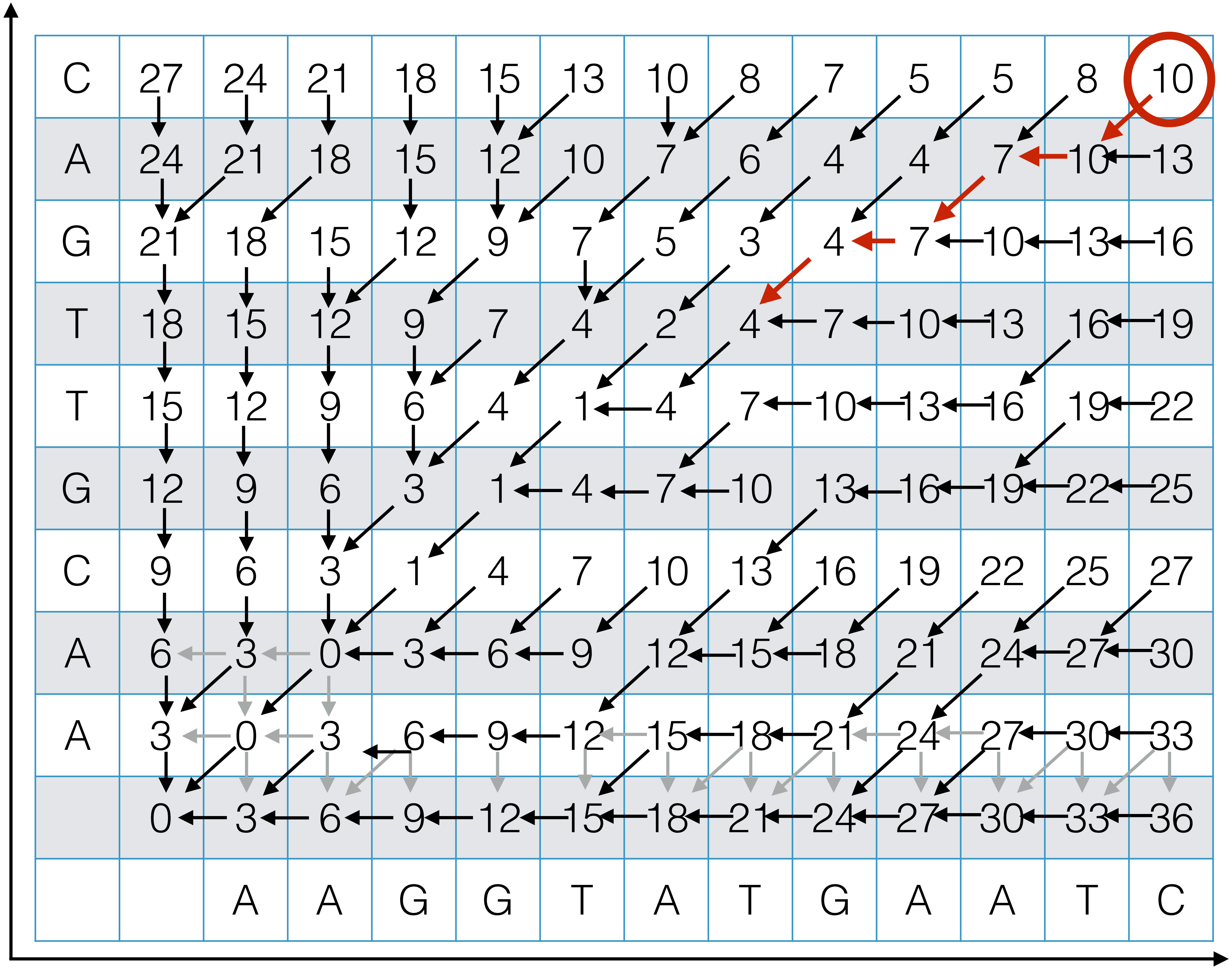
Example



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T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
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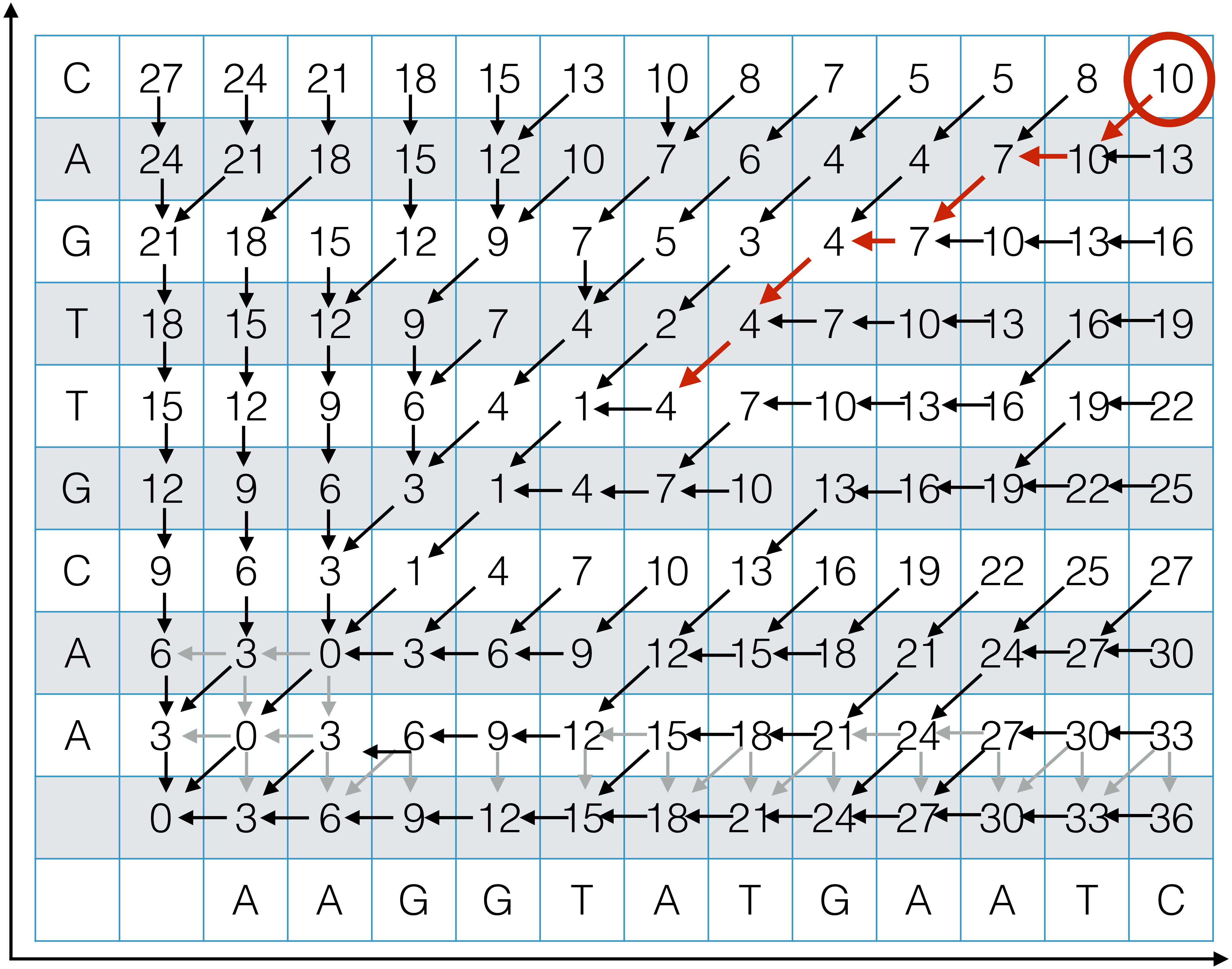
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
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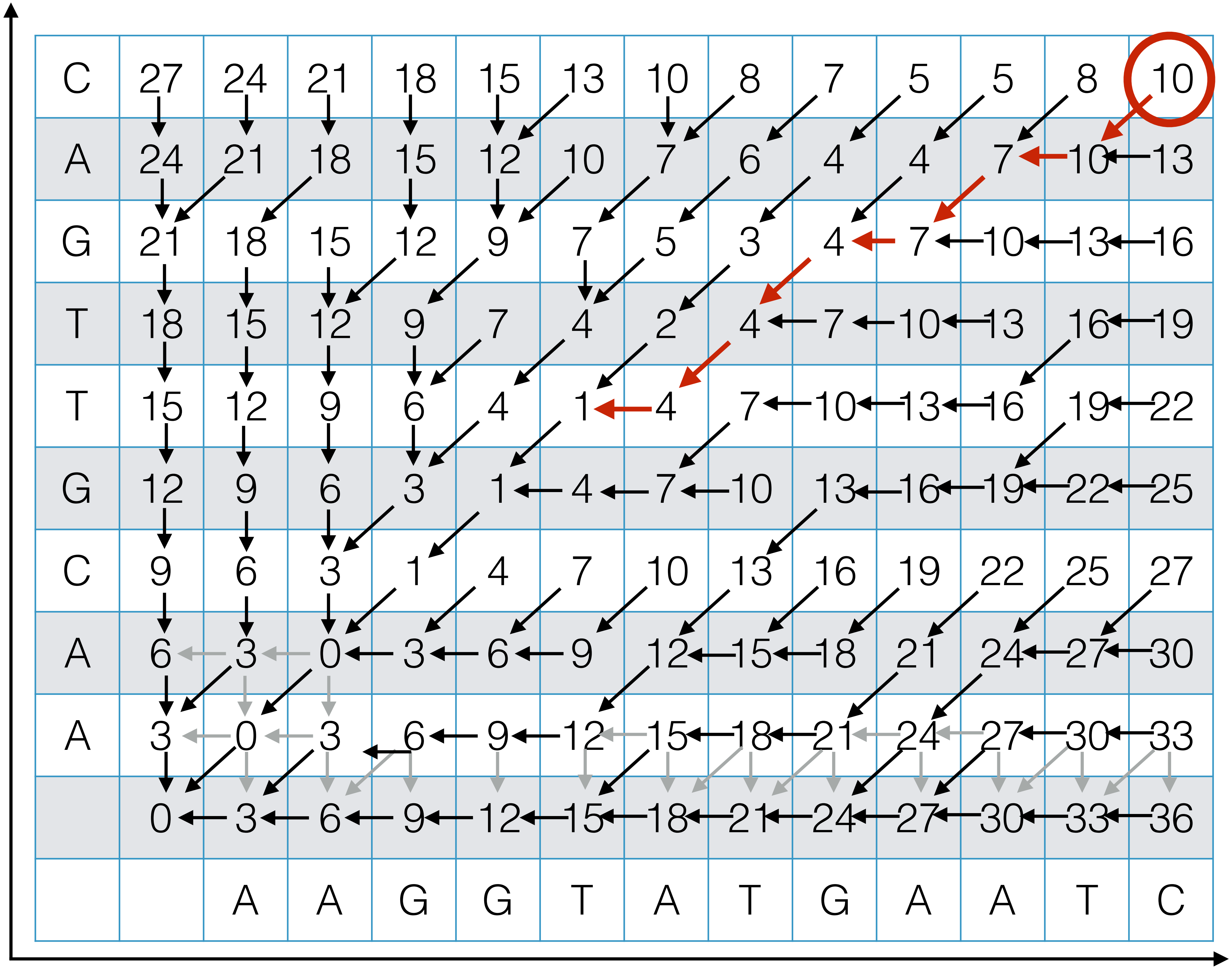
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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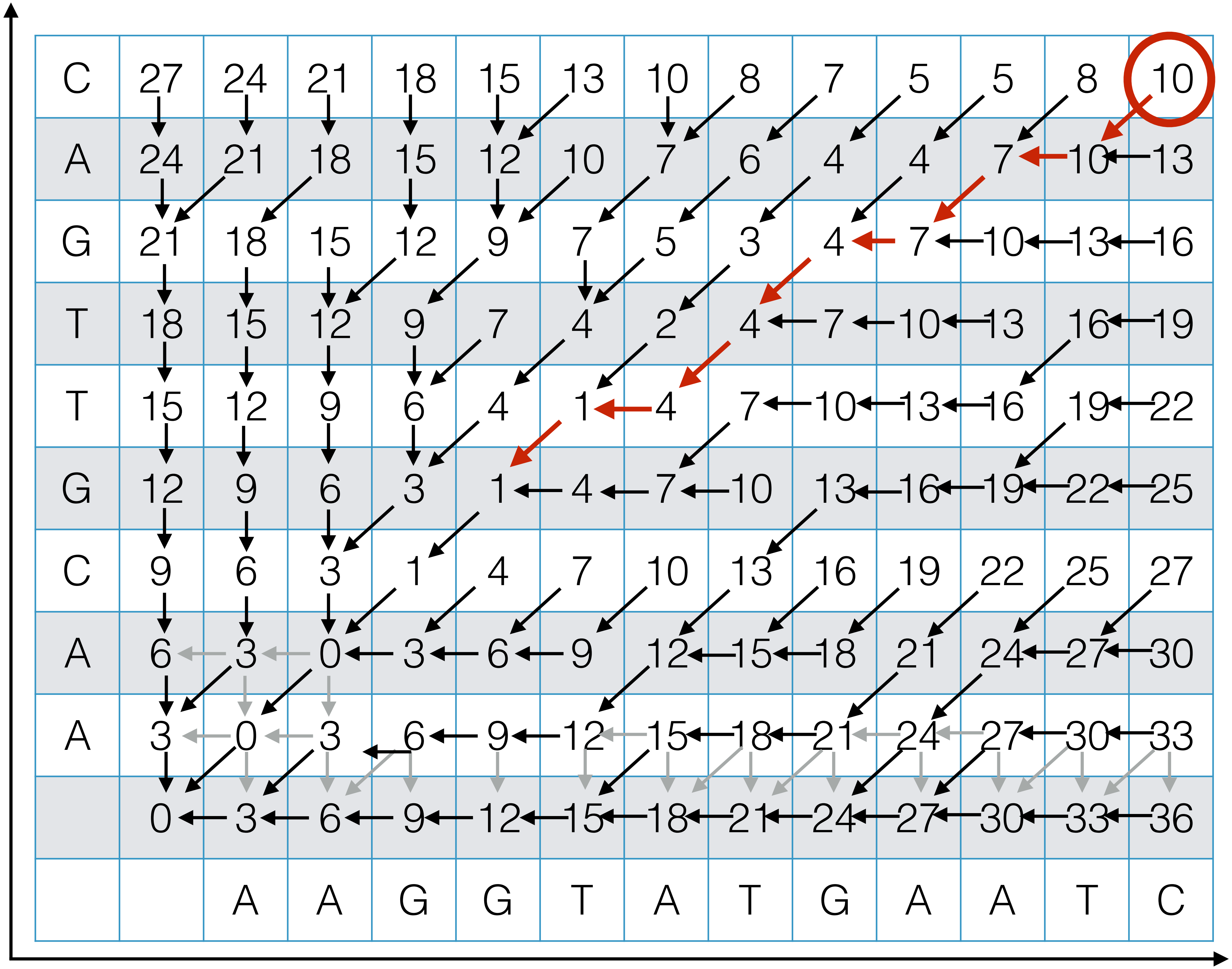
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



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A	24	21	18	15	12	10	7	6	4	4	7	10	13
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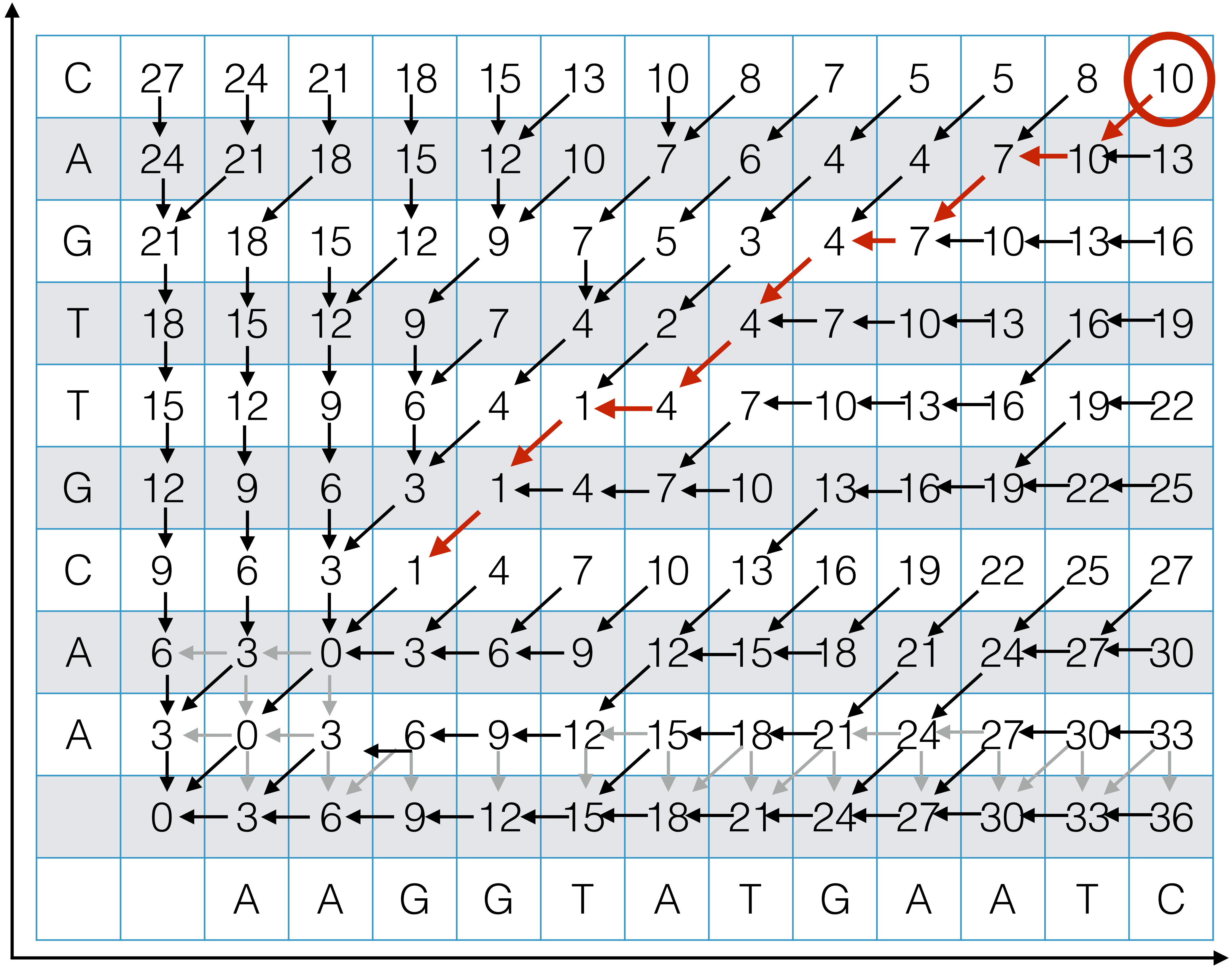
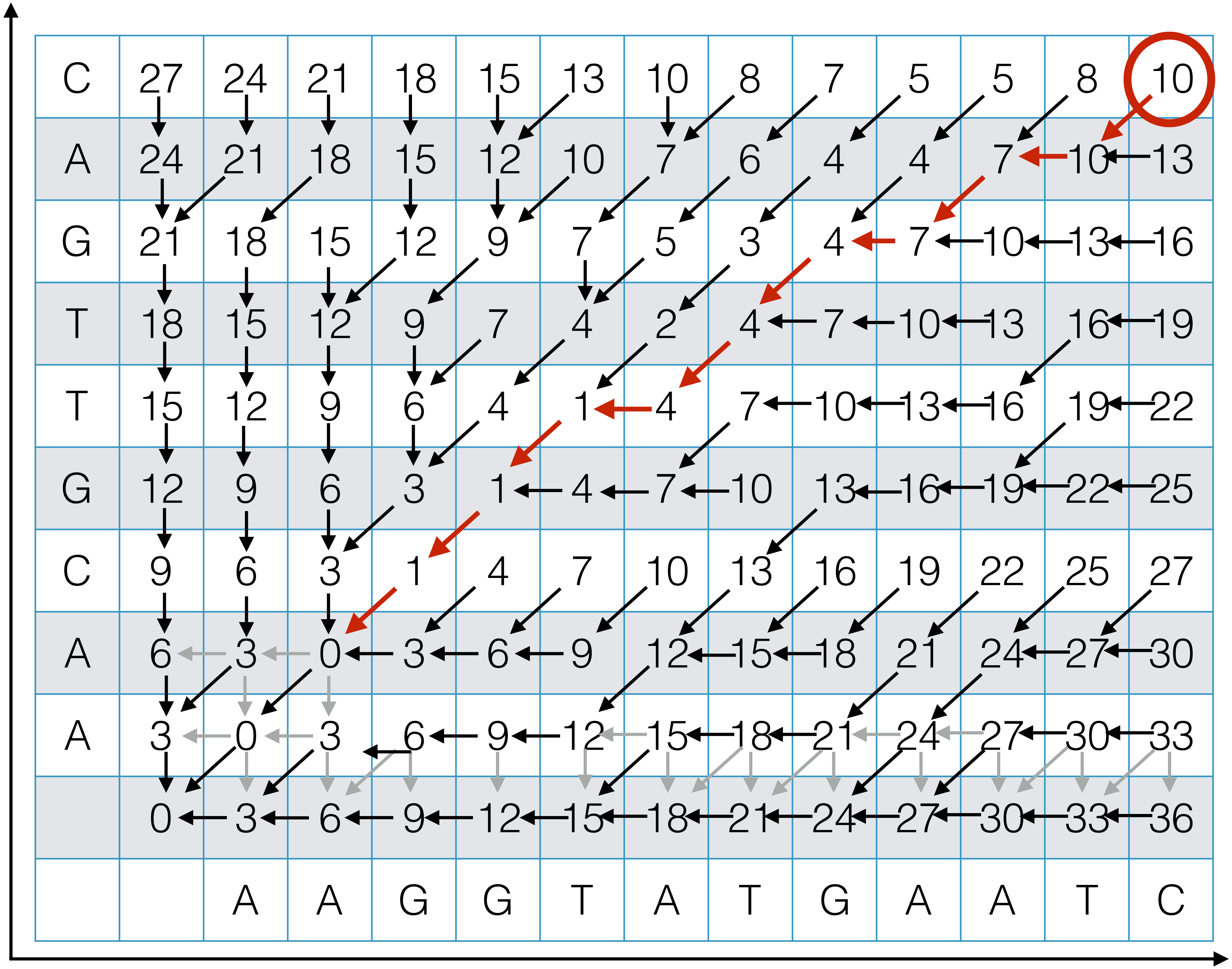
T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



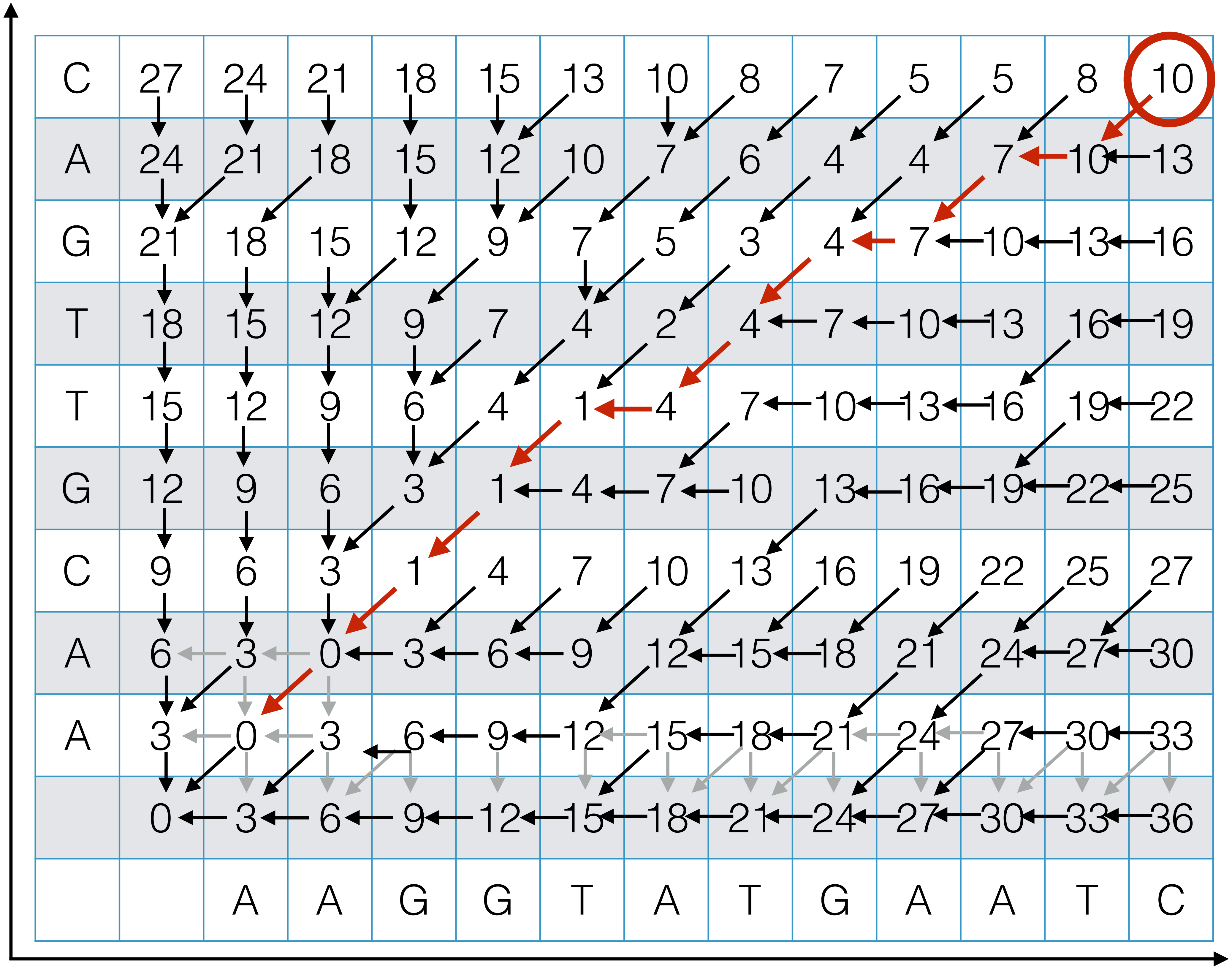
C	27	24	21	18	15	13	10	8	7	5	5	8	10
A	24	21	18	15	12	10	7	6	4	4	7	10	13
G	21	18	15	12	9	7	5	3	4	7	10	13	16
T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



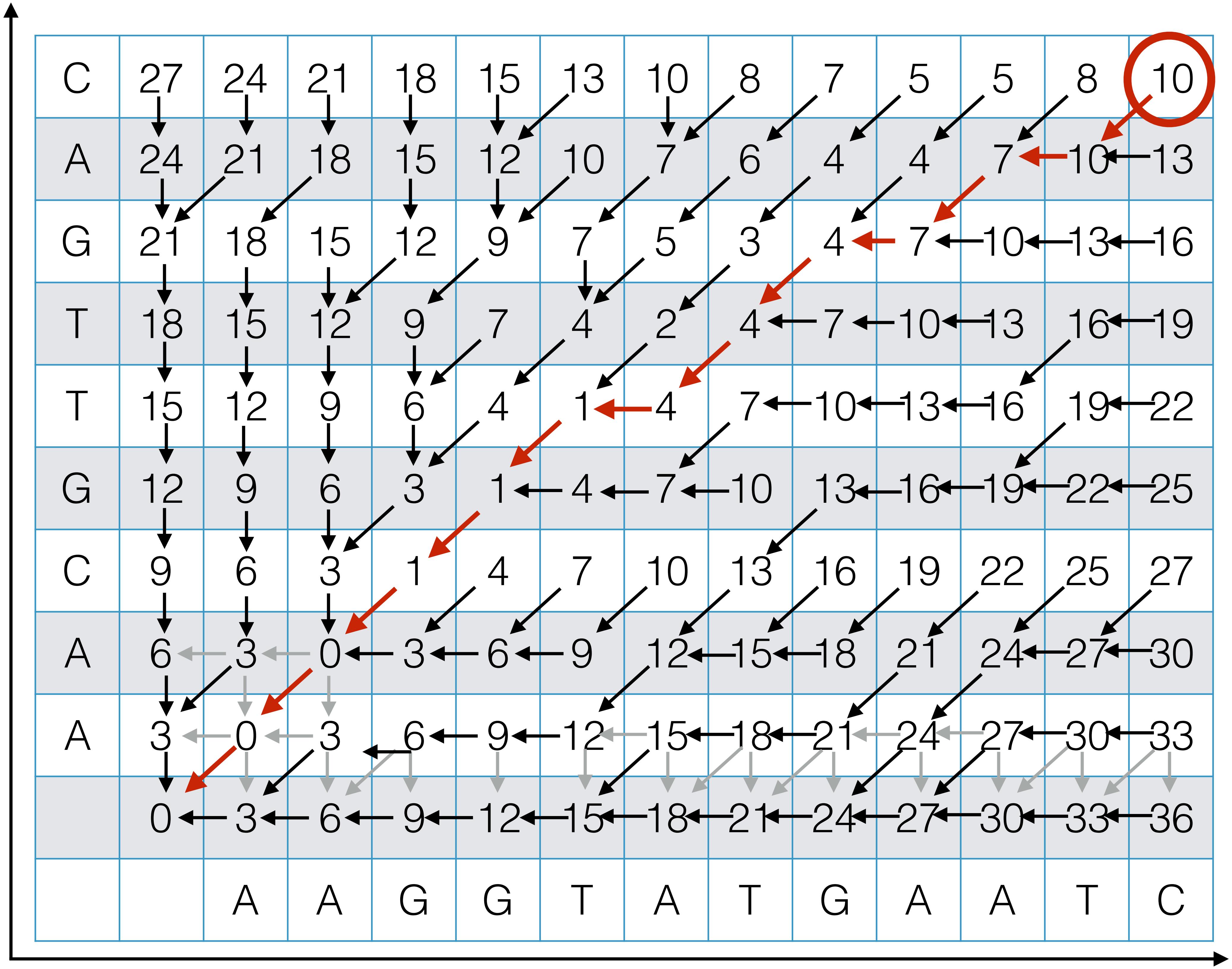
C	27	24	21	18	15	13	10	8	7	5	5	8	10
A	24	21	18	15	12	10	7	6	4	4	7	10	13
G	21	18	15	12	9	7	5	3	4	7	10	13	16
T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



C	27	24	21	18	15	13	10	8	7	5	5	8	10
A	24	21	18	15	12	10	7	6	4	4	7	10	13
G	21	18	15	12	9	7	5	3	4	7	10	13	16
T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Example



C	27	24	21	18	15	13	10	8	7	5	5	8	10
A	24	21	18	15	12	10	7	6	4	4	7	10	13
G	21	18	15	12	9	7	5	3	4	7	10	13	16
T	18	15	12	9	7	4	2	4	7	10	13	16	19
T	15	12	9	6	4	1	4	7	10	13	16	19	22
G	12	9	6	3	1	4	7	10	13	16	19	22	25
C	9	6	3	1	4	7	10	13	16	19	22	25	27
A	6	3	0	3	6	9	12	15	18	21	24	27	30
A	3	0	3	6	9	12	15	18	21	24	27	30	33
	0	3	6	9	12	15	18	21	24	27	30	33	36
		A	A	G	G	T	A	T	G	A	A	T	C

Outputting the Alignment

Build the alignment from right to left.

```
ACGT
A-GA
```

Follow the backtrack pointers starting from entry (n,m).

- If you follow a diagonal pointer, add both characters to the alignment,
- If you follow a left pointer, add a gap to the y-axis string and add the x-axis character
- If you follow a down pointer, add the y-axis character and add a gap to the x-axis string.

*

Recap: Dynamic Programming

The previous sequence alignment / edit distance algorithm is an example of dynamic programming.

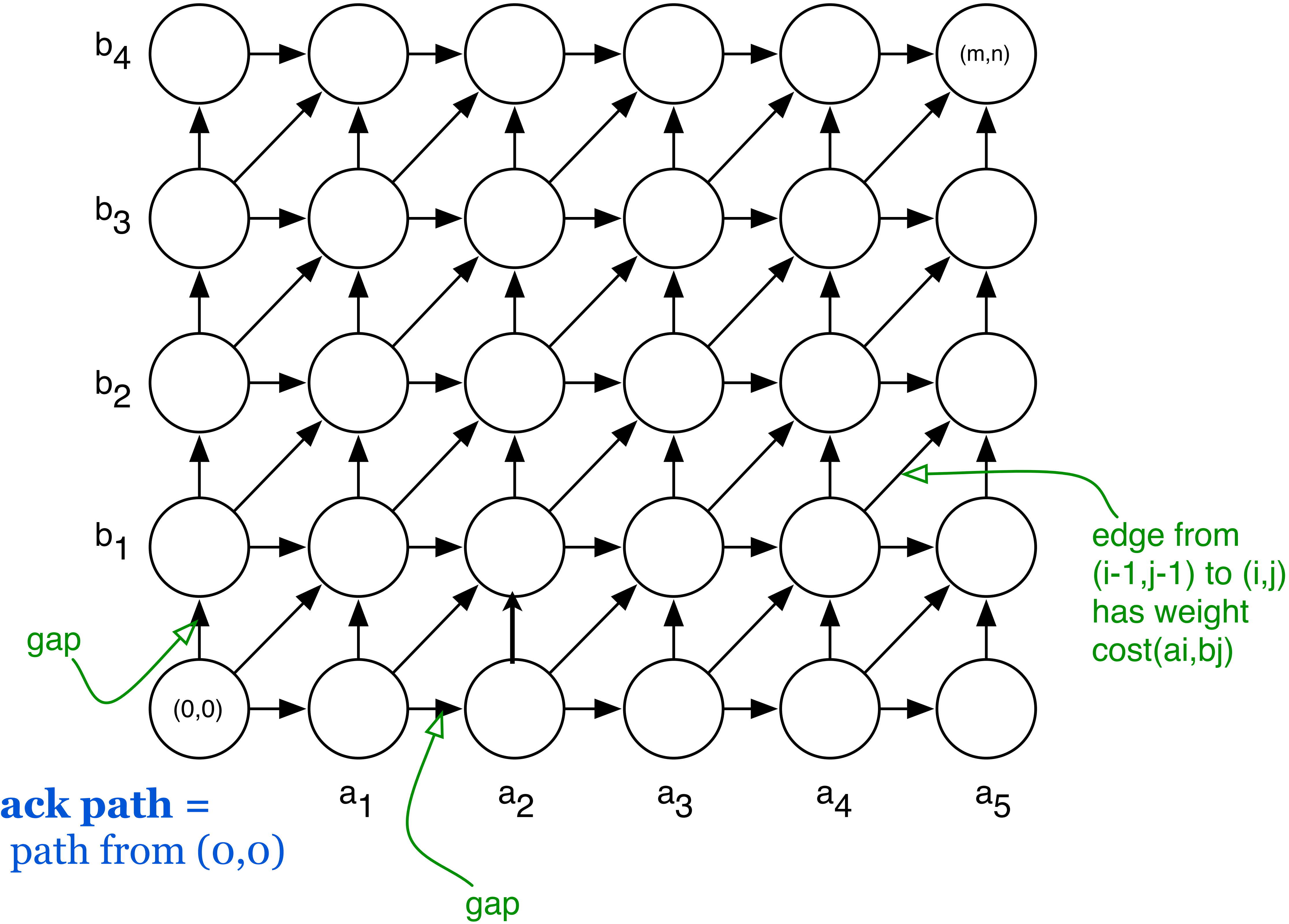
Main idea of dynamic programming: solve the subproblems in an order so that when you need an answer, it's ready.

Requirements for DP to apply:

1. Optimal value of the original problem can be computed from some similar subproblems.
2. There are only a polynomial # of subproblems
3. There is a "natural" ordering of subproblems, so that you can solve a subproblem by only looking at **smaller** subproblems.

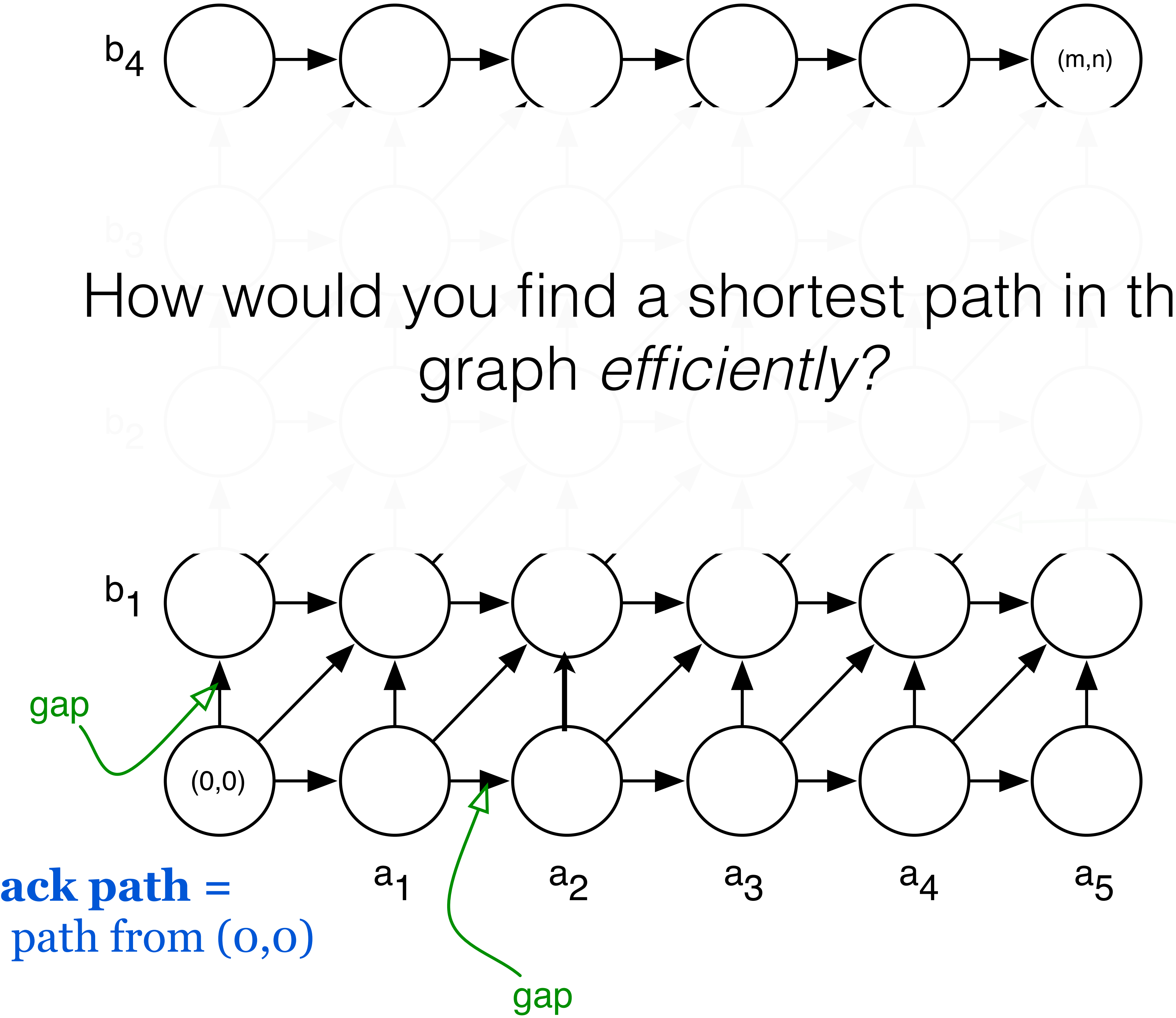
*

Another View: Recasting as a Graph



Traceback path = shortest path from (0,0) to (m,n)

Another View: Recasting as a Graph



How would you find a shortest path in this graph *efficiently*?

edge from (i-1,j-1) to (i,j) has weight cost(ai,bj)

Traceback path =
shortest path from (0,0) to (m,n)

*