COMP1730/COMP6730
Programming for Scientists

Control, part 3: Dynamic programming

Outline

* Dynamic programming.
* (DNA) sequence alignment.

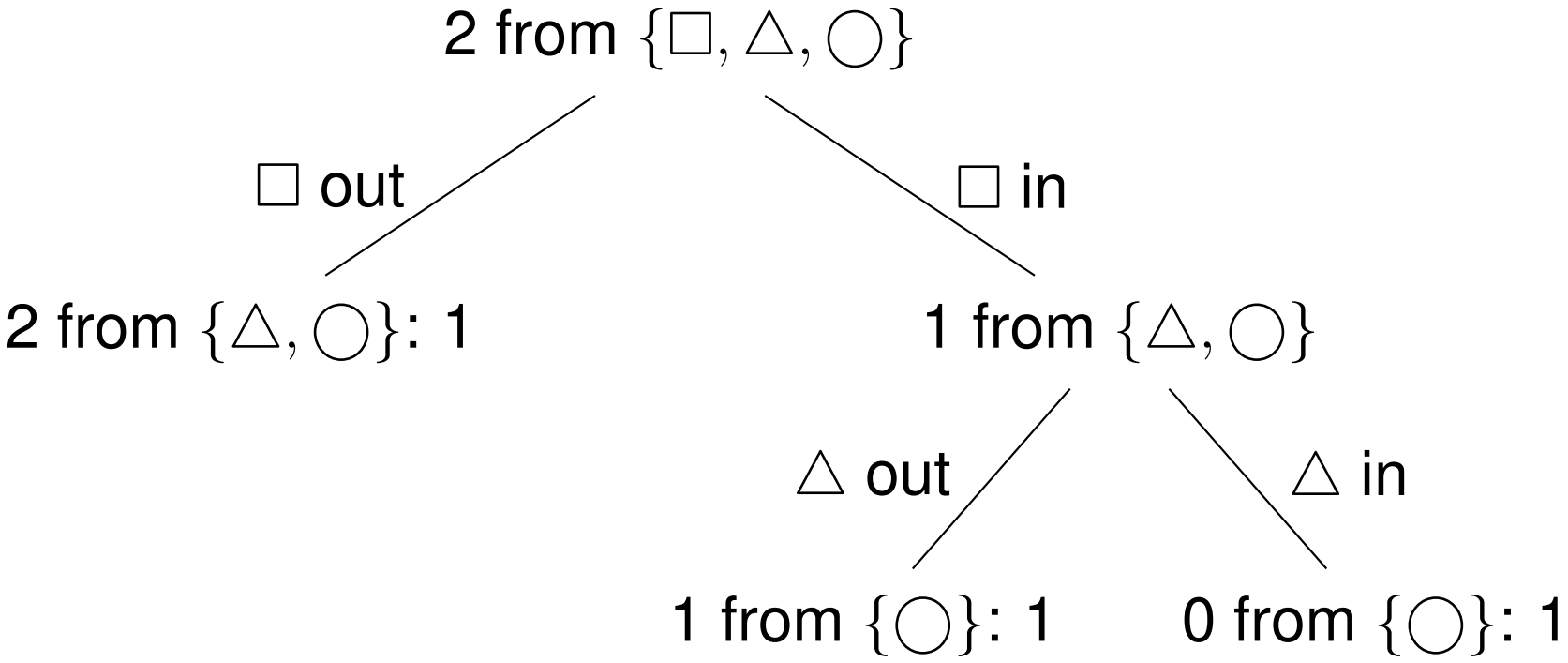
Dynamic programming

Recursion or iteration?

* Examples of problems that could be solved both with recursion and with iteration:
  - Counting boxes in a stack.
  - Solving an equation (the interval-halving algorithm).
* Examples pf problems that we have only seen recursive solutions for:
  - Counting selections ("*n* choose *k*").
  - The subset sum problem.

Example: Counting selections

* Compute the number of ways to choose k elements from a set of n, $C(n, k)$.



* Simple recursive formulation:

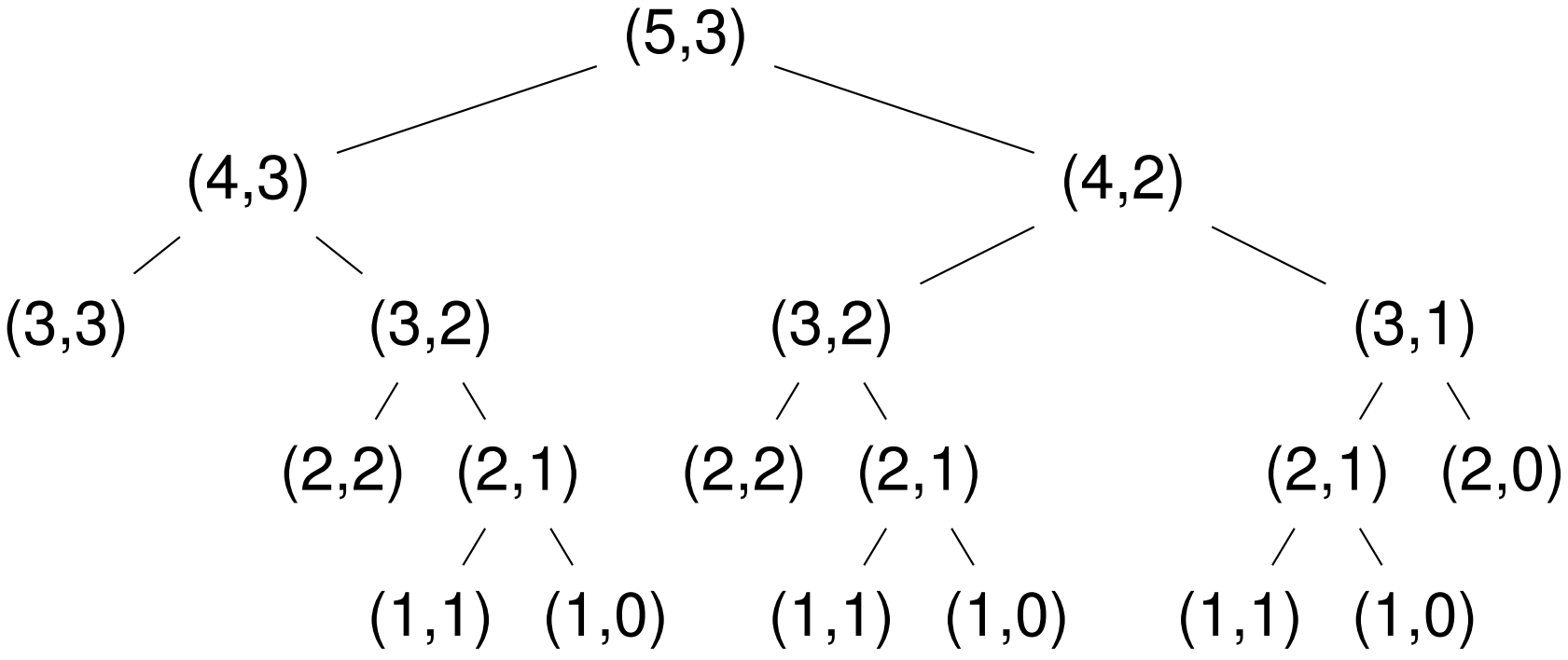
$$C(n,k) = C(n-1,k) + C(n-1,k-1)$$
$$C(n,0) = 1$$
$$C(n,n) = 1$$

* Simple recursive implementation:

```
def choices(n, k):
    if k == n or k == 0:
        return 1
    else:
        return choices(n - 1, k) + \
               choices(n - 1, k - 1)
```

* How to implement with iteration?

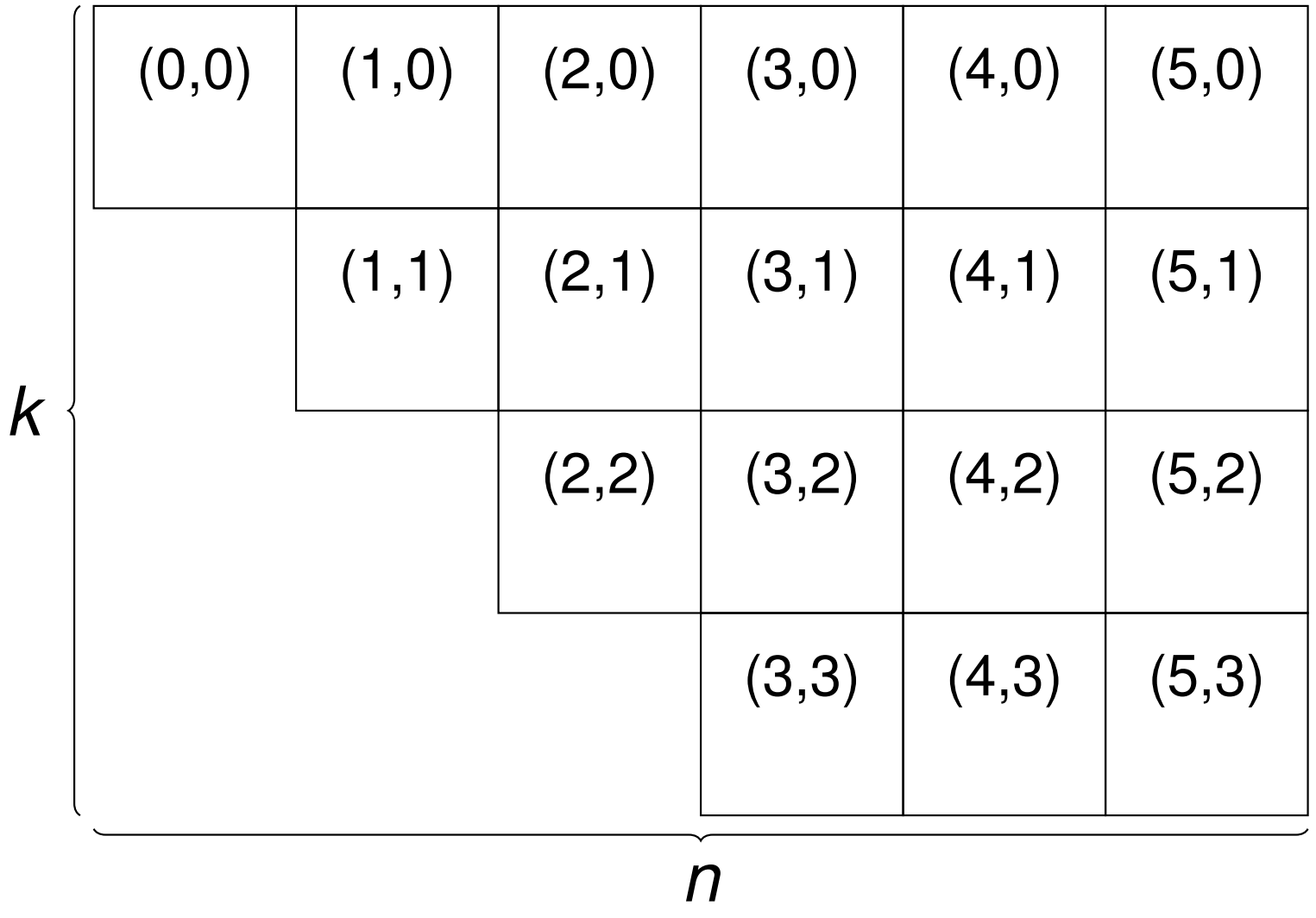
* Recursive calls by `choices(5, 3)`:



* Note repeated work.

* The idea of **dynamic programming** is to store answers to (recursively defined) subproblems, to avoid computing them repeatedly.
  - Trade memory for computation time.
* By computing subproblem solutions “from the bottom up”, we can also transform a recursive algorithm into an iterative one:
  - solve the base cases first;
  - then, repeatedly, solve problems whose subproblems are already solved;
  - until the whole problem is solved.
* Need a way to index subproblems.

* Array of subproblems:



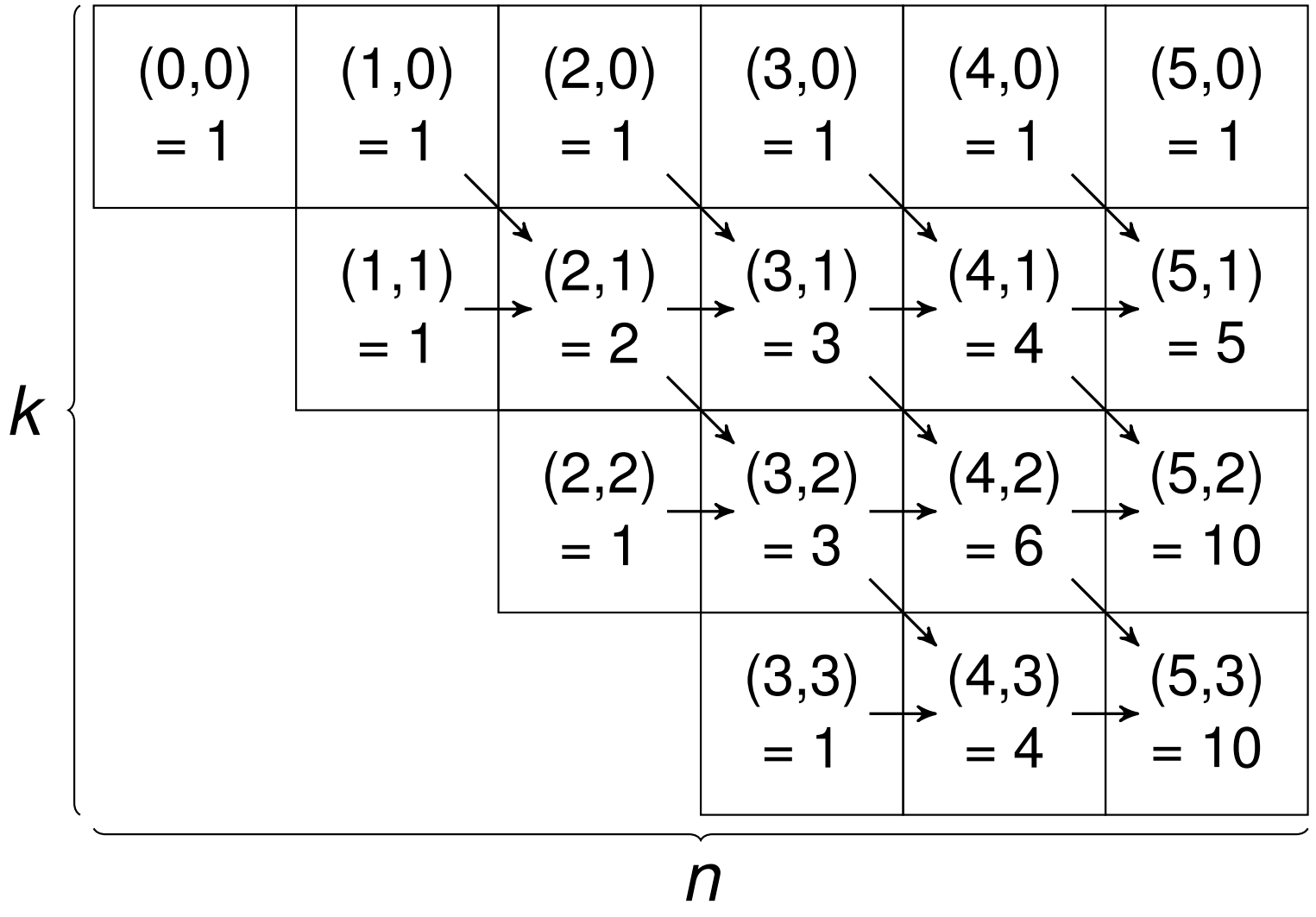
* With base cases solved:

(0,0) = 1	(1,0) = 1	(2,0) = 1	(3,0) = 1	(4,0) = 1	(5,0) = 1
	(1,1) = 1	(2,1)	(3,1)	(4,1)	(5,1)
		(2,2) = 1	(3,2)	(4,2)	(5,2)
			(3,3) = 1	(4,3)	(5,3)

k

n

* Complete:


(0,0) = 1
(1,0) = 1
(2,0) = 1
(3,0) = 1
(4,0) = 1
(5,0) = 1
(1,1) = 1
(2,1) = 2
(3,1) = 3
(4,1) = 4
(5,1) = 5
(2,2) = 1
(3,2) = 3
(4,2) = 6
(5,2) = 10
(3,3) = 1
(4,3) = 4
(5,3) = 10
k
n

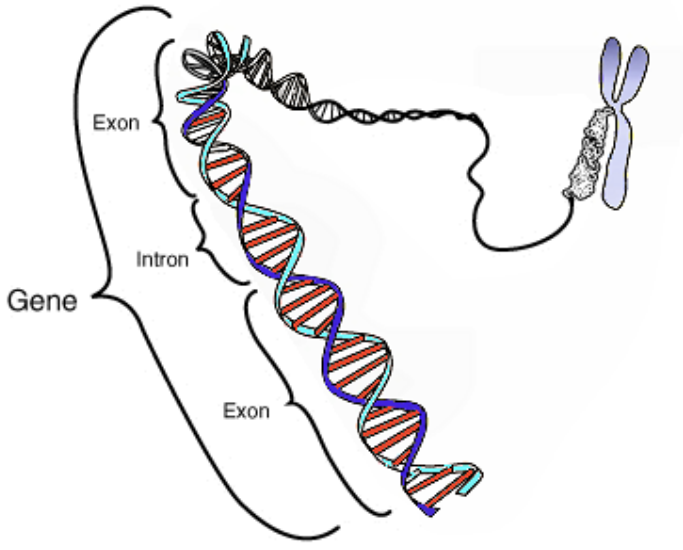
(DNA) sequence alignment

BRCA 1

CTTAGCGGTAGCCCCTTGGTTTCCGTGGCAACGGAAAAGCGCGGGAATTACAGATAAATTAAAACTGCGACTGCGCGGCGTGAGCTCGC
TGAGACTTCCTGGACGGGGGACAGGCTGTGGGGTTTCTCAGATAACTGGGCCCCTGCGCTCAGGAGGCCTTCACCCTCTGCTCTGGTTC
ATTGGAACAGAAAGAAATGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGCAGAAAATCTTAGAGTGTC
CCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACCACATATTTTGCAAATTTTGCATGCTGAAACTTCTCAACCAG
AAGAAAGGGCCTTCACAGTGTCCTTTATGTAAGAATGATATAACCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTCAACTTGTTGA
AGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGACACAGGTTTGGAGTATGCAAACAGCTATAATTTTGCAAAAAAGGAAAATAACT
CTCCTGAACATCTAAAAGATGAAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTGAACCCGAA
AATCCTTCCTTGGAAACCAGTCTCAGTGTCCAACTCTCTAACCTTGGAACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACCTCA
AAAGACGTCTGTCTACATTGAATTGGGATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAGTGTGGGAGATCAAGAAT
TGTTACAAATCACCCCTCAAGGAACCAGGGATGAAATCAGTTTGGATTCTGCAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTA
ACAAATACTGAACATCATCAACCCAGTAATAATGATTTGAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGTATCAGGG
TGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGTCTCTGAAGACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAACCACTCAGC
AGAGGGATACCATGCAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAGCTGTGTTAGAACAGCATGGGAGCCAGCCT
TCTAACAGCTACCCTTCCATCATAAGTGACTCTTCTGCCCTTGAGGACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATT
AACTTCACAGAAAAGTAGTGAATACCCTATAAGCCAGAATCCAGAAGGCCTTTCTGCTGACAAGTTTGAGGTGTCTGCAGATAGTTCTA
CCAGTAAAAATAAAGAACCAGGAGTGGAAAGGTCATCCCCTTCTAAATGCCCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCT
GGGAGTCTTCAGAATAGAAACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCC
ACACGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATCTAGAGGGAACCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATG
ACCCTGAATCTGATCCTTCTGAAGACAGAGCCCCAGAGTCAGCTCGTGTTGGCAACATACCATCTTCAACCTCTGCATTGAAAGTTCCC
CAATTGAAAGTTGCAGAATCTGCCCAGAGTCCAGCTGCTGCTCATACTACTGATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAG
CAGGGAGAAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACAAAAGAATGTCCATGGTGGTGTCTGGCCTGACCCCAGAAGAATTTA
TGCTCGTGTACAAGTTTGCCAGAAAACACCACATCACTTTAACTAATCTAATTACTGAAGAGACTACTCATGTTGTTATGAAAACAGAT
GCTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAGTTAGCTATTTCTGGGTGACCCAGTC
TATTAAAGAAAGAAAAATGCTGAATGAG

Biological sequence data

* DNA and RNA.
* Protein amino acid sequence.
* Arrangement of genes in chromosome / genome.



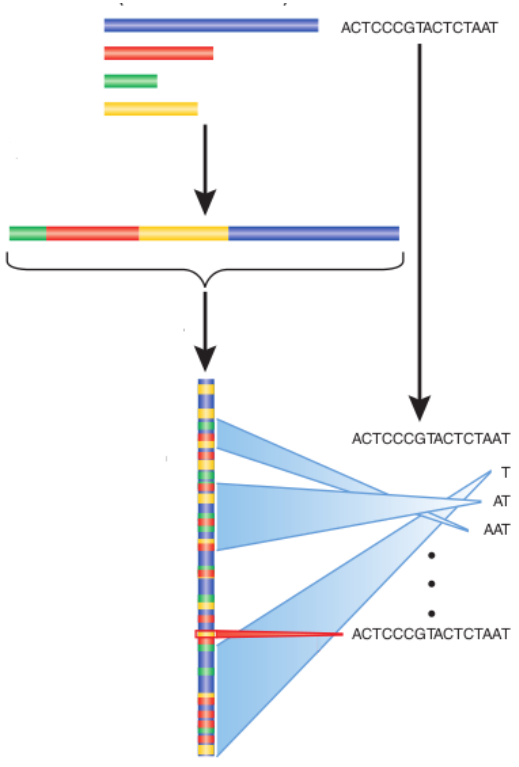
* Human DNA is ∼3 billion bp.
* BRCA 1 & 2 genes are ∼80kb (incl. exons).
* Harmful mutations change as few as 2 bases.
* DNA sequencer reads are 100–2k bases.

* Alignment

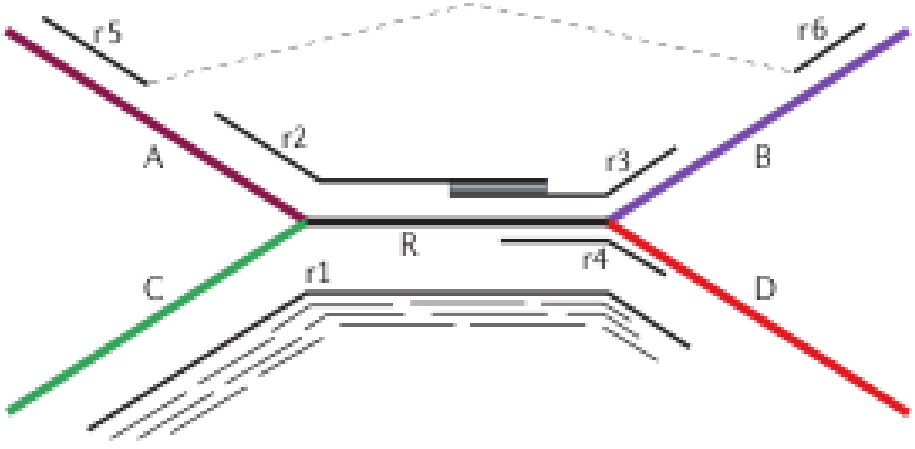
```
GAATTCAG  GAATTCAG
| | || |  | || | |
GGA-TC-G  GCAT-C-G

GAATTC-A  GAATTC-A
| | || |  | || | |
GGA-TCGA  GCAT-CGA
```

* Mapping



* Assembly



Edit distance

* Minimum (weighted) number of “edit operations” needed to transform one sequence into the other.
* Levenshtein (string edit) distance:
  - insert a character (gap in other string);
  - delete a character (gap in this string);
  - substitute a character.
* Minimum edit equals best sequence alignment.

* distance(GAATTCA, GGATCGA) = 3.
* Edits:

		G A A T T C A
(subst. 1 G)	$\Rightarrow$	G G A T T C A
(del 4)	$\Rightarrow$	G G A T C A
(ins 4 G)	$\Rightarrow$	G G A T G C A

* Alignment:

G	**A**	A	T	T	C	_	A
G	**G**	A	T	_	C	G	A
	+1			+1		+1	

Recursive formulation

$$\text{dist}(s, '\,') = \text{len}(s) * w_{\text{gap}}$$
$$\text{dist}('\,', t) = \text{len}(t) * w_{\text{gap}}$$

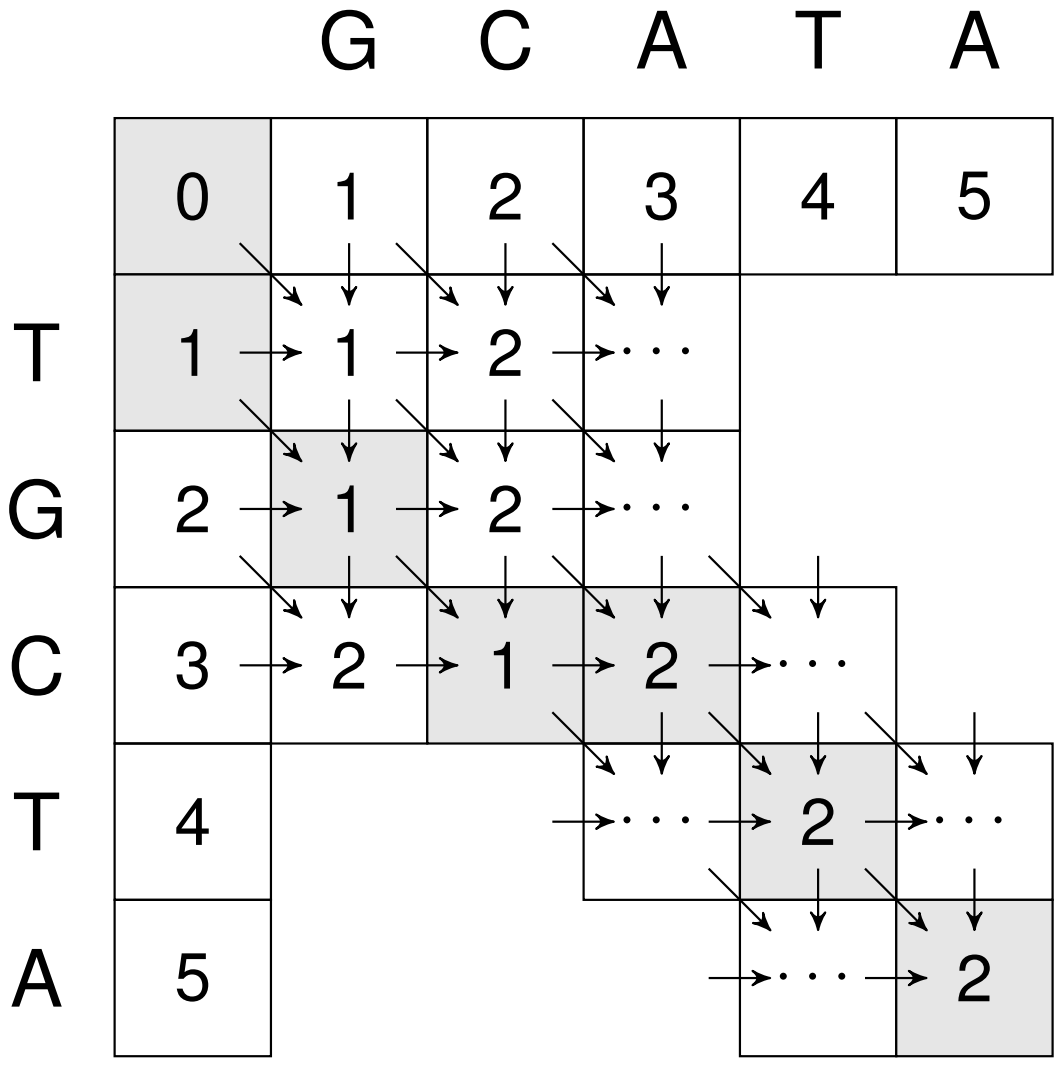
$$\text{dist}(s + x, t + y) =$$
$$\min \begin{cases} \text{dist}(s, t) + \begin{cases} 0 & \text{if} x = y \\ w_{\text{sub}} & \text{otherwise} \end{cases} \\ \text{dist}(s + x, t) + w_{\text{gap}} \\ \text{dist}(s, t + y) + w_{\text{gap}} \end{cases}$$

* In example, $w_{\text{sub}} = w_{\text{gap}} = 1$.

```
def align(s, t):
    if len(s) == 0:
        return len(t) * w_gap
    elif len(t) == 0:
        return len(s) * w_gap
    else:
        if s[-1] == t[-1]:
            d1 = align(s[:-1], t[:-1])
        else:
            d1 = align(s[:-1], t[:-1]) + w_sub
        d2 = align(s, t[:-1]) + w_gap
        d3 = align(s[:-1], t) + w_gap
        return min(d1, d2, d3)
```

Iterative formulation

* How to index subproblems?
  - Each call aligns two sequence prefixes.
  - (i, j): `align(s[:i], t[:j])`.
* Base cases?
  - One sequence is empty ($i = 0$ or $j = 0$).
* Update: min of $(i - 1, j - 1)$ (plus subst. weight if `s[i] != t[j]`), $(i - 1, j)$ plus gap weight, and $(i, j - 1)$ plus gap weight.


G C A T A
T G C T A
0 1 2 3 4 5
1 1 2 ···
2 1 2 ···
3 2 1 2 ···
4 ··· 2 ···
5 ··· 2

Summary

* Recursion, iteration and dynamic programming are all useful algorithm design ideas.
* There is no single “best” idea.
* It is not always easy to know which is the right one to apply to a given problem.