Comparaison de séquences 2 à 2

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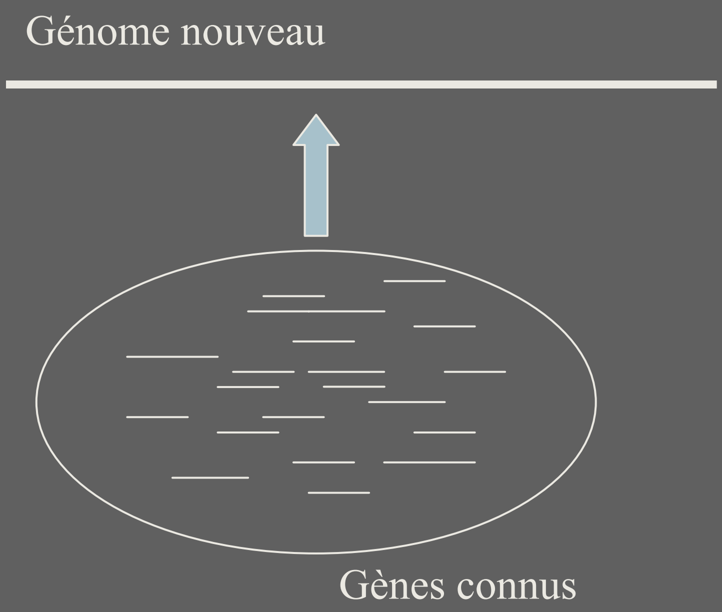
Motivations

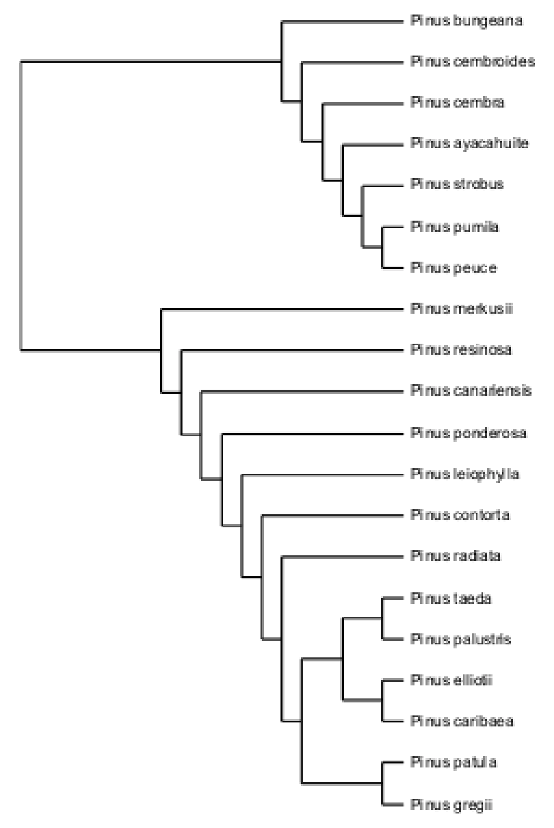
- Détection de gènes :



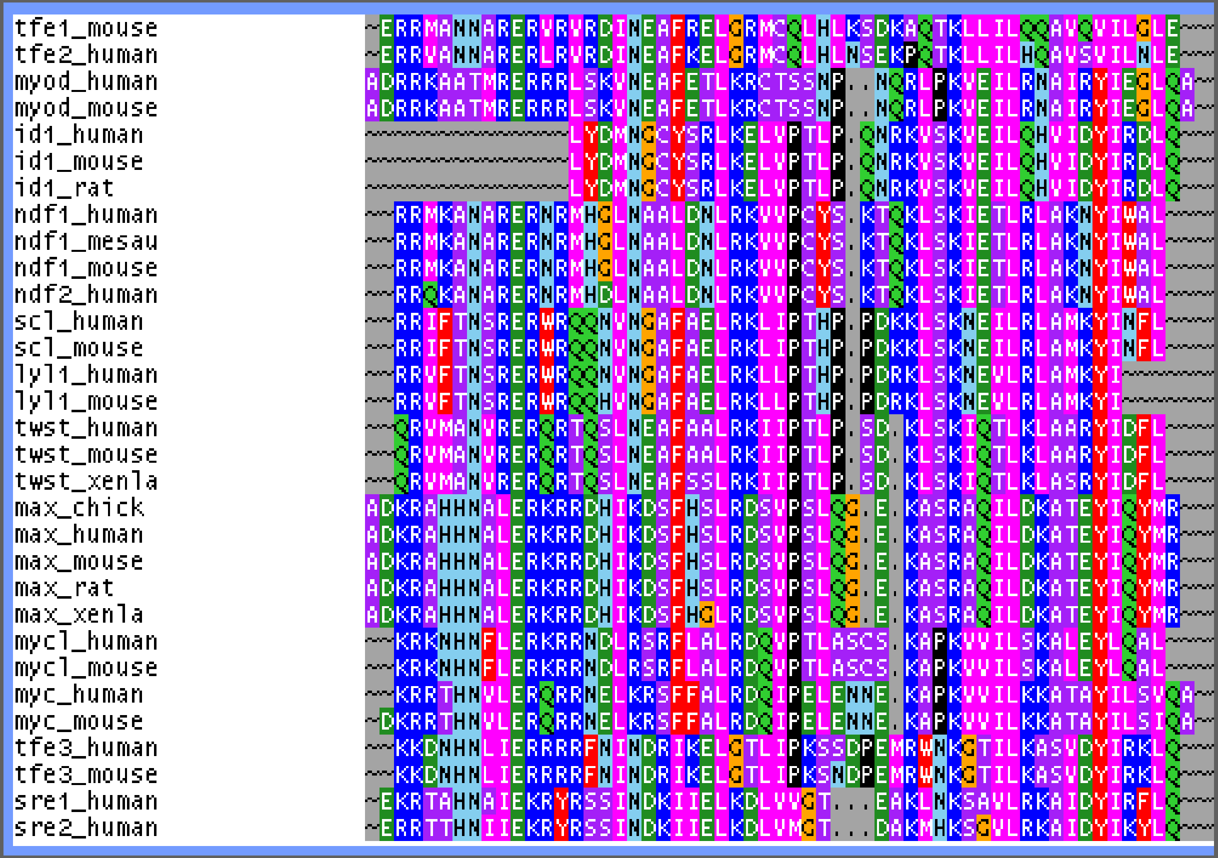
Génome nouveau

Gènes connus

- Phylogénie :



(Alignements multiples)



```
tfe1_mouse   ~ERRMANNARERVRVRDINEAFRELGRMCQLHLKSDKAQTKLLILQQAVQVILGLE~~
tfe2_human   ~ERRVANNARERLRVRDINEAFKELGRMCQLHLNSEKPQTKLLILHQAVSVILNLE~~
myod_human   ADRRKAATMRERRRLSKVNEAFETLKRCTSSNP..NQRLPKVEILRNAIRYIEGLQA~
myod_mouse   ADRRKAATMRERRRLSKVNEAFETLKRCTSSNP..NQRLPKVEILRNAIRYIEGLQA~
id1_human    ~~~~~~~~~~~~~~LYDMNGCYSRLKELVPTLP.QNRKVSKVEILQHVIDYIRDLQ~~
id1_mouse    ~~~~~~~~~~~~~~LYDMNGCYSRLKELVPTLP.QNRKVSKVEILQHVIDYIRDLQ~~
id1_rat      ~~~~~~~~~~~~~~LYDMNGCYSRLKELVPTLP.QNRKVSKVEILQHVIDYIRDLQ~~
ndf1_human   ~~RRMKANARERNRMHGLNAALDNLRKVVPCYS.KTQKLSKIETLRLAKNYIWAL~~~
ndf1_mesau   ~~RRMKANARERNRMHGLNAALDNLRKVVPCYS.KTQKLSKIETLRLAKNYIWAL~~~
ndf1_mouse   ~~RRMKANARERNRMHGLNAALDNLRKVVPCYS.KTQKLSKIETLRLAKNYIWAL~~~
ndf2_human   ~~RRQKANARERNRMHDLNAALDNLRKVVPCYS.KTQKLSKIETLRLAKNYIWAL~~~
scl_human    ~~RRIFTNSRERWRQQNVNGAFAELRKLIPTHP.PDKKLSKNEILRLAMKYINFL~~~
scl_mouse    ~~RRIFTNSRERWRQQNVNGAFAELRKLIPTHP.PDKKLSKNEILRLAMKYINFL~~~
lyl1_human   ~~RRVFTNSRERWRQQNVNGAFAELRKLLPTHP.PDRKLSKNEVLRLAMKYI~~~~~~
lyl1_mouse   ~~RRVFTNSRERWRQQHVNGAFAELRKLLPTHP.PDRKLSKNEVLRLAMKYI~~~~~~
twst_human   ~~QRVMANVRERQRTQSLNEAFAALRKIIPTLP.SD.KLSKIQTLKLAARYIDFL~~~
twst_mouse   ~~QRVMANVRERQRTQSLNEAFAALRKIIPTLP.SD.KLSKIQTLKLAARYIDFL~~~
twst_xenla   ~~QRVMANVRERQRTQSLNEAFSSLRKIIPTLP.SD.KLSKIQTLKLASRYIDFL~~~
max_chick    ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQG.E.KASRAQILDKATEYIQYMR~~
max_human    ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQG.E.KASRAQILDKATEYIQYMR~~
max_mouse    ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQG.E.KASRAQILDKATEYIQYMR~~
max_rat      ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQG.E.KASRAQILDKATEYIQYMR~~
max_xenla    ADKRAHHNALERKRRDHIKDSFHGLRDSVPSLQG.E.KASRAQILDKATEYIQYMR~~
mycl_human   ~~KRKNHNFLERKRRNDLRSRFLALRDQVPTLASCS.KAPKVVILSKALEYLQAL~~~
mycl_mouse   ~~KRKNHNFLERKRRNDLRSRFLALRDQVPTLASCS.KAPKVVILSKALEYLQAL~~~
myc_human    ~~KRRTHNVLERQRRNELKRSFFALRDQIPELENNE.KAPKVVILKKATAYILSVQA~
myc_mouse    ~DKRRTHNVLERQRRNELKRSFFALRDQIPELENNE.KAPKVVILKKATAYILSIQA~
tfe3_human   ~~KKDNHNLIERRRRFNINDRIKELGTLIPKSSDPEMRWNKGTILKASVDYIRKLQ~~
tfe3_mouse   ~~KKDNHNLIERRRRFNINDRIKELGTLIPKSNDPEMRWNKGTILKASVDYIRKLQ~~
sre1_human   ~EKRTAHNAIEKRYRSSINDKIIELKDLVVGT...EAKLNKSAVLRKAIDYIRFLQ~~
sre2_human   ~ERRTTHNIIEKRYRSSINDKIIELKDLVMGT...DAKMHKSGVLRKAIDYIKYLQ~~
```
]

Distance d'édition

Deux séquences $v = v_1 v_2 \ldots v_n$ et $w = w_1 w_2 \ldots w_m$

Opérations d'édition :

- ins(x,i)
- suppr(x,i)
- subs(x,y,i)

CHAT - suppr(C,1) → HAT - subs(H,R,1) → RAT

Distance d'édition

- Chaque modification a un poids, dépendant de l'opération et des lettres en cause.

- Distance d'édition entre v et w : poids minimal d'une suite d'opérations permettant de transformer v en w.

CHAT - suppr(C,1) → HAT - subs(H,R,1) → RAT

Alignement

X : alphabet des séquences
X' = X ∪ {-}
X'' = X' × X' \ {-,-}

2 morphismes de monoïdes :

F_1: X''* → X*
(x,y) → x si x ≠ -
ε sinon

F_2: X''* → X*
(x,y) → y si x ≠ -
ε sinon

Un alignement de $v = v_1v_2\ldots v_n$ et $w = w_1w_2\ldots w_m$ est un mot A de X'' tel que $F_1(A) = v$ et $F2(A) = w$.

v = aatca

w = agca

aa-tca
agc-a-
OK

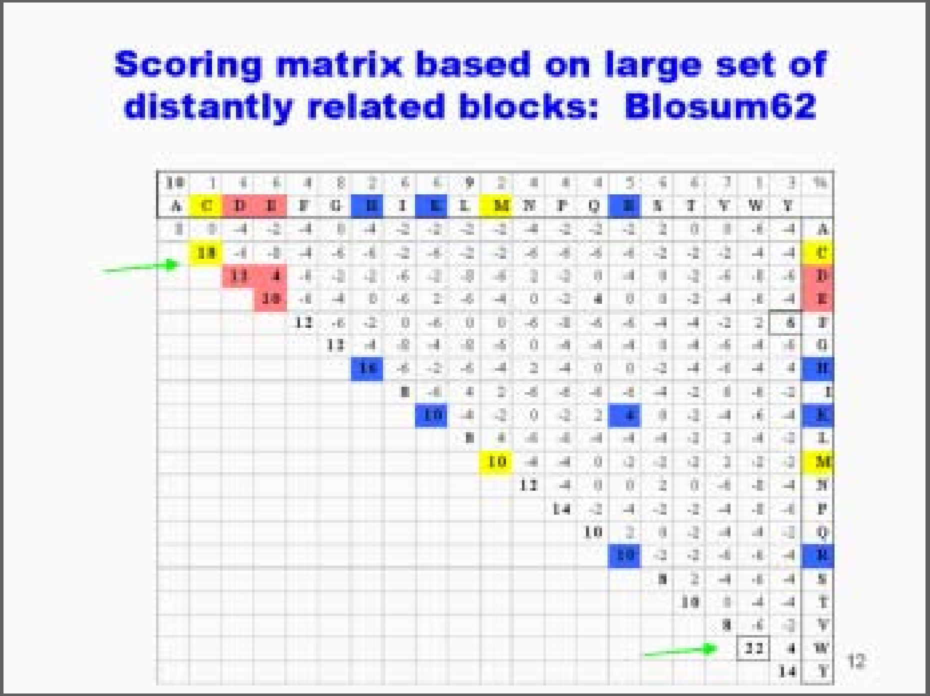
aatc-a
-agc-a
~~OK~~

aatca
-agca
OK

Score d’alignement

- Le score d’un alignement est la somme des scores lettre à lettre.

- On cherche l’alignement de score maximal.

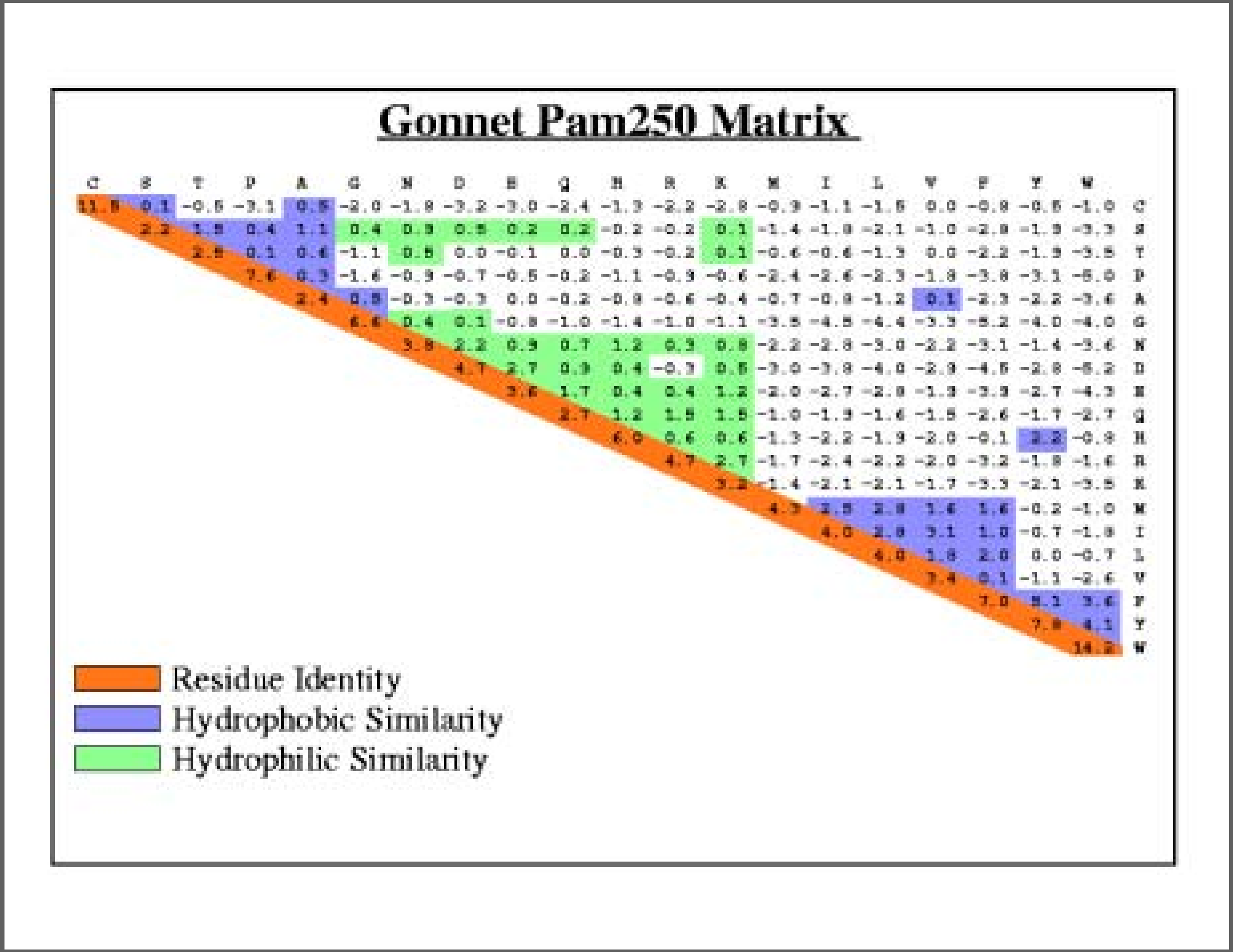


Scoring matrix based on large set of distantly related blocks: Blosum62

Score d'alignement

	A	C	G	T
A	1	0	0	0
C	0	1	0	0
G	0	0	1	0
T	0	0	0	1

	A	C	G	T
A	3	0	1	0
C	0	3	0	1
G	1	0	3	0
T	0	0	1	3



Gonnet Pam250 Matrix

🟧 Residue Identity
🟦 Hydrophobic Similarity
🟩 Hydrophilic Similarity

Un alignement de deux protéines

```
seq 1:       3 EHYYSEKPSVKSNKQTWSFRLRNKDFTFTSDSGVFSKKEVDFGSRLLIDSFEEPEVEGGI 62
                ||||  |.|     .     |   | | . |||||    | |. |||..      .  |
seq 2:       2 GHYYSREPNVPLKTKQIDVCIRGYCFKFITASGVFSFGKLDRGTELLIENM-ILKPDWKI 60


seq 1:      63 LDVGCGYGPIGLSLASDFKDRTIHMIDVNERAVELSNENAEQNGITNVKIYQSDLFSNVD 122
               || ||||| ||   || |    . | |.| |||     |.  ||. |. .    |.  |.
seq 2:      61 LDLGCGYGVIGI-VASRFVNYVV-MTDINKRAVQIARKNIKINGVKNAEVRLGNLYEPVE 118


seq 1:     123 SAQTFASILTNPPIRAGKKVVHAIFEKSAEHLKASGELWIVIQKKQGAPSAIEKLEELFD 182
                .  | || ||||..||| . . |       |.  | |  ||  | ||  . .   . |
seq 2:     119 -GEKFHSIITNPPVHAGKDILREIVINAPNYLHDGGMLQLVIKTKLGAKFIKDLMKDTFT 177


seq 1:     183 EVSVVQKKKGY 193
               ||    |  ||
seq 2:     178 EVVELAKGSGY 188
```

Equivalence édition - alignement

```
AACTA-CGAT
A-GTACCGTT
```

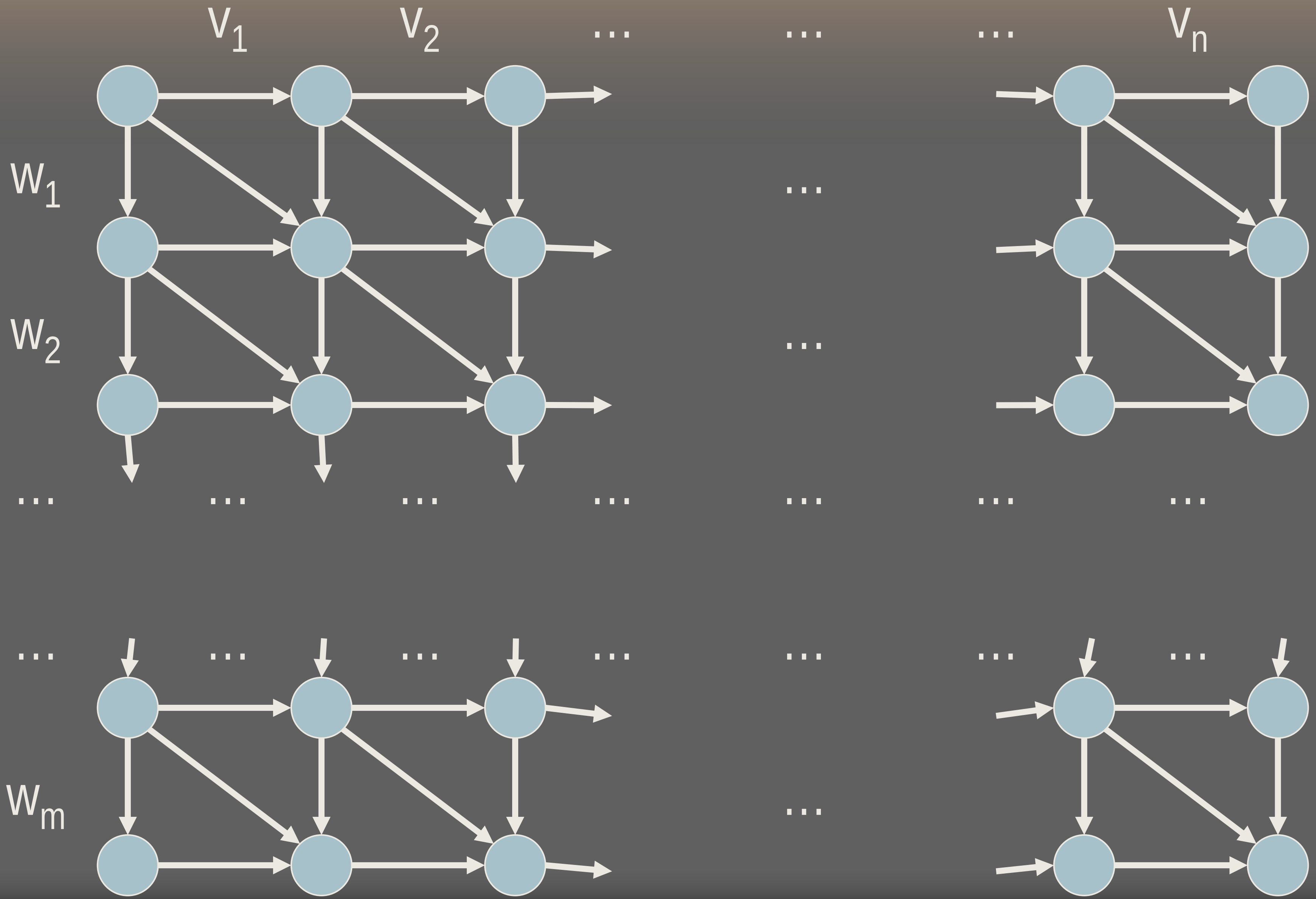
suppr(A,2)
subs(C,G,2)
ins(C,5)
subs(A,T,8)

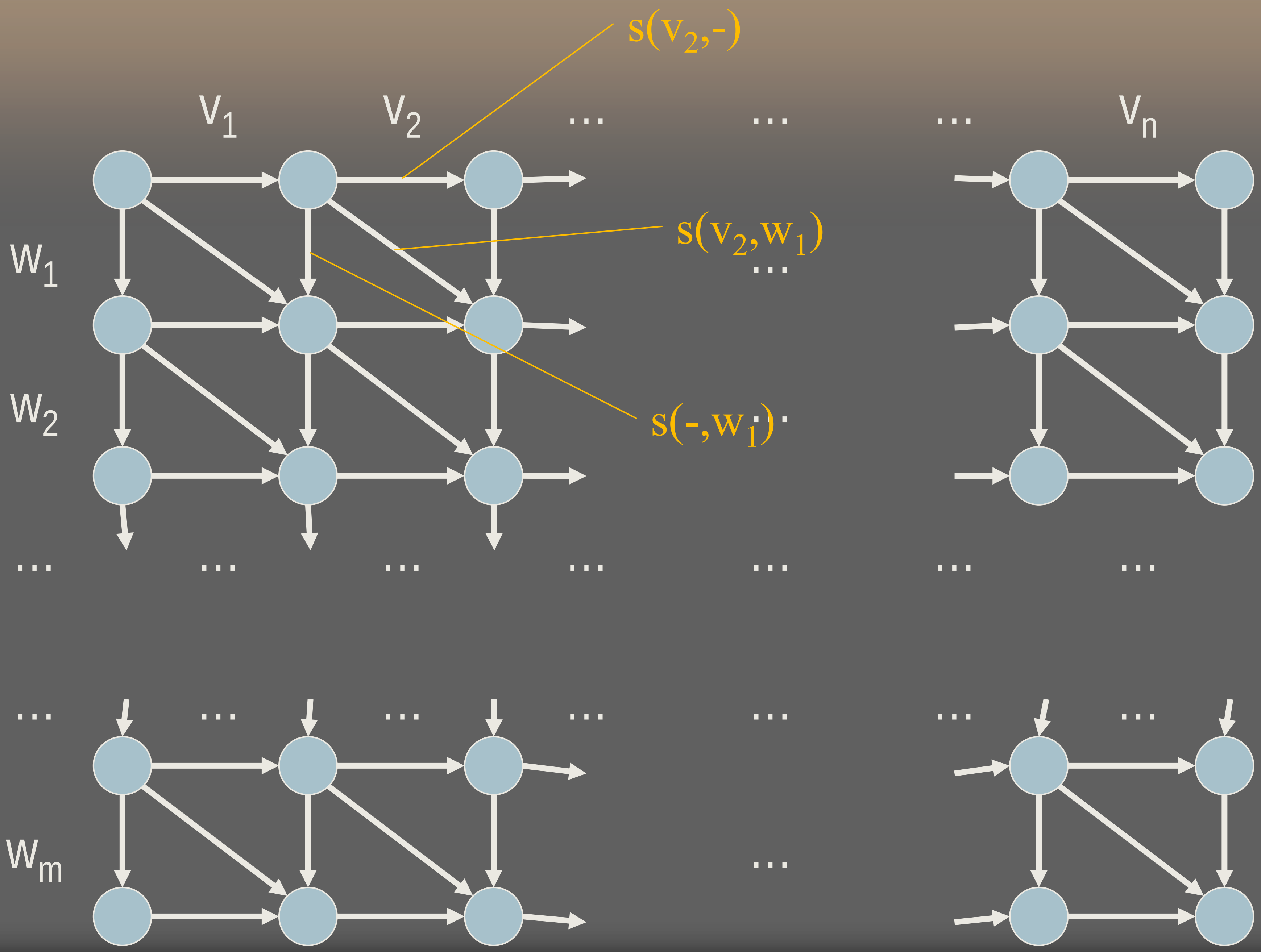
Algorithme de Needleman et Wunsch (1970), Gotoh (1982)

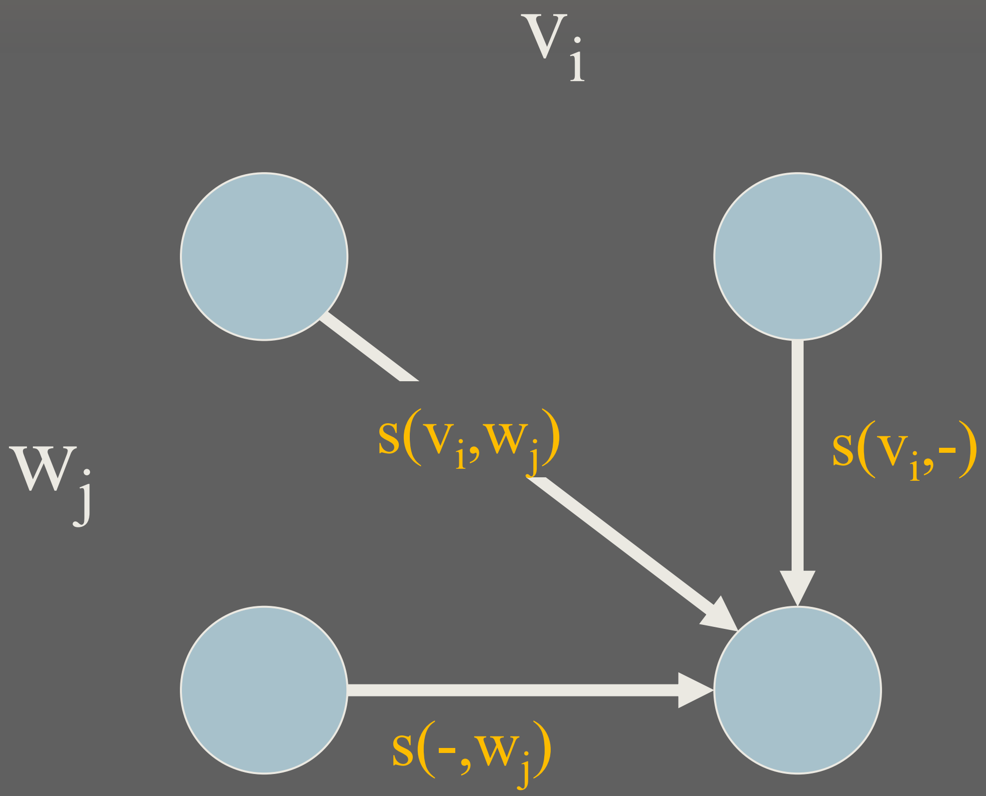
$v = v_1 v_2 \ldots v_n$
$w = w_1 w_2 \ldots w_m$

s(x,y) : score de substitution de x en y
s(x,-) : score de suppression de x
s(-,y) : score d'insertion de y

S(v,w) : score d'alignement de v et w


v_1
v_2
…
…
…
v_n
w_1
w_2
w_m
…


s(v2,-)
V1
V2
…
…
…
Vn
W1
s(v2,w1)
…
W2
s(-,w1)
…
…
…
…
…
…
…
…
…
…
…
…
…
…
…
…
Wm
…



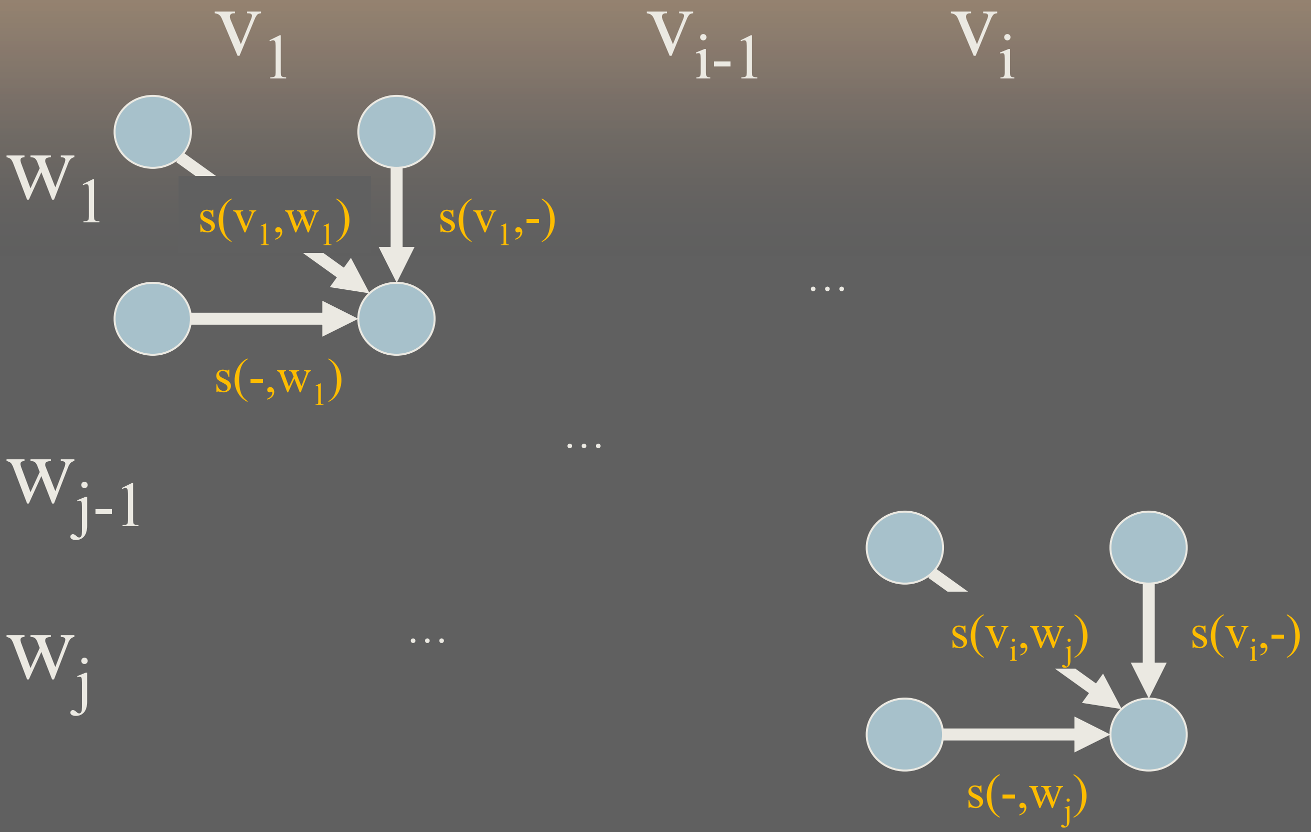
v_i

w_j

$s(v_i,w_j)$

$s(v_i,-)$

$s(-,w_j)$



v_1 v_{i-1} v_i

w_1

w_{j-1}

w_j

$s(v_1,w_1)$ $s(v_1,-)$ $s(-,w_1)$

…

$s(v_i,w_j)$ $s(v_i,-)$ $s(-,w_j)$

$$S(v_1\ldots v_i,w_1\ldots w_j) = \text{Max}\ \left\{ \begin{array}{l} S(v_1\ldots v_{i-1},w_1\ldots w_{j-1}) + s(v_i,w_j) \\ S(v_1\ldots v_{i-1},w_1\ldots w_j) + s(v_i,-) \\ S(v_1\ldots v_i,w_1\ldots w_{j-1}) + s(-,w_j) \end{array} \right\}$$

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1							
I	-2							
N	-3							
U	-4							
X	-5							

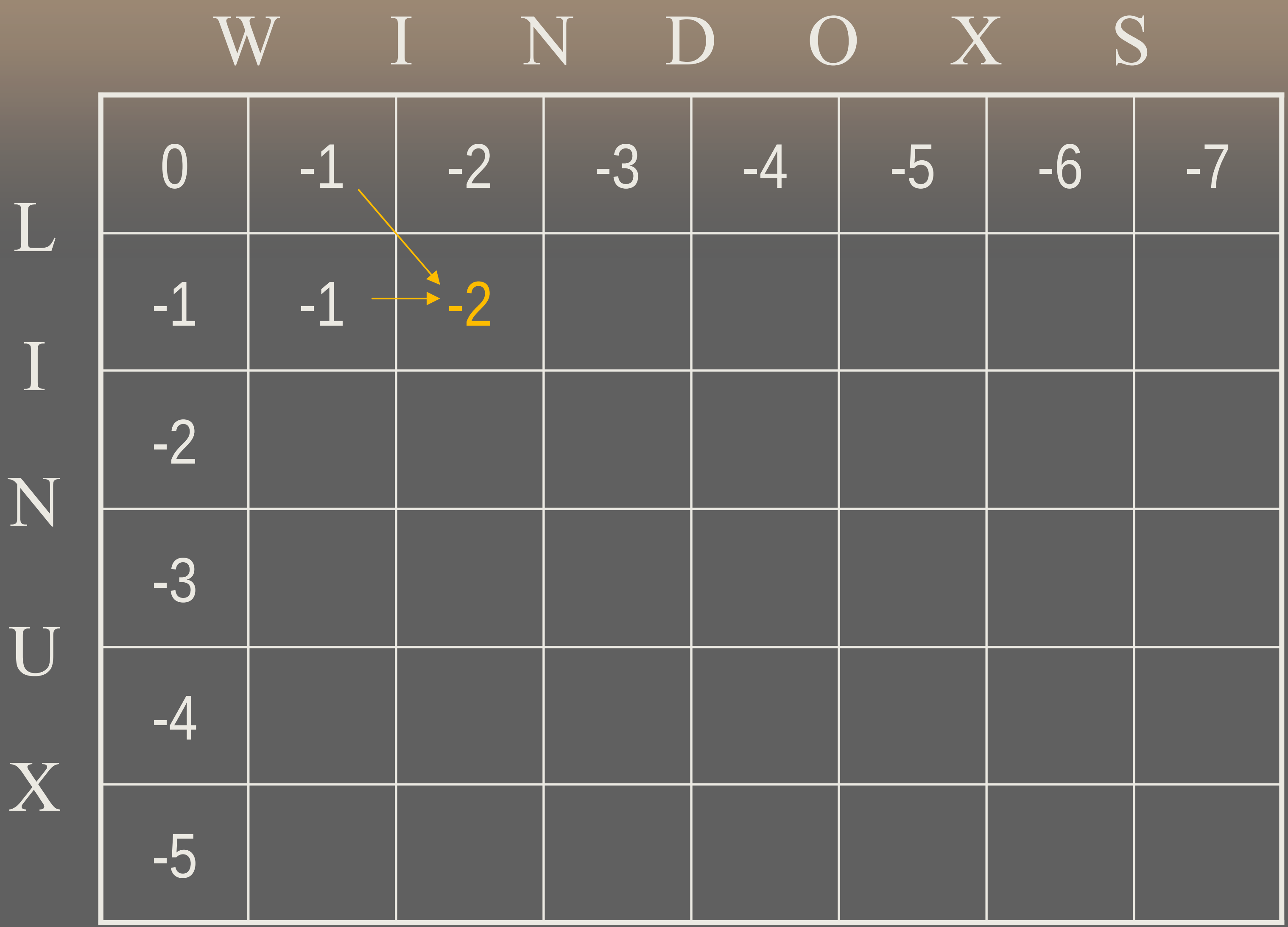
$s(x,y) = 2$ si $x=y$
-1 sinon

$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1						
I	-2							
N	-3							
U	-4							
X	-5							

s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2					
I	-2							
N	-3							
U	-4							
X	-5							

s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2						
N	-3							
U	-4							
X	-5							

$$s(x,y) = \begin{cases} 2 & \text{si } x=y \\ -1 & \text{sinon} \end{cases}$$

$$s(x,-) = s(-,x) = -1$$

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1					
N	-3							
U	-4							
X	-5							

$s(x,y) = 2$ si $x=y$
-1 sinon

$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	→ 0				
N	-3							
U	-4							
X	-5							

$s(x,y) = 2$ si $x=y$
-1 sinon

$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

$s(x,y) = 2$ si $x=y$

-1 sinon

$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3 →	2

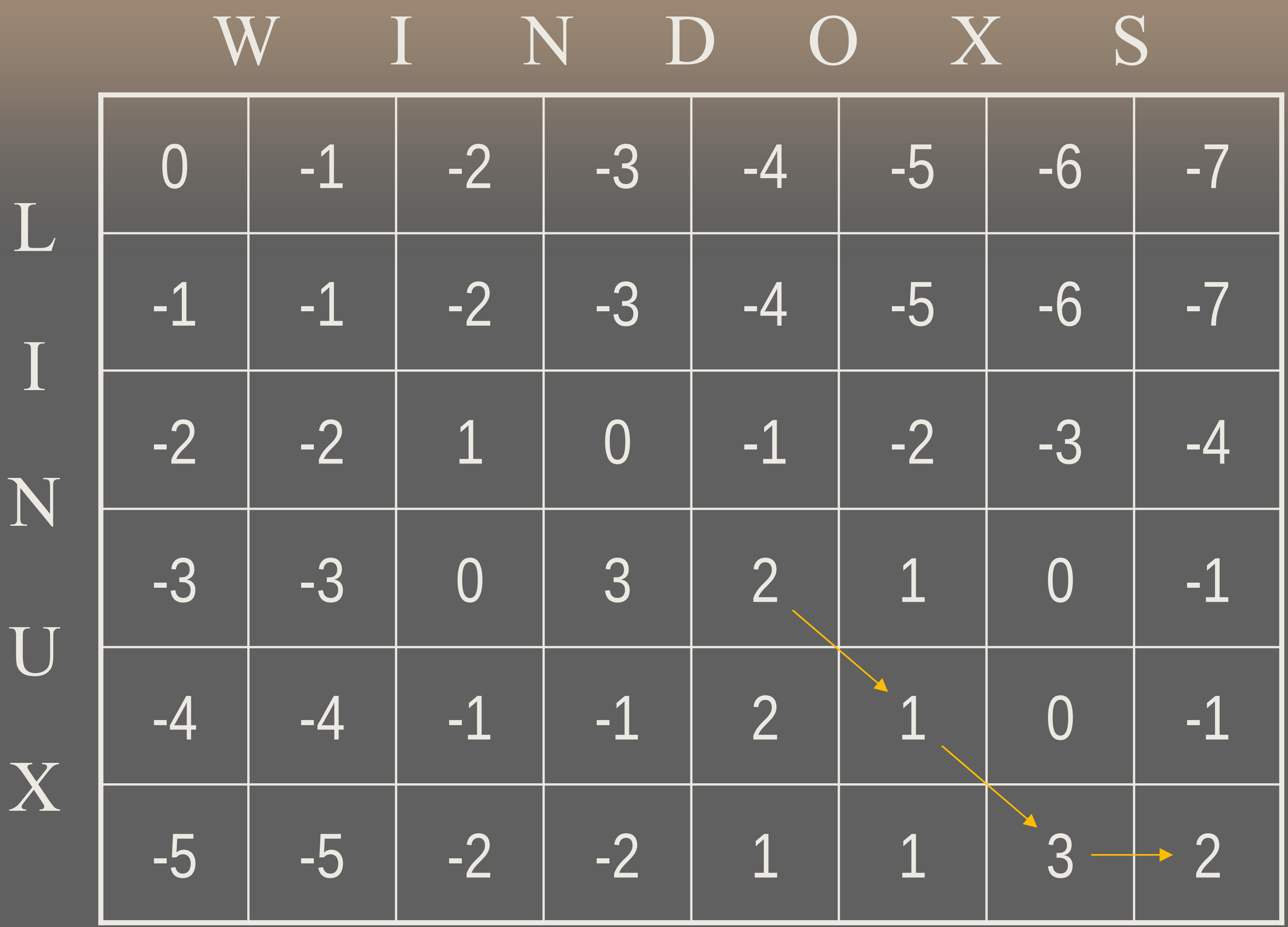
$s(x,y) = 2$ si $x=y$ $\qquad s(x,-) = s(-,x) = -1$

-1 sinon

		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1 ↘	0	-1
X	-5	-5	-2	-2	1	1	3 →	2

s(x,y) = 2 si x=y
-1 sinon

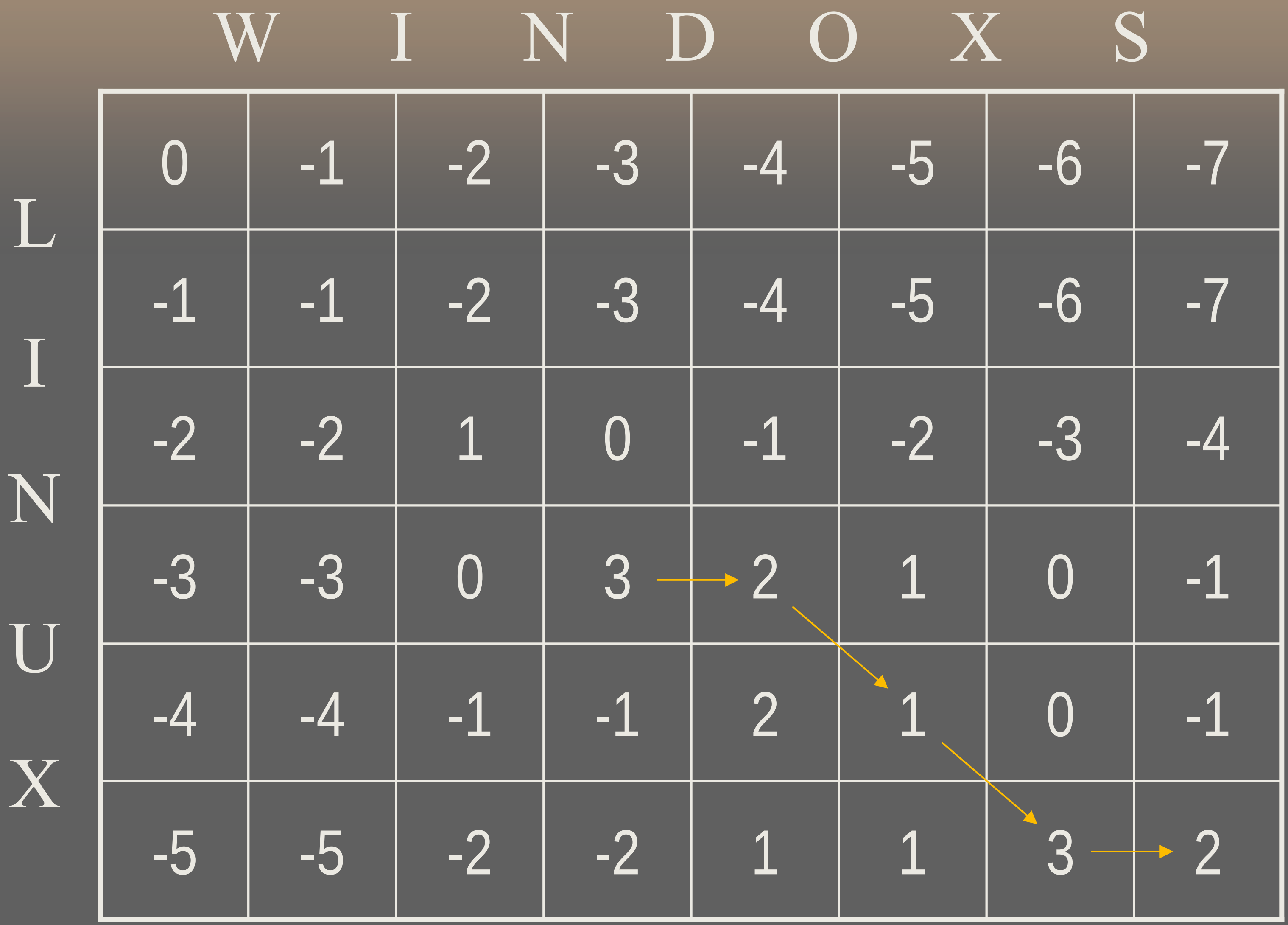
s(x,-) = s(-,x) = -1



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

$s(x,y) = 2$ si $x=y$
-1 sinon

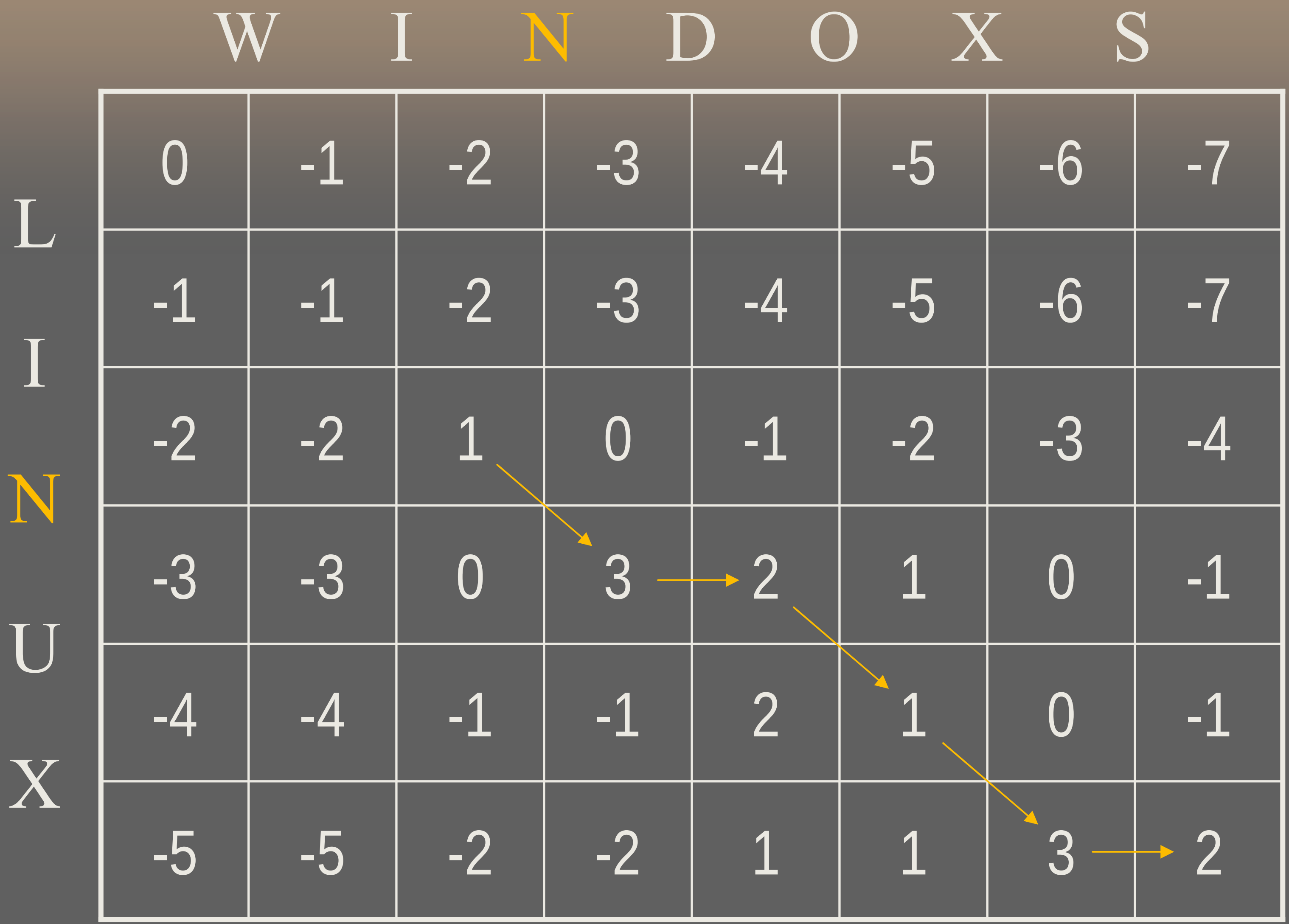
$s(x,-) = s(-,x) = -1$



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

s(x,y) = 2 si x=y
-1 sinon

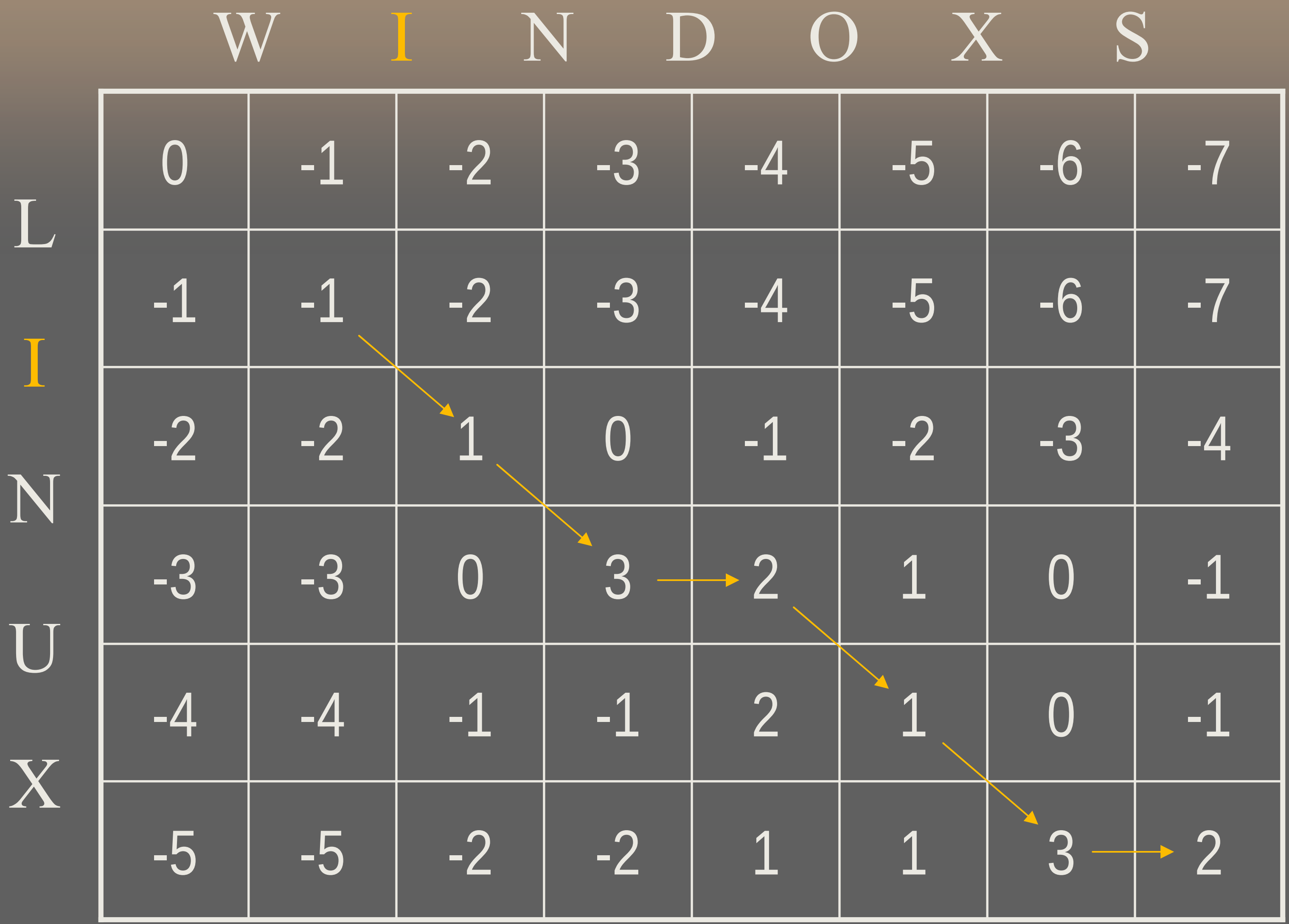
s(x,-) = s(-,x) = -1



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

$s(x,y) = 2$ si $x=y$
$\quad -1$ sinon

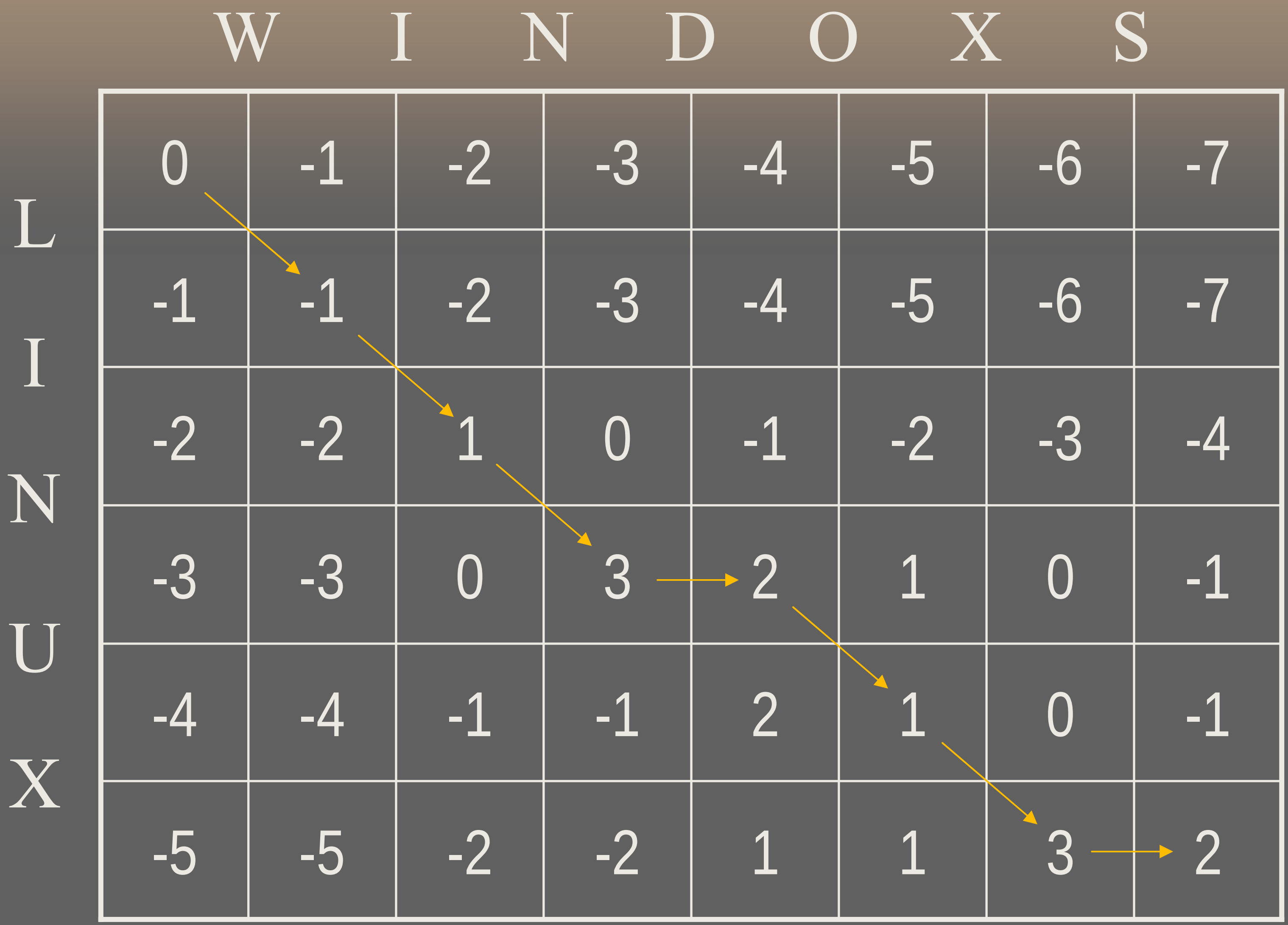
$s(x,-) = s(-,x) = -1$



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

$s(x,y) = 2$ si $x=y$
-1 sinon

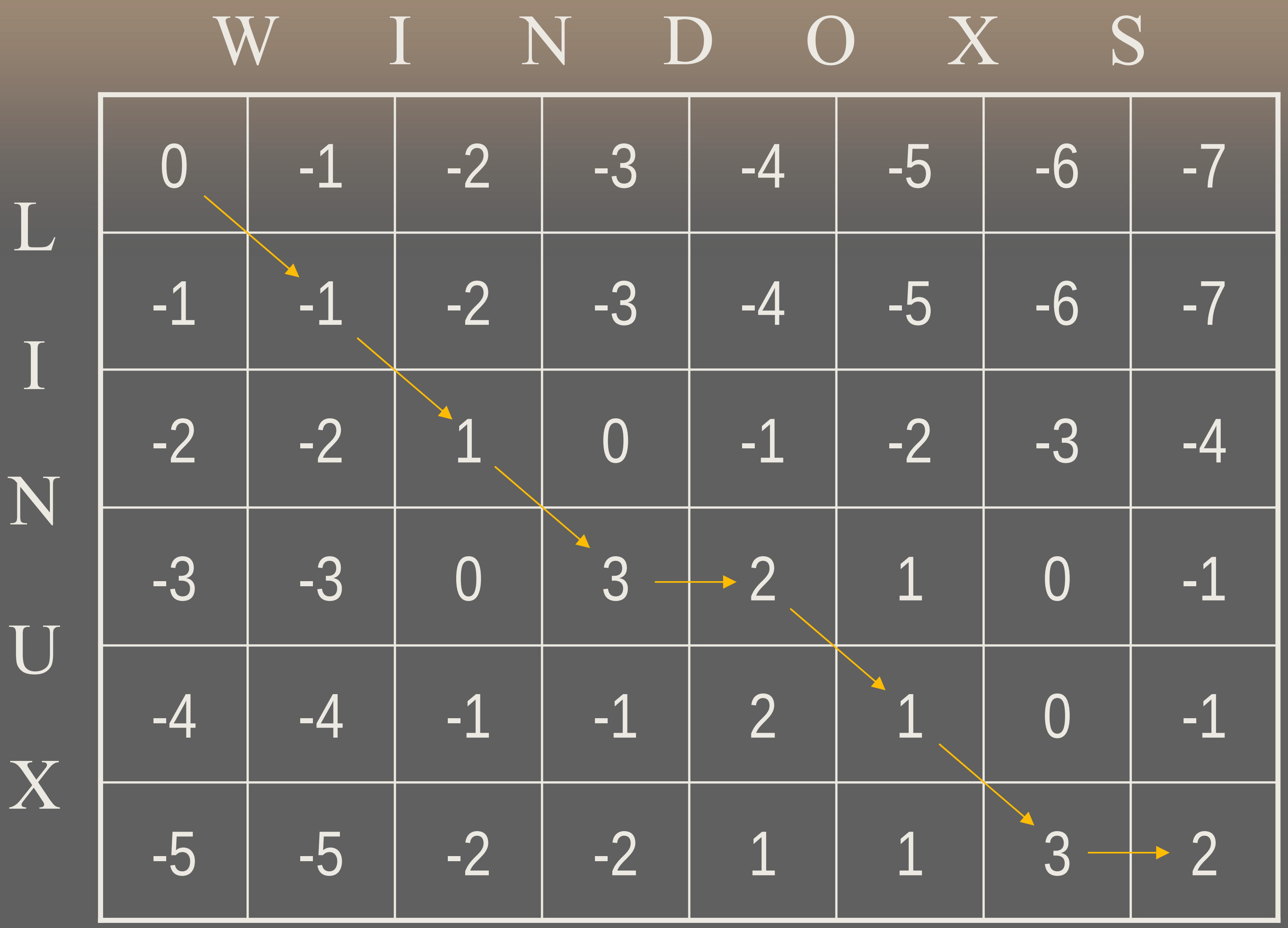
$s(x,-) = s(-,x) = -1$



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

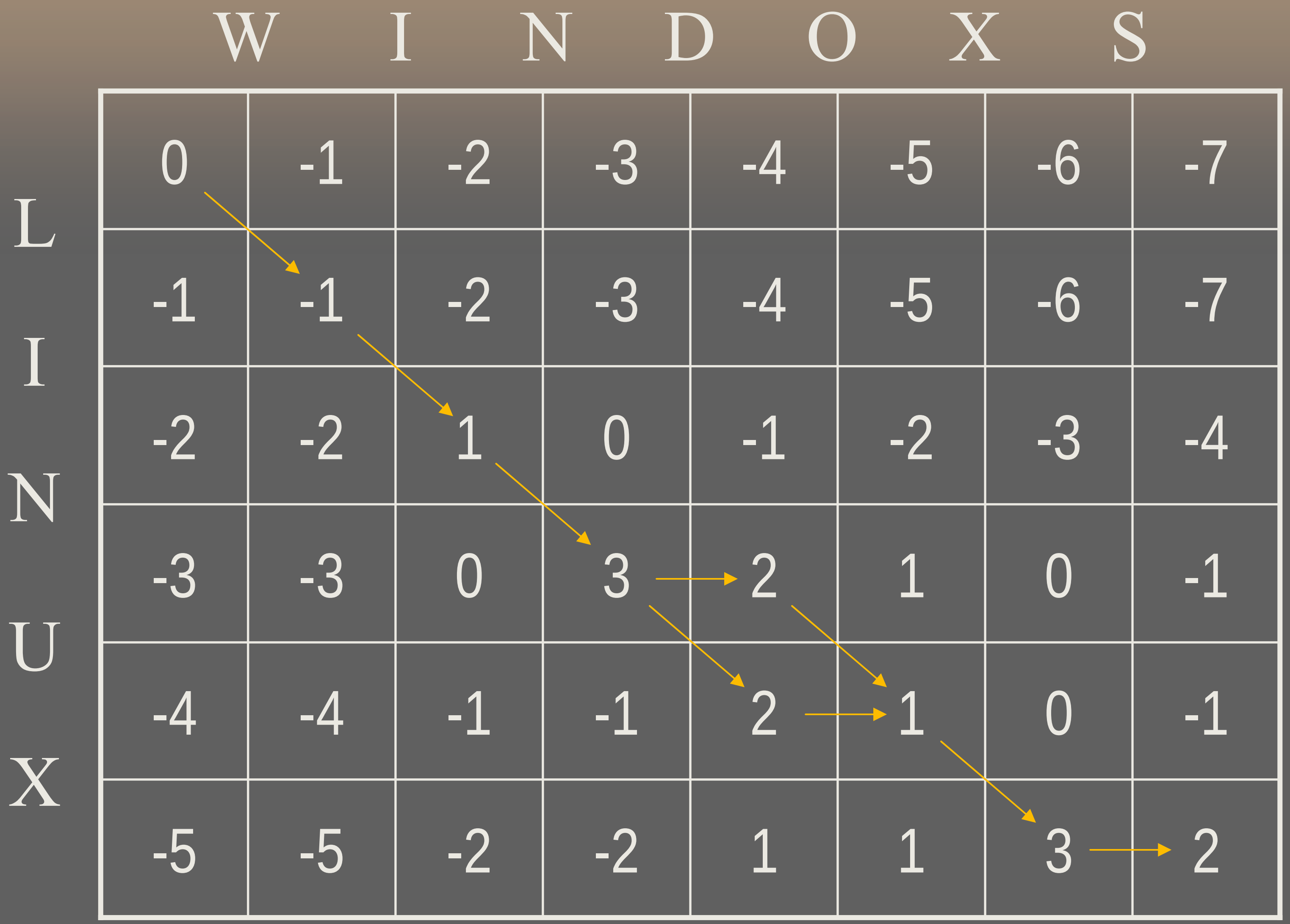
s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

```
W I N D O X S
L I N – U X -
```



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1	0	-1	-2	-3	-4
N	-3	-3	0	3	2	1	0	-1
U	-4	-4	-1	-1	2	1	0	-1
X	-5	-5	-2	-2	1	1	3	2

```
W I N D O X S        W I N D O X S
L I N – U X -        L I N U - X -
```

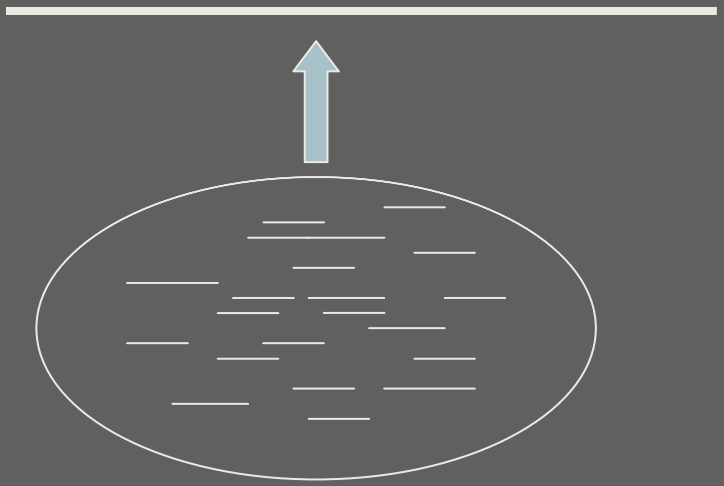
Complexité

En espace : $m \times n$

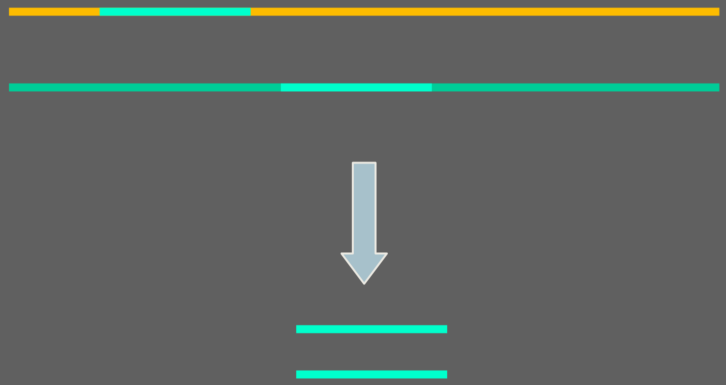
En temps : $m \times n$

Alignement local (Smith et Waterman 1981)

Aligner des petites séquences sur des grandes :



Trouver des similarités locales :

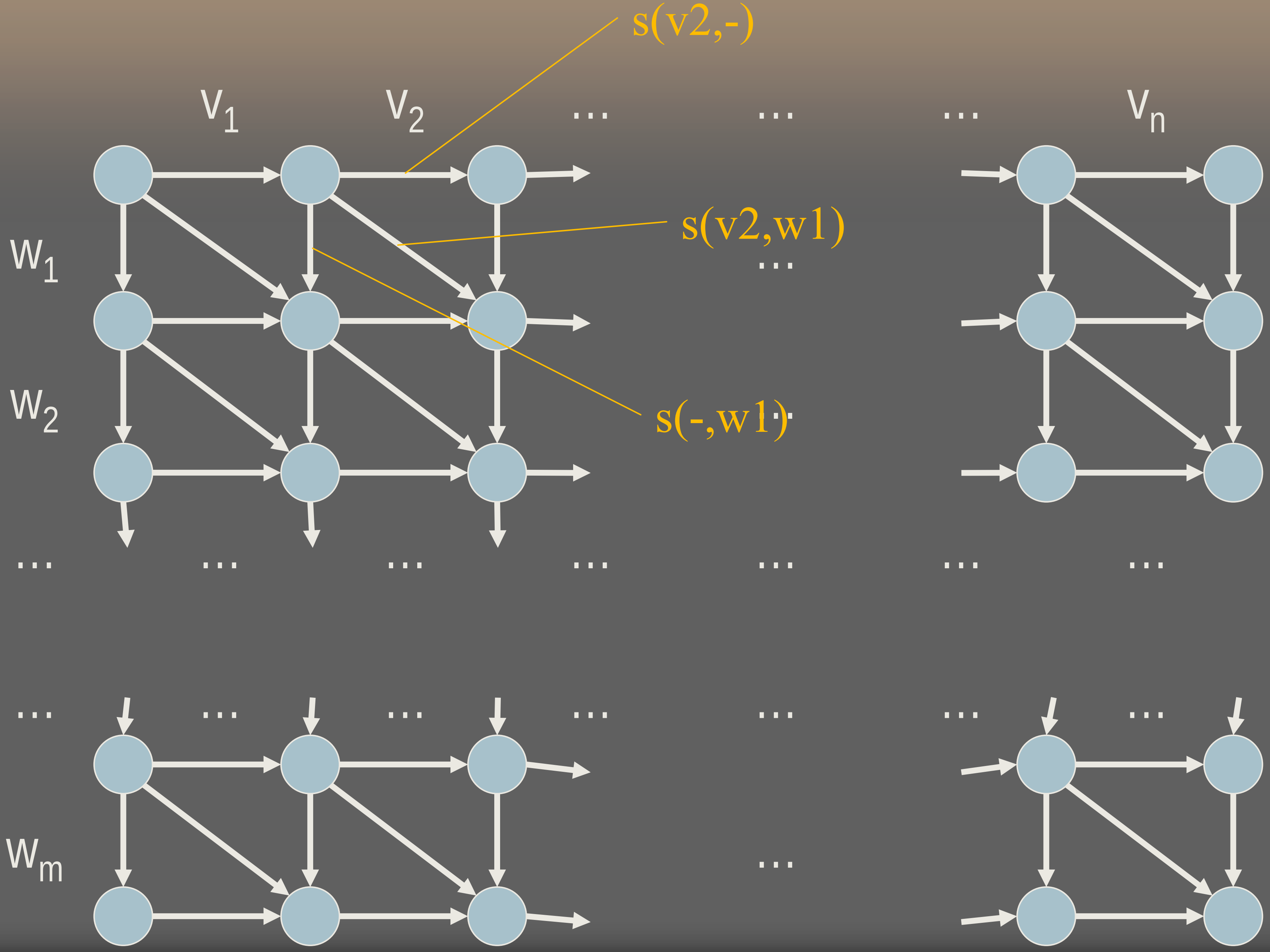


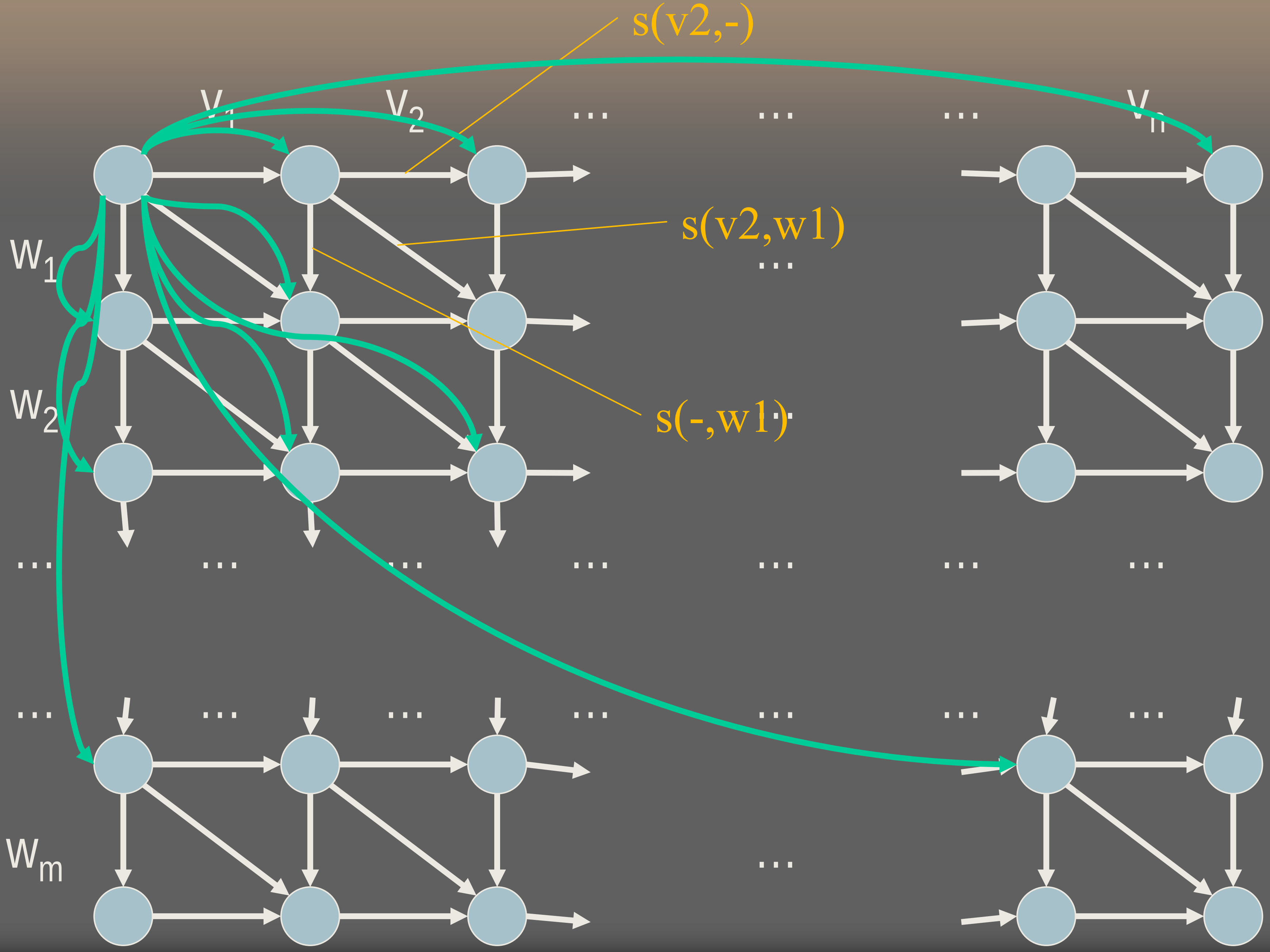
Alignement local de deux séquences d'ADN

```
ACCAGTTAAAGCTAGTGATTTATTTTATGATCCCCAACCACTTCTTAATTCTATCAGTTT
TTATAGTATATAACAACGTAAATCTGTAACGACGTCAGTTGTTCCAATATCTATTTTCTT
ATTTGTGGAAAAACATATCTACCTTACTTAATAAGTTGCAGGTATGTTTATTAAAACACA
AGCAAAGTAGCTATATATCTCATTTTATCCTGCAAATTGTAAGATCGAAAATGATACTAT
AAAGGATGAGAACACCGACTTAATAATACGTTCATATTCTAGTTACAATCAATCTAACTC
TAAGCGTTGATTTTAACTTAAGACTAGCGGTGTTATAATTTTAATATGTATGAATTGCAA
```

```
TTCTCTGCCAATCCCCTATACTATACATGGCTAGCTCAATAGGGATGAGATGGGAGTGAT
GGTAACTAGTAATGTAACGTTTTATATAATTACCTAAAAAAATACTTATGCTAAGTTCGT
AGCACCCTCTTAGGTATAAAATTTATTCCAACGTGGCATATAAATGTATTAATATTTAAC
TAAAGTATCTAAAAATCTCAATTTATAATATAACAGTTATTGTTGAAATCAGGCGGAATG
TTTATCACCATGAATATATTTTTAGTCGAAACATGTGATTAGAATAATTAACGTAAATAT
```

```
seq 1:     153 AAGTTGCAGGTATGTTTATTAAAACACAAGCAAAGTAGCTATATATCTCATTTTAT 208
               | || |||  ||  | |||||| |   ||  |||||| ||| | |||||| |||||
seq 2:     151 ACGTGGCATATAAATGTATTAATATTTAACTAAAGTATCTAAAAATCTCAATTTAT 206
```

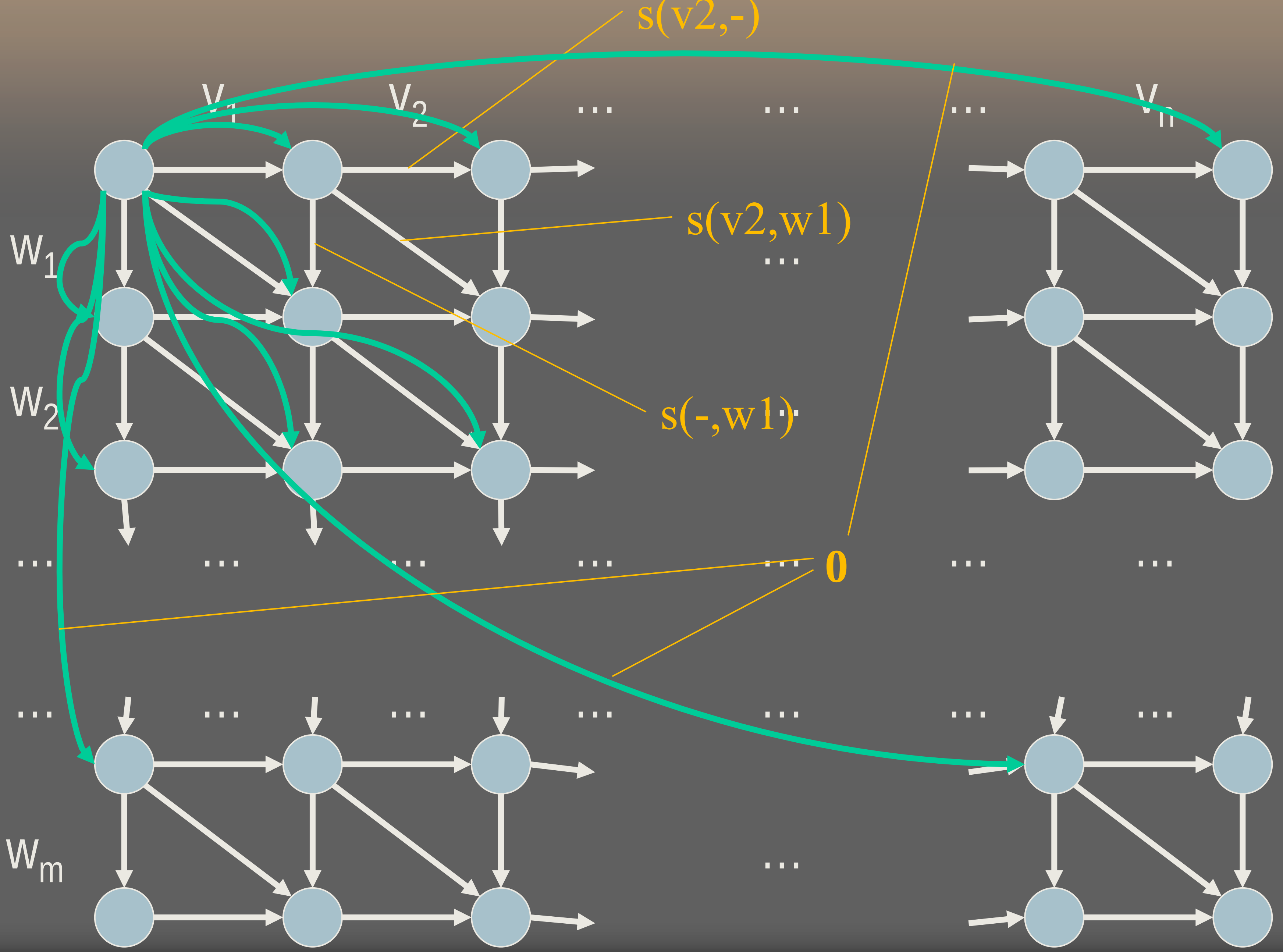

s(v2,-)
V1
V2
…
…
…
Vn
s(v2,w1)
W1
…
W2
s(-,w1)
…
…
…
…
…
…
…
…
…
…
…
…
…
…
…
Wm
…



s(v2,-)

s(v2,w1)

s(-,w1)

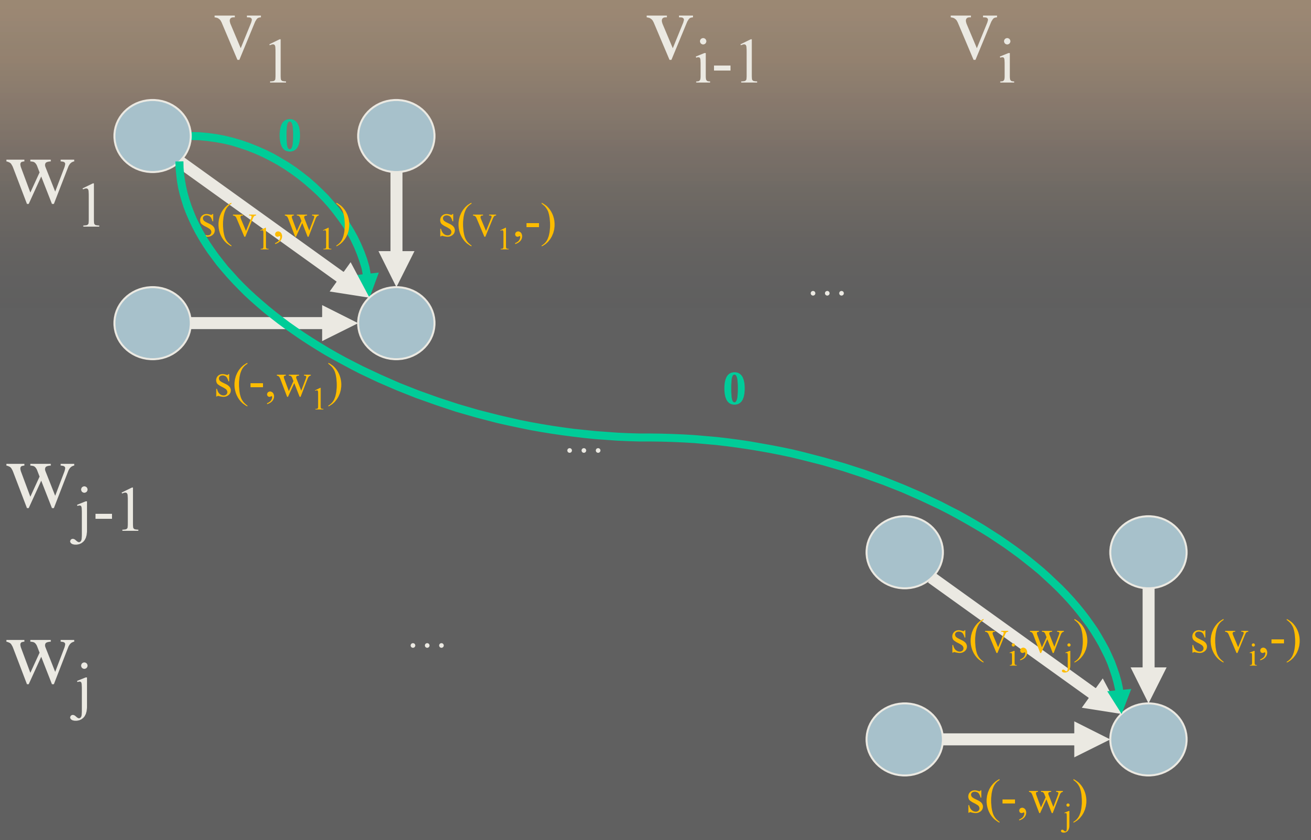


s(v2,-)

s(v2,w1)

s(-,w1)

0



$$S(v_1 \ldots v_i, w_1 \ldots w_j) = \mathrm{Max} \left\{ \begin{array}{l} \mathbf{0} \\ S(v_1 \ldots v_{i-1}, w_1 \ldots w_{j-1}) + s(v_i, w_j) \\ S(v_1 \ldots v_{i-1}, w_1 \ldots w_j) + s(v_i, -) \\ S(v_1 \ldots v_i, w_1 \ldots w_{j-1}) + s(-, w_j) \end{array} \right\}$$

		W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0							
I	0							
N	0							
U	0							
X	0							

$s(x,y) = 2$ si $x=y$
-1 sinon

$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0	0						
I	0							
N	0							
U	0							
X	0							

$s(x,y) = 2$ si $x=y$
-1 sinon

$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	0	0
I	0	0	2					
N	0							
U	0							
X	0							

s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1

		W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	0	0
I	0	0	2	1	0	0	0	0
N	0	0	1	4	3	2	1	0
U	0	0	0	3	3	2	1	0
X	0	0	0	2	2	2	4	3

$s(x,y) = 2$ si $x=y$
-1 sinon

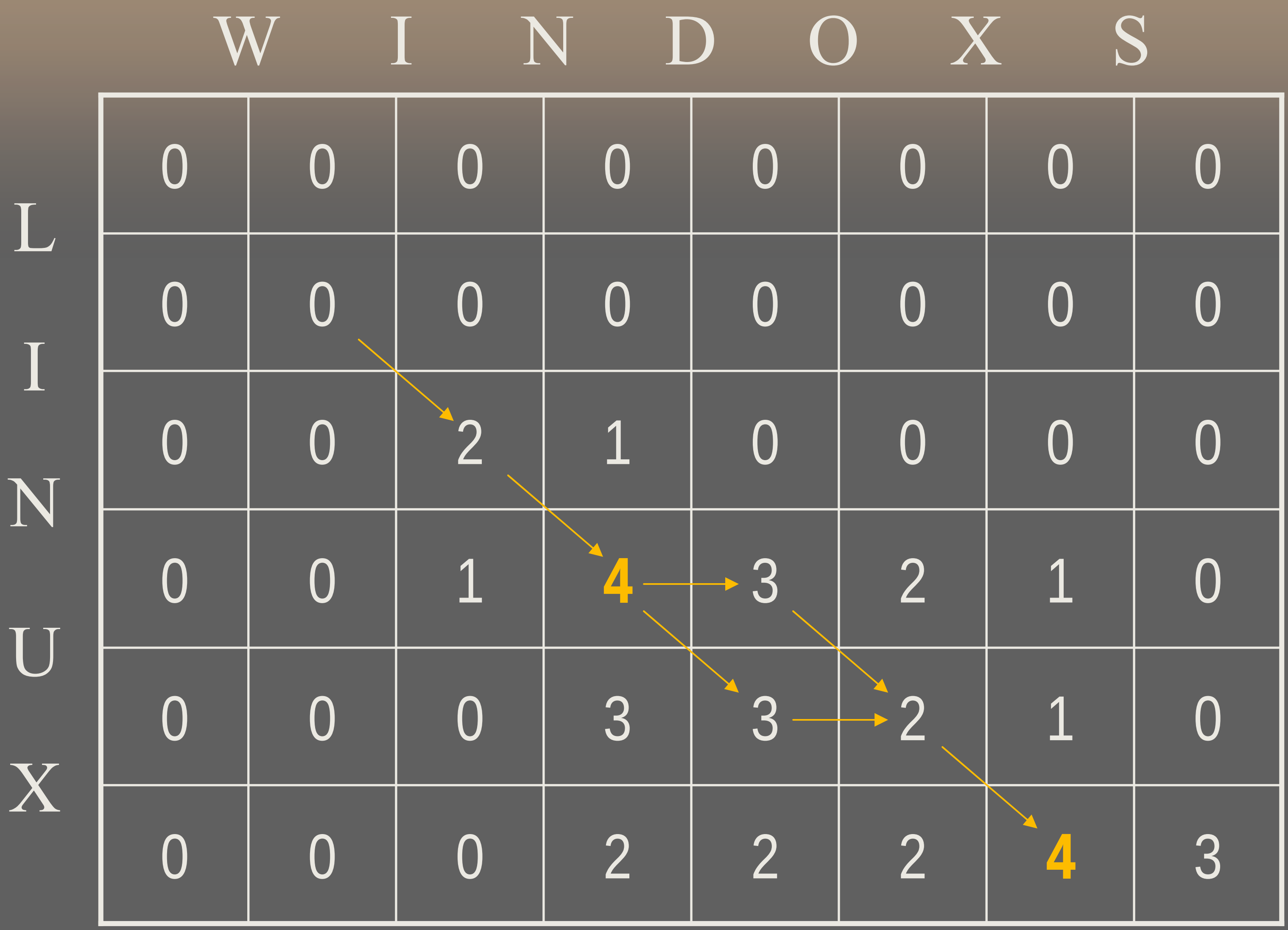
$s(x,-) = s(-,x) = -1$

		W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	0	0
I	0	0	2	1	0	0	0	0
N	0	0	1	**4**	3	2	1	0
U	0	0	0	3	3	2	1	0
X	0	0	0	2	2	2	**4**	3

$s(x,y) = 2$ si $x=y$

-1 sinon

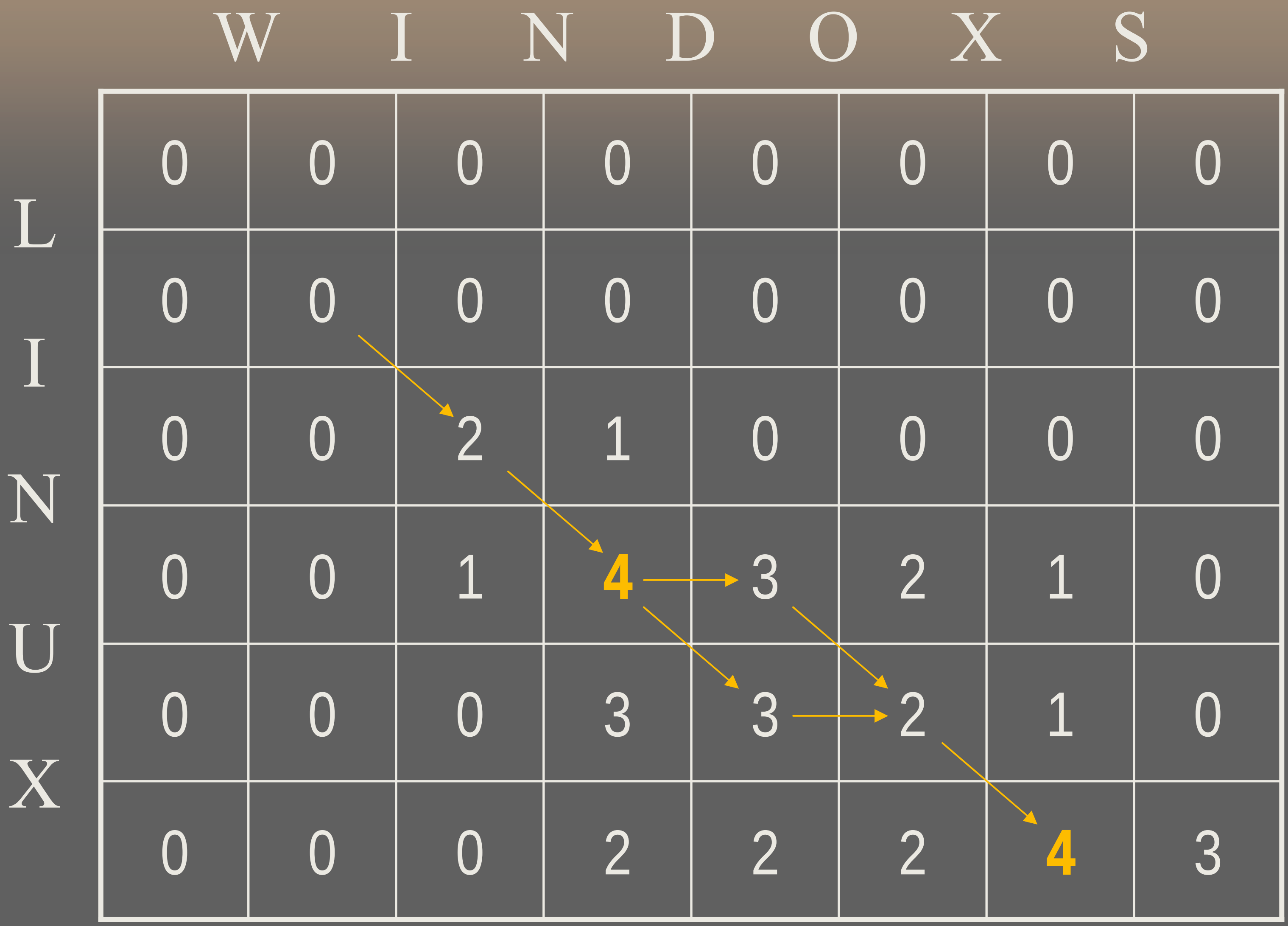
$s(x,-) = s(-,x) = -1$



		W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	0	0
I	0	0	2	1	0	0	0	0
N	0	0	1	**4**	3	2	1	0
U	0	0	0	3	3	2	1	0
X	0	0	0	2	2	2	**4**	3

s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1



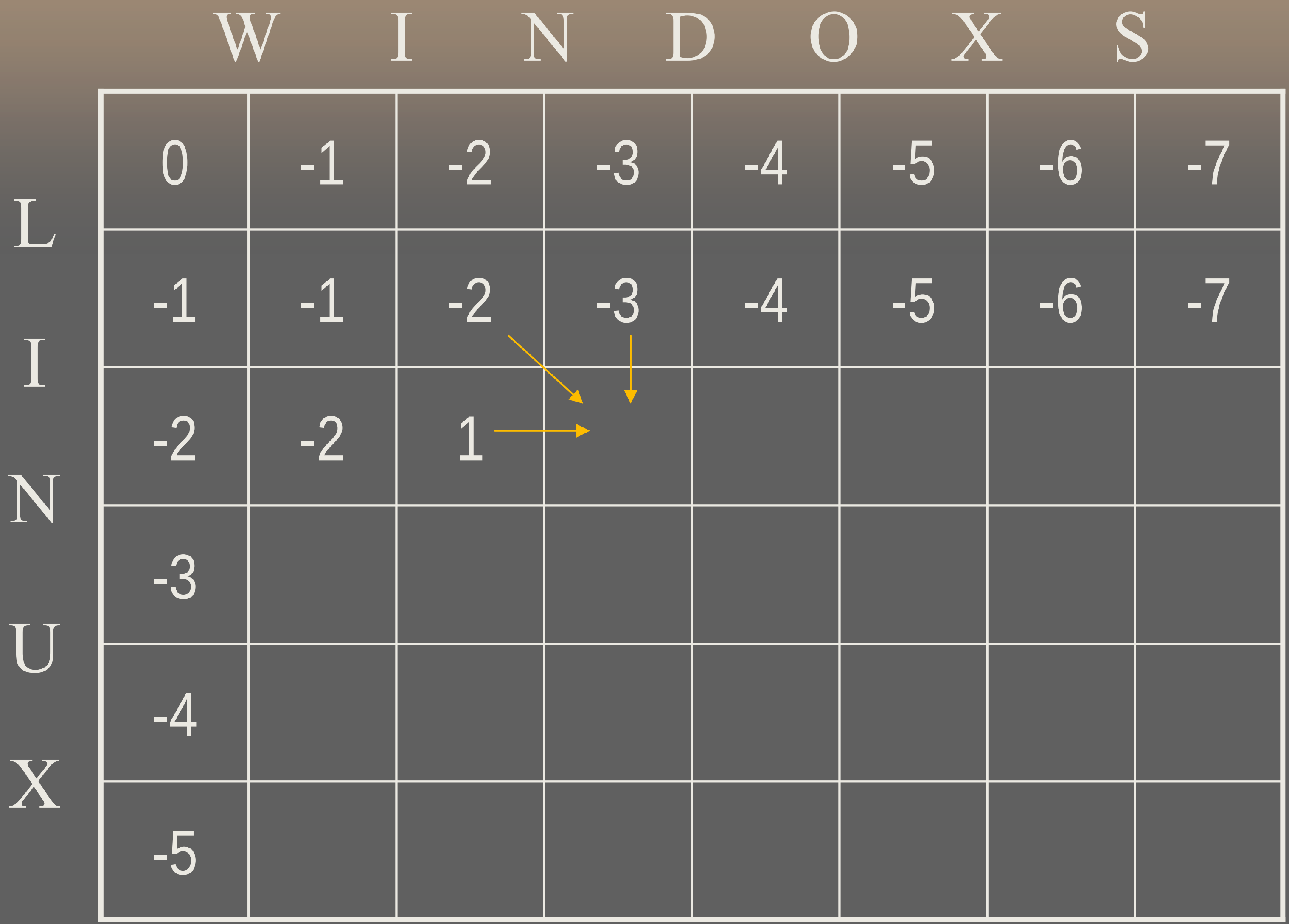
	W	I	N	D	O	X	S
	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	0	0
I	0	0	2	1	0	0	0	0
N	0	0	1	**4**	3	2	1	0
U	0	0	0	3	3	2	1	0
X	0	0	0	2	2	2	**4**	3

IN
IN

INDOX
IN-UX

INDOX
INU-X

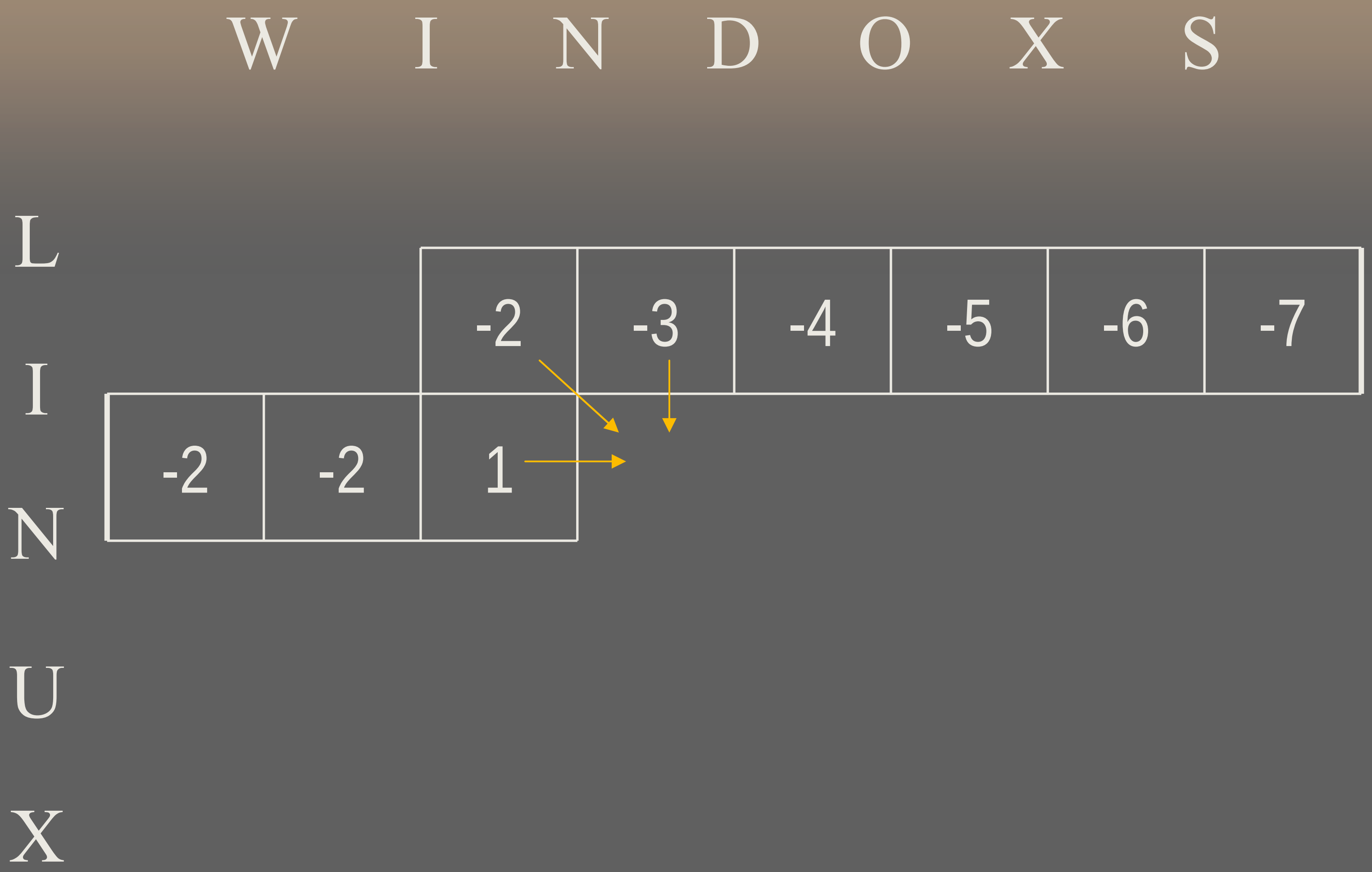
Alignement en espace linéaire



		W	I	N	D	O	X	S
	0	-1	-2	-3	-4	-5	-6	-7
L	-1	-1	-2	-3	-4	-5	-6	-7
I	-2	-2	1					
N	-3							
U	-4							
X	-5							

$s(x,y) = 2$ si $x=y$
-1 sinon

$s(x,-) = s(-,x) = -1$



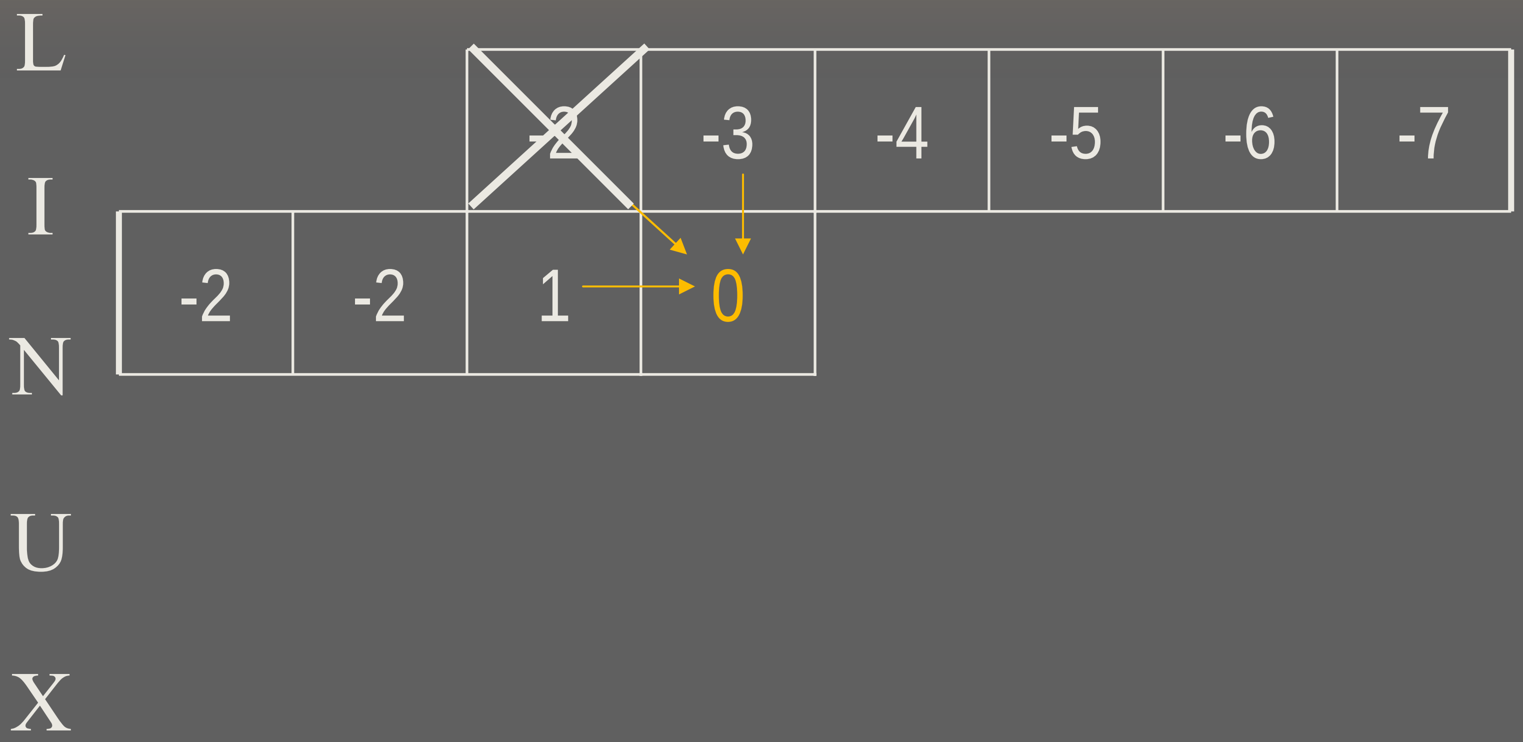
Espace linéaire …

s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1

WINDOXS

LINUX

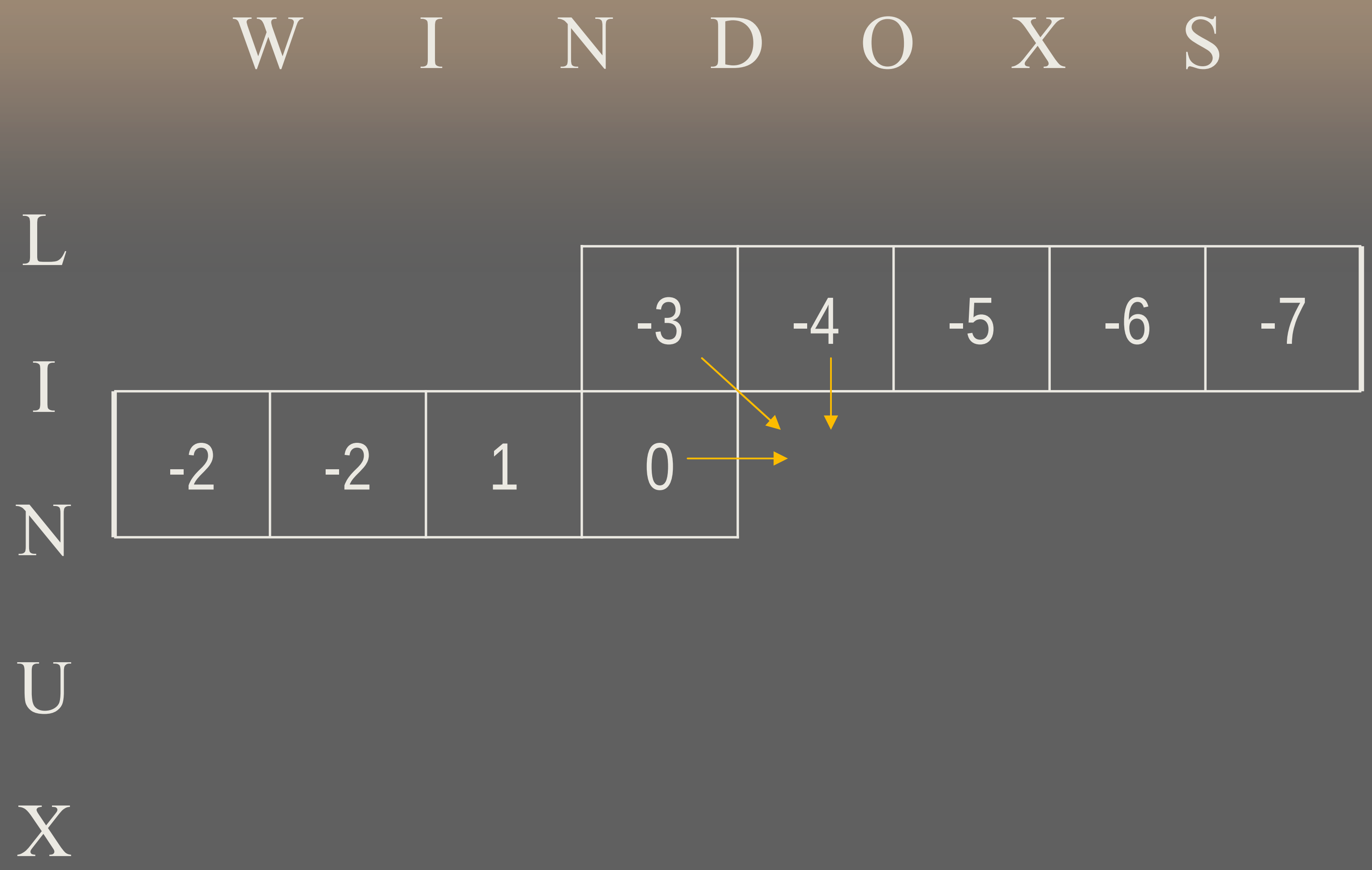


		~~-2~~	-3	-4	-5	-6	-7
-2	-2	1	0				

Espace linéaire …

s(x,y) = 2 si x=y
-1 sinon

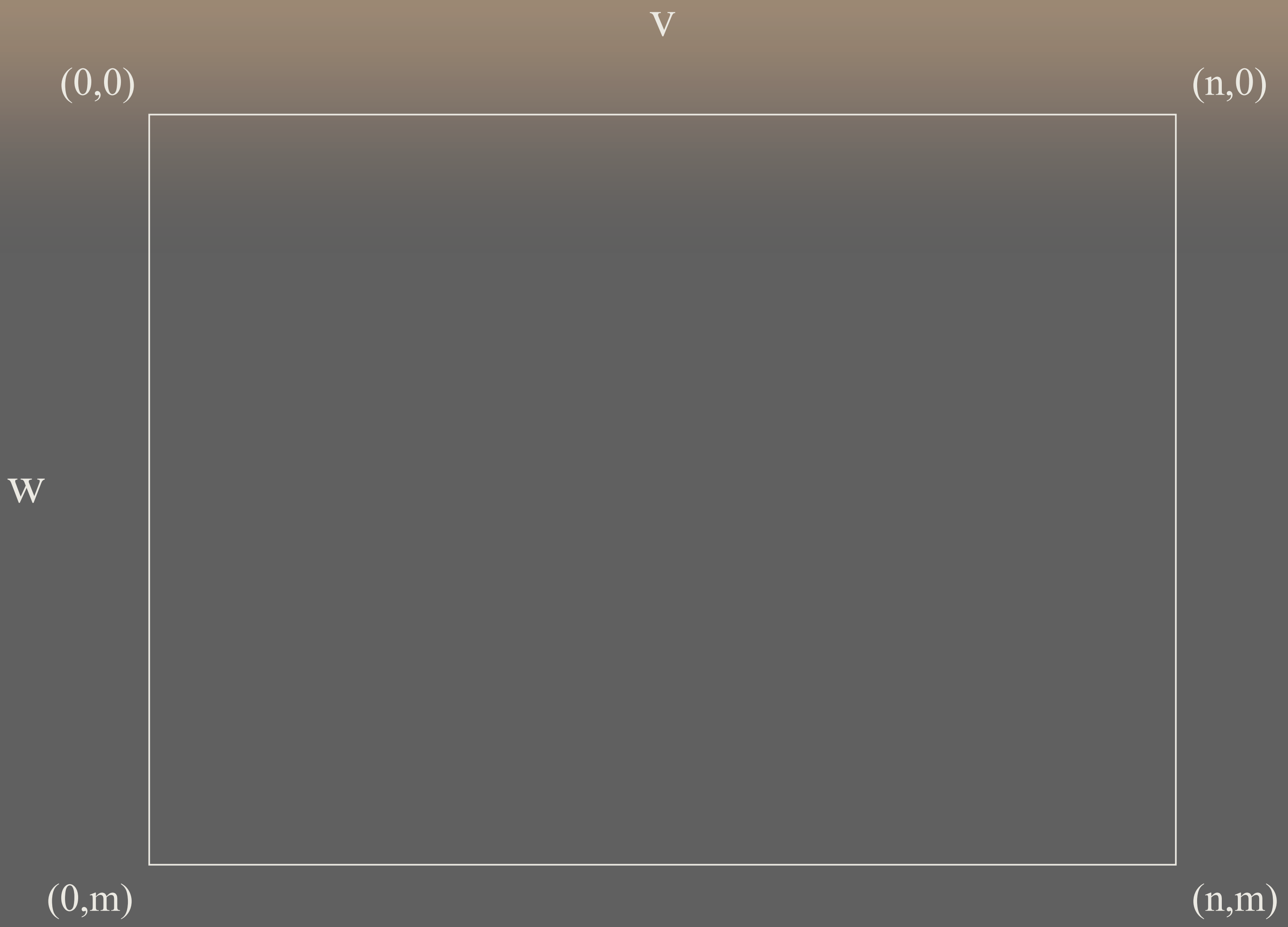
s(x,-) = s(-,x) = -1



Espace linéaire … mais seulement le score

s(x,y) = 2 si x=y
-1 sinon

s(x,-) = s(-,x) = -1



V

(0,0)

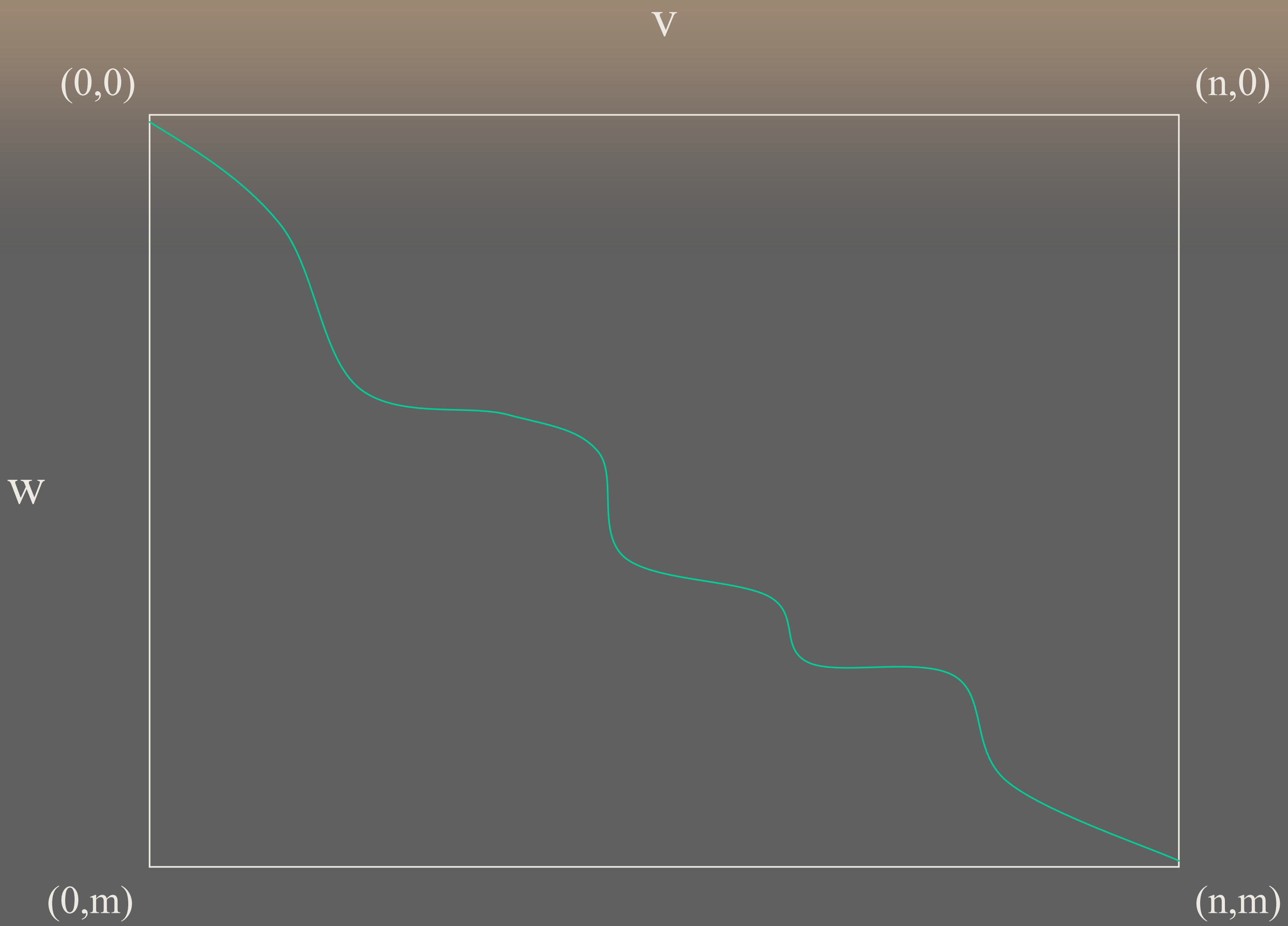
(n,0)

W

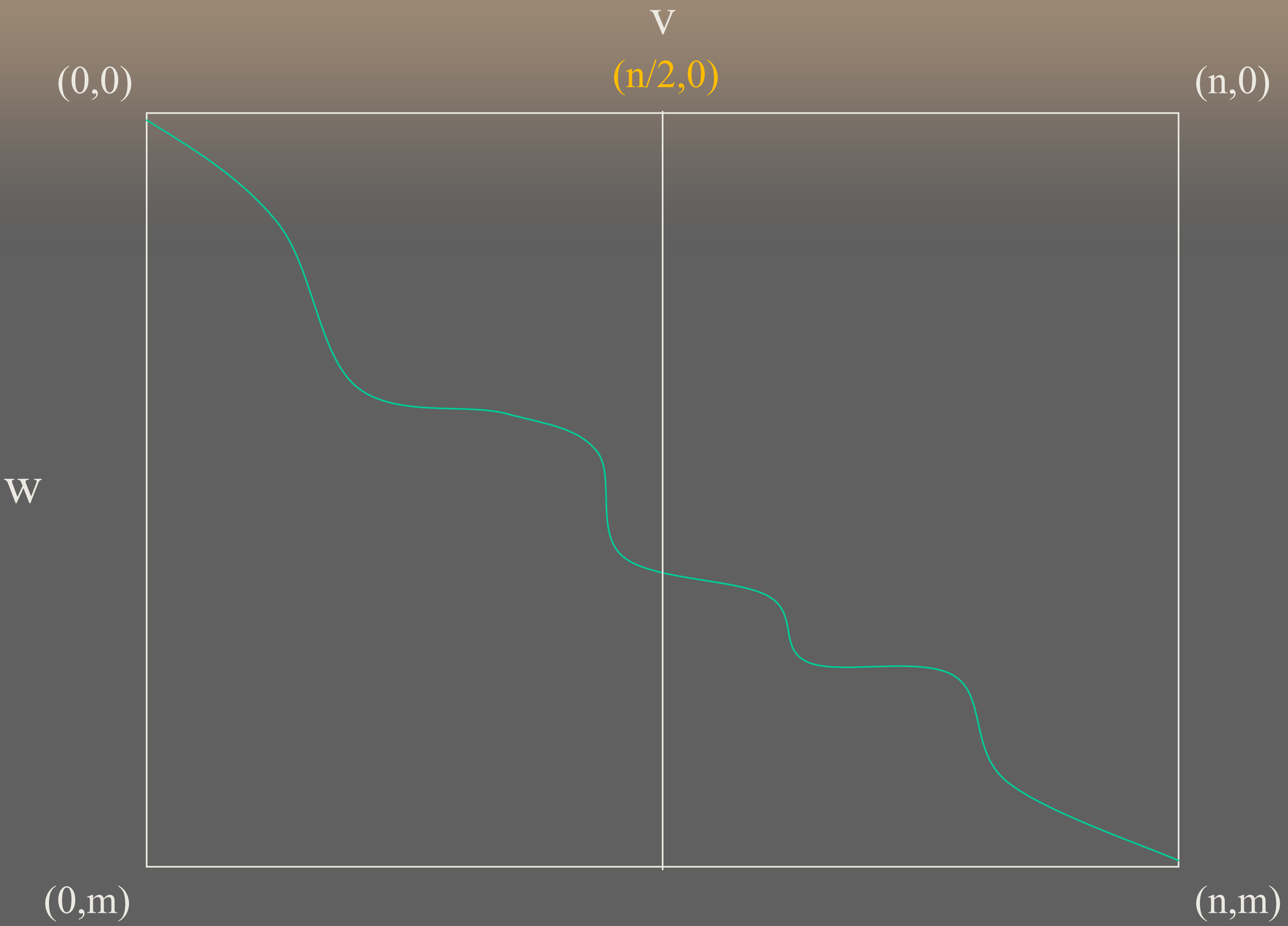
(0,m)

(n,m)

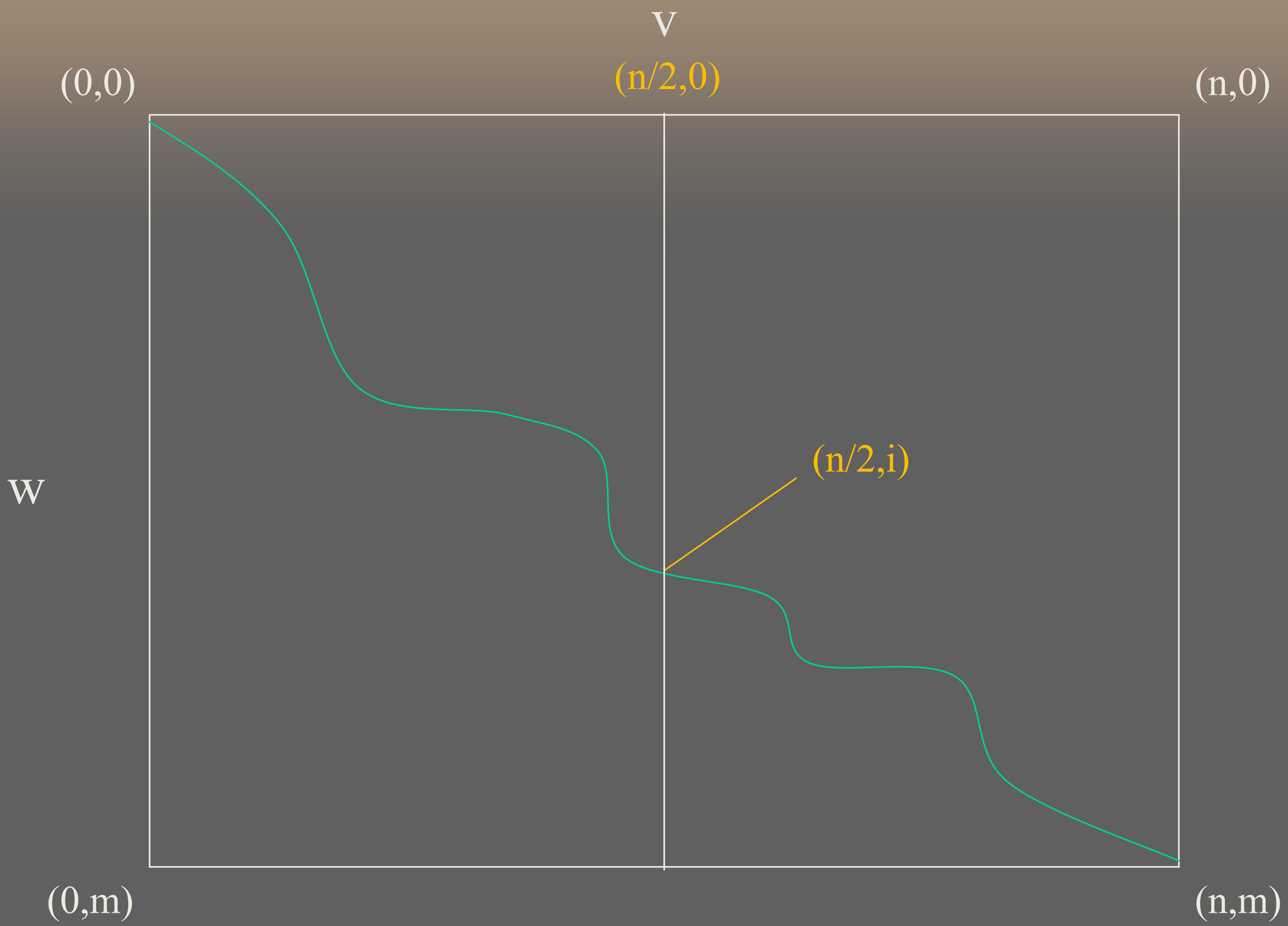
Score **et** alignement en espace linéaire



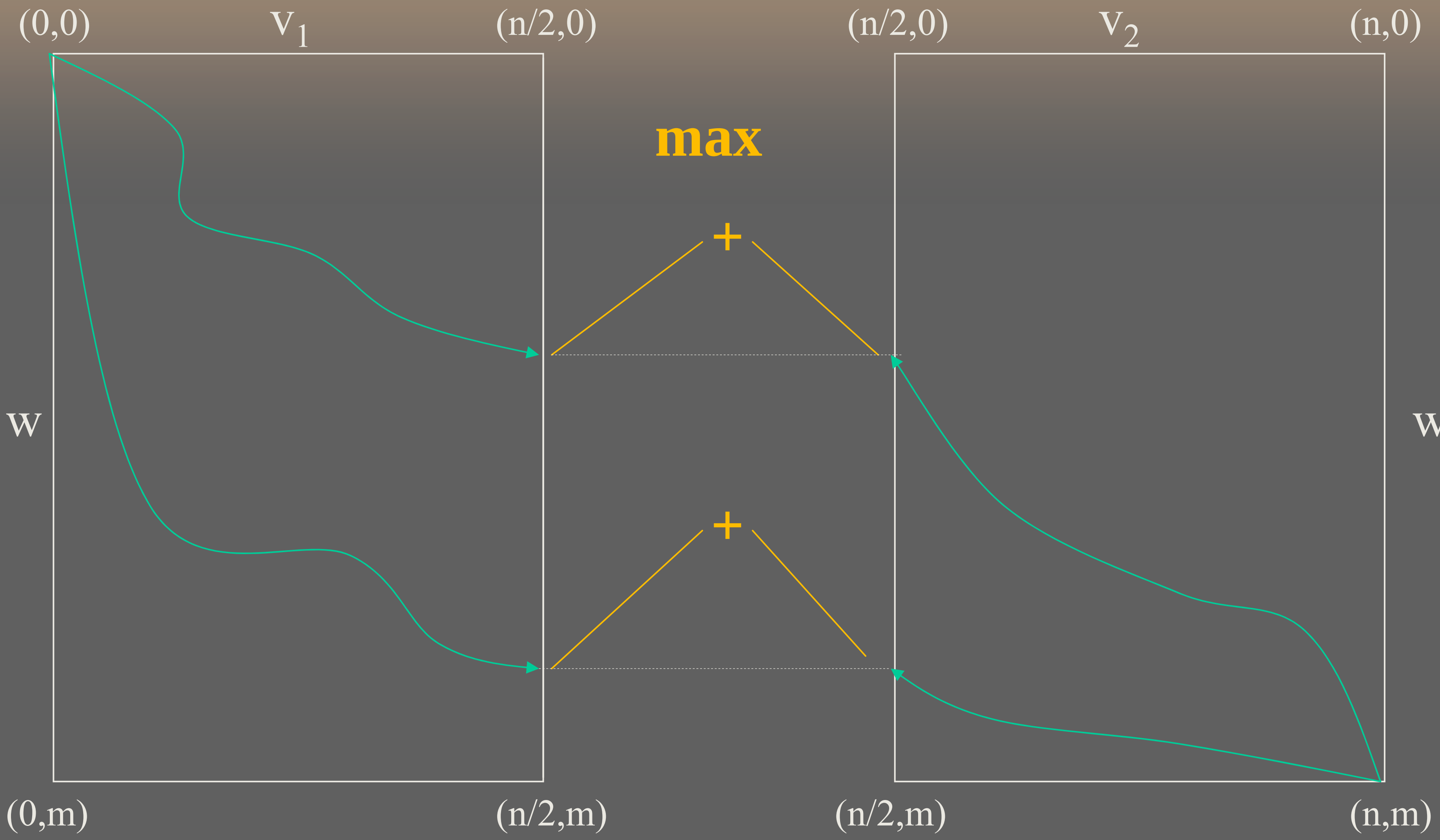
Score **et** alignement en espace linéaire



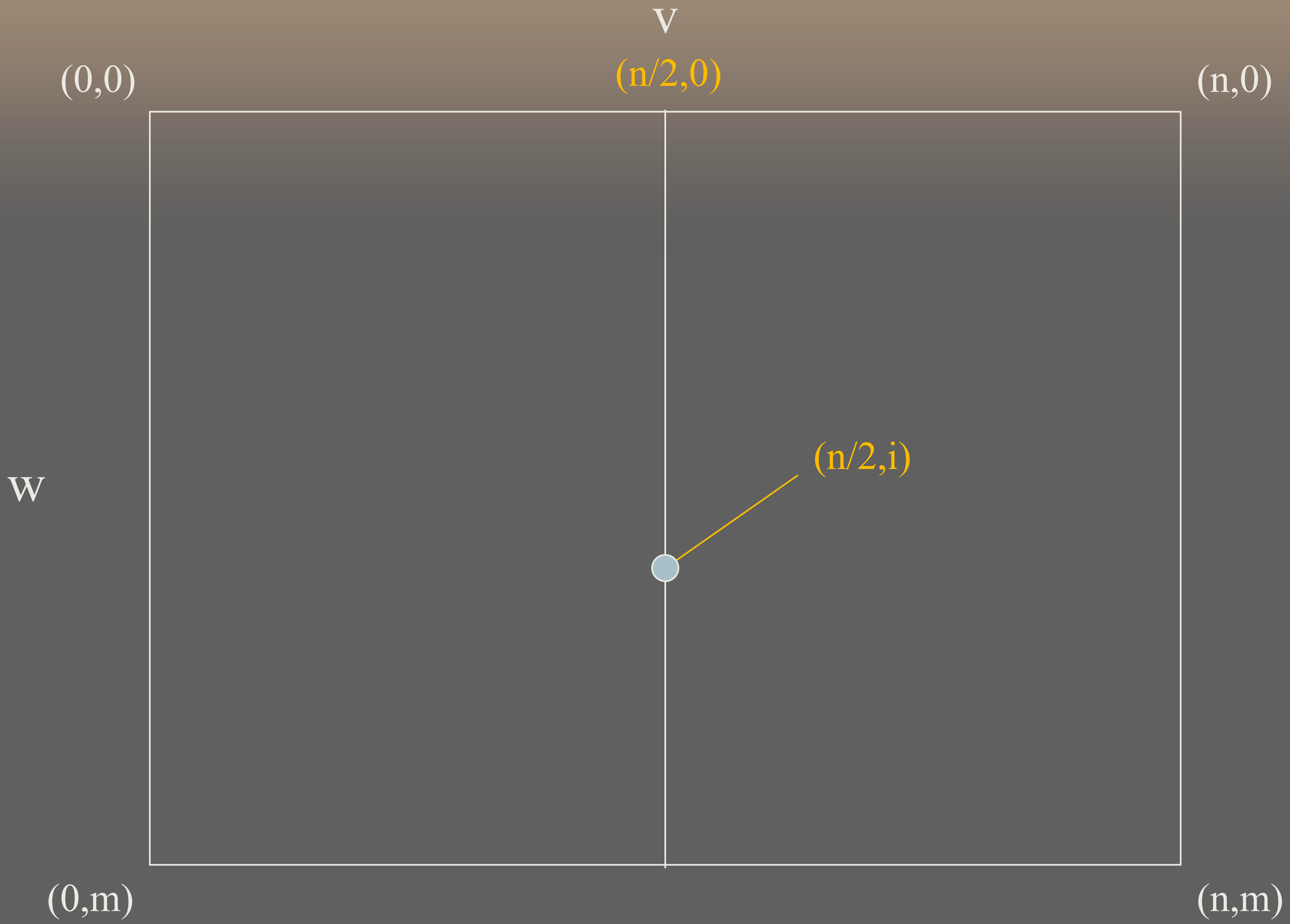
Score **et** alignement en espace linéaire



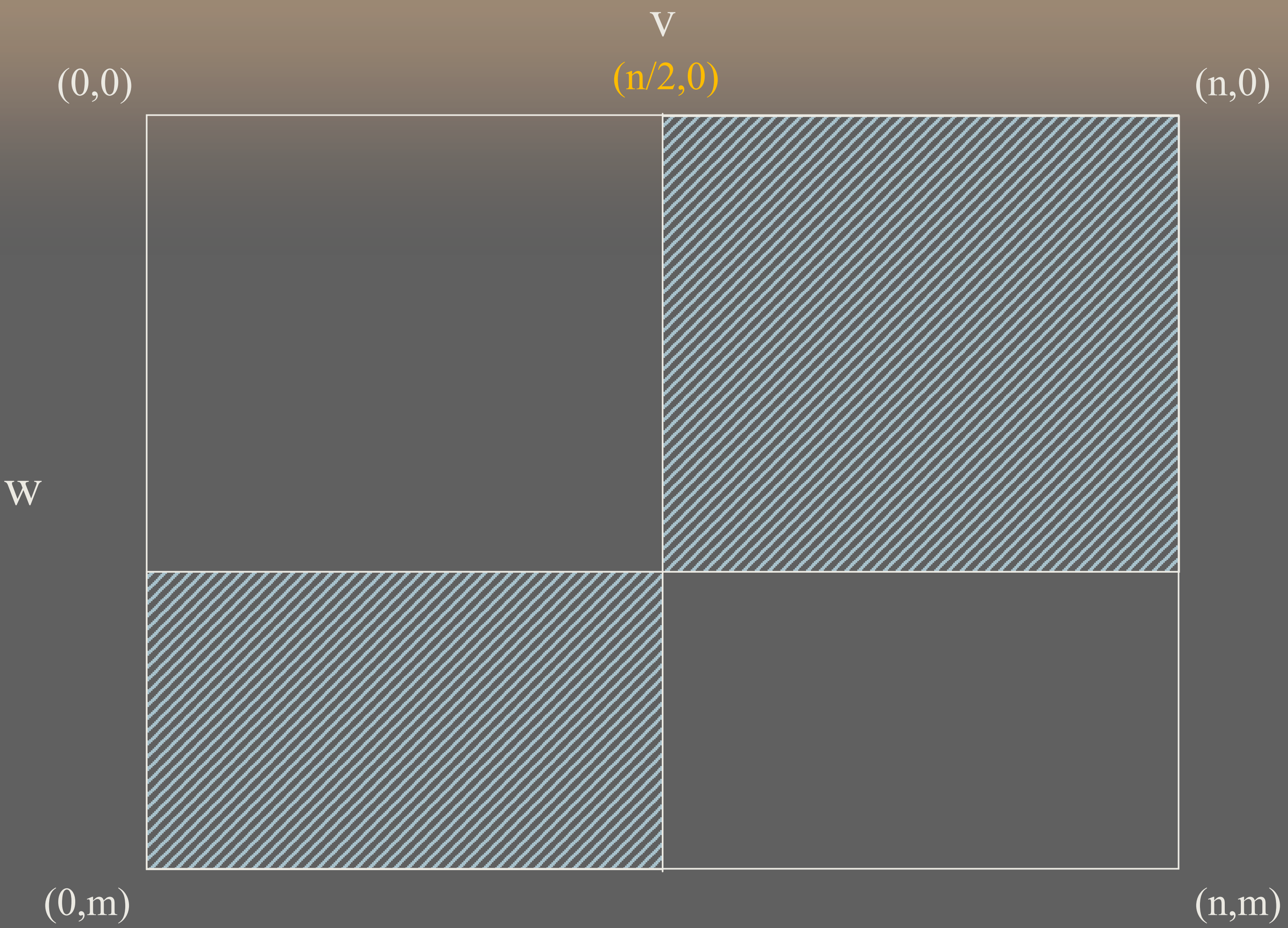
Score **et** alignement en espace linéaire



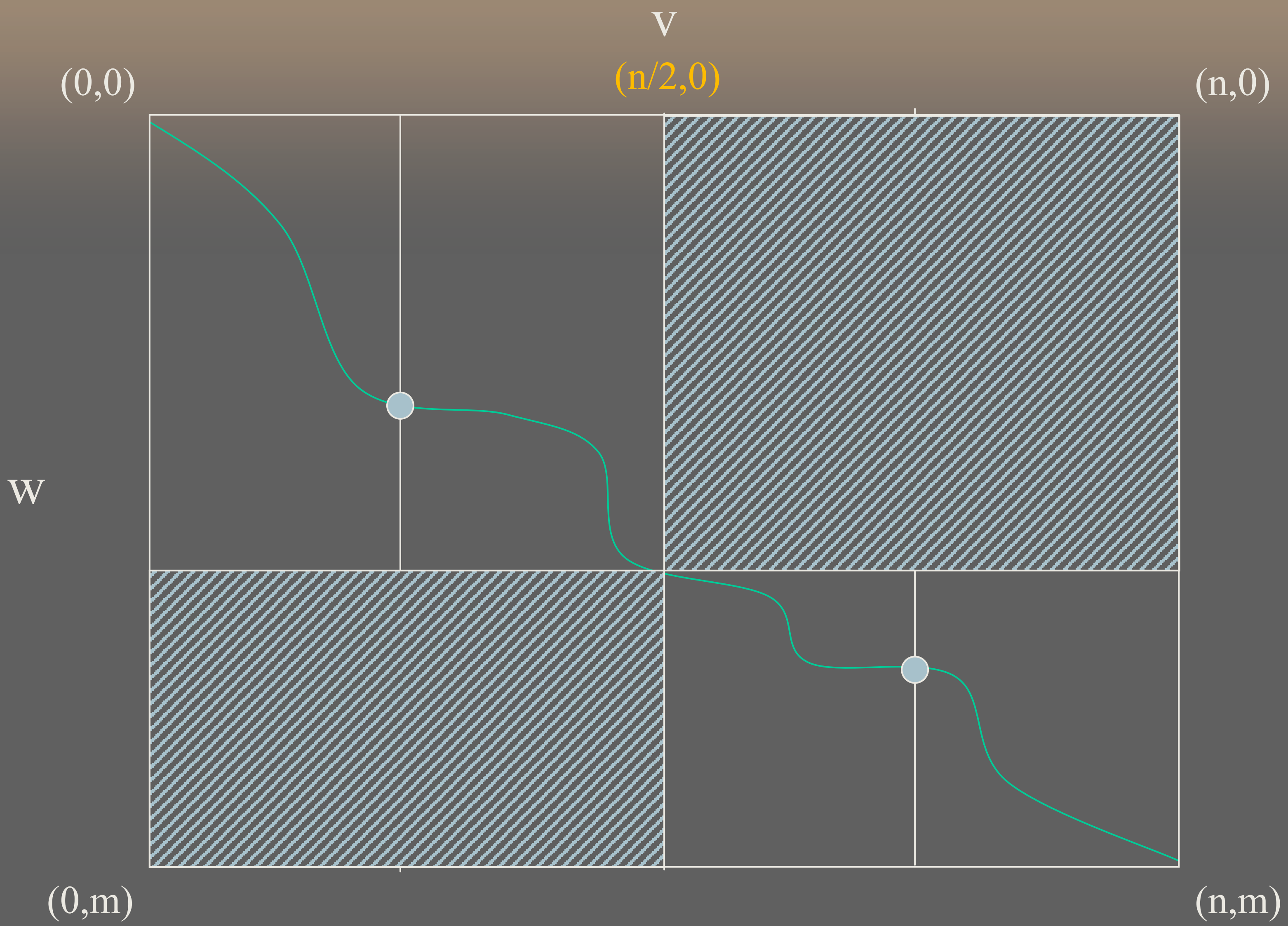
Score **et** alignement en espace linéaire



Score **et** alignement en espace linéaire



Score **et** alignement en espace linéaire



Score **et** alignement en espace linéaire

Complexité

En espace : linéaire.

En temps : $mn + mn/2 + mn/4 + mn/8 + \ldots < 2mn$

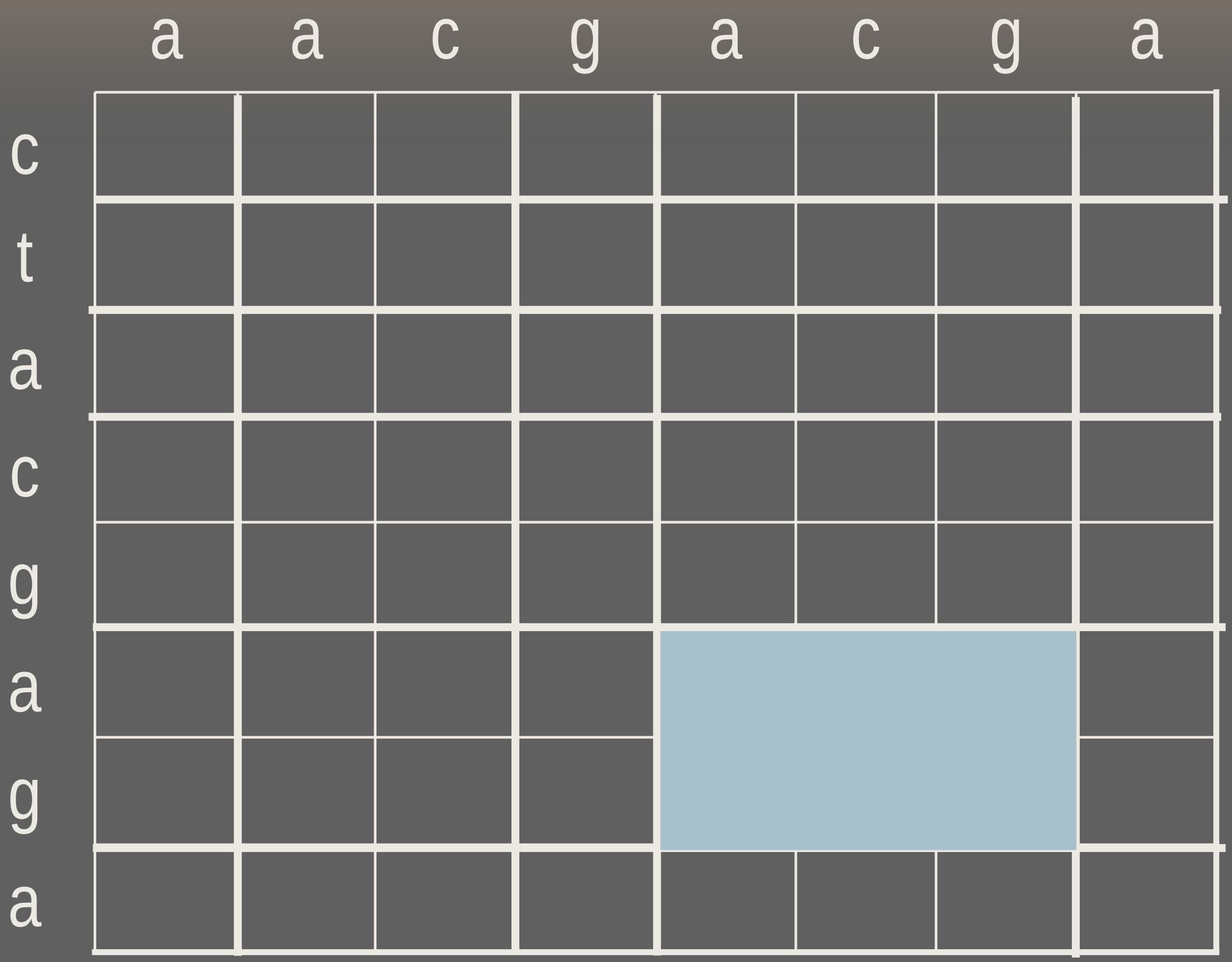
Alignement sous-quadratique

(Crochemore, Landau, Ziv-Ukelson 2002)

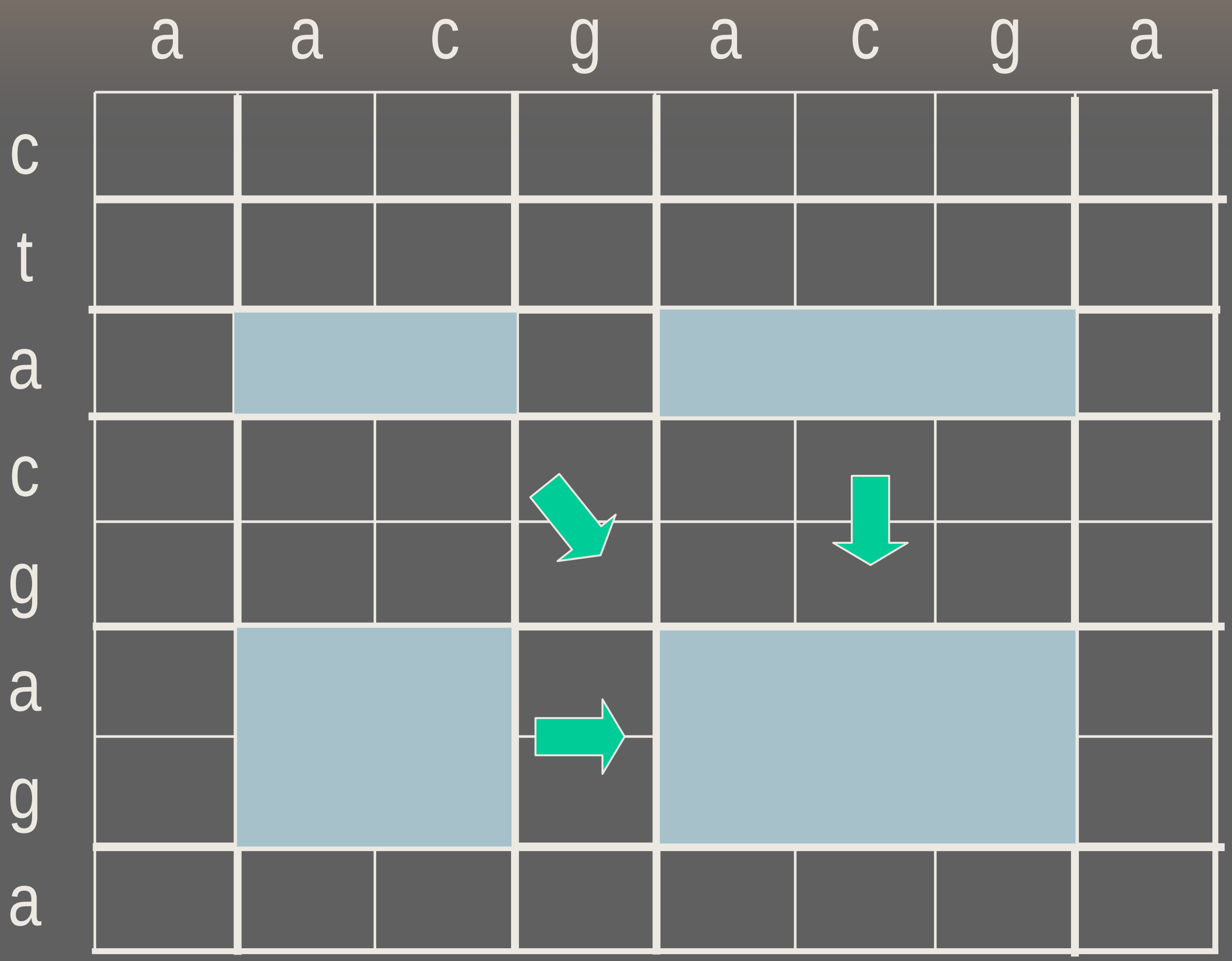
	a	a	c	g	a	c	g	a
c								
t								
a								
c								
g								
a								
g								
a								

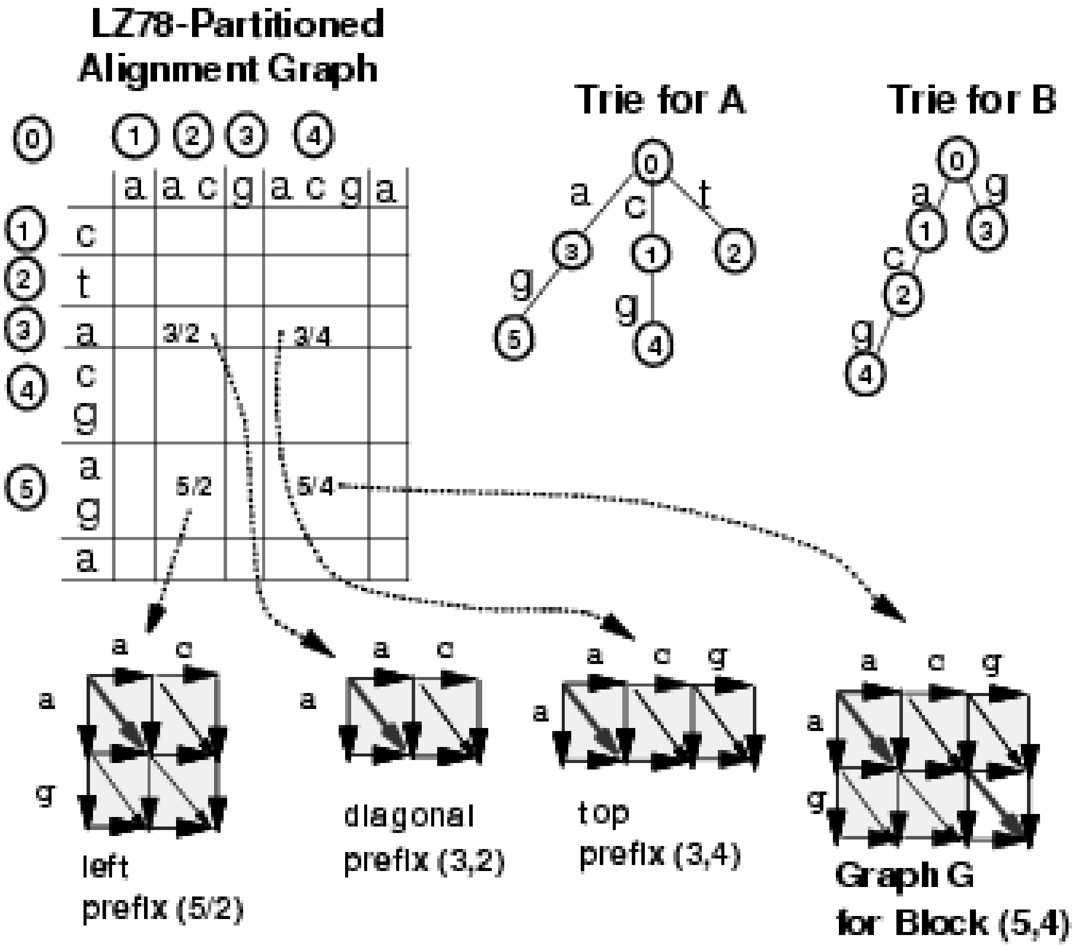
	a	a	c	g	a	c	g	a
c								
t								
a								
c								
g								
a								
g								
a								

	a	a	c	g	a	c	g	a
c								
t								
a								
c								
g								
a								
g								
a								

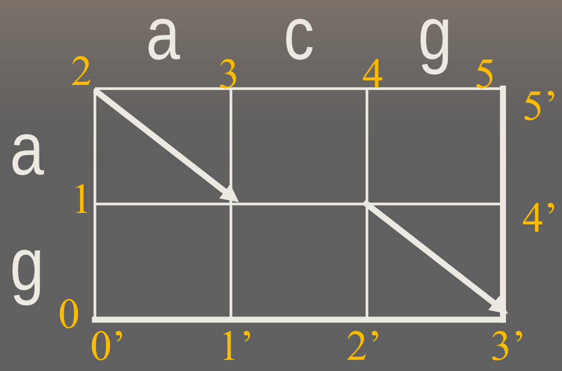


	a	a	c	g	a	c	g	a
c								
t								
a								
c								
g								
a					▨	▨	▨	
g					▨	▨	▨	
a								


a a c g a c g a
c
t
a
c
g
a
g
a


LZ78-Partitioned Alignment Graph
Trie for A
Trie for B
0 1 2 3 4
a a c g a c g a
1 c
2 t
3 a
4 c g
5 a g
a
3/2
3/4
5/2
5/4
a c t g
a c g
left prefix (5/2)
diagonal prefix (3,2)
top prefix (3,4)
Graph G for Block (5,4)

matrice DIST

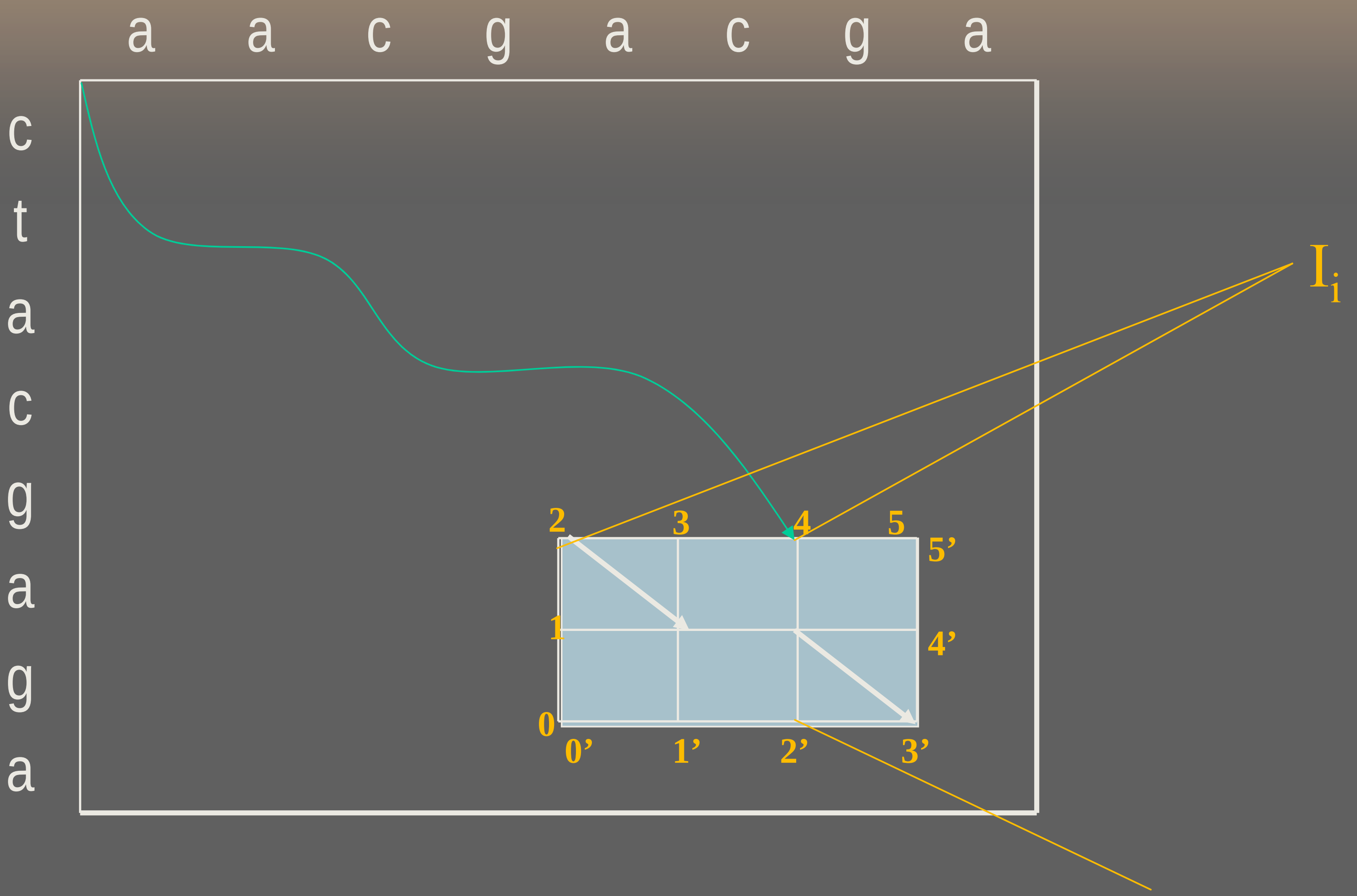


$s(x,y) = 1$ si $x=y$

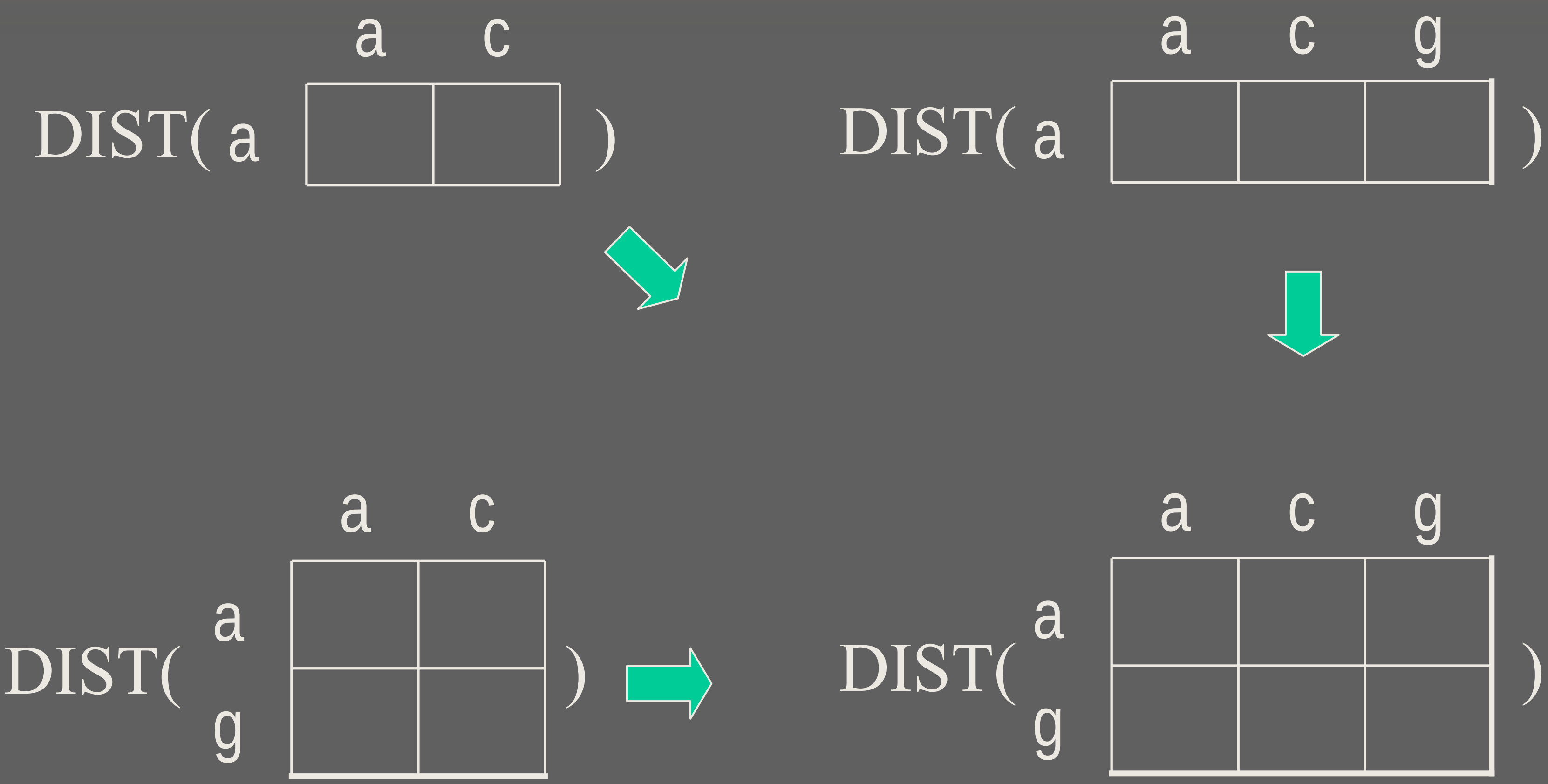
-1 sinon

$s(x,-) = s(-,x) = -1$

	0’	1’	2’	3’	4’	5’
0	0	-1	-2	-3		
1	-1	-1	-2	-1	-3	
2	-2	0	0	1	-1	-3
3		-2	-2	0	-2	-2
4			-2	0	-1	-1
5				-2	-1	0



$$S_j = \max_i \{I_i + DIST_{ij}\}$$



a c

DIST(a)

a c g

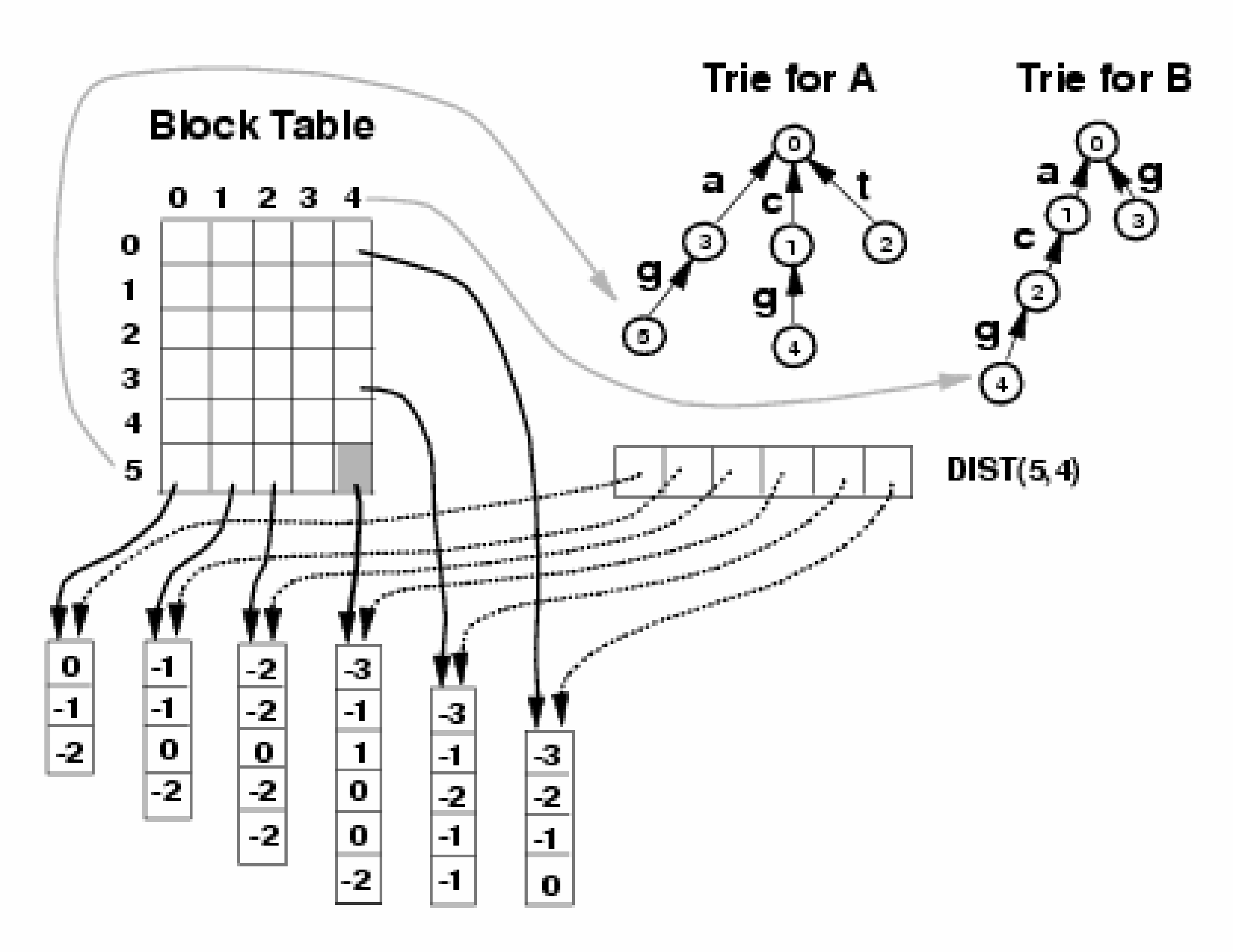
DIST(a)

a c

DIST(a g)

a c g

DIST(a g)


Block Table
Trie for A
Trie for B
DIST(5,4)
0 1 2 3 4
0
1
2
3
4
5
a
c
t
g
g
a
g
c
g
0 -1 -2
-1 -1 0 -2
-2 -2 0 -2 -2
-3 -1 1 0 0 -2
-3 -1 -2 -1 -1
-3 -2 -1 0

Complexité

- Construction des tries : O(n)
- Pour chacune des O(n / logn) lignes :
  - Pour chacun des blocs de la ligne, de demi-périmètre t :
    - Calcul de DIST : O(t)
    - calcul des S_j : O(t)
  - La somme des O(t) est en O(n)

→ **Complexité $O(n^2 / \log n)$**