#### Agenda for today

- Introduction to approximate matching
  - Edit distance
  - Intro to dynamic programming
  - -Substitution matrices and gap penalties
    - \* PAM250 and BLOSUM50
  - Local alignment
  - -BLAST and FASTA

#### Approximate matching

- Allows for mismatches in string comparisons
- Linguistic motivation
  - -Spell check
  - Morpheme sequence homology across languages
- Biological motivation
  - Sequence similarities imply functional similarities
  - Pairs of proteins related by common ancestry
  - -DNA sequence homology across species

#### Approximate matching on string sequences

- Matching two strings corresponds to finding the best alignment between the strings according to some distance metric
- In exact matching, we searched for an alignment where the 'distance' between two strings was zero
- In approximate matching, we will be searching for some minimal distance between two strings

#### Edit distance

- Given two strings, one can ask: how many changes to the first string would it take to yield the second?
- For example, if I typed 'eammpld' but meant 'example'
  - first need to add back the 'x': eammpld  $\rightarrow$  exammpld
  - next need to remove the extra 'm': exampld → exampld
  - next need to switch the 'd' to an 'e': example → example
  - One insertion, one deletion and one substitution: 3 edits
- Many other ways to map 'eammpld' onto 'example,' some more reasonable than others
  - first remove all of the letters in 'eammpld,' then insert all of the letters in 'example'
  - Seven deletions and seven insertions: 14 edits
- Of all possible mappings, which has the LEAST number of edits?

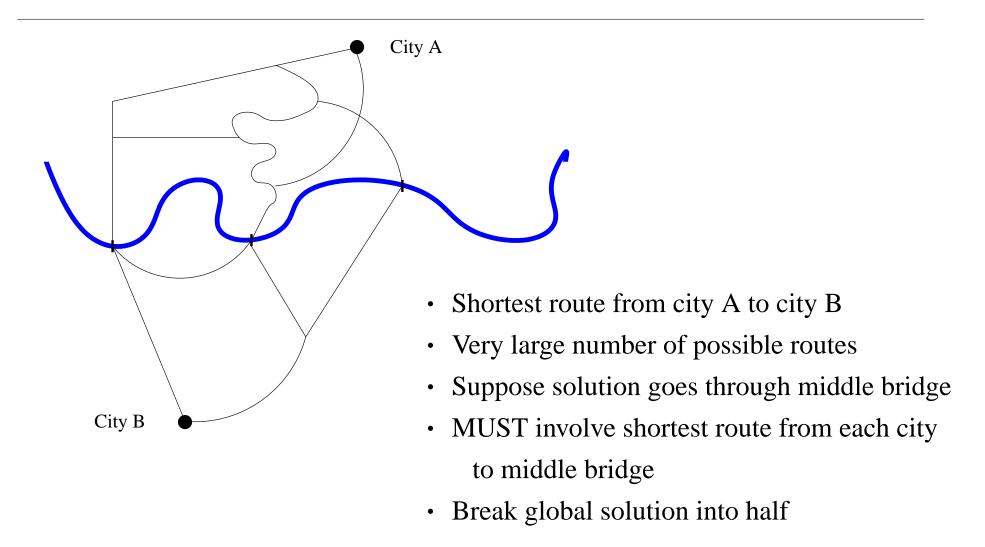
#### Complexity of approximate matching

- In approximate matching, the number of possible mappings between two strings is exponential in the length of the string
  - Due to allowing insertions and deletions
  - Enumerating all possible mappings with exact matching was slow, but not impossible (naive match):  $O(n^2)$
  - With approximate matching, becomes computationally intractable to enumerate all possible mappings:  $O(2^n)$
- To find the minimum edit distance, will need some 'trick' to make the search tractable: dynamic programming

#### Dynamic programming

- General technique to find globally optimal solutions by solving a sequence of sub-problems
- In scenarios where searching from among very large (exponential) set of solutions, can make search tractable
- For example, finding the shortest route between two cities with a fixed number of mid-points (e.g., bridges)
  - -Rather than building every route and comparing
  - Find shortest routes to each midpoint, then find shortest combination

#### Example: shortest distance



#### Edit distance dynamic programming algorithm

- ullet Given two strings  $S_1$  and  $S_2$  of length m and n respectively
- ullet Let F(i,j) be the fewest edits mapping  $S_1[1,i]$  to  $S_2[1,j]$
- ullet Let F(0,j)=j and F(i,0)=i for all i,j
- ullet Let M[x,y] be the cost of mapping from symbol x to symbol y

$$M[x,y] = egin{cases} 0 & ext{if } x = y \ 1 & ext{otherwise} \end{cases}$$

Then

$$F(i,j) = \min \left\{ egin{aligned} F(i,j-1) + 1, \ F(i-1,j) + 1, \ F(i-1,j-1) + M[S_1(i),S_2(j)] \end{aligned} 
ight\}$$

#### Tabular representation: 'perambulate' $\rightarrow$ 'preamble'

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0									
p	1									
e	2									
r	3									
a	4									
m	5									
b	6									
u	7									
1	8									
a	9									
t	10									
e	11									

### Initialize zero positions

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1								
e	2	2								
r	3	3								
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8								
a	9	9								
t	10	10								
e	11	11								

## Fill cell, i = 1, j = 1

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	<b>→</b> •							
e	2	2								
r	3	3								
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(1,$	(0) + 1,
a	9	9					ig  F(1,1)	= min	$\left\{\begin{array}{l} F(0, \cdot) \\ -\frac{1}{2} \end{array}\right.$	$egin{array}{l} (0)+1,\ (1)+1,\ (0)+M[p] \end{array}$
t	10	10							$\int F(0,$	(0) + M[p]
e	11	11								

## Fill cell, i = 2, j = 1

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0							
e	2	2	<b>→</b> •							
r	3	3								
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(2,$	(0) + 1,
a	9	9					$oxed{F(2,1)}$	$= \min$	$\left\{\begin{array}{c} F(1, \cdot) \\ -1 \end{array}\right.$	$egin{align} (0)+1,\ (1)+1,\ (0)+M[\epsilon ] \end{array}$
t	10	10							F(1,	$(0)+M[\epsilon$
e	11	11								

# Fill cell, i = 1, j = 2

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	<b>→</b> •						
e	2	2	1							
r	3	3								
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(1,$	1) + 1,
a	9	9					$oxed{F(1,2)}$	= min	$\left\{\begin{array}{l} F(0, \cdot) \\ - \cdot \end{array}\right.$	$egin{aligned} 1) + 1, \ 2) + 1, \ 1) + M[p] \end{aligned}$
t	10	10							F(0,	(1) + M[p]
e	11	11								

## Fill cell, $i=2,\,j=2$

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1						
e	2	2	1	<b>→</b> •						
r	3	3								
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(2,$	(1) + 1,
a	9	9					F(2,2)	= min	$\left\{\begin{array}{c} F(1, \cdot) \\ -\cdot \end{array}\right.$	$egin{array}{l} (1)+1, \ (2)+1, \ (1)+M[\epsilon ] \end{array}$
t	10	10							F(1,	$,1)+M[\epsilon$
e	11	11								

## Fill cell, i = 3, j = 1

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1						
e	2	2	1	1						
r	3	3	<b>→</b> •							
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(3)$	,0) + 1,
a	9	9					$\int F(3,1)$	$= \min$	$\begin{cases} F(2) \end{cases}$	$egin{aligned} (0,0)+1,\ (1)+1,\ (0)+M[r] \end{aligned}$
t	10	10							F(2)	,0)+M[r]
e	11	11								

# Fill cell, i = 3, j = 2

			p	r	e	a	m	b	1	e
	$\stackrel{i}{\downarrow}_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1						
e	2	2	1	1						
r	3	3	2	<b>→</b> •						
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(3)$	(1) + 1,
a	9	9					F(3,2)	$= \min$	$\begin{cases} F(2, -1) \end{cases}$	$egin{array}{l} (1)+1, \\ (2)+1, \\ (1)+M[r] \end{array}$
t	10	10							F(2)	(1) + M[r]
e	11	11								

## Fill cell, i = 1, j = 3

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	<b>→</b> •					
e	2	2	1	1						
r	3	3	2	1						
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(1,$	2) + 1,
a	9	9					$\int F(1,3)$	= min	$\left\{\begin{array}{l} F(0, \cdot) \\ -\frac{1}{2} \end{array}\right.$	$egin{aligned} 2) + 1, \ 3) + 1, \ 2) + M[p] \end{aligned}$
t	10	10							$\int F(0,$	(2) + M[p]
e	11	11								

## Fill cell, i = 2, j = 3

			p	r	e	a	m	b	1	e
	$\begin{vmatrix} i \\ \downarrow j \end{vmatrix}$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2					
e	2	2	1	1	<b>→</b> •					
r	3	3	2	1						
a	4	4								
m	5	5								
b	6	6								
u	7	7								
1	8	8							$\int F(2,$	(2) + 1,
a	9	9					F(2,3)	= min	$\left\{\begin{array}{l}F(1, \cdot) \\ -\cdot\end{array}\right.$	$egin{array}{l} (2)+1, \ (3)+1, \ (2)+M[\epsilon ] \end{array}$
t	10	10							F(1,	$(2)+M[\epsilon$
e	11	11								

## Fill cell, i = 3, j = 3

			p	r	e	a	m	b	1	e	
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8	
	0	0	1	2	3	4	5	6	7	8	
p	1	1	0	1	2						
e	2	2	1	1	1						
r	3	3	2	1	<b>→</b> •						
a	4	4									
m	5	5									
b	6	6									
u	7	7									-
1	8	8							$\int F(3,$	2) + 1,	
a	9	9					F(3,3)	= mir	$1 \left\{ egin{array}{l} F(2, -1) \ -1 \end{array}  ight.$	(3) + 1,	
t	10	10							ig( F(2,	(2) + M	[r,e]
e	11	11									

## Fill cell, i = 4, j = 4

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3				
e	2	2	1	1	1	2				
r	3	3	2	1	2	2				
a	4	4	3	2	2	<b>→</b> •				
m	5	5								
b	6	6								
u	7	7								
1	8	8								
a	9	9								
t	10	10								
e	11	11								

## Fill cell, i = 5, j = 5

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4			
e	2	2	1	1	1	2	3			
r	3	3	2	1	2	2	3			
a	4	4	3	2	2	2	3			
m	5	5	4	3	3	3	<b>→</b> •			
b	6	6								
u	7	7								
1	8	8								
a	9	9								
t	10	10								
e	11	11								

## Fill cell, i = 6, j = 6

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5		
e	2	2	1	1	1	2	3	4		
r	3	3	2	1	2	2	3	4		
a	4	4	3	2	2	2	3	4		
m	5	5	4	3	3	3	2	3		
b	6	6	5	4	4	4	3	<b>→</b> •		
u	7	7								
1	8	8								
a	9	9								
t	10	10								
e	11	11								

## Fill cell, i = 7, j = 7

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	
e	2	2	1	1	1	2	3	4	5	
r	3	3	2	1	2	2	3	4	5	
a	4	4	3	2	2	2	3	4	5	
m	5	5	4	3	3	3	2	3	4	
b	6	6	5	4	4	4	3	2	3	
u	7	7	6	5	5	5	4	3	<b>→</b> •	
1	8	8								
a	9	9								
t	10	10								
e	11	11								

### Fill cell, i = 8, j = 8

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	<b>→</b> •
a	9	9								
t	10	10								
e	11	11								

## Fill cell, i = 9, j = 8

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	<b>→</b> •
t	10	10								
e	11	11								

### Fill cell, i = 10, j = 8

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	<b>→</b> •
e	11	11								

### Fill cell, i = 11, j = 8

			p	r	e	a	m	b	1	e
	$\left  egin{array}{c} i \\ \downarrow \end{array} \right  j  ightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	$\rightarrow$ :

#### Minimal edit distance: cell i = 11, j = 8

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

#### Find the optimal alignment

- Now we know that the lowest cost of aligning 'perambulate' to 'preamble' is 5
- Just knowing this cost might be useful in some cases
- But in general, we want to know which edits led to the optimal alignment
- Thus, backtrace to find the path(s) corresponding to the score in bottom-right cell  $(i=11,\,j=8)$ 
  - (Why might we have more than one optimal path?)

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\left  egin{array}{c} i \ j \end{array}  ight.  ight.$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\left  egin{array}{c} i \ j \end{array}  ight.  ight.$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\left  egin{array}{c} i \ j \end{array}  ight.  ight.$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0	0	1	2	3	4	5	6	7	8
p	1	1	0	1	2	3	4	5	6	7
e	2	2	1	1	1	2	3	4	5	6
r	3	3	2	1	2	2	3	4	5	6
a	4	4	3	2	2	2	3	4	5	6
m	5	5	4	3	3	3	2	3	4	5
b	6	6	5	4	4	4	3	2	3	4
u	7	7	6	5	5	5	4	3	3	4
1	8	8	7	6	6	6	5	4	3	4
a	9	9	8	7	7	6	6	5	4	4
t	10	10	9	8	8	7	7	6	5	5
e	11	11	10	9	8	8	8	7	6	5

#### **Backtrace**

- ullet Can find the path(s) corresponding to final score in O(n+m)
- ullet While filling in the matrix, keep a backpointer B(i,j) for each cell such that

$$B(i,j) = \operatorname{argmin} \left\{ egin{aligned} F(i,j-1) + 1, \ F(i-1,j) + 1, \ F(i-1,j-1) + M[S_1(i),S_2(j)] \end{aligned} 
ight\}$$

- On a match/substitution, B(i,j) will point to cell  $(i\!-\!1,j\!-\!1)$
- On an insertion, B(i,j) will point to cell (i,j-1)
- On a deletion, B(i,j) will point to cell (i-1,j)
- On a tie, B(i,j) may point to multiple cells

# Saving backpointers, initialize table

			p	r	e	a	m	b	1	e
	$\stackrel{i}{\downarrow}_{j} \rightarrow$	0	1	2	3	4	5	6	7	8
	0	_	<b>←</b>	<b>←</b>	$\leftarrow$	<b>←</b>	<b>←</b>	<b>←</b>	<b>←</b>	$\leftarrow$
p	1	<b>↑</b>								
e	2	<b>↑</b>								
r	3	1								
a	4	1								
m	5	1								
b	6	1								
u	7	1								
1	8	1								
a	9	1								
t	10	1								
e	11	1								

# Saving backpointers, i = 1, j = 1

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0		<b>←</b>							
p	1	<b>↑</b>								
e	2	<b>↑</b>								
r	3	<b>↑</b>								
a	4	<b>↑</b>								
m	5	<b>↑</b>								
b	6	<b>↑</b>								
u	7	<b>↑</b>								
1	8	<b>↑</b>								
a	9	<b>↑</b>								
t	10	<b>↑</b>								
e	11	<b>↑</b>								

# Saving backpointers, i = 2, j = 2

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0		<del></del>	<b>←</b>	<del></del>	<del></del>	<del></del>	<del></del>	<del></del>	<b>←</b>
p	1	1		<b>←</b>						
e	2	1	1							
r	3	<b>↑</b>								
a	4	<b>↑</b>								
m	5	<b>↑</b>								
b	6	<b>↑</b>								
u	7	<b>↑</b>								
1	8	<b>↑</b>								
a	9	<b>↑</b>								
t	10	<b>↑</b>								
e	11	1								

# Saving backpointers, i = 3, j = 3

			p	r	e	a	m	b	1	e
	$\begin{vmatrix} i \\ \downarrow j \end{vmatrix}$	0	1	2	3	4	5	6	7	8
	0	_	<b>←</b>	$\leftarrow$	$\leftarrow$	<b>←</b>	<b>←</b>	<b>←</b>	<b>←</b>	<b></b>
p	1	<b>↑</b>		$\leftarrow$	$\leftarrow$					
e	2	<b>↑</b>	<b>↑</b>		_					
r	3	1	<b>↑</b>		<u></u>					
a	4	1								
m	5	1								
b	6	1								
u	7	1								
1	8	1								
a	9	1								
t	10	1								
e	11	1								

# Saving backpointers, i = 11, j = 8

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0		<del></del>	<del></del>	<del></del>	<del></del>	<del></del>	<del></del>	<del></del>	<b>←</b>
p	1	1		<del></del>	<del></del>	<del></del>	<del></del>	<del></del>	<del></del>	<b>←</b>
e	2	<b>↑</b>	1		_	<del></del>	<del></del>	<del></del>	<del></del>	<b>←</b>
r	3	<b>↑</b>	1		<u></u>	_	<u> </u>	<u> </u>	<u> </u>	<u> </u>
a	4	<b>↑</b>	1	1		_	<u> </u>	<u> </u>	<u> </u>	<u> </u>
m	5	<b>↑</b>	1	1	$\uparrow \uparrow$	$\uparrow \uparrow$	_	<del></del>	<del></del>	<b>←</b>
b	6	<b>↑</b>	1	1	$\uparrow \uparrow$	$\uparrow \uparrow$	1		<del></del>	<b>←</b>
u	7	<b>↑</b>	1	1	$\uparrow \uparrow$	$\uparrow \uparrow$	1	<b>↑</b>		<u> </u>
1	8	<b>↑</b>	1	1	$\uparrow \uparrow$	$\uparrow \uparrow$	1	<b>↑</b>		
a	9	<b>↑</b>	1	1	$\uparrow \uparrow$	_	1	<b>↑</b>	1	
t	10	<b>↑</b>	1	1	$\uparrow \uparrow$	1	$\uparrow \uparrow$	<b>↑</b>	1	$\uparrow \uparrow$
e	11	1	1	1		1	$\uparrow \uparrow$	<b>↑</b>	1	

# Backpointers along optimal path(s)

			p	r	e	a	m	b	1	e
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7	8
	0									
p	1			<b>←</b>						
e	2		1							
r	3				<u></u>					
a	4									
m	5						_			
b	6									
u	7							1		
1	8									
a	9								1	
t	10								1	
e	11									

### Paths correspond to alignments

• Three different alignments result in edit distance of 5:

b r  $\mathbf{a}$  $\mathbf{m}$  $\mathbf{p}$  $\mathbf{e}$  $\mathbf{e}$ 1. 1 b  $\mathbf{t}$  $\mathbf{m}$  $\mathbf{e}$ r  $\mathbf{a}$ u  $\mathbf{a}$  $\mathbf{e}$ p

 p
 r
 e
 a
 m
 b
 l
 e
 e

 p
 e
 r
 a
 m
 b
 u
 l
 a
 t
 e

b  $\mathbf{m}$ r  $\mathbf{a}$  $\mathbf{p}$  $\mathbf{e}$ 3. b  $\mathbf{t}$  $\mathbf{m}$ u a  $\mathbf{p}$  $\mathbf{e}$  $\mathbf{a}$  $\mathbf{e}$ 

- Can choose to slightly skew costs to avoid such ambiguities
  - e.g., score substitutions at cost 0.99

2.

#### Substitution models

- For natural language sequences, typically looking for full approximate matches (e.g., spell checking)
- For protein and DNA/RNA sequences, more often looking to match subsequences (e.g., for similarity across species)
- Need some way to find "likely" related subsequences, i.e., approximate matches that probably didn't arise by chance
  - Build "random" model, whereby two sequences are modeled independently
  - Build joint model, whereby two sequences are modeled together
  - Compare likelihoods via log likelihood or log odds ratio
- This is a principled way to capture the fact that particular symbols tend to substitute for each other
  - i.e., are evolutionarily related

#### Substitution likelihood

- ullet Let q(a) be the probability of observing symbol a
- ullet Let p(ab) be the probability that symbols a and b are substituted
- Then, for a given ungapped alignment between  $S_1$  and  $S_2$ , the *odds ratio* between the joint and random models is

$$\text{odds}(S_1, S_2) \, = \, \frac{\prod_i p(S_1(i)S_2(i))}{\prod_i q(S_1(i)) \prod_i q(S_2(i))} \, = \, \, \prod_i \frac{p(S_1(i)S_2(i))}{q(S_1(i))q(S_2(i))}$$

• Taking the log, we get

where 
$$L[a,b] = \sum_i L[S_1(i),S_2(i)]$$

- ullet L[a,b] will be positive for symbols with high probability of substitution
- Note that we now switch from min to max for dynamic programming

### PAM250 substitution matrix

P S T R N E G H L K M F W Y A Q I R E Η K M W Y 

#### Blosum50 substitution matrix

T R N E H K M S W Y Α G -2 -1 0 -1 0 -3 Α 3 -2 -2 -3 R -1 -4 0 -3 0 -4 -2 -3 -3 -3 -3 N -2 0 0 -3 -4 -2 -4 -2 -4 -3 0 ()-2 -4 -5 -5 -3 0 -4 -4 -1 D -1 -1 -4 -1 0 -4 -2 -4 13 -3 -3 -3 -3 -2 -2 -3 -2 -2 -5 -3 -4 -1 -3 -1 ()0 7 -2 1 -3 ()-4 -1 ()-1 -3 0 E -3 -3 -3 -2 -3 0 6 0 -4 -3 -1 -3 G  $\mathbf{0}$ -3 -3 -2 -3 8 -4 -2 -3 -2 0 -2 -3 -3 0 -4 -4 -3 -2 10 -3 -2 -2 -3 Η 0 0 -4 0 -1 -1 -4 -3 2 -3 -1 -3 -4 -3 -4 -4 5 ()-3 -3 -4 -2 5 -3 3 -2 -3 -2 -3 -3 -3 -2 -1 -4 -4 -4 -4 2 -3 3 -3 0 -3 -2 -3 K -1 -2 -3 0 6 -4 -1 0 -1 -2 3 -2 -2 0 -2 -3 2 -2 -3 -2 M -4 -1 -3 -3 -5 -2 -3 0 -4 -3 F -4 -4 -4 -1 0 -4 -3 -2 -1 -4 -1 -2 -3 -1 -3 10 -1 -1 -3 -4 -4 -4 -1 -1 -3 -3 -2 -3 -1 5 -2 0 -1 0 0 -4 -2 -3 -2 -2 -1 0 -1 -1 -1 W -3 -5 -3 -3 -3 -2 -3 -3 -5 -3 15 -3 -4 -1 -4 -4 -3 -2 -2 -2 Y -2 -3 -1 -3 -1 -1 0-3 -1 -3 -4 -4 -3 -2 0 -3

### Gap penalties

- Not just substitution to consider also insertion and deletion
- ullet These are penalized as "gaps" of a certain length  $oldsymbol{g}$
- Linear gap penalties give the same cost d to every single symbol gap
  - Thus, the penalty for a gap of length g is  $\gamma(g)=-gd$
- Also, commonly, an "affine" gap penalty is used
  - A penalty for starting a gap d
  - Another penalty for continuing an already started gap e
  - Thus, the penalty for a gap of length g is  $\gamma(g)=-d-(g-1)e$
- For affine gap penalties, need to keep track of whether gap is started or not
  - slightly different dynamic programming (stay tuned ...)

### Protein sequence alignment

- Will use example from Durbin et al., section 2.3
  - Strings  $S_1$  = 'HEAGAWGHEE' and  $S_2$  = 'PAWHEAE'
  - Use BLOSUM50 substitution matrix
  - Linear gap penalty with d=8
- ullet Let F(0,j)=-jd and F(i,0)=-id for all i,j
- Alignment scores are calculated

$$F(i,j) = \max \left\{ egin{aligned} F(i,j-1) - d, \ F(i-1,j) - d, \ F(i-1,j-1) + M[S_1(i),S_2(j)] \end{aligned} 
ight\}$$

# Initialize zero positions

			P	A	W	Н	Е	A	Е
	$\left  egin{array}{c} i \\ \downarrow \end{array} \right  j  ightarrow$	0	1	2	3	4	5	6	7
	0	0	-8	-16	-24	-32	-40	-48	-56
Н	1	-8							
Е	2	-16							
A	3	-24							
G	4	-32							
A	5	-40							
W	6	-48							
G	7	-56							
Н	8	-64							
Е	9	-72							
Е	10	-80							

# Fill cell, i = 1, j = 1

			P	A	W	Н	Е	A	Е		
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7		
	0	0	-8	-16	-24	-32	-40	-48	-56		
Н	1	-8	<b>→</b> •								
Е	2	-16									
A	3	-24									
G	4	-32									
A	5	-40									
W	6	-48									
G	7	-56									,
Н	8	-64					- ID(1 1)		$\int F(1,$	0) - 8,	
Е	9	-72					$egin{bmatrix} F(1,1) \ \end{bmatrix}$	) = ma	$X \left\{ \begin{array}{c} F'(0, \\ F(0) \end{array} \right.$	$egin{aligned} 0) &- 8, \ 1) &- 8, \ 0) &+ M[H, F] \end{aligned}$	<b>)</b> ]
Е	10	-80						P] = -		<i>O)</i>   171 [11, 1	1 <b>)</b>

# Fill cell, i = 2, j = 2

			P	A	W	Н	Е	A	Е		
	$\begin{vmatrix} i \\ \downarrow j \end{vmatrix}$	0	1	2	3	4	5	6	7		
	0	0	-8	-16	-24	-32	-40	-48	-56		
Н	1	-8	-2	-10							
Е	2	-16	-9	<b>→</b> •							
A	3	-24									
G	4	-32									
A	5	-40									
W	6	-48									
G	7	-56									
Н	8	-64					T(0, 0)		$\int F(2,$	$egin{aligned} 1) - 8, \ 2) - 8, \ 1) + M[E, A] \end{aligned}$	
Е	9	-72					$egin{bmatrix} oldsymbol{F}(2,2) \ \end{array}$	) = ma	$X \left\{ \begin{array}{c} F'(1, \\ F(1) \end{array} \right.$	2) $-8$ , 1) $+ M[E]$	<b>4</b> 1
Е	10	-80						A] = -		±)   1v1 [±2, 2	<b>-</b> j

# (skip to interesting bits) Fill cell, i = 5, j = 2

			P	A	W	Н	Е	A	Е	
	$\downarrow^i_{j} \rightarrow$	0	1	2	3	4	5	6	7	
	0	0	-8	-16	-24	-32	-40	-48	-56	
Н	1	-8	-2	-10						
Е	2	-16	-9	-3						
A	3	-24	-17	-4						
G	4	-32	-25	-12						
A	5	-40	-33	<b>→</b> •						
W	6	-48								
G	7	-56								,
Н	8	-64							$\int F(5,1)$ -	- 8,
Е	9	-72					$egin{bmatrix} F(5,2) \ \end{bmatrix}$	) = ma	$\mathbf{x} \left\{egin{array}{l} F(5,1) - \ F(4,2) - \ F(4,1) - \ \end{array} ight.$	$\begin{bmatrix} -8, \\ M \begin{bmatrix} A & A \end{bmatrix} \end{bmatrix}$
Е	10	-80						A] = 5	( * (+, 1)	[m,n]

# Fill cell, i = 6, j = 3

			P	A	W	Н	Е	A	Е	
	$\stackrel{i}{\downarrow}_{j} \rightarrow$	0	1	2	3	4	5	6	7	
	0	0	-8	-16	-24	-32	-40	-48	-56	
Н	1	-8	-2	-10	-18					
Е	2	-16	-9	-3	-11					
A	3	-24	-17	-4	-6					
G	4	-32	-25	-12	-7					
A	5	-40	-33	-20	-15					
W	6	-48	-41	-28	<b>→</b> •					
G	7	-56								,
Н	8	-64					T(0, 2)		$\int F(6)$	(2,2) - 8,
Е	9	-72					$\mathbf{F}(\mathbf{b}, 3)$	) = ma	$X \left\{ \begin{array}{c} F'(5) \\ F(5) \end{array} \right.$	$\left. egin{aligned} (2,2) - 8, \ (3) - 8, \ (2) + M[W,W] \end{aligned}  ight.  ight.$
Е	10	-80					igg  M[W,	W] = 3	( * ( <sup>9</sup> 15	,-, , -, -, -, , , , , , , , , , , ,

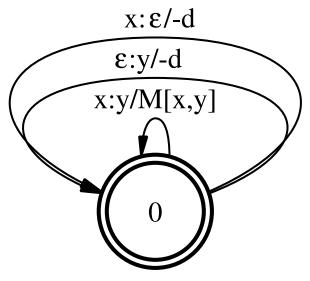
# Fill cell, i = 9, j = 5

			P	A	W	Н	Е	A	Е
	$\left  egin{array}{c} i \ j \end{array}  ight.  ight.$	0	1	2	3	4	5	6	7
	0	0	-8	-16	-24	-32	-40	-48	-56
Н	1	-8	-2	-10	-18	-14	-22		
Е	2	-16	-9	-3	-11	-18	-8		
A	3	-24	-17	-4	-6	-13	-16		
G	4	-32	-25	-12	-7	-8	-16		
A	5	-40	-33	-20	-15	-9	-9		
W	6	-48	-41	-28	-5	-13	-12		
G	7	-56	-49	-36	-13	-7	-15		
Н	8	-64	-57	-44	-21	-3	-7		
Е	9	-72	-65	-52	-29	-11	<b>→</b> •		
Е	10	-80							

# Best path (one among many)

			P	A	W	Н	Е	A	Е
	$\left  egin{array}{c} i \ j \end{array}  ight.  ight.$	0	1	2	3	4	5	6	7
	0	0	-8	-16	-24	-32	-40	-48	-56
Н	1	-8	-2	-10	-18	-14	-22	-30	-38
Е	2	-16	-9	-3	-11	-18	-8	-16	-24
A	3	-24	-17	-4	-6	-13	-16	-3	-11
G	4	-32	-25	-12	-7	-8	-16	-11	-6
A	5	-40	-33	-20	-15	-9	-9	-11	-12
W	6	-48	-41	-28	-5	-13	-12	-12	-14
G	7	-56	-49	-36	-13	-7	-15	-12	-15
Н	8	-64	-57	-44	-21	-3	-7	-15	-12
Е	9	-72	-65	-52	-29	-11	3	-5	-9
Е	10	-80	-73	-60	-37	-19	-5	2	1

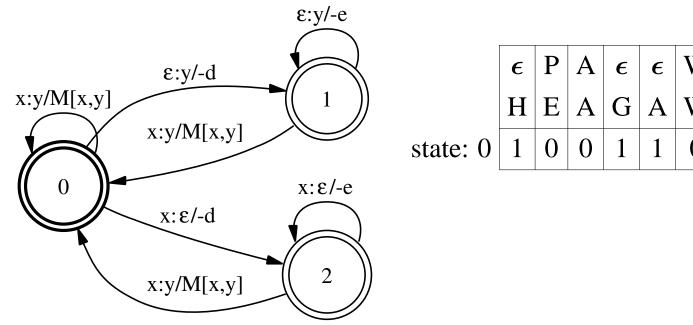
### Finite-state transducer: linear gaps



	$\epsilon$	P	A	$\epsilon$	$\epsilon$	W	$\epsilon$	Н	E	A	E
	Н	E	A	G	A	W	G	Н	E	$\epsilon$	E
state: 0	0	0	0	0	0	0	0	0	0	0	0

- Only one state required; add scores together
- $\epsilon$  represents a gap of length 1
- $\bullet$  gaps receive -d cost for each symbol in gap
- ullet Mapping input symbol x to output symbol y gets substitution matrix score for that pair

### Finite-state transducer: affine gaps



 $\epsilon \mid H \mid E$ W E A $A \mid W \mid G \mid H \mid E$ E 0 0 2 0

- Three states required; add scores together
- Initial gap on input goes to state 1; initial gap on output to state 2
- $\bullet$  gaps receive -d cost to start; plus -e for each additional symbol in gap
- Mapping input symbol x to output symbol y gets substitution matrix score for that pair

## Larger chart required for dynamic programming

						P			A			W			Н			Е			A		
	$\downarrow^i_{j} \rightarrow$		0			1			2			3			4			5			6		
	state:	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0
	0	0	•	•	•	-8	•	•	-12	•	•	-16	•	•	-20	•	•	-24	•	•	-28	•	•
Н	1	•	•	-8	>	$\rightarrow$	$\downarrow$																
Е	2	•	•	-12																			
A	3	•	•	-16																			
G	4	•	•	-20																			
A	5	•	•	-24																			
W	6	•	•	-28																			
G	7	•	•	-32																			
Н	8	•	•	-36																			
Е	9	•	•	-40																			
Е	10	•	•	-44																			

## State 1 only from states 0,1; State 2 from 0,2

						P			A			W			Н			Е			A		
	$\downarrow^i_{j} \rightarrow$		0			1			2			3			4			5			6		
	state:	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0
	0	0	•	•	•	-8	•	•	-12	•	•	-16	•	•	-20	•	•	-24	•	•	-28	•	
Н	1	•	•	-8	-2	•	•	>	$\rightarrow$	$\downarrow$													
E	2	•	•	-12																			
A	3	•	•	-16																			
G	4	•	•	-20																			
A	5	•	•	-24																			
W	6	•	•	-28																			
G	7	•	•	-32																			
Н	8	•	•	-36																			
Е	9	•	•	-40																			
Е	10	•	•	-44																			

## State 1 costs -d from state 0; only -e from state 1

						P			A			W			Н			Е			A		
	$\downarrow^i_{j} \rightarrow$		0			1			2			3			4			5			6		
	state:	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	(
	0	0	•	•	•	-8	•	•	-12	•	•	-16	•	•	-20	•	•	-24	•	•	-28	•	
Н	1	•	•	-8	-2	•	•	-10	-10	•	\ <u></u>	$\rightarrow$	$\downarrow$										
Е	2	•	•	-12																			
A	3	•	•	-16																			
G	4	•	•	-20																			
A	5	•	•	-24																			
W	6	•	•	-28																			
G	7	•	•	-32																			
Н	8	•	•	-36						_					_								
Е	9	•	•	-40																			
Е	10	•	•	-44																			

## State 1 only from states 0,1; State 2 from 0,2

						P			A			W			Н			Е			A		
	$\downarrow^i_{j} \rightarrow$		0			1			2			3			4			5			6		
	state:	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	(
	0	0	•	•	•	-8	•	•	-12	•	•	-16	•	•	-20	•	•	-24	•	•	-28	•	
Н	1	•	•	-8	-2	•	•	-10	-10	•	-15	-14	•										
E	2	•	•	-12	>	$\rightarrow$	<b>1</b>																
A	3	•	•	-16																			
G	4	•	•	-20																			
A	5	•	•	-24																			
W	6	•	•	-28																			
G	7	•	•	-32																			
Н	8	•	•	-36										_		-		_					
Е	9	•	•	-40																			
Е	10	•	•	-44																			

## State 2 costs -d from state 0; only -e from state 2

						P			A			W			Н			Е			A		
	$\begin{vmatrix} i \\ \downarrow j \end{vmatrix}$		0			1			2			3			4			5			6		
	state:	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	
	0	0	•	•	•	-8	•	•	-12	•	•	-16	•	•	-20	•	•	-24	•	•	-28	•	
Н	1	•	•	-8	-2	•	•	-10	-10	•	-15	-14	•										
Е	2	•	•	-12	-9	•	-10																
A	3	•	•	-16	>	$\rightarrow$	<b>1</b>																
G	4	•	•	-20																			
A	5	•	•	-24																			
W	6	•	•	-28																			
G	7	•	•	-32																			
Н	8	•	•	-36																			
Е	9	•	•	-40																			
Е	10	•	•	-44																			

## And so on – same dynamic programming

						P			A			W			Н			Е			A	
	$\downarrow^i_{j} \rightarrow$		0			1			2			3			4			5			6	
	state:	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2	0	1	2
	0	0	•	•	•	-8	•	•	-12	•	•	-16	•	•	-20	•	•	-24	•	•	-28	•
Н	1	•	•	-8	-2	•	•	-10	-10	•	-15	-14	•									
Е	2	•	•	-12	-9	•	-10															
A	3	•	•	-16	-13	•	-14															
G	4	•	•	-20																		
A	5	•	•	-24																		
W	6	•	•	-28																		
G	7	•	•	-32																		
Н	8	•	•	-36																		
Е	9	•	•	-40																		
Е	10	•	•	-44																		

### Finite-state transducers for alignment

- Can move to arbitrarily complex finite-state transducer models
  - Durbin et al. mention 4 state model, with two match states corresponding to low and high fidelity regions
- Must keep track of scores at each state in dynamic programming
- Next lecture we will look at Hidden Markov Models
  - States represent hidden variables
  - Stochastic model conditioned on hidden state
  - Still finite-state

### Local alignment

- Simple idea: allow resetting alignment at any point
- Get high quality local alignments, rather than global alignments
- Same algorithm, except now:

$$F(i,j) = \max egin{cases} 0, \ F(i,j-1) - d, \ F(i-1,j) - d, \ F(i-1,j-1) + M[S_1(i),S_2(j)] \end{pmatrix}$$

- Similar modification for multi-state models
- Note: assumes scores less than zero
  - PAM250 won't work unmodified

# Initialize zero positions (Global)

			P	A	W	Н	Е	A	Е
	$\begin{vmatrix} i \\ \downarrow j \end{vmatrix}$	0	1	2	3	4	5	6	7
	0	0	-8	-16	-24	-32	-40	-48	-56
Н	1	-8							
Е	2	-16							
A	3	-24							
G	4	-32							
A	5	-40							
W	6	-48							
G	7	-56							
Н	8	-64							
Е	9	-72							
Е	10	-80							

# Initialize zero positions (Local)

			P	A	W	Н	Е	A	Е
	$\downarrow^i_j \rightarrow$	0	1	2	3	4	5	6	7
	0	0	0	0	0	0	0	0	0
Н	1	0							
Е	2	0							
A	3	0							
G	4	0							
A	5	0							
W	6	0							
G	7	0							
Н	8	0							
Е	9	0							
Е	10	0							

# P no matches; H 1 match

			P	A	W	Н	Е	A	Е
	$\left  egin{array}{c} i \\ \downarrow \end{array} \right  j \longrightarrow$	0	1	2	3	4	5	6	7
	0	0	0	0	0	0	0	0	0
Н	1	0	0	0	0	10	0	0	0
Е	2	0	0						
A	3	0	0						
G	4	0	0						
A	5	0	0						
W	6	0	0						
G	7	0	0						
Н	8	0	0						
Е	9	0	0						
Е	10	0	0						

### 4 non-zero cells in next row

			P	A	W	Н	Е	A	Е
	$\left  egin{array}{c} i \\ \downarrow \end{array} \right  j  ightarrow$	0	1	2	3	4	5	6	7
	0	0	0	0	0	0	0	0	0
Н	1	0	0	0	0	10	0	0	0
Е	2	0	0	0	0	2	16	8	6
A	3	0	0						
G	4	0	0						
A	5	0	0						
W	6	0	0						
G	7	0	0						
Н	8	0	0						
Е	9	0	0						
Е	10	0	0						

# ${\bf Great\ local\ match-not\ in\ global\ solutions}$

			P	A	W	Н	Е	A	Е
	$\left  egin{array}{c} i \\ \downarrow \end{array} \right  j  ightarrow$	0	1	2	3	4	5	6	7
	0	0	0	0	0	0	0	0	0
Н	1	0	0	0	0	10	0	0	0
Е	2	0	0	0	0	2	16	8	6
A	3	0	0	5	0	0	8	21	13
G	4	0	0						
A	5	0	0						
W	6	0	0						
G	7	0	0						
Н	8	0	0						
Е	9	0	0						
Е	10	0	0						

#### **BLAST** and **FASTA**

- Pronounced 'that was pretty fast, eh?'
- Widely used heuristic local match algorithms
- Begin with exact (or near exact) match seeds
  - "Diagonals" on our chart
- Grow larger matches out from these seeds
- Heuristic because they may miss some matches
- Great speedups through use of very fast exact match algorithms
- Very highly tuned to domains, but roughly speaking are instances of "exclusion" methods

### Alignment: what's left to cover

- Better space usage: current approach O(nm) in space
- Faster approximate matching
  - Bounded number of differences
  - Exclusion methods
- Better models
  - Hidden Markov Models
- Multiple sequences to jointly align
- (In other words, today was the tip of the iceberg)