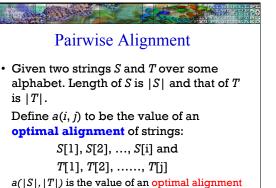
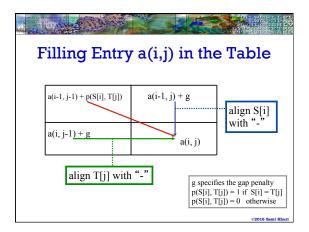
of S and T.



## Filling in the DP Table

- DP uses a table of size  $(|S|+1) \times (|T|+1)$ .
- a(i, j) corresponds to the optimal alignment of the  $i^{th}$  prefix of S with the  $j^{th}$  prefix of T.
- The dynamic programming algorithm fills in the entries of the table (matrix) by computing the values of a(i, j) from top to bottom, left to right.
- The value of the optimal alignment is given by a(|S|, |T|).

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## DP: Bookkeeping and Retracing

- Draw lines crossing the entries in the matrix to show from which entry in the matrix we derived the maximum score for each entry a(i, j).
- To determine the solution of the optimal alignment, simply retrace the steps from entry a(|S|, |T|) to entry a(0, 0).

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```
DP for Pairwise Alignment
      Algorithm Similarity
            input: sequences s and t
            output: similarity between s and t
            m \leftarrow |s|
            n \leftarrow |t|
                                                   Algorithm for filling in the
            for i \leftarrow 0 to m do
                                                  DP table row by row, from
            a[i, 0] \leftarrow i \times g
for j \leftarrow 0 to n do
                                                  top to bottom, left to right.
                                                  g specifies the gap penalty.
                   a[0,j] \leftarrow j \times g
            for i \leftarrow 1 to m do
                   for j \leftarrow 1 to n do
                         a[i, j] \leftarrow \max(a[i-1, j] + g,
a[i-1, j-1] + p(i, j),
                                             a[i, j-1]+g)
             \textbf{return} \ a[m,n] \\ \hspace{0.5cm} \textbf{Introduction to Computational Molecular Biology by Setubal et al.}
```

```
Pairwise Alignment: Traceback

Algorithm Align

input: alignment in align \cdot s_i align t_i and length in len

if i = 0 and j = 0 then

len \leftarrow 0

else if i > 0 and a[i, j] = a[i - 1, j] + g then

Align(i - 1, j, len)

len \leftarrow len + 1

align \cdot s[len] \leftarrow s[i]

Introduction to Computational Molecular Biology by Setubal et al.
```