Introduction to Algorithms and Data Structures

Lecture 20: "Seam Carving" and Edit distance (via Dynamic Programming)

Mary Cryan

School of Informatics University of Edinburgh

Seam Carving

We need to fit images into new dimensions (relevant for tablet/mobile layouts).

Naïve approaches to adapting to varying dimensions include cropping and scaling. Both have their flaws - see video by Shai Avidan and Ariel Shamir: https://www.youtube.com/watch?v=6NcIJXTlugc&feature=emb_logo

A better, more flexible, approach is to search for seams in the image, a seam being a connected sequence of pixels running from top-to-bottom *(vertical)* or from left-to-right *(horizontal)*.

More general than deleting a column.

- Seams can be deleted (or duplicated) and the rows and columns of the altered image will have uniform lengths 1 less (or more) than before.
- For re-sizing images, we will want to find seams of low-energy (where there is little difference between the seam pixels and their surrounding pixels).

Seam Carving

We are given an image $I : [m] \times [n]$ where each pixel is a colour (maybe RGB). Our dimensions are $m \times n$ but we want to fit to different dimensions $m' \times n'$.

Definition

In a image I of dimensions $m \times n$, we define a vertical seam to be any sequence

$$\mathbf{s} = j_1, \ldots, j_m \in [n]$$

such that for every $i \in [m] \setminus \{1\}$, we have $|j_i - j_{i-1}| \le 1$ and $2 \le j_i \le n-1$ (don't touch left/right sides). A horizontal seam is any sequence

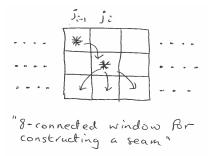
$$\mathbf{s} = i_1, \ldots, i_n \in [m]$$

such that for every $j \in [n] \setminus \{1\}$, we have $|i_j - i_{j-1}| \le 1$ and $2 \le i_j \le m-1$.

(recall [k] is the set of values $\{1, \ldots, k\}$)

Seams and Energy

In building a (vertical) seam we are allowed to move (straight) down, 1-pixel left, or 1-pixel right.



We need to evaluate the energy of a pixel, as we prefer low-energy seams.

We assume some energy function $e = e_{I}$ applied to pixels of that image. Then

$$e(\mathbf{s}) =_{def} \begin{cases} \sum_{\substack{i=1 \ j=1}^{m}}^{m} e_{\mathbf{I}}(i, j_i) & \mathbf{s} \text{ is a vertical seam} \\ \sum_{j=1}^{n} e_{\mathbf{I}}(i_j, j) & \mathbf{s} \text{ is a horizontal seam} \end{cases}$$

Energy functions

Many options for (pixel) energy function, often a (local) gradient score.

• L_1 gradient scoring (for pixel (i, j)) can be written as

$$\mathbf{e}_{\mathbf{I}}(i,j) =_{def} \left| \frac{\partial}{\partial x} \mathbf{I} \right|_{i,j} + \left| \frac{\partial}{\partial y} \mathbf{I} \right|_{i,j}$$

• $\frac{\partial}{\partial x}, \frac{\partial}{\partial y}$ are defined in the image processing context:

For example the Sobel operators can be used to calculate $\frac{\partial}{\partial x}$ and $\frac{\partial}{\partial y}$:

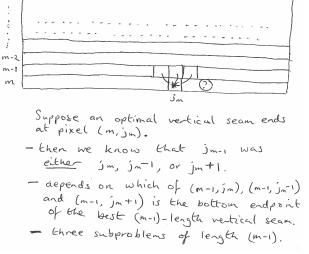
$$\begin{bmatrix} -1 & 0 & +1 \\ -2 & 0 & +2 \\ -1 & 0 & +1 \end{bmatrix} \qquad \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ +1 & +2 & +1 \end{bmatrix}$$

► The first (vertical) would calculate $\frac{\partial}{\partial x}|_{i,j}$ as $(I_{i-1,j+1} - I_{i-1,j-1}) + 2(I_{i,j+1} - I_{i,j-1}) + (I_{i+1,j+1} - I_{i+1,j-1}).$

A colour image will have 3 color channels, so 3 $\frac{\partial}{\partial x}$ and 3 $\frac{\partial}{\partial y}$ scores to sum.

Computing an optimal seam

We assume we are looking for a vertical seam (without loss of generality). Take a recursive view and understand the optimal seam in terms of (slightly) shorter seam



Recurrence for optimal (vertical) seam

Assume that we have precomputed $e_{\mathbf{I}}(i,j)$ for every pixel $1 \le i \le m$, every $1 \le j \le n$ ($\Theta(1)$ time for each (i,j)).

($e_{I}(i, j)$ slightly different for top/bottom rows)

Definition

For every $i, j, 1 \le i \le m, 1 \le j \le n$, we define $opt_{\mathbf{I}}(i, j)$ to be the cost of the minimum-cost vertical seam from (somewhere in) row 1 to pixel (i, j), where cost is scored as at the end of slide 4.

We have the following recurrence:

$$opt_{\mathbf{I}}(i,j) = e_{\mathbf{I}}(i,j) + \begin{cases} 0 & \text{if } i = 1\\ \min\{opt_{\mathbf{I}}(i-1,j-1), & \\ opt_{\mathbf{I}}(i-1,j), & \text{if } i > 1\\ opt_{\mathbf{I}}(i-1,j+1) \end{cases}$$

(we will set $e_{\mathbf{I}}(i,j) \leftarrow \infty$ if j = 1 or n)

We will need a table/array of size $m \cdot n$, let the table be opt. (I assume indexing starts at 1 for this algorithm)

- Entry opt[i, j] will store the value of $opt_{I}(i, j)$ (when we have computed it).
- We will need to have the local e_I(i, j) energy values pre-computed (for each 1 ≤ i ≤ m, 1 ≤ j ≤ n) and stored in a table e (of dimensions m × n). We will set e[i, 1] ← ∞, e[i, n] ← ∞ for all i ∈ [m] to make sure the seam avoids the sides.
- For image processing applications we definitely need to know the pixel sequence for the *actual* seam of optimal score.

Define another table/array p of dimensions $m \times n$ to hold -1, 0, 1 values (indicating whether j_i was $j_{i-1} - 1, j_{i-1}, j_{i-1} + 1$ for the good seam).

Algorithm Vertical-Seam(I, m, n)

1. for $i \leftarrow 1$ to n2. for $i \leftarrow 1$ to m 3. $e[i, j] \leftarrow$ "compute $e_{\mathbf{I}}(i, j)$ " $/\Theta(1)$ time 4. $opt[1, j] \leftarrow e[1, j], p[1, j] \leftarrow 0$ //Base case 5. for $i \leftarrow 1$ to m 6. for $i \leftarrow 1$ to n 7. $opt[i, j] \leftarrow opt[i-1, j], p[i, j] \leftarrow 0$ //default case 8. **if** opt[i-1, j-1] < opt[i, j] then 9. $opt[i, i] \leftarrow opt[i-1, i-1]$. $p[i, i] \leftarrow -1$ 10. **if** opt[i-1, i+1] < opt[i, j] then 11. $opt[i, j] \leftarrow opt[i-1, j+1], p[i, j] \leftarrow +1$ 12. $opt[i, j] \leftarrow opt[i, j] + e[i, j]$ //Always add e[i, j]13. $i^* \leftarrow 2$ 14. for $i \leftarrow 1$ to n 15. **if** $opt[m, j] < opt[m, j^*]$ **then** $j^* \leftarrow j$ 16. Print("Best vertical seam ends at cell (m, j^*) ").

Wrapping up

- After the algorithm has terminated, we find the optimal vertical seam by searching row *m* for the minimum opt[*m*, *j*] value (one final loop).
- ▶ The double-loop between lines 5-12 does the main work, computing the *opt* values using the recurrence. There are $m \cdot n$ iterations of lines 7-12, and we can check that for a specific (i, j), lines 7-12 take O(1) time. So the algorithm has worst-case running-time O(mn).

(ok, should also say lines 1-4 take O(mn) and lines 13-16 take O(n))

- The values in the p array make it very easy to reconstruct the actual sequence of pixels forming the seam (even easier than edit distance, etc).
- ► We specify how to compute e[i, j] as the specific energy function can vary (see Avidan-Shamir paper). These are functions of local (to (i, j)) pixels and hence will always be computable in O(1)-time (per (i, j) entry).

As discussed in the video, the seam will either be deleted (if we are aiming to reduce the width) or alternatively duplicated (if aiming to increase width). There is a similar algorithm for Horizontal-Seam.

Edit distance

Our setting is strings over some input alphabet. We want to measure the edit distance between two given strings s, t over that alphabet.

We have three operations on strings - insertion, deletion, and substitution.

Examples:

- DNA or RNA strings over their 4-character alphabet: for example, "AATCCGCTAG" versus "AAACCCTTAG".
- ▶ Words from a natural language for example, "kitten" versus "sitting".

kittensitt**i**ng

(3 operations: 2 "substitutions" and 1 "insertion")

Sequence Alignment

We often talk about possible alignments of two (or more) sequences. For example, here are two competing alignments for a given pair of DNA sequences:

А	С	С	G	G	Т	Α	Т	С	С	Т	А	G	G	А	С
А	С	С	Т	Α	Т	С	Т	-	-	Т	А	G	G	А	С
А	С	С	G	G	Т	А	Т	С	С	т	А	G	G	А	С
			_												

An alignment of two sequences $s \in \Sigma^m$, $t \in \Sigma^n$ is any padding (with some – insertions) s' of s, and t' of t such that

$$|s'| = |t'|$$

 $(s'_i \neq -) \lor (t'_i \neq -) \quad ext{for all } 1 \leq i \leq |s'|$

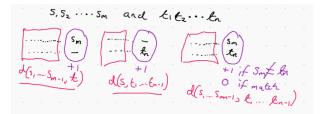
The score of an alignment is the total number of insertions $(s'_i \in \Sigma \text{ with } t'_i = -)$, deletions $(s'_i = - \text{ with } t'_i \in \Sigma)$ and substitutions $(s'_i \neq t'_i, s'_i \in \Sigma, t'_i \in \Sigma)$.

Edit distance

The edit distance d(s, t) between two strings $s, t \in \Sigma^*$ is the minimum number of operations possible for an alignment of those strings.

We start with strings over the alphabet Σ . How to align these? We don't know.

But we do know there are only 3 ways the final column can be arranged!



And the "best possible" for each of these 3 possibilities is another "edit distance" problem for an input that is slightly smaller.

Edit distance

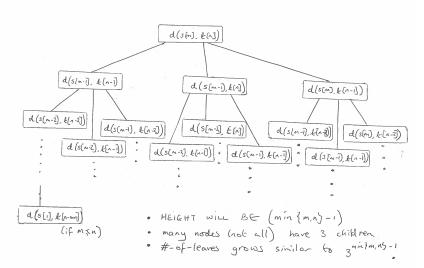
We get a natural recurrence for the edit distance for $s = s[1 \dots m], t = t[1 \dots n]$:

$$d(s[1...m], t[1...n]) = \begin{cases} m & \text{if } n = 0 \\ n & \text{if } m = 0 \\ d(s[1...m-1], t[1...n-1]) & \text{if } s_m = t_n \\ 1 + \min\{d(s[1...m-1], t[1...n-1]) \\ d(s[1...m-1], t[1...n]) & \text{if } s_m \neq t_n \\ d(s[1...m], t[1...n-1])\} \end{cases}$$

Justification?

Whatever the best alignment is, its right column must *either* be a substitution, *or* a deletion, *or* an insertion.

A recursive implementation?



Recursion tree is exponential in size ... however there are at most $m \cdot n$ sub-problems that can arise! So we are in a situation where DP can be exploited IADS - Lecture 20 - slide 15

We will need a table/array of size $(m+1) \cdot (n+1)$, let the table be d.

- Entry d[i, j] is intended to store the value of d(s[1...i]), t[1...j]) (when we have computed it).
- ► We need to fill the table in a careful order need to be sure that d[i-1,j-1], d[i-1,j] and d[i,j-1] have already been computed before we exploit the recurrence to compute d[i,j].

We will also keep a table/array called *a* which will store values 0, 1, 2, 3 to mark whether the optimum for s[1...i], t[1...j] ended in a match (0), a substitution (1), an insertion (2) or a deletion (3).

The a table will help us reconstruct the actual (best) alignment that achieves the edit distance.

(the 0/1/2/3 are just quaternary "flags" and their values are not significant)

Algorithm Edit-Distance(s[1...m], t[1...n])

1. for $i \leftarrow 0$ to m 2 $d[i,0] \leftarrow i, a[i,0] \leftarrow 3$ 3. for $i \leftarrow 0$ to n 4. $d[0, j] \leftarrow j, a[0, j] \leftarrow 2$ 5. for $i \leftarrow 1$ to m do 6. for $i \leftarrow 1$ to n do if $s_i = t_i$ then 7. $d[i, j] \leftarrow d[i-1, j-1]$ 8. $a[i, i] \leftarrow 0$ 9. 10. else $d[i, j] \leftarrow 1 + \min\{d[i, j-1], d[i-1, j], d[i-1, i-1]\}$ 11. if d[i, j] = d[i-1, j-1] + 1 then $a[i, j] \leftarrow 1$ 12. else if d[i, j] = d[i, j-1] + 1 then $a[i, j] \leftarrow 2$ 13. else $a[i, j] \leftarrow 3$ 14. IADS – Lecture 20 – slide 17

Reconstructing the best alignment

We use the information in the a table to fill two arrays b, c.

- b will hold the padded version of s (the s'), in reverse
- c will hold the padded version of t (the t'), in reverse
- ▶ we will build b, c by "working-back" through the table a (having started at a[m, n] (i ← m, j ← n).
- At each step, we will check whether a[i, j] is either
 - 0/1 In this case we insert character s_i into b, and character t_j into c, then decrement both i and j
 - 2 In this case we insert character '-' into b, and character t_j into c, then decrement j (but not i)
 - 3 In this case we insert character s_i into b, and character '-' into c, then decrement i (but not j)
- At some point either i or j will hit 0, then we need to "finish off" b and c with a "run of insertions" or a "run of deletions".
- This results with the exact alignment stored in b and c, in reverse order. We then can print out in reverse.

Running time

It is not too hard to show that the running time for Edit-Distance is the same as the space of its primary tables, ie, $\Theta(mn)$.

Reading Materials

Seam Carving:

- "Seam-Carving for Content-Aware Image Resizing" (clickable). I have used slightly different notation.
- There are many Seam-Carving implementations in Python available on the Internet, worth Googling them and taking a look. They are usually using numpy for file i/o and other functionality, plus some image processing resource too.

Edit Distance: None of our texts cover edit distance in exactly the way we have done - however, each of them has a section on sequence alignment:

[KT] Chapter 6.6 [CLRS] 14.4 [Roughgarden] 17.1