Stitching and Blending

Kari Pulli Senior Director NVIDIA Research



First project



Build your own (basic) programs

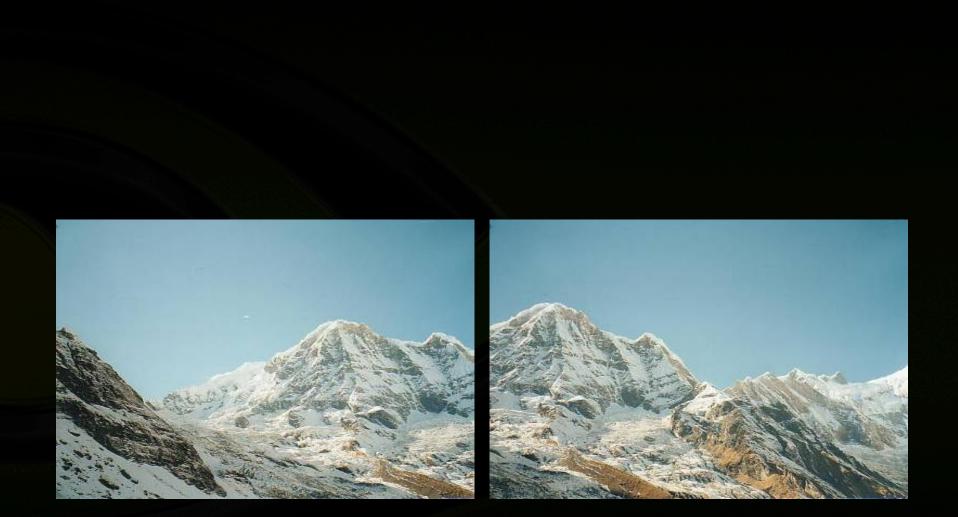
- panorama
- HDR (really, exposure fusion)

The key components

- register images so their features align
- determine overlap
- blend

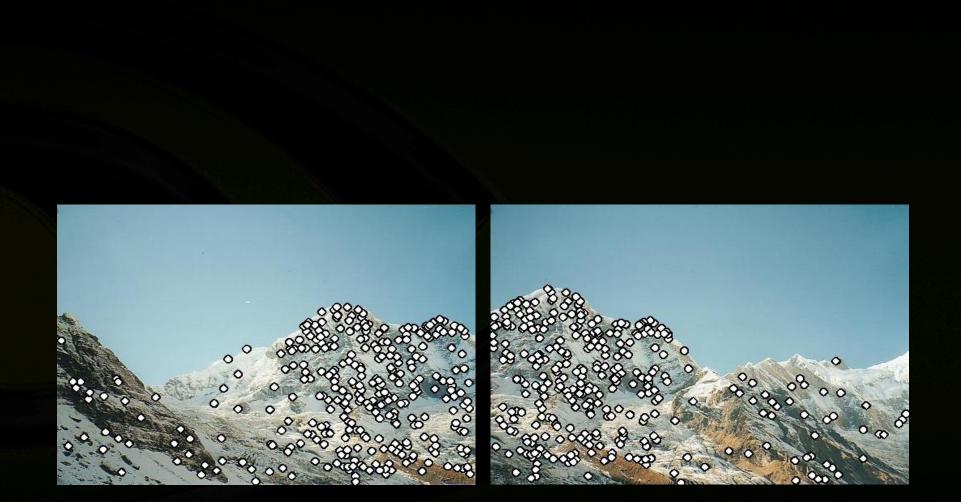
We need to match (align) images





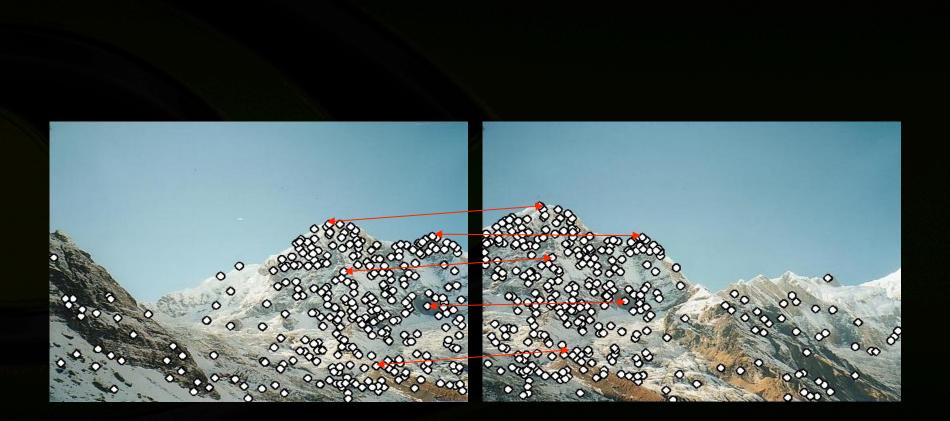
Detect feature points in both images





Find corresponding pairs





Use these pairs to align images





Matching with Features



Problem 1:

Detect the same point independently in both images





no chance to match!

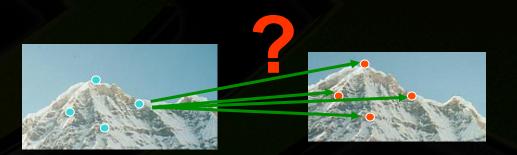
We need a repeatable detector

Matching with Features



Problem 2:

For each point correctly recognize the corresponding one

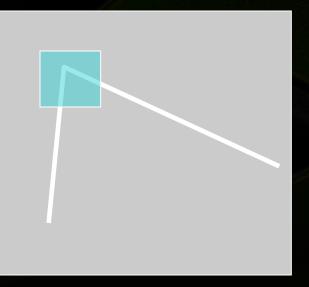


We need a reliable and distinctive descriptor

Harris Corners: The Basic Idea

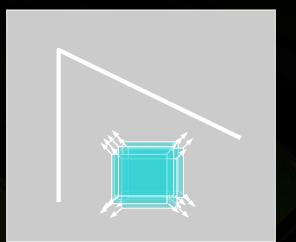


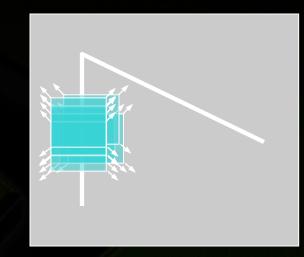
- We should easily recognize the point by looking through a small window
- Shifting a window in any direction should give a large change in intensity

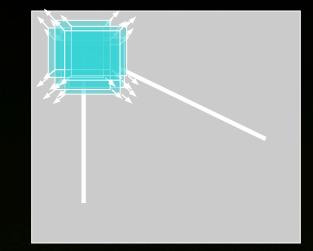


Harris Detector: Basic Idea









"flat" region: no change in all directions

edge":

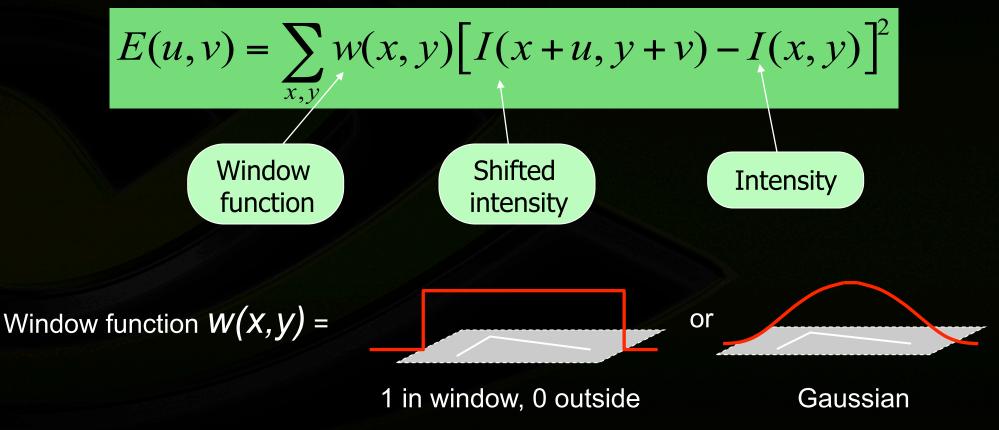
no change along the edge direction

"corner":

significant change in all directions



Window-averaged change of intensity for the shift [*u*,*v*]:





Expanding E(u,v) in a 2nd order Taylor series expansion, we have, for small shifts [u,v], a *bilinear* approximation:

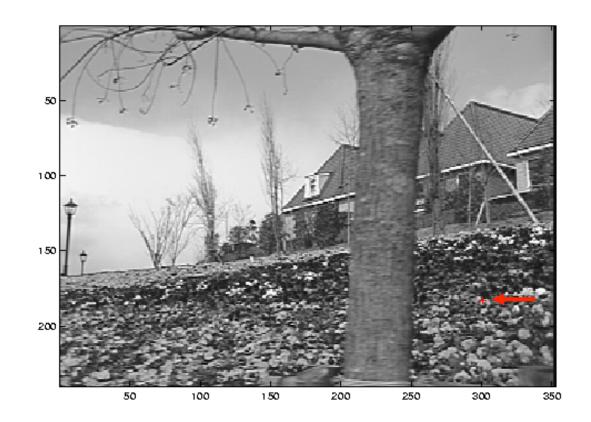
$$E(u,v) \cong \begin{bmatrix} u,v \end{bmatrix} M \begin{bmatrix} u\\v \end{bmatrix}$$

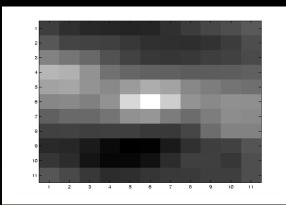
where M is a 2×2 matrix computed from image derivatives:

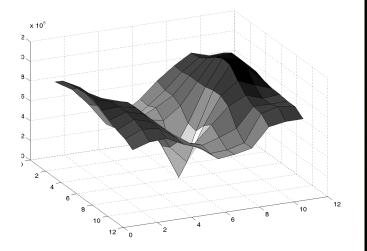
$$M = \sum_{x,y} w(x,y) \begin{bmatrix} I_x^2 & I_x I_y \\ I_x I_y & I_y^2 \end{bmatrix}$$

Eigenvalues λ_1, λ_2 of M at different locations







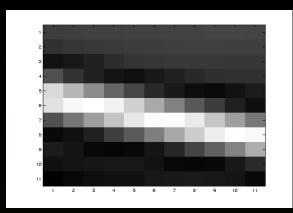


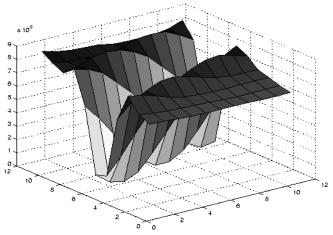
 λ_1 and λ_2 are large

Eigenvalues λ_1 , λ_2 of M at different locations





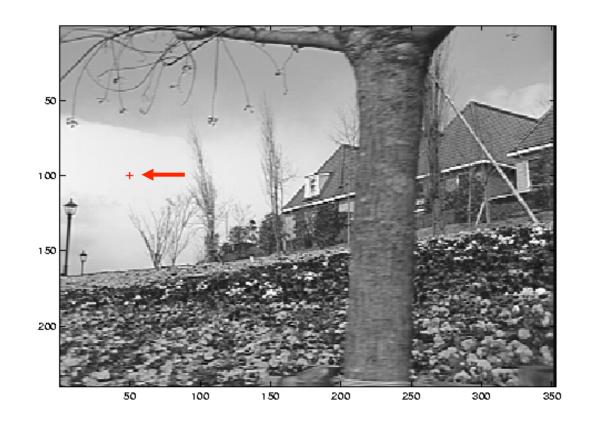


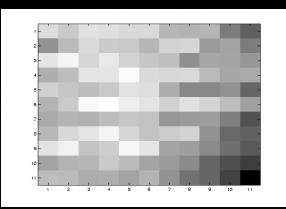


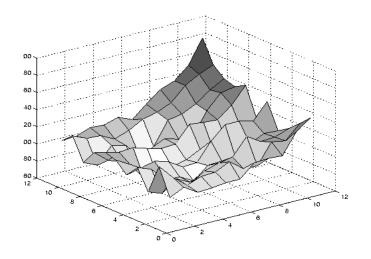
large λ_1 , small λ_2

Eigenvalues λ_1 , λ_2 of M at different locations





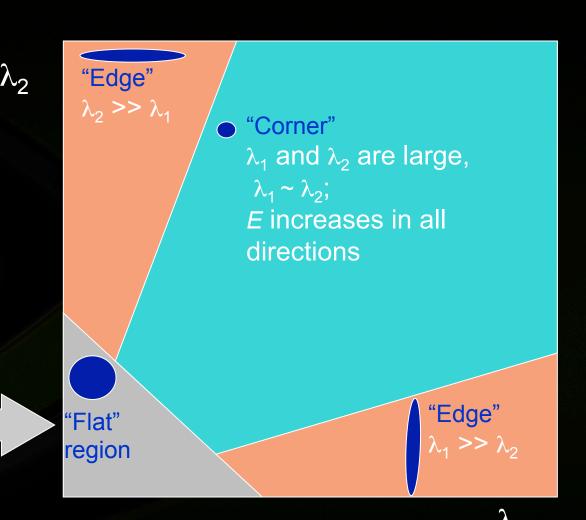




small λ_1 , small λ_2



Classification of image points using eigenvalues of *M*:



 λ_1 and λ_2 are small; *E* is almost constant in all directions

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Measure of corner response:

$$M = \sum_{x,y} w(x,y) \begin{bmatrix} I_x^2 & I_x I_y \\ I_x I_y & I_y^2 \end{bmatrix}$$

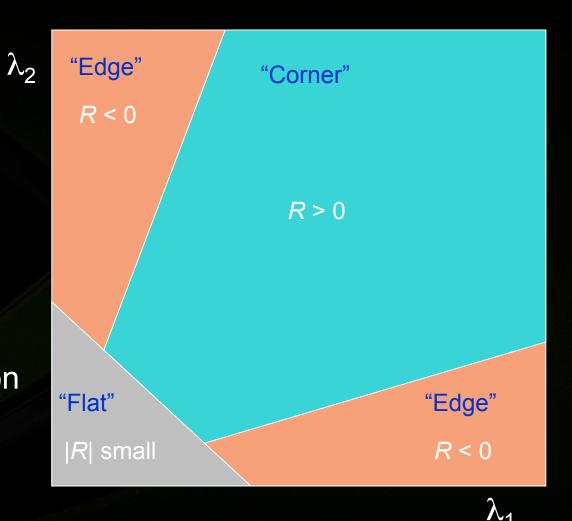
$$R = \det M - k (\operatorname{trace} M)^2$$

$$\det M = \lambda_1 \lambda_2$$

trace $M = \lambda_1 + \lambda_2$

(k - empirical constant, k = 0.04 - 0.06)

- *R* depends only on eigenvalues of M
- *R* is large for a corner
- *R* is negative with large magnitude for an edge
- |R| is small for a flat region





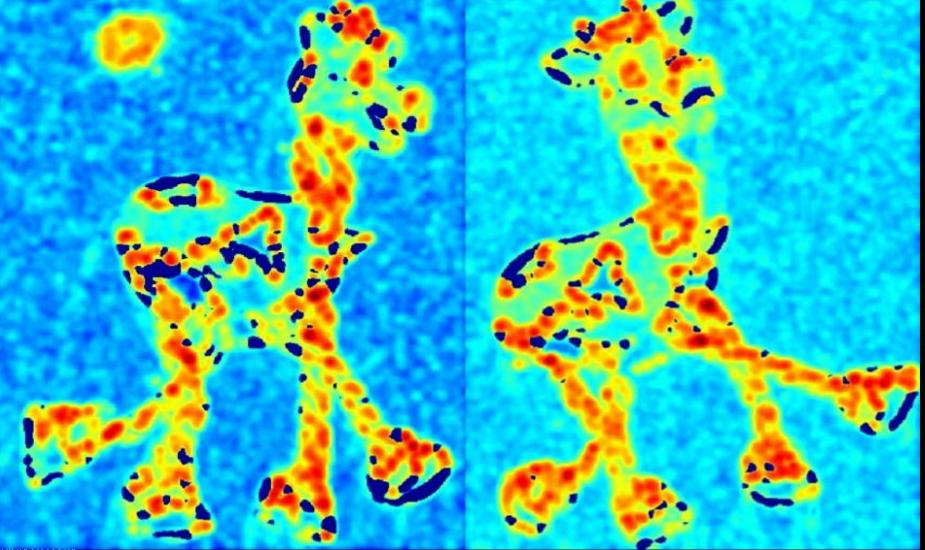




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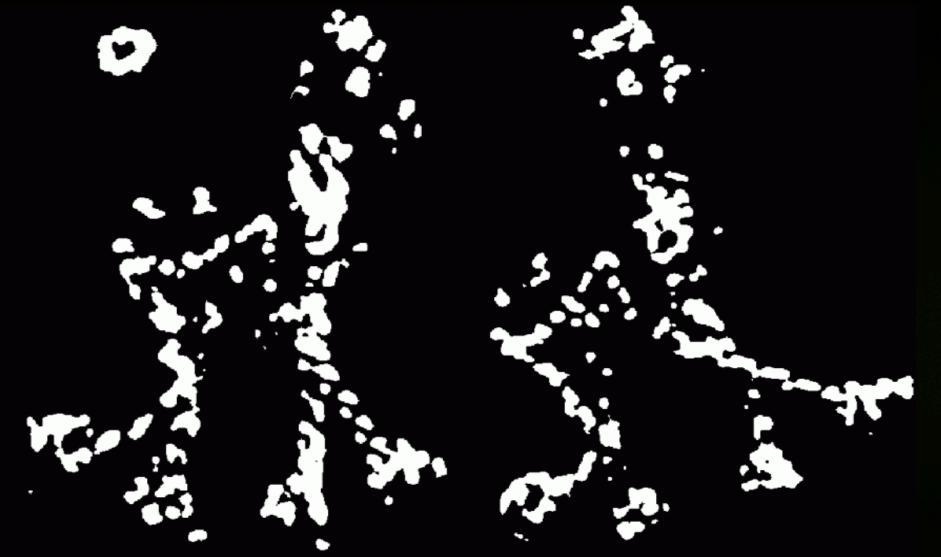
Harris Detector: Workflow Compute corner response R

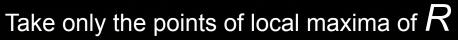






Find points with large corner response: R > threshold











Harris Detector: Summary



Average intensity change in direction [*u*,*v*] can be expressed as a bilinear form:

$$E(u,v) \cong \begin{bmatrix} u, v \end{bmatrix} M \begin{bmatrix} u \\ v \end{bmatrix}$$

Describe a point in terms of eigenvalues of *M*: *measure of corner response*

$$R = \lambda_1 \lambda_2 - k \left(\lambda_1 + \lambda_2\right)^2$$

A good (corner) point should have a *large intensity change* in *all directions*, i.e., *R* should be large positive

Harris Detector: Invariant to rotation





Ellipse rotates but its shape (i.e., eigenvalues) remains the same

Corner response R is invariant to image rotation

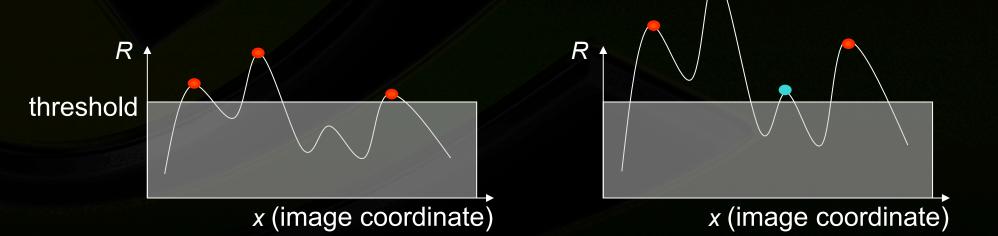
Almost invariant to intensity change



Partial invariance

✓ Only derivatives are used => invariance to intensity shift $I \rightarrow I + b$

✓ Intensity scale: $I \rightarrow a I$



Not invariant to image scale!



All points will be classified as edges

Corner !

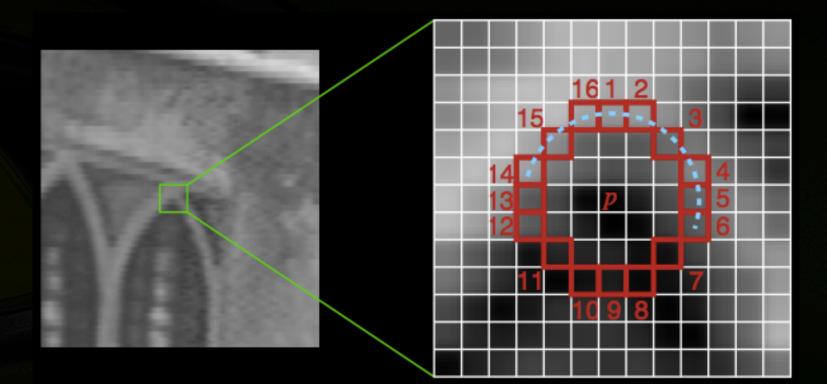
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FAST Corners



Look for a contiguous arc of N pixels

all much darker (or brighter) than the central pixel p



How FAST?

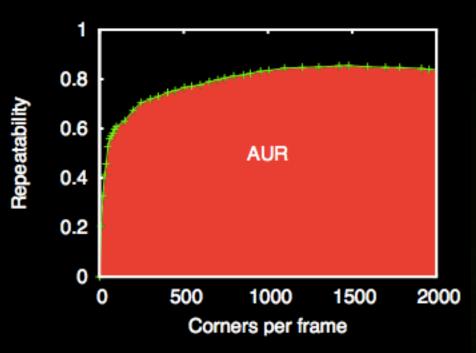


Detector	Set 1		Set 2	
	Pixel rate (MPix/s)	%	MPix/s	%
FAST $n = 9$	188	4.90	179	5.15
FAST $n = 12$	158	5.88	154	5.98
Original FAST ($n = 12$)	79.0	11.7	82.2	11.2
FAST-ER	75.4	12.2	67.5	13.7
SUSAN	12.3	74.7	13.6	67.9
Harris	8.05	115	7.90	117
Shi-Tomasi	6.50	142	6.50	142
DoG	4.72	195	5.10	179

How repeatable?



AUR		
1313.6		
1304.57		
1275.59		
1219.08		
1195.2		
1153.13		
1121.53		
1116.79		
271.73		

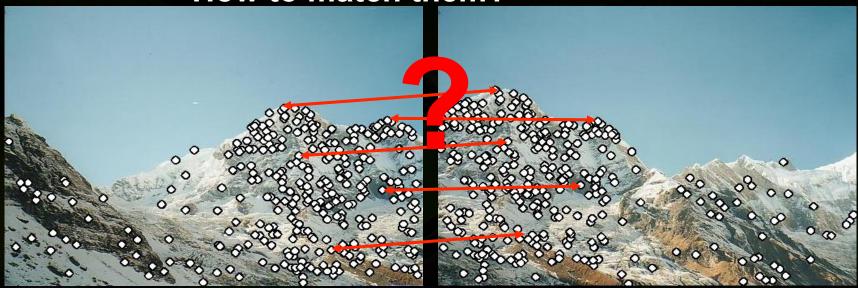


Point Descriptors



- We know how to detect points
- Next question:

How to match them?



Point descriptor should be:

- 1. Invariant
- 2. Distinctive

SIFT – Scale Invariant Feature Transform

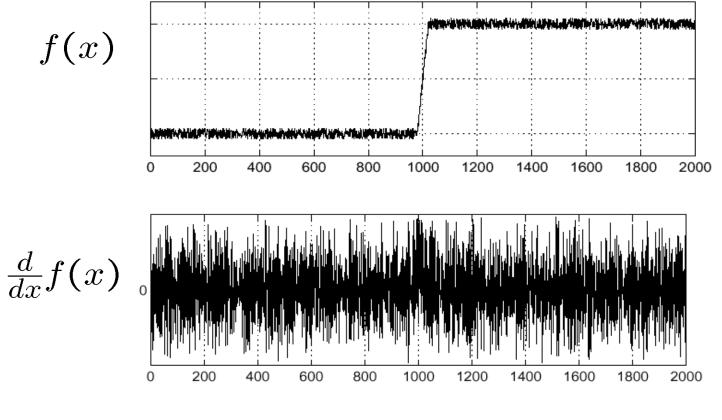


Figure 12: The training images for two objects are shown on the left. These can be recognized in a cluttered image with extensive occlusion, shown in the middle. The results of recognition are shown on the right. A parallelogram is drawn around each recognized object showing the boundaries of the original training image under the affi ne transformation solved for during recognition. Smaller squares indicate the keypoints that were used for recognition.

Effects of Noise

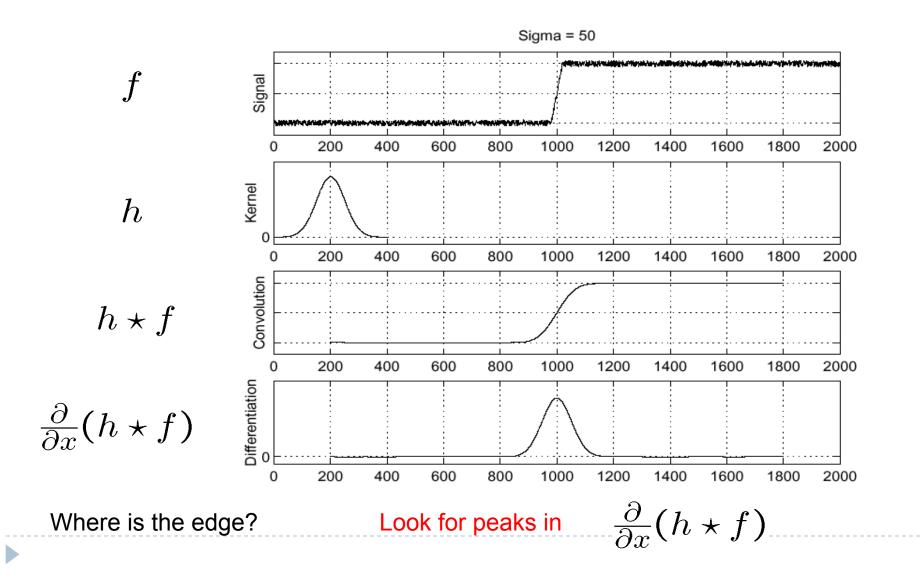
Consider a single row or column of the image

Plotting intensity as a function of position gives a signal



Where is the edge?

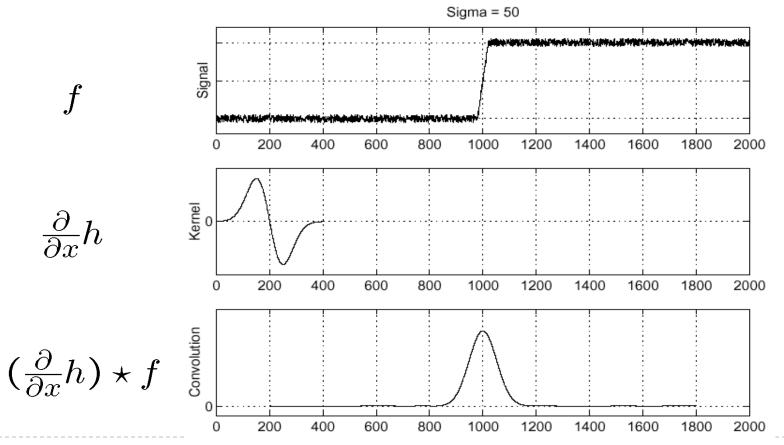
D



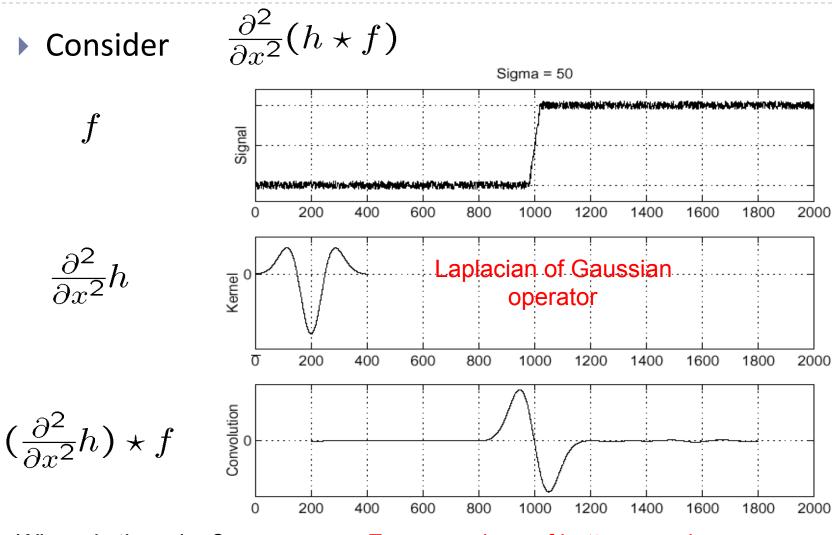
Associative Property of Convolution

$$\frac{\partial}{\partial x}(h \star f) = (\frac{\partial}{\partial x}h) \star f$$

This saves us one operation:



Laplacian of Gaussian



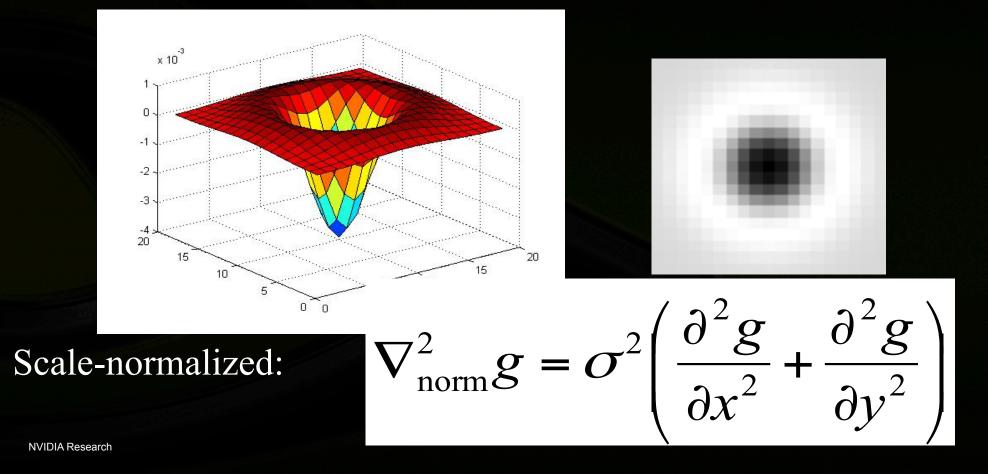
Where is the edge?

Zero-crossings of bottom graph

Blob detection in 2D



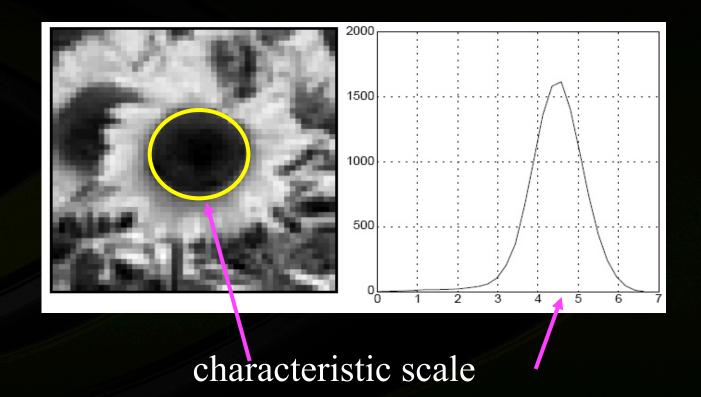
Laplacian of Gaussian: Circularly symmetric operator for blob detection in 2D



Characteristic scale



We define the characteristic scale as the scale that produces peak of Laplacian response

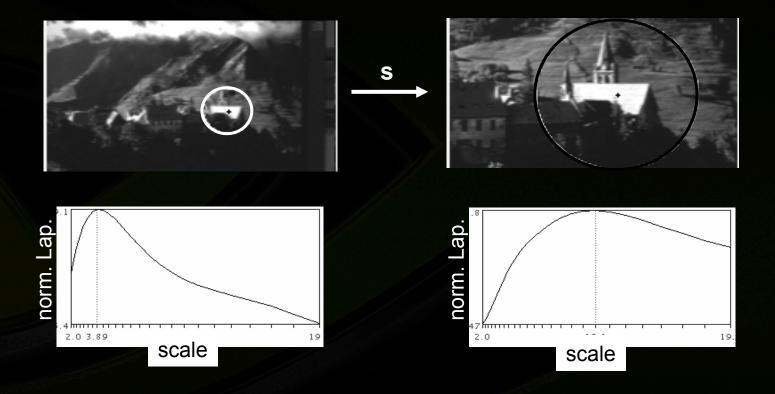


T. Lindeberg (1998). Feature detection with automatic scale selection. *International Journal of Computer Vision* **30** (2): pp 77--116.

Scale selection



Scale invariance of the characteristic scale



Difference of Gaussians (DoG)



Laplacian of Gaussian can be approximated by the difference between two different Gaussians

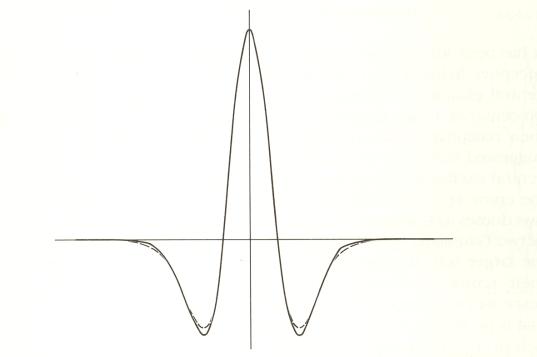
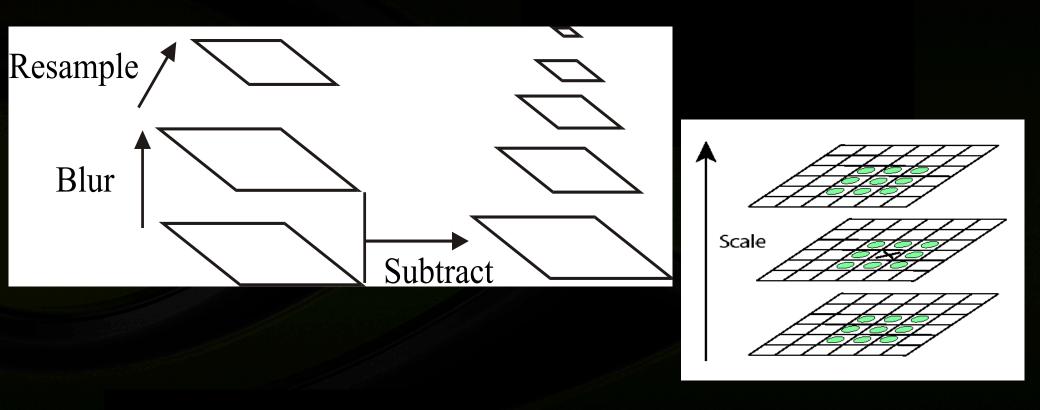


Figure 2–16. The best engineering approximation to $\nabla^2 G$ (shown by the continuous line), obtained by using the difference of two Gaussians (DOG), occurs when the ratio of the inhibitory to excitatory space constraints is about 1:1.6. The DOG is shown here dotted. The two profiles are very similar. (Reprinted by permission from D. Marr and E. Hildreth, "Theory of edge detection, "*Proc. R. Soc. Lond. B* 204, pp. 301–328.)

SIFT – Scale Invariant Feature Transform

Descriptor overview:

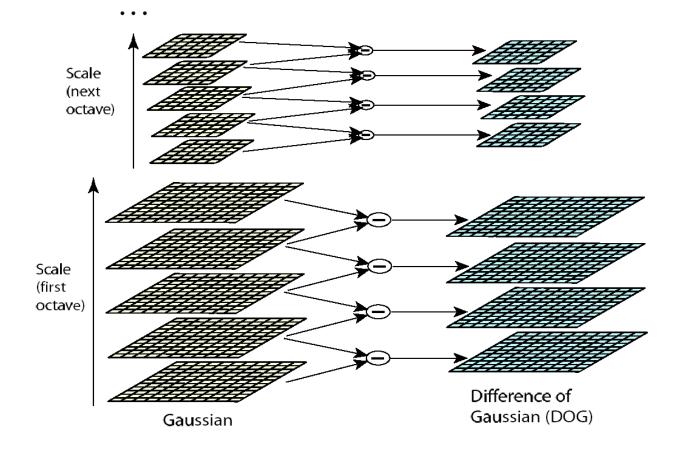
Determine scale (by maximizing DoG in scale and in space)



D. Lowe. "Distinctive Image Features from Scale-Invariant Keypoints" IJCV 2004

DOG detector

• Fast computation, scale space processed one octave at a time

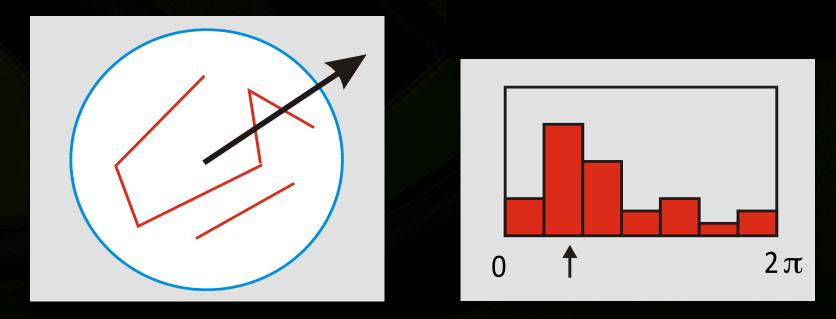


David G. Lowe. "Distinctive image features from scale-invariant keypoints." IJCV 60 (2).

SIFT – Scale Invariant Feature Transform

Descriptor overview:

- Determine scale (by maximizing DoG in scale and in space), local orientation as the dominant gradient direction
- Use this scale and orientation to make all further computations invariant to scale and rotation



D. Lowe. "Distinctive Image Features from Scale-Invariant Keypoints" IJCV 2004















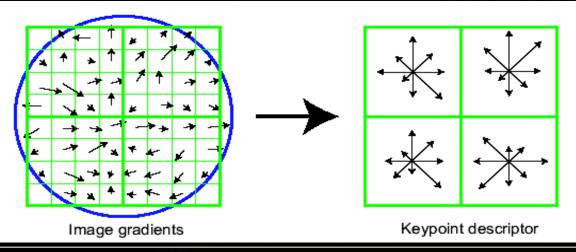


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SIFT – Scale Invariant Feature Transform

Descriptor overview:

- Determine scale (by maximizing DoG in scale and in space), local orientation as the dominant gradient direction
- Use this scale and orientation to make all further computations invariant to scale and rotation
- Compute gradient orientation histograms of several small windows (128 values for each point)
- Normalize the descriptor to make it invariant to intensity change



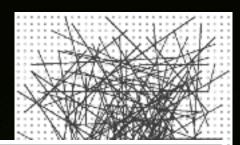
D. Lowe."Distinctive Image Features from Scale-Invariant Keypoints" IJCV 2004

ORB (Oriented FAST and Rotated BRIEF)

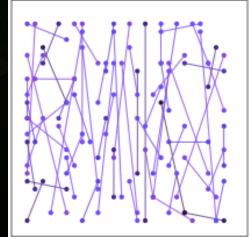
- Use FAST-9
 - use Harris measure to order them
- Find orientation
 - calculate weighted new center
 - reorient image so that gradients vary vertically

BRIEF

- Binary Robust Independent Elementary Features
- choose pixels to compare, result creates 0 or 1
- combine to a binary vector, compare using Hamming distance (XOR + pop count)
- **Rotated BRIEF**
 - train a good set of pixels to compare

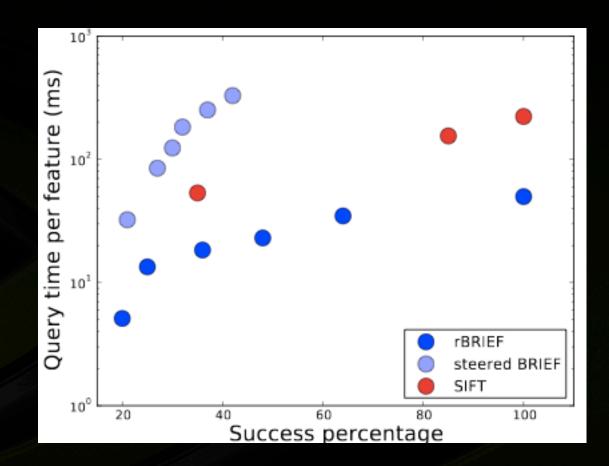


 $\left(\frac{\sum xI(x,y)}{\sum I(x,y)}, \frac{\sum yI(x,y)}{\sum I(x,y)}\right)$



rBRIEF vs. SIFT





Aligning images: Translation?





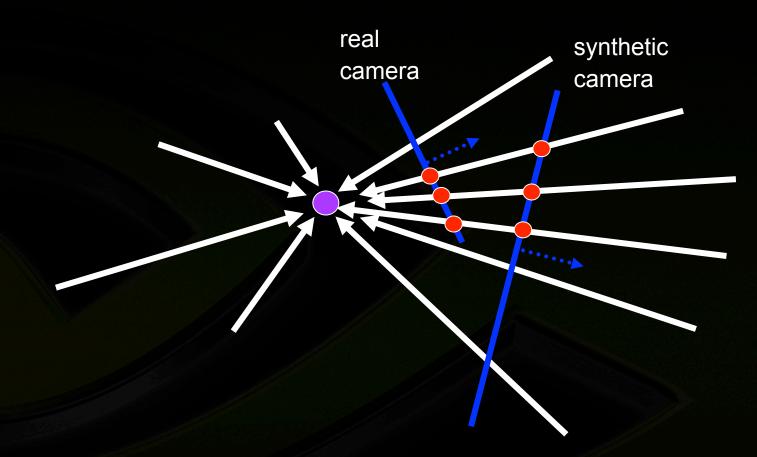
Translations are not enough to align the images



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A pencil of rays contains all views



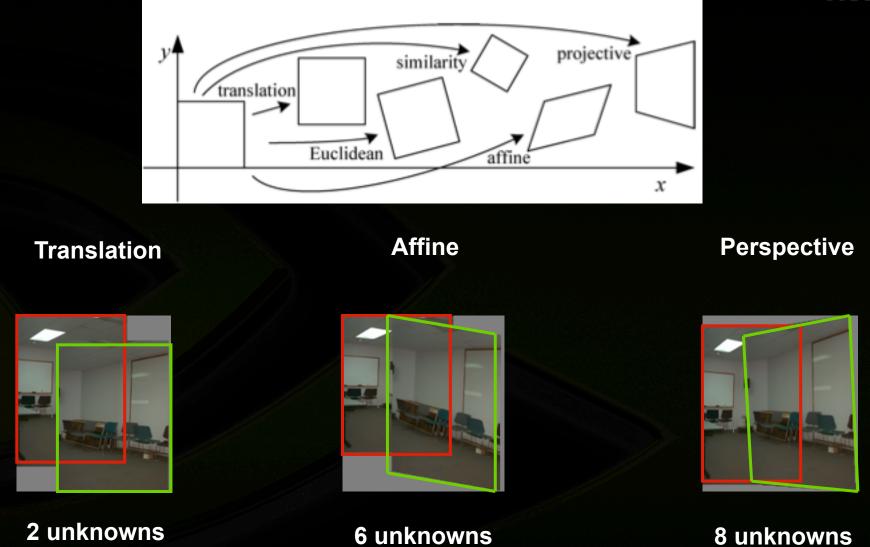


Can generate any synthetic camera view as long as it has **the same center of projection**! ... and scene geometry does not matter ...

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Which transform to use?





Homography

- Projective mapping between any two PPs with the same center of projection
 - rectangle should map to arbitrary quadrilateral
 - parallel lines aren't
 - but must preserve straight lines

is called a Homography

$$\begin{bmatrix} wx' \\ wy' \\ w \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

$$\underbrace{\mathbf{p'} \qquad \mathbf{H} \qquad \mathbf{p}}$$

To apply a homography H

compute p' = Hp (regular matric multiply)

convert p' from homogeneous to image coordinates [x', y'] *(divide by w)*



Homography from mapping quads

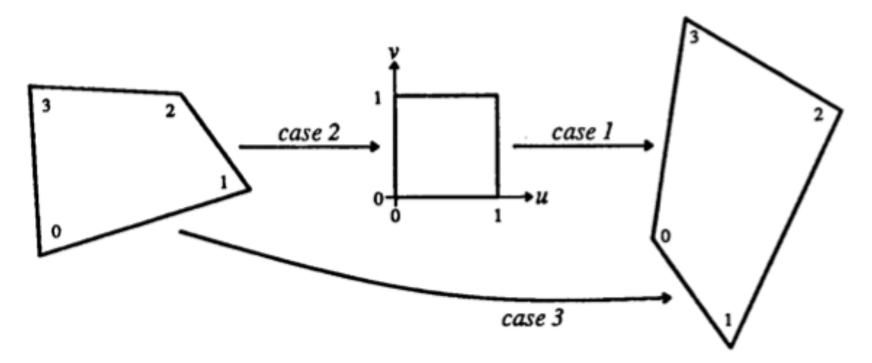


Figure 2.8: Quadrilateral to quadrilateral mapping as a composition of simpler mappings.

Fundamentals of Texture Mapping and Image Warping Paul Heckbert, M.Sc. thesis, U.C. Berkeley, June 1989, 86 pp. http://www.cs.cmu.edu/~ph/texfund/texfund.pdf

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Homography from *n* point pairs (x,y; x',y')

p

 $\begin{bmatrix} wx' \\ wy' \\ w \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$ **Multiply out** $wx' = h_{11} x + h_{12} y + h_{13}$ wy' = $h_{21} x + h_{22} y + h_{23}$ $w = h_{31} x + h_{32} y + h_{33}$ Get rid of w Н p' $(h_{31} x + h_{32} y + h_{33})x' - (h_{11} x + h_{12} y + h_{13}) = 0$ h₁₁ $(h_{31} x + h_{32} y + h_{33})y' - (h_{21} x + h_{22} y + h_{23}) = 0$ h_{12} Create a new system Ah = 0 h₁₃ Each point constraint gives two rows of A h_{21} [-x -y -1 0 0 0 xx' yx' x'] h = 1 h_{22} [000-x-y-1 xy' yy' y'] h_{23} Solve with singular value decomposition of A = USV^T h_{31} h₃₂ solution is in the nullspace of A the last column of V (= last row of V^{T}) h₃₃

```
from numpy import *
```

```
# create 4 random homogen. points Python test code
                                                                              NVIDIA
\underline{\mathbf{x}} = \operatorname{ones}([3, 4])
                     # the points are on columns
X[:2,:] = random.rand(2,4) # first row x coord, second y coord, third w = 1
x, y = X[0], X[1]
# create projective matrix
H = random.rand(3,3)
# create the target points
Y = dot(H,X)
# homogeneous division
YY = (Y / Y[2])[:2,:]
u, v = YY[0], YY[1]
A = zeros([8,9])
for i in range(4):
    A[2*i] = [-x[i], -y[i], -1, 0, 0, 0, x[i] * u[i], y[i] * u[i], u[i]]
    A[2*i+1] = [0, 0, -x[i], -y[i], -1, x[i] * v[i], y[i] * v[i], v[i]]
```

```
[u,s,vt] = linalg.svd(A)
```

```
# reorder the last row of vt to 3x3 matrix
HH = vt[-1,:].reshape([3,3])
```

```
# test that the matrices are the same (within a multiplicative factor)
print H - HH * (H[2,2] / HH[2,2])
```

Example





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perspective reprojection

Pics: Marc Levoy

Reprojecting an image onto a different picture plane







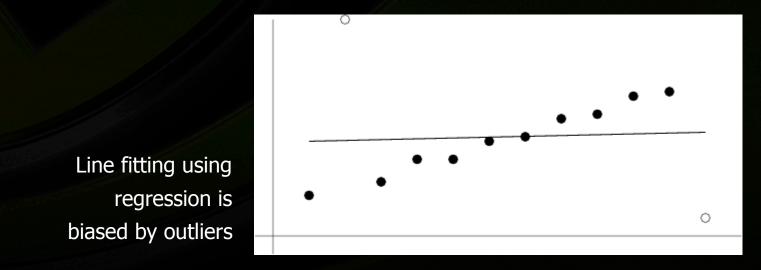
the sidewalk art of Julian Beever

The view on any picture plane can be projected onto any other plane in 3D without changing its appearance as seen from the center of projection

What to do with outliers?



- Least squares OK when error has Gaussian distribution
- But it breaks with outliers
 - data points that are not drawn from the same distribution
- Mis-matched points are outliers to the Gaussian error distribution
 - severely disturbs the Homography

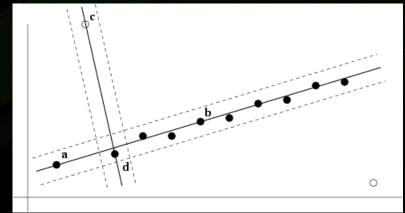


RANSAC

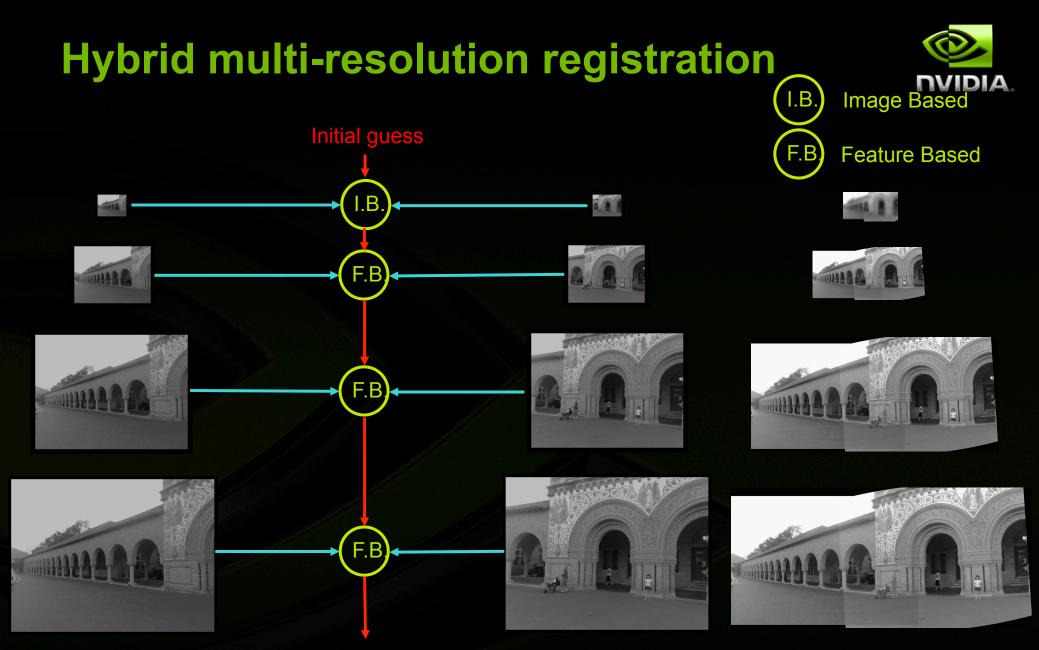


RANdom SAmple Consensus

- 1. Randomly choose a subset of data points to fit model (a sample)
- 2. Points within some distance threshold **t** of model are a *consensus set* Size of consensus set is model's *support*
- 3. Repeat for N samples; model with biggest support is most robust fit
 - Points within distance t of best model are inliers
 - Fit final model to all inliers



Two samples and their supports for line-fitting



Registration parameters

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K. Pulli, M. Tico, Y. Xiong, X. Wang, C-K. Liang, "Panoramic Imaging System for Camera Phones", ICCE 2010

Progression of multi-resolution registration



Actual size



Applied to hi-res



Feature-based registration



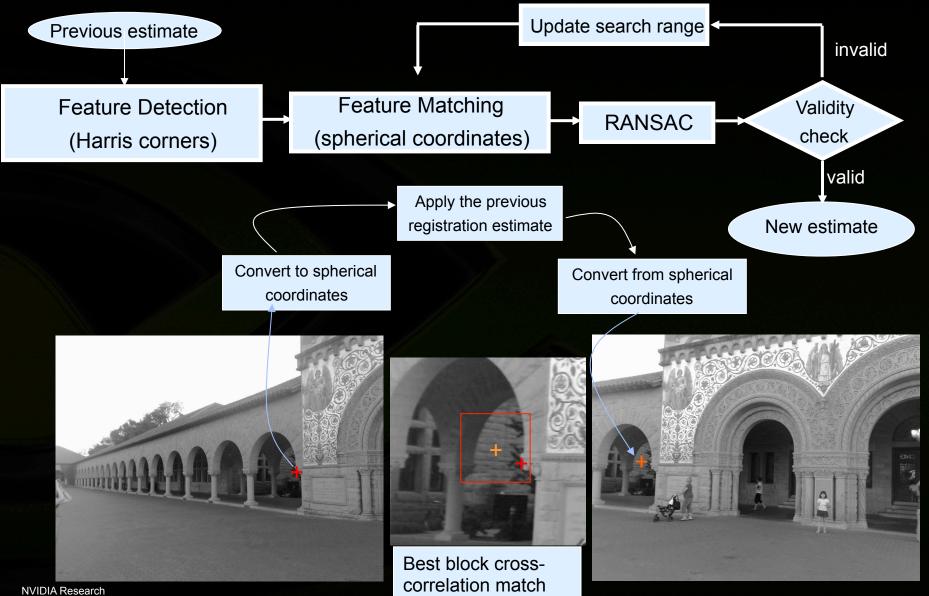


Image blending



Directly averaging the overlapped pixels results in ghosting artifacts
 Moving objects, errors in registration, parallax, etc.



Photo by Chia-Kai Liang

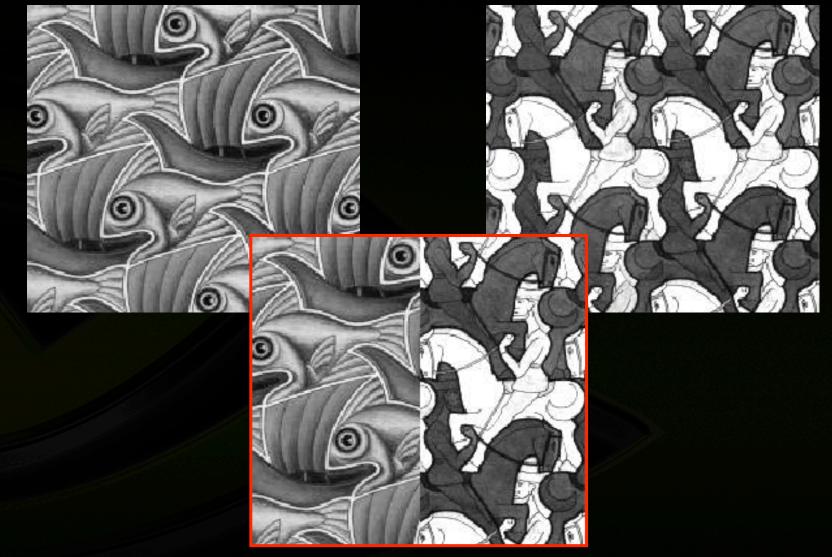






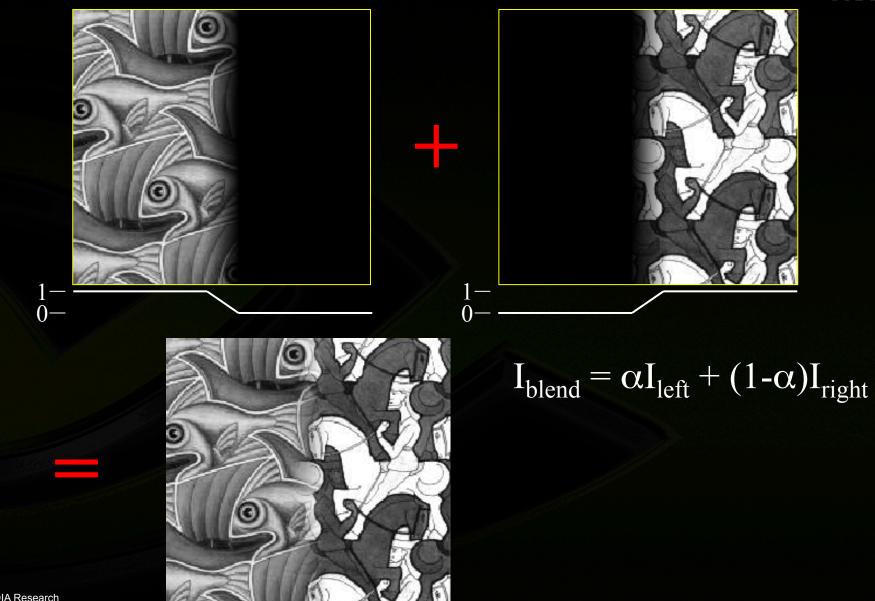
Alpha Blending / Feathering





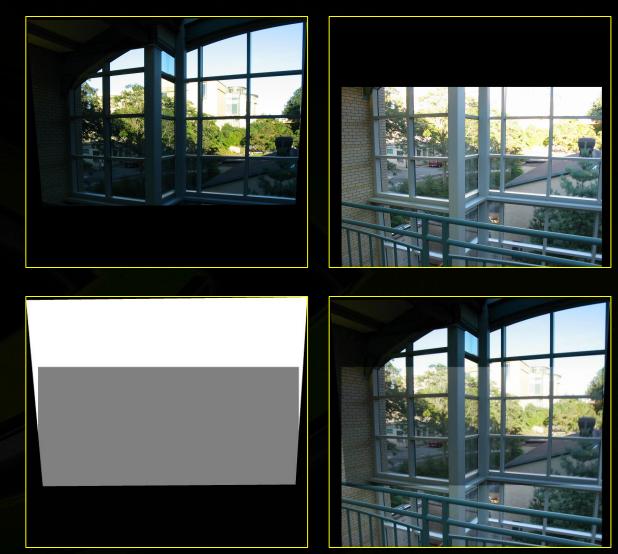
Alpha Blending / Feathering





Setting alpha: simple averaging



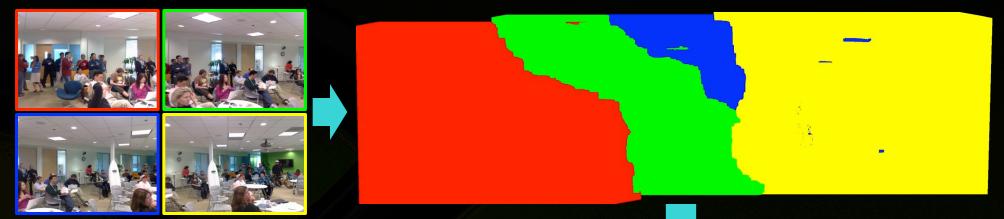


Alpha = .5 in overlap region

Solution for ghosting: Image labeling



- Assign one input image each output pixel
 - Optimal assignment can be found by graph cut [Agarwala et al. 2004]







New artifacts



Inconsistency between pixels from different input images

- Different exposure/white balance settings
- Photometric distortions (e.g., vignetting)





Solution: Poisson blending



- Copy the gradient field from the input image
- Reconstruct the final image by solving a Poisson equation



Combined gradient field

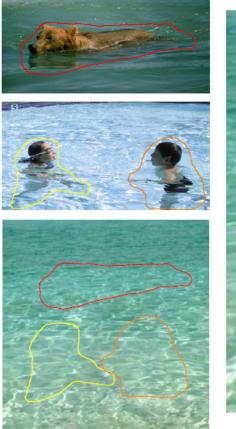




Problems with direct cloning



P. Pérez, M. Gangnet, A. Blake. Poisson image editing. SIGGRAPH 2003 http://www.irisa.fr/vista/Papers/2003_siggraph_perez.pdf





cloning

sources/destinations

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sources/destinations

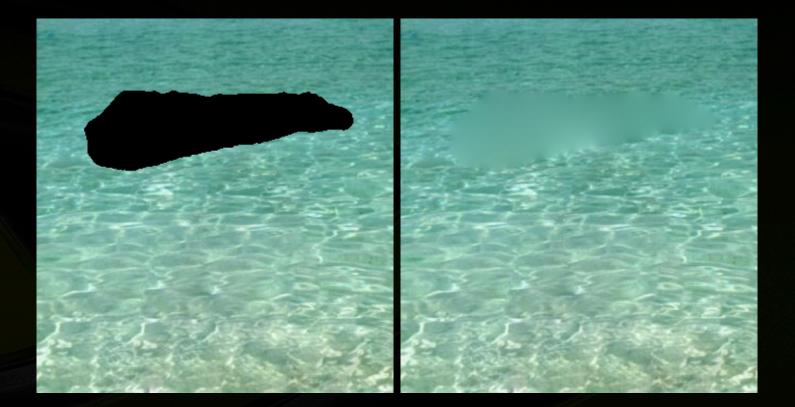
cloning

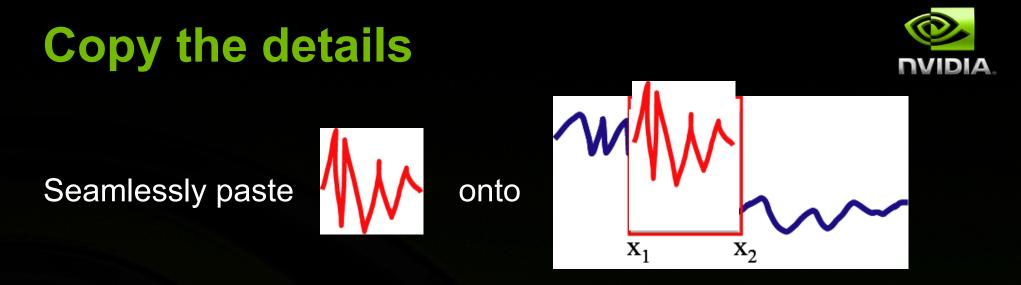
seamless cloning

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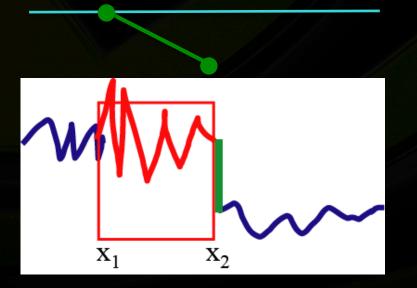
Membrane interpolation



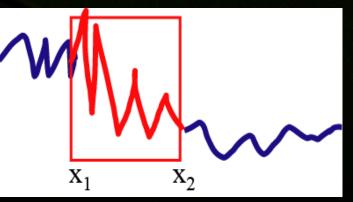




Just add a linear function so that the boundary condition is respected

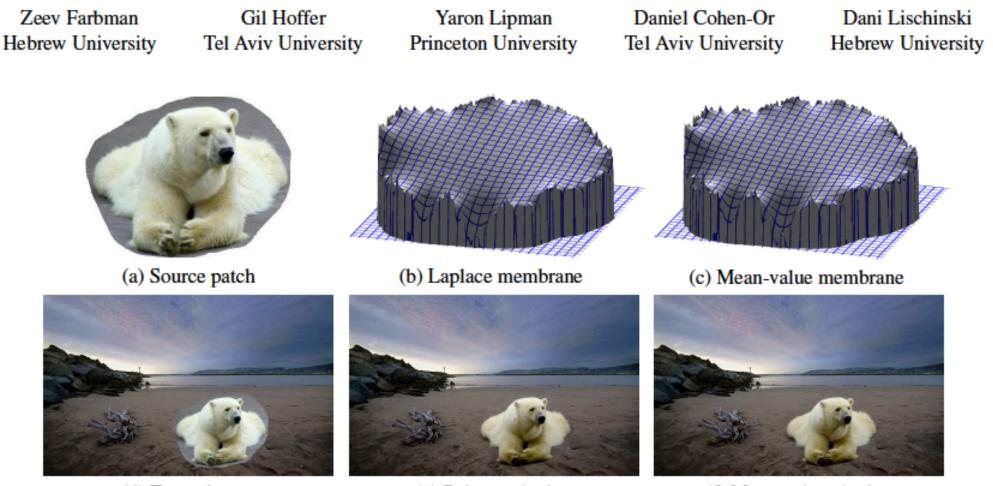


Gradients didn't change much, and function is continuous





Coordinates for Instant Image Cloning SIGGRAPH 2009



(d) Target image

(e) Poisson cloning

(f) Mean-value cloning

Figure 1: Poisson cloning smoothly interpolates the error along the boundary of the source and the target regions across the entire cloned region (the resulting membrane is shown in (b)), yielding a seamless composite (e). A qualitatively similar membrane (c) may be achieved via transfinite interpolation, without solving a linear system. (f) Seamless cloning obtained instantly using the mean-value interpolant.



Mean-value coordinates for smooth interpolation

these coordinates may be used to smoothly interpolate any function f defined at the boundary vertices:

$$\tilde{f}(\mathbf{x}) = \sum_{i=0}^{m-1} \lambda_i(\mathbf{x}) f(\mathbf{p}_i).$$
(3)

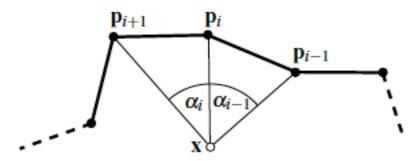


Figure 2: Angle definitions for mean-value coordinates.

Evaluate them sparsely... ... and interpolate within triangles

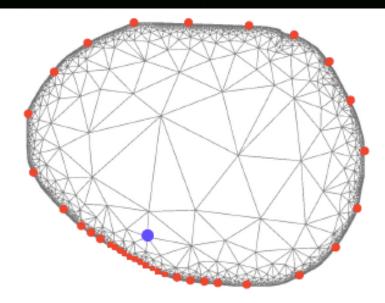


Figure 3: An adaptive triangular mesh constructed over the region to be cloned. The red dots on the boundary show the positions of boundary vertices that were selected by adaptive hierarchical subsampling for the mesh vertex indicated in blue.

Interactive Poisson cloning!



Table 1: Performance statistics for MVC cloning. Times exclude disk I/O and sending the images to the graphics subsystem. Cloning rate is the number of region updates per second.

#cloned	#bdry	#mesh	coords	prep.	cloning rate	
pixels	pixels	vertices	/vertex	time(s)	CPU	GPU
51,820	1,113	2,063	38.63	0.15	199.0	163
133,408	1,562	2,963	44.21	0.30	92.1	134
465,134	2,683	5,323	45.50	0.63	22.6	82
1,076,572	4,145	8,241	44.59	1.16	9.7	44
4,248,461	8,133	16,369	57.71	3.63	2.7	26
12,328,289	14,005	28,240	58.68	8.99	0.94	-

Faster than "real" Poisson

2008], as well as our own experiments, indicate that common Poisson solvers on the CPU are able to handle regions with 256² pixels at a rate of 3–5 solutions per second. Another possibility, which we have not seen mentioned in the literature, is to precompute a factorization of the Poisson equation matrix during the preprocessing stage, and then quickly compute the solution via back-substitution at each target location. In our experiments, for a region with 125K pixels, computing the back-substitution takes 0.3 seconds. Thus, all of the above are significantly slower than the rates we are able to achieve.





After labeling





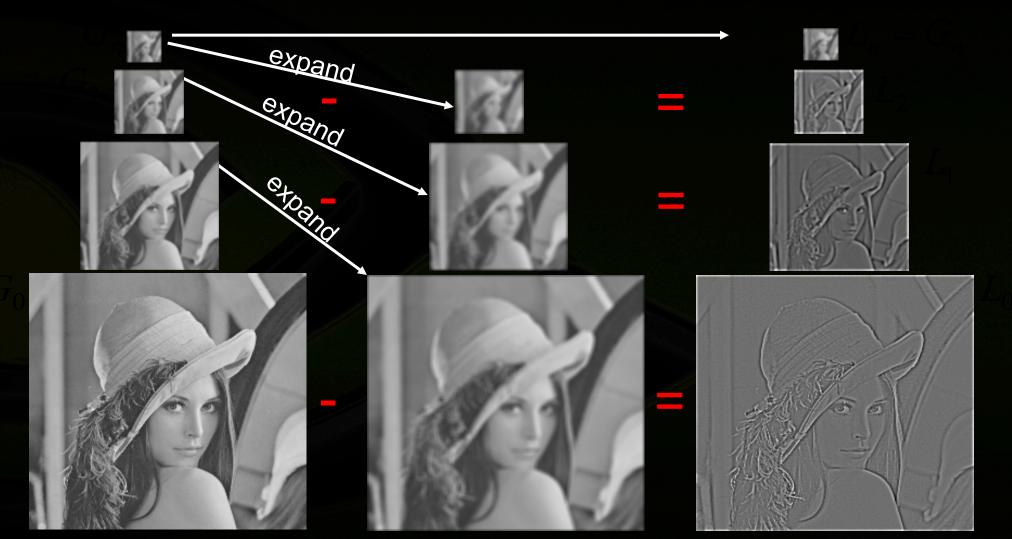
Poisson blending

The Laplacian pyramid





Laplacian Pyramid



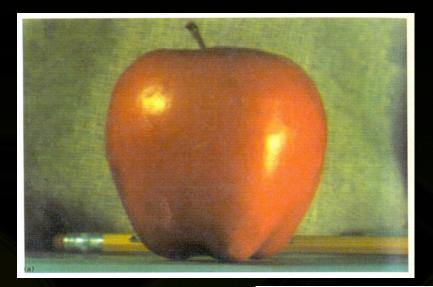
```
void createLaplacePyr( const Mat &img, int num levels, std::vector<Mat> &pyr )
{
    pyr.resize(num_levels + 1);
    Mat downNext, lvl up, lvl down;
    Mat current = img;
    pyrDown(img, downNext);
    for( int i = 1; i < num levels; ++i )</pre>
    {
        pyrDown( downNext, lvl down );
        pyrUp( downNext, lvl_up, current.size() );
        subtract( current, lvl up, pyr[i-1], noArray(), CV 16S );
        current = downNext;
        downNext = lvl down;
    }
    pyrUp( downNext, lvl_up, current.size() );
    subtract( current, lvl_up, pyr[num_levels-1], noArray(), CV_16S );
    downNext.convertTo( pyr[num levels], CV 16S );
```

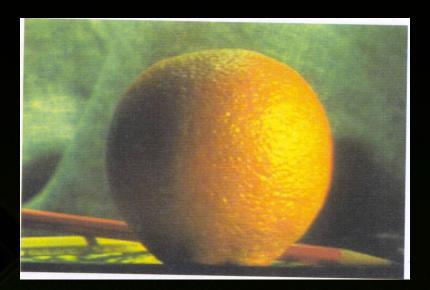


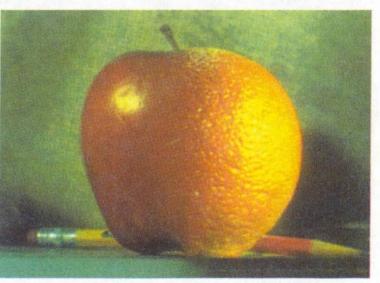
}

Pyramid Blending









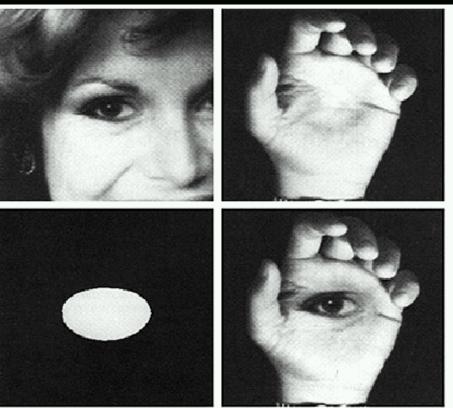
NVIDIA Research

(1)

Laplacian Pyramid: Blending

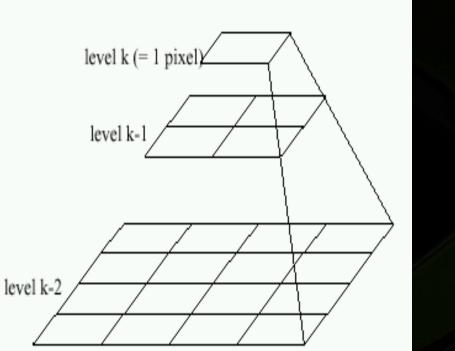


- General Approach:
 - 1. Build Laplacian pyramids LA and LB from images A and B
 - 2. Build a Gaussian pyramid *GR* from selected region *R*
 - 3. Form a combined pyramid *LS* from *LA* and *LB* using nodes of *GR* as weights:
 - LS(i,j) = GR(I,j,) * LA(I,j) + (1-GR(I,j)) * LB(I,j)
 - 4. Collapse the *LS* pyramid to get the final blended image

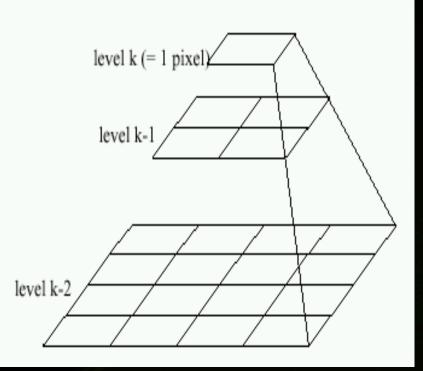


Pyramid Blending







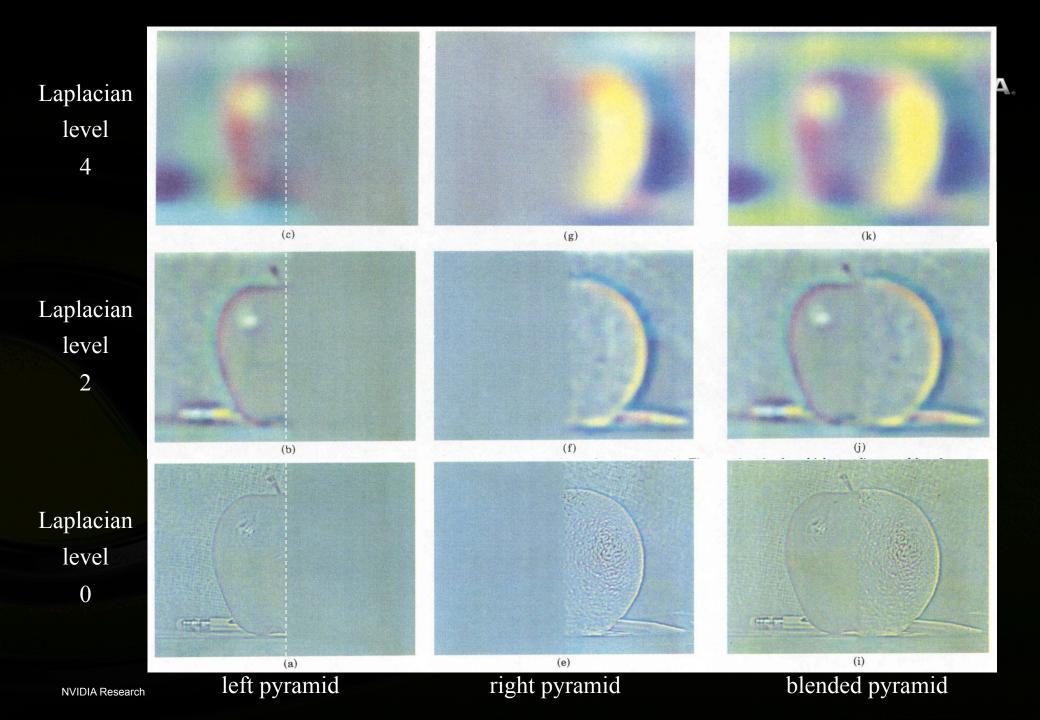


Left pyramid



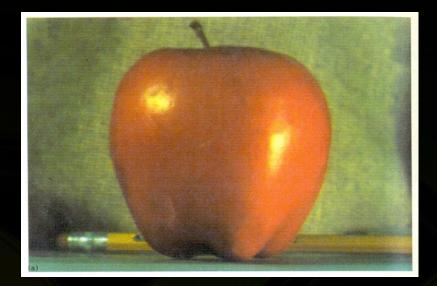
Right pyramid

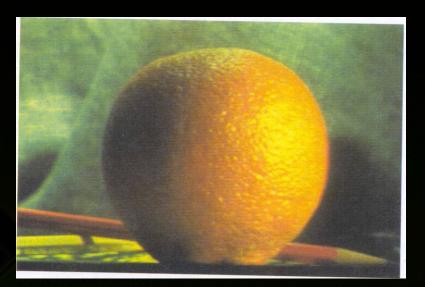
NVIDIA Research

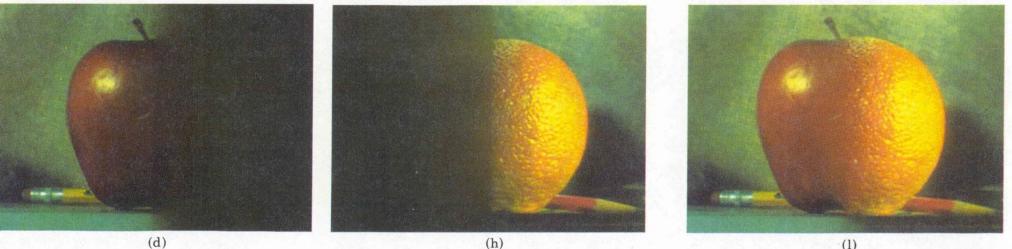


Pyramid Blending









Simplification: Two-band Blending



Brown & Lowe, 2003

- Only use two bands: high freq. and low freq.
- Blends low freq. smoothly



2-band Blending





Low frequency ($\lambda > 2$ pixels)



High frequency (λ < 2 pixels)

NVIDIA Research

Linear Blending

2-band Blending