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# Searching for Sub-images Using Sequence Alignment

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# Presentation Outline



- Motivation
- Current approaches to the sub-image retrieval
- Sequence alignment methods
- Conclusion

# Motivation

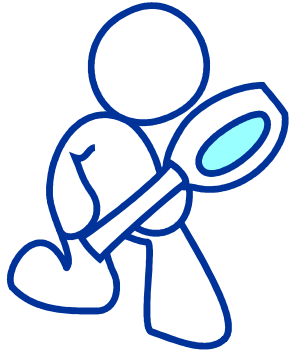


Image  
(query)



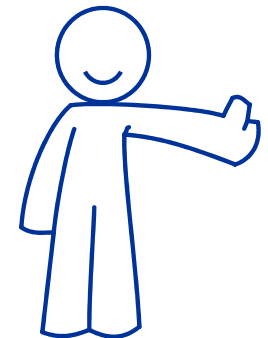
& Search engine  
(technology)



& Database of images =



Found images  
(response)



& Happy user

# Motivation

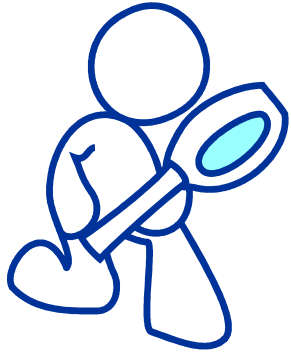


Image  
(query)



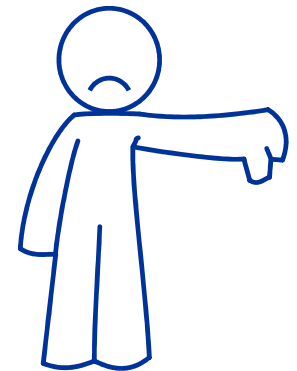
& Search engine  
(technology)



& Database of images =



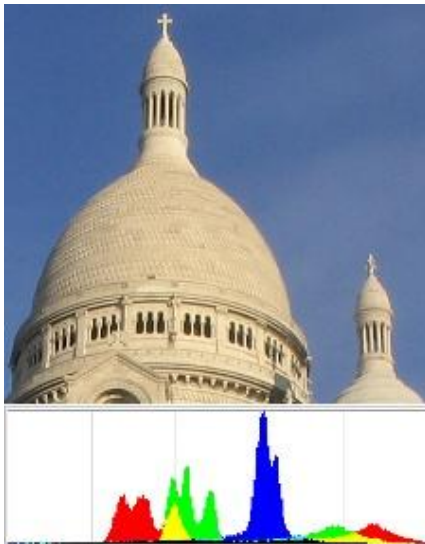
Found images  
(response)



& Disappointed  
user

# Sub-Image Retrieval – Approaches

- Image characterization



Global descriptors



Local descriptors

# Sub-Image Retrieval – L.F. Approaches



Query Image

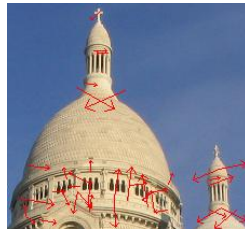


Database Image(s)

# Sub-Image Retrieval – L.F. Approaches

Extract  
local  
features

Suppose our features are scale- and rotation-invariant  
SIFT and its derivatives, MSER, ...



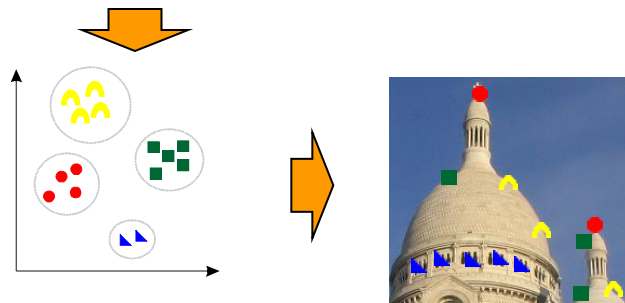
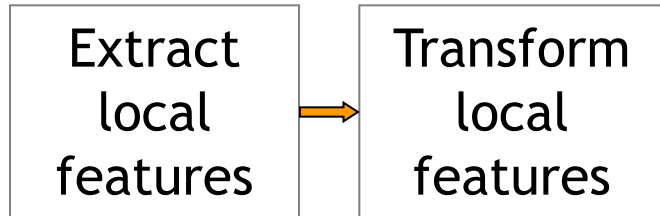
Query Image



Database Image(s)

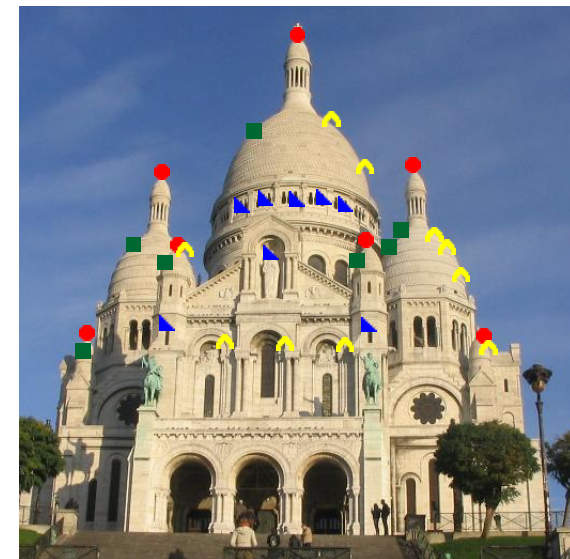


# Sub-Image Retrieval – L.F. Approaches



- local features => visual words
- image => bag-of-words

Query Image



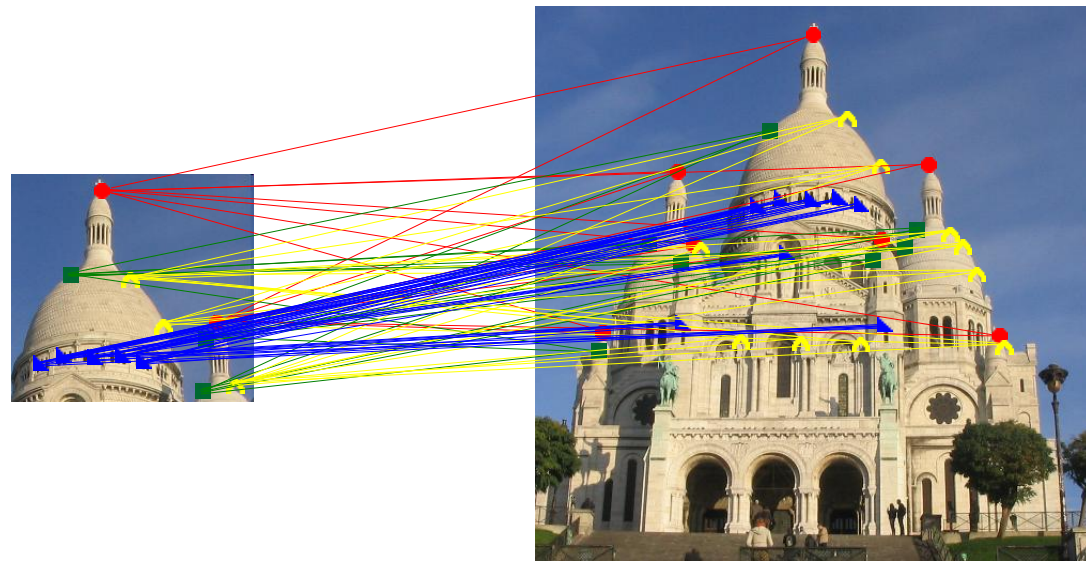
Database Image(s)



# Sub-Image Retrieval – L.F. Approaches



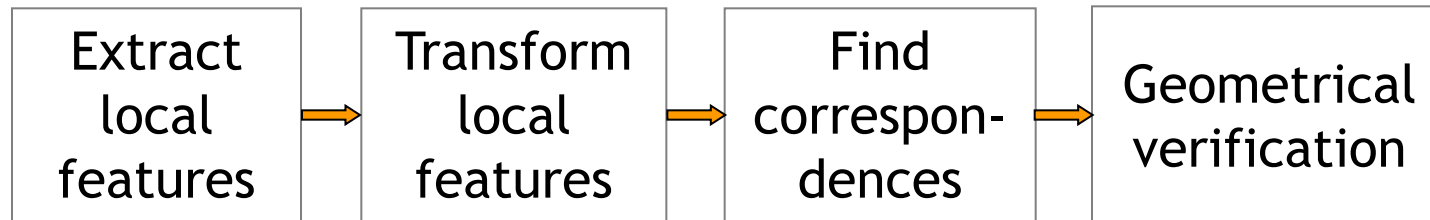
Usually inspired by the text retrieval (tf-idf,...)



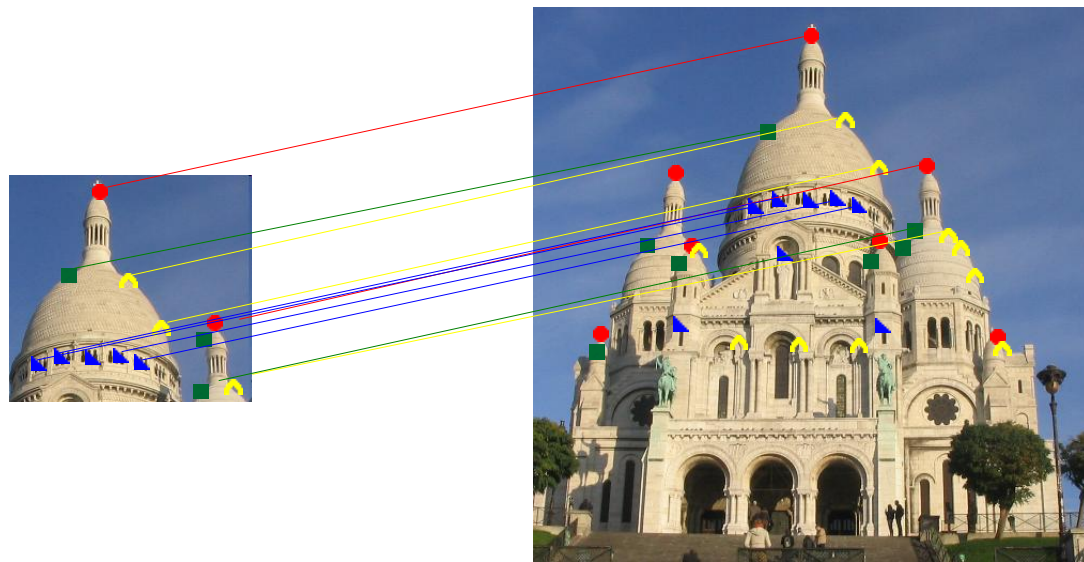
Query Image

Database Image(s)

# Sub-Image Retrieval – L.F. Approaches



RANSAC,  
Least Medians of  
Squares,  
Generalized Hough  
Transformation,  
...



Query Image

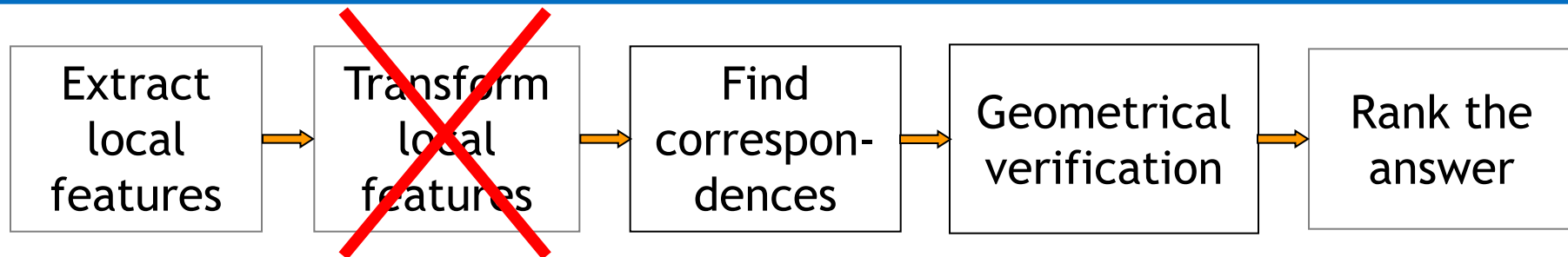
Database Image(s)

# Sub-Image Retrieval – L.F. Approaches



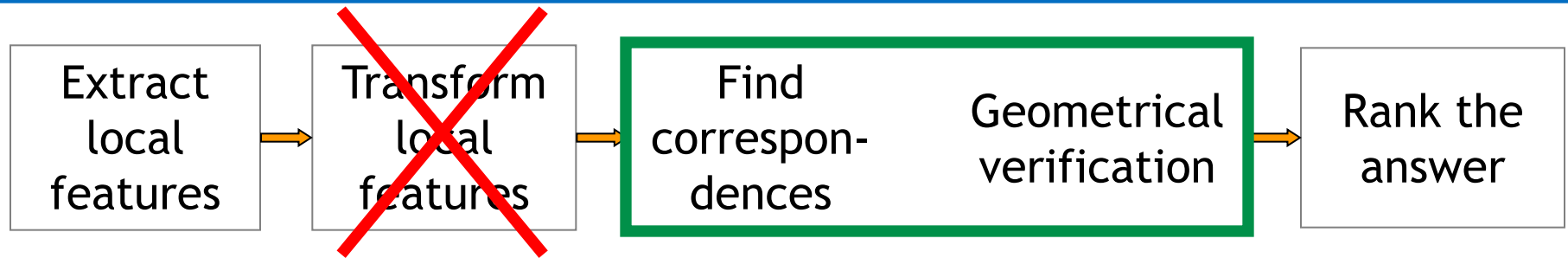
Query image    Ranked answer

# Sub-Image Retrieval – Our Approach



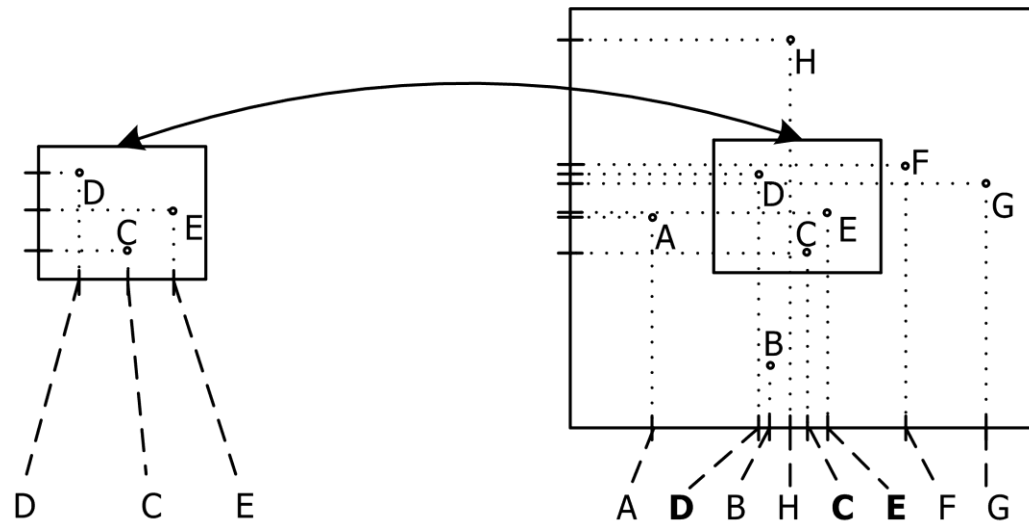
- **Bag-of-words methods:**
  - Rely on training data
  - Lost of information
- **Local features (High-dimensional vectors) themselves create an alphabet in our approach**

# Sub-Image Retrieval – Our Approach



- Sequence alignment methods used for the geometrical verification

# Sequence alignment



- Local features are projected into x/y axis  
=> ordered sequence
- Sequences are compared using sequence-alignment methods

# Sequence alignment methods



- Commonly used in bioinformatics (i.e. protein sequences alignment)
- User defined scoring scheme (match, mismatch and gap scores/penalties)
- Scoring matrix





# Sequence-alignment methods - cont.

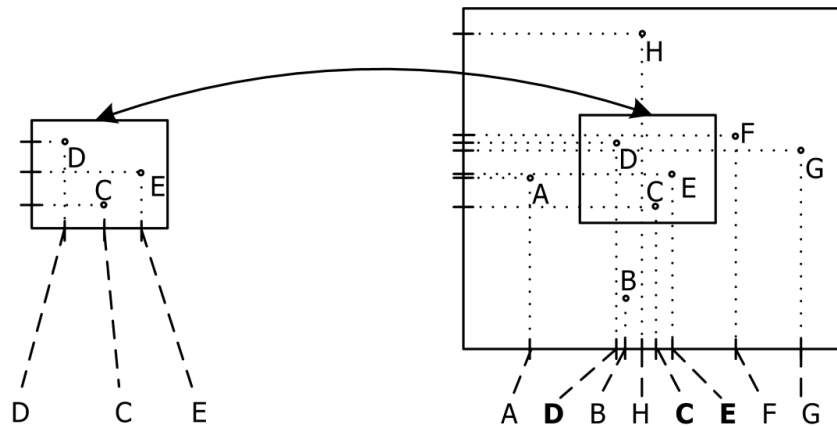
- Needleman-Wunsch (Global alignment)

-D-- <b>CE</b> --	-	Gap
x   x x     x x	x	Mismatch
<b>ADBHCEFG</b>		Match

- Smith-Watermann (Local alignment - deals better with starting/ending gaps -> sequences of the non-equal length)

-D-- <b>CE</b> --	=	Gap opening
=   = -     = -	-	Gap cont.
<b>ADBHCEFG</b>	x	Mismatch
		Match

# Sliding windows



- Small query & large database image (and vice versa) leads to “noise” in projected sequences (letters B and H)
- => Split images (queries and database) into the fixed-size windows
- Run sequence alignment for each of the window separately

# Evaluation

- BelgaLogos dataset
- Queries: 26 logos, database: 10 000 images
- Original method Joly&al - Visual words + RANSAC  
Mean Average Precision: 25.67
- Our method: 30.95

(Smith-Waterman,  
Window size  
128×128 px)



# Method cons and pros

- ⊕ Scale-change, shear invariant
- ⊕ Flipping, rotation of  $90^\circ$  invariant (with projections re-ordering)
- ⊖ Not fully rotation and camera viewpoint change (tilt) invariant
- ⊕ Method handles with multiple occurrences of the queried sub-image in one DB image
- ⊕ Sequence of letters  $\approx$  time series  $\Rightarrow$  **indexable** (contrary to RANSAC,...)

# Future work



- Performance
  - Indexing
  - Features quantization
- Quality
  - Rotation invariance
  - Lower precision (too many false positives)
  - Large windows (more than one window)



- Sub-Image Retrieval
  - Features forms an alphabet
  - Geometric consistency validation using sequence alignment methods
  - (Sliding) windows to avoid the noise

