U-Phylogeny: Undirected Provenance Graph Construction

A. Bharati¹, D. Moreira¹, A. Pinto², J. Brogan¹, K. Bowyer¹, P. Flynn¹, W. Scheirer¹ and A. Rocha^{1,2} ¹University of Notre Dame, USA ²University of Campinus, Brazil

Problem

Provenance: tracing the place of origin or earliest known history of something

Why solve Image Provenance?

- Existence of multiple copies of the same media
- Prevalence of photo manipulation in popular culture
- Which is the original image and where did it come from?





Limitations of Existing Methods

- No multi-composite scenarios
- Only works in constrained environments
- Not much exploration of dissimilarity computation
- Not invariant to many transformations
- Unavailability of sufficient information to perform mappings (compression artifacts for non-JPEG images)

What is U-Phylogeny*?

- Undirected provenance graph construction method that can be extended to obtain directed phylogenetic tree
- Generalized and more efficient method for > 2 donors without image format restrictions



* Bharati, A., Moreira, D., Pinto, A., Brogan, J., Bowyer, K., Flynn, P., Scheirer, W. and Rocha, A., 2017. U-Phylogeny: Undirected Provenance Graph Construction in the Wild. IEEE International Conference on Image Processing, 2017. Code: <u>https://gitlab.com/notredame-provenance/u-phylogeny</u>

Methodology

<u>Pipeline:</u>

- 1. Detection and description of points of interest (SURF)
- 2. Keypoint matching using L2 distance
- 3. Match filtering
 - Geometrically Consistent Matching (GCM)
- 4. Dissimilarity computation
 - Number of GCM's, Distance of GCM's
 - Difference in pixel distribution(MSE, Mutual Information) (extended U-phylogeny)
- 5. Kruskal's min/max spanning tree algorithm



Dataset Used: 59 provenance cases from NIST's Nimble 2017 challenge dataset

- 59 queries and 10446 gallery images (750 related)
- Average graph order = 12.7, Range [3, 82]
- Small (<=12 nodes) Medium (13-20 nodes) Large (>20 nodes)

Evaluation Metrics: web graph similarity metrics

 $VEO(G,G') = \frac{|nodes(G') \cap nodes(G)| + |edges(G') \cap edges(G)|}{(d_1 + (d_2 + d_3))}$

|nodes(G')|+|nodes(G)|+|edges(G')|+|edges(G)|

Results



Experiment 2: With distractors (25 images/case)



Conclusion

- Effectiveness decreases with the size of graphs irrespective of dissimilarity metrics
- Extended U-Phylogeny performs better on average but reduced efficiency
- U-Phylogeny is robust to the presence of distractors (VEO = 88%)
- Mutual Information yields better performance than MSE

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