Wall Painting Reconstruction Using a Genetic Algorithm

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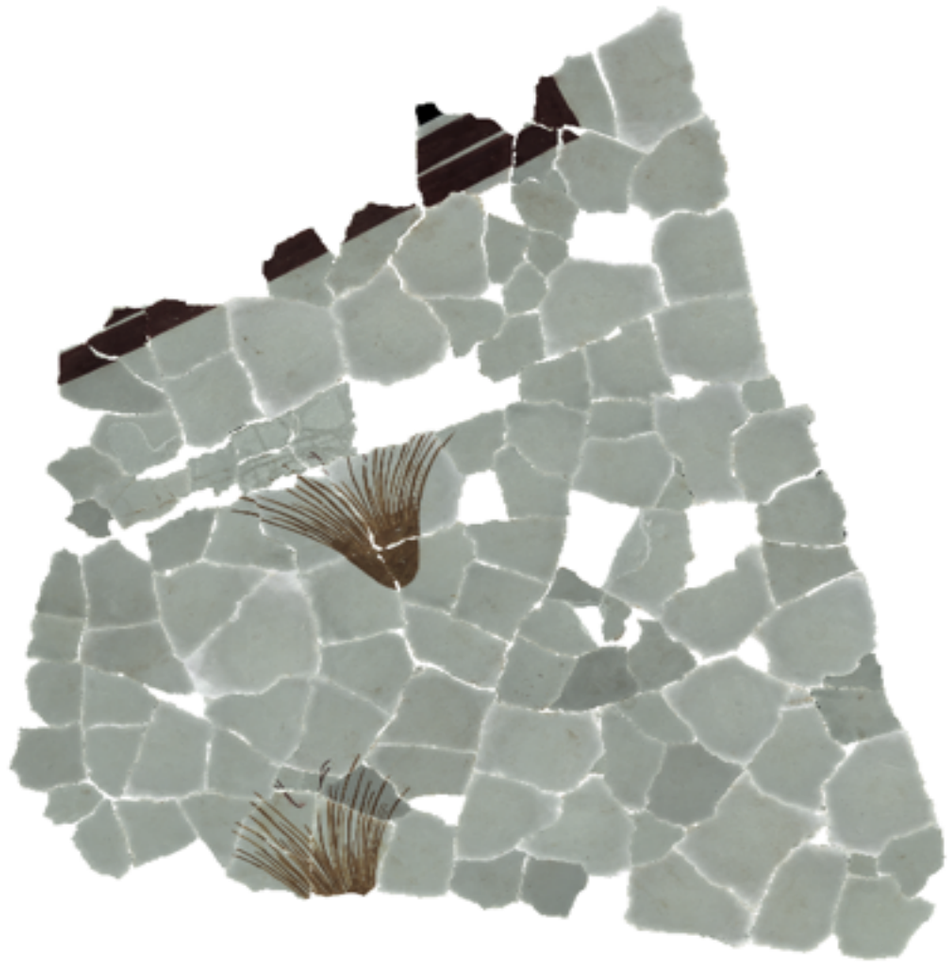
Motivation

Wall paintings recovered from Akrotiri (Santorini), Greece

Antelope Fresco



Part of a reconstructed fresco

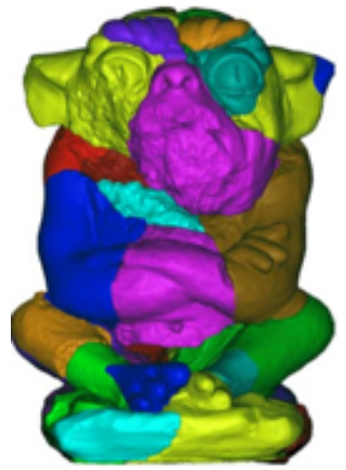
https://artoffresco.com
https://www.santorini.com/archaeology/akrotiri.htm

Related Problems

Reconstruction of Torn Documents

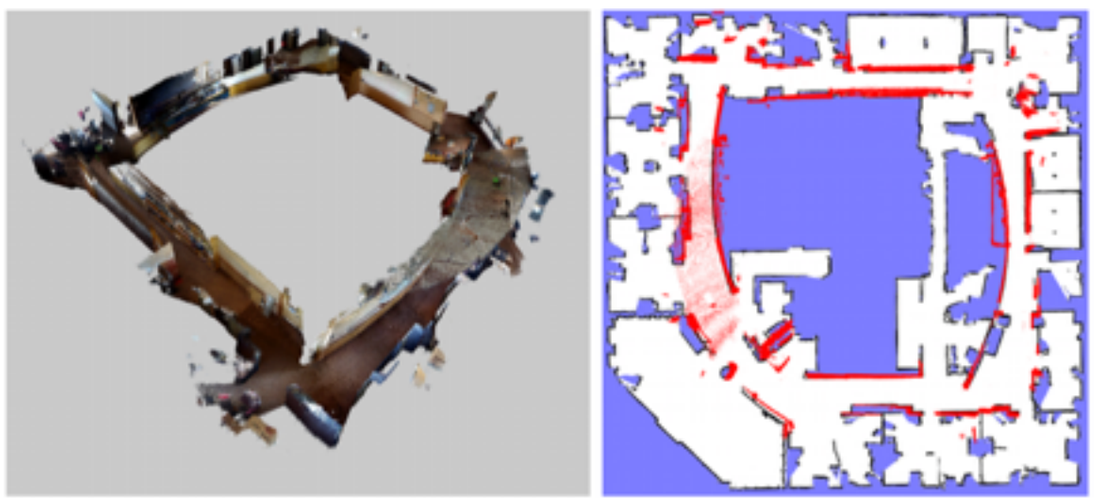
[Biswas ‘05]

Reconstruction of Fragmented Objects



[Huang ‘06]

RGB-D Reconstruction



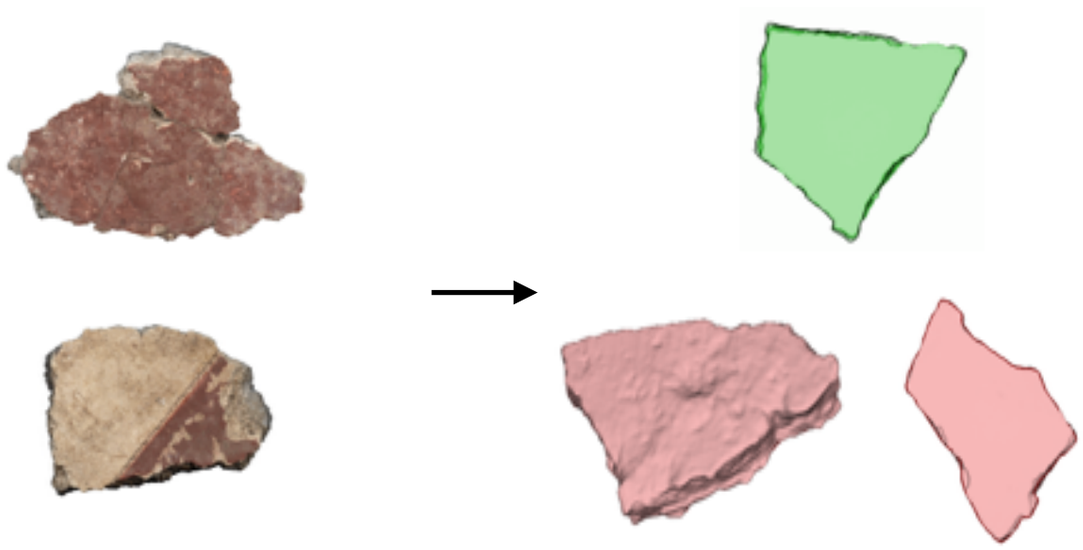
[Henry ‘10]

Computer Based Reconstruction Methods

Real Fragments

Reconstruction Pipeline

Computer Based Reconstruction Methods



Real Fragments

3D Models

Reconstruction Pipeline

Computer Based Reconstruction Methods

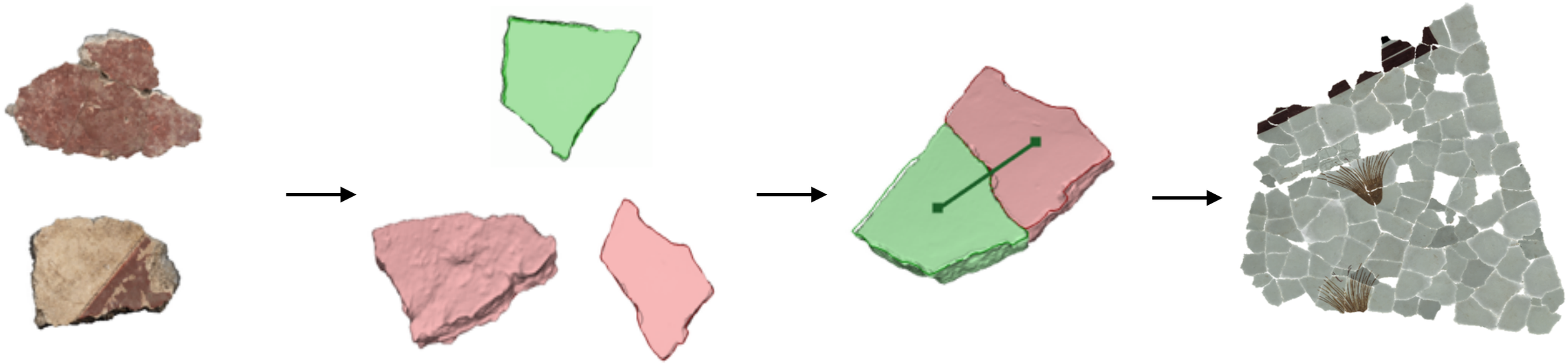
Real Fragments

3D Models

Pairwise Matches

Reconstruction Pipeline

Computer Based Reconstruction Methods



Real Fragments

3D Models

Pairwise Matches

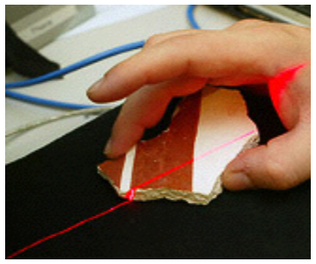
Reconstruction

Reconstruction Pipeline

Step 1: Scanning

Use a laser scanner to acquire a 3D surface

Physical Fragments



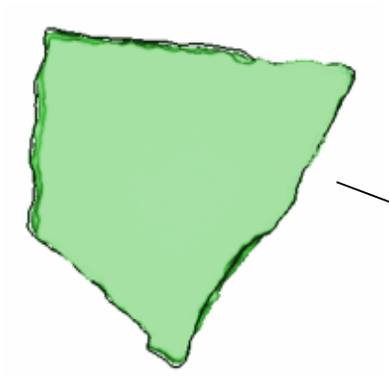
Surface Scanning

Digital Scan of a Fragment

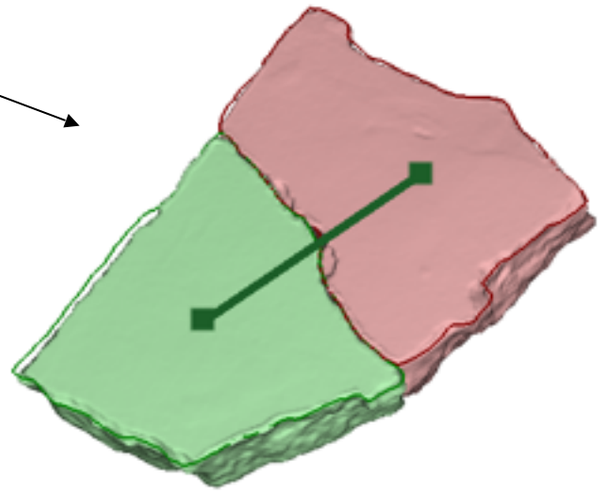
[Brown et al. 08]

Step 2: Matching

Use an algorithm to find and rank potential pairwise matches between fragments



Resulting match is a geometric transformation between coordinate systems of two fragments



Score: 1.15975

$$M = \begin{pmatrix} \cos\delta_{i,j} & -\sin\delta_{i,j} & t_1 \\ \sin\delta_{i,j} & \cos\delta_{i,j} & t_2 \\ 0 & 0 & 1 \end{pmatrix}$$

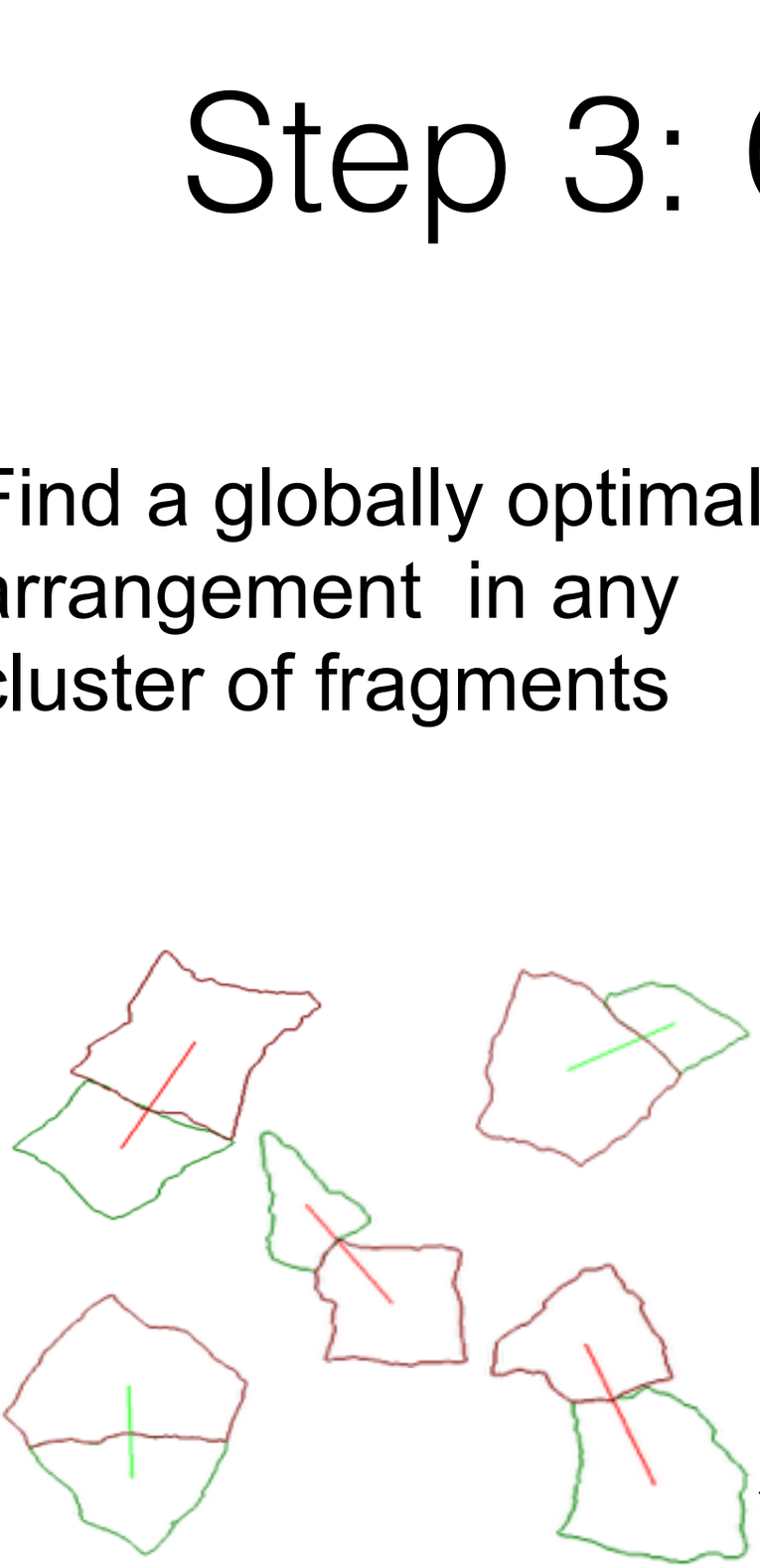
$\delta_{ij} = \theta_i - \theta_j$ - Angular offset

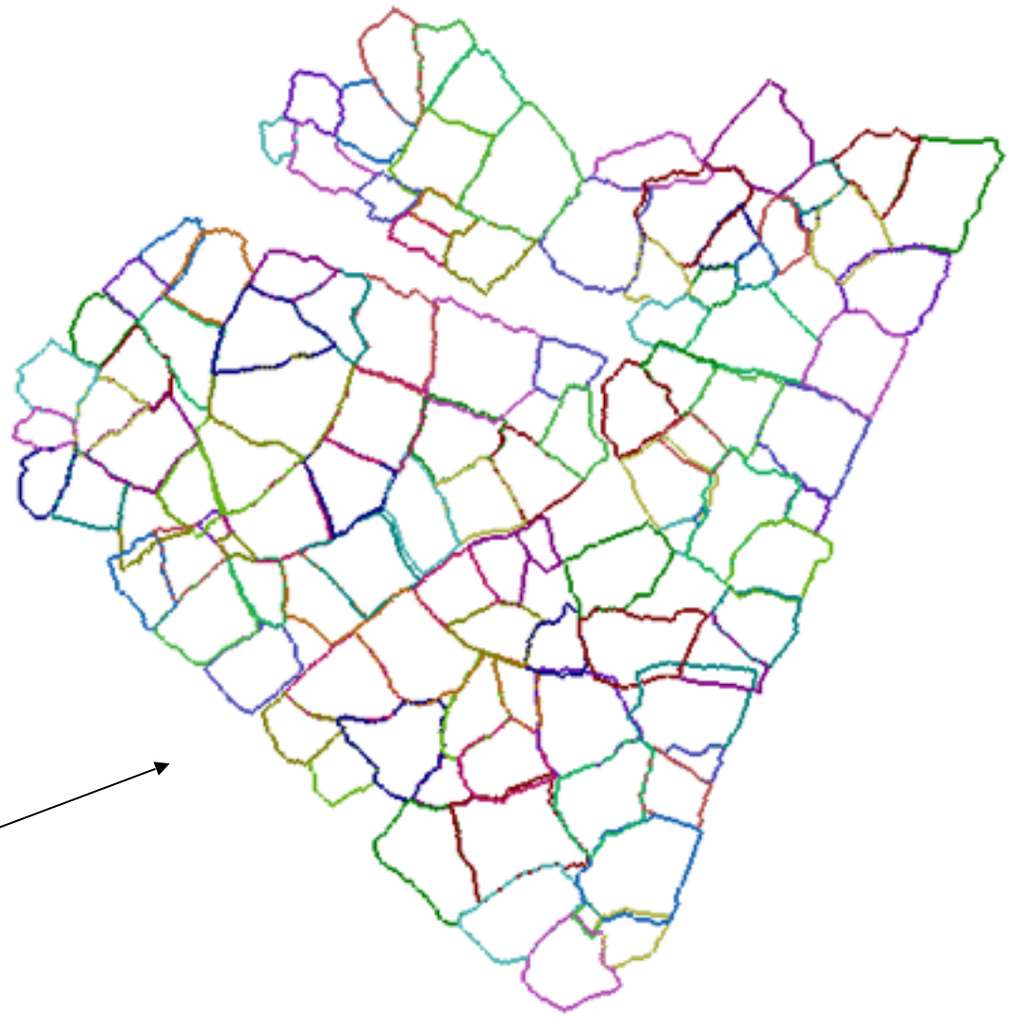
$T = (t_1, t_2)$ - Translational offset

[Funkhouser et al. 2011]

Step 3: Global Assembly

Find a globally optimal arrangement in any cluster of fragments

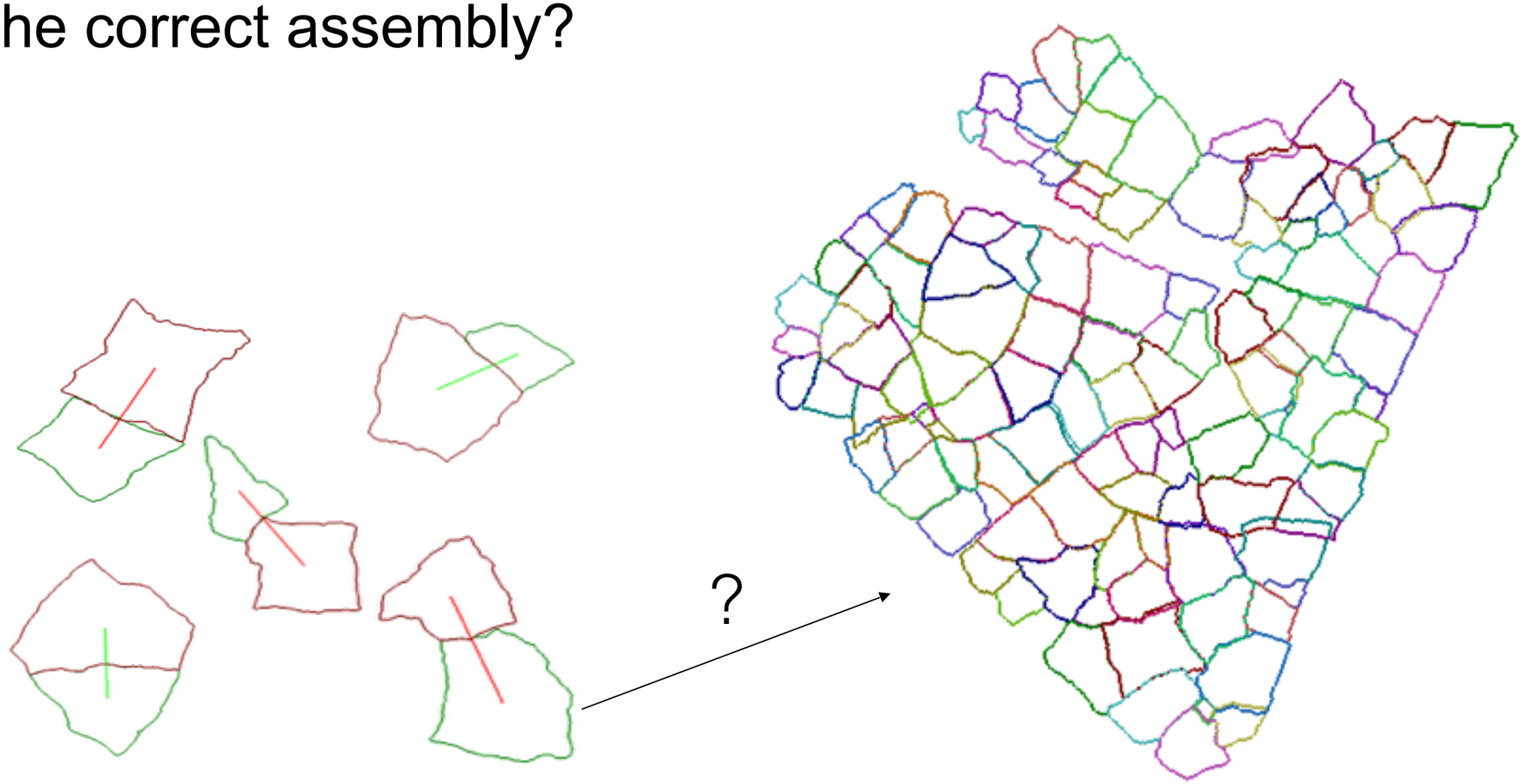




50K ranked matches, most are wrong

Challenge

Which matches are part of the correct assembly?



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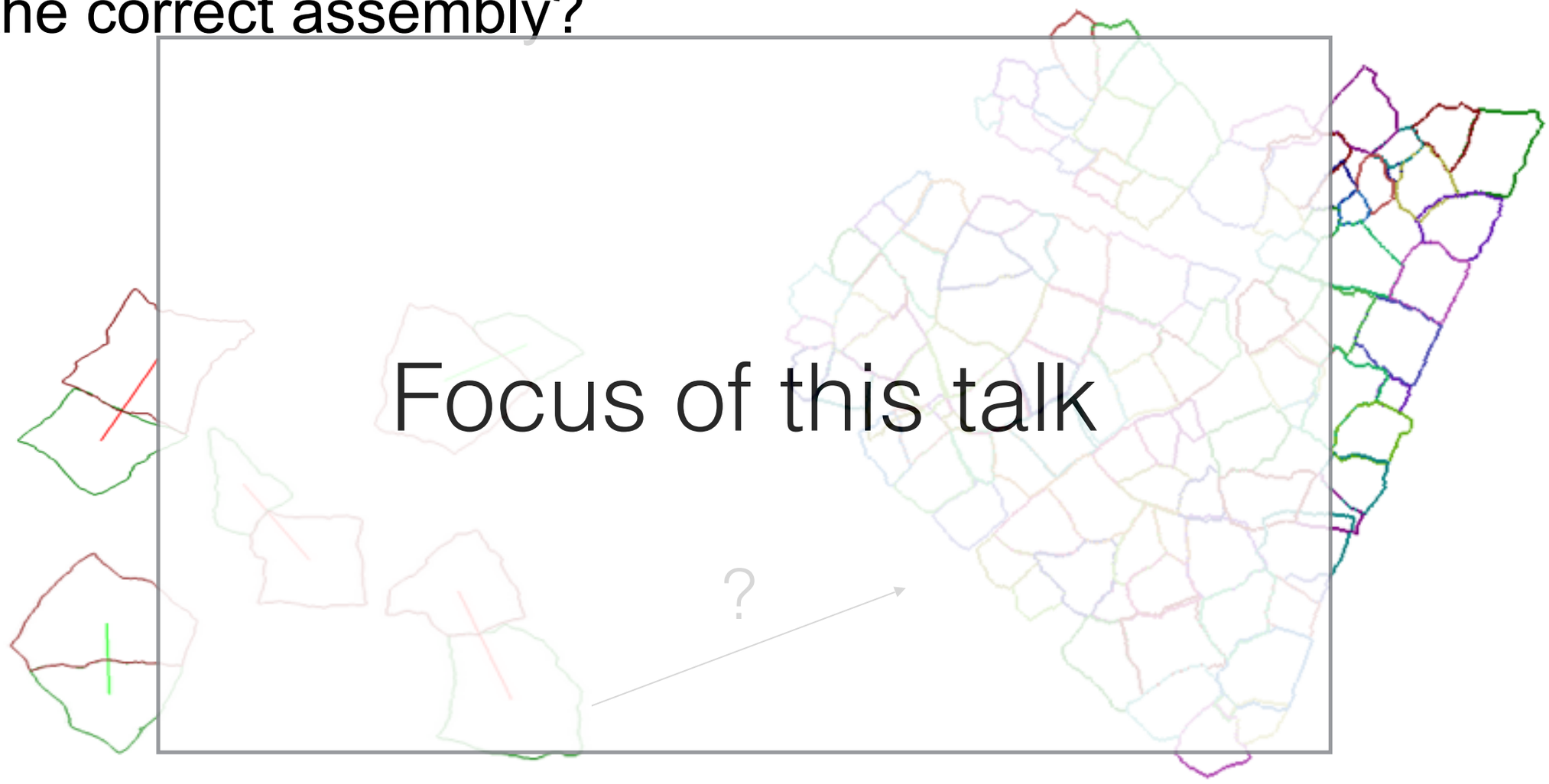
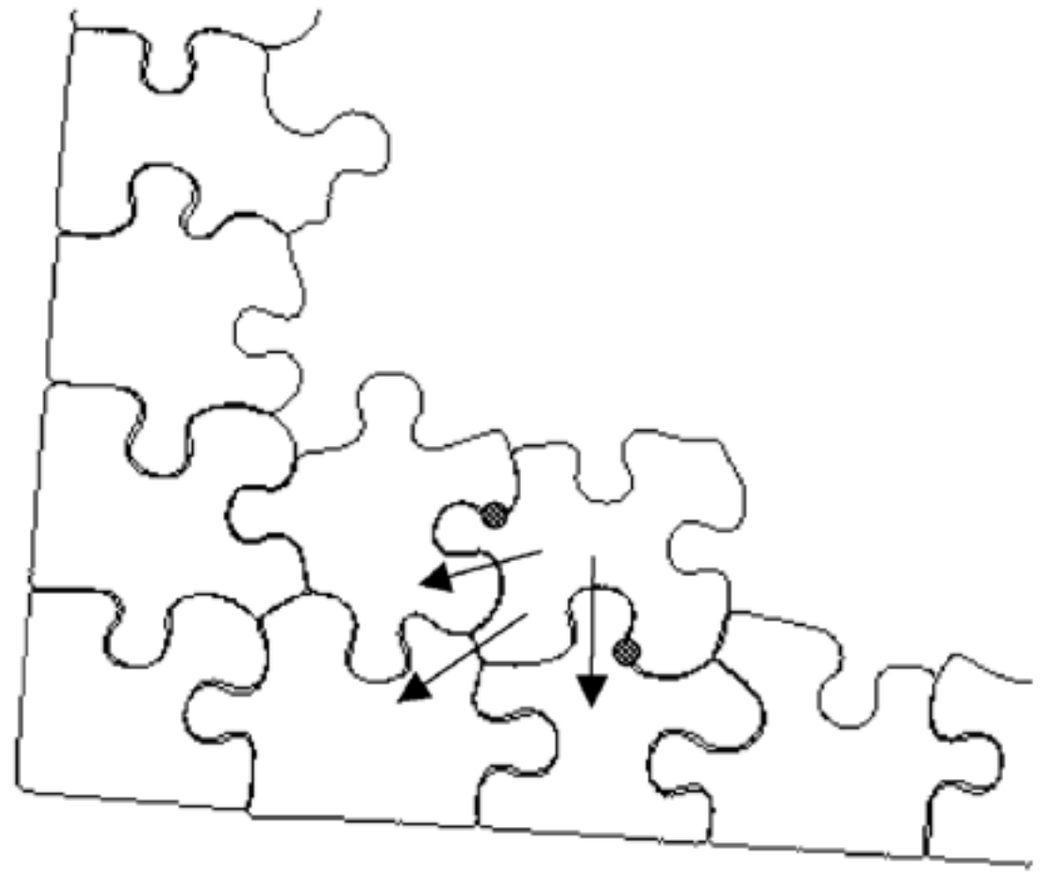


50K ranked matches, most are wrong

Existing Assembly Strategies

Dense Cluster Growth

- clusters of fragments are merged by means of best candidate match

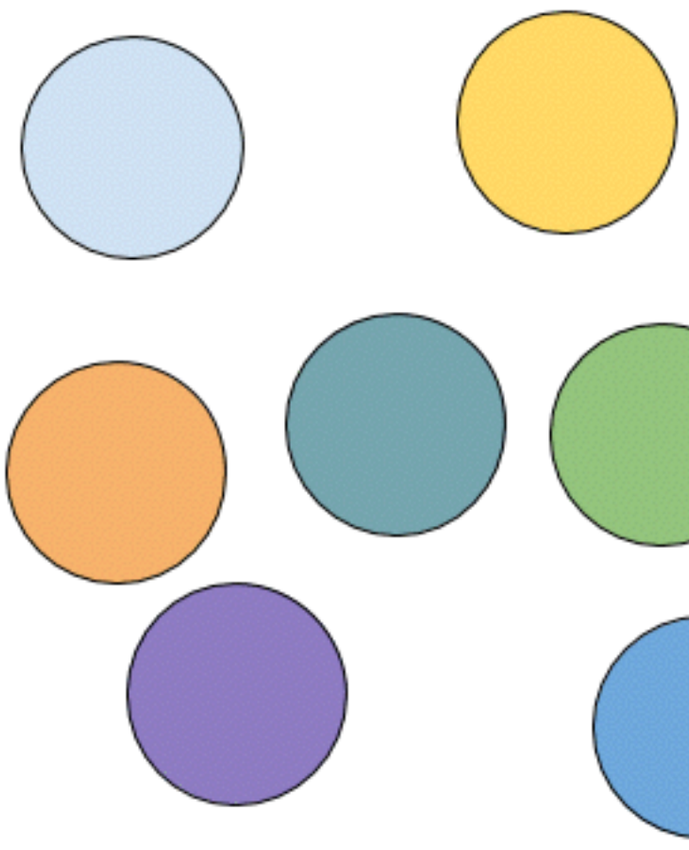


[Goldberg et al. 2002]

Existing Assembly Strategies

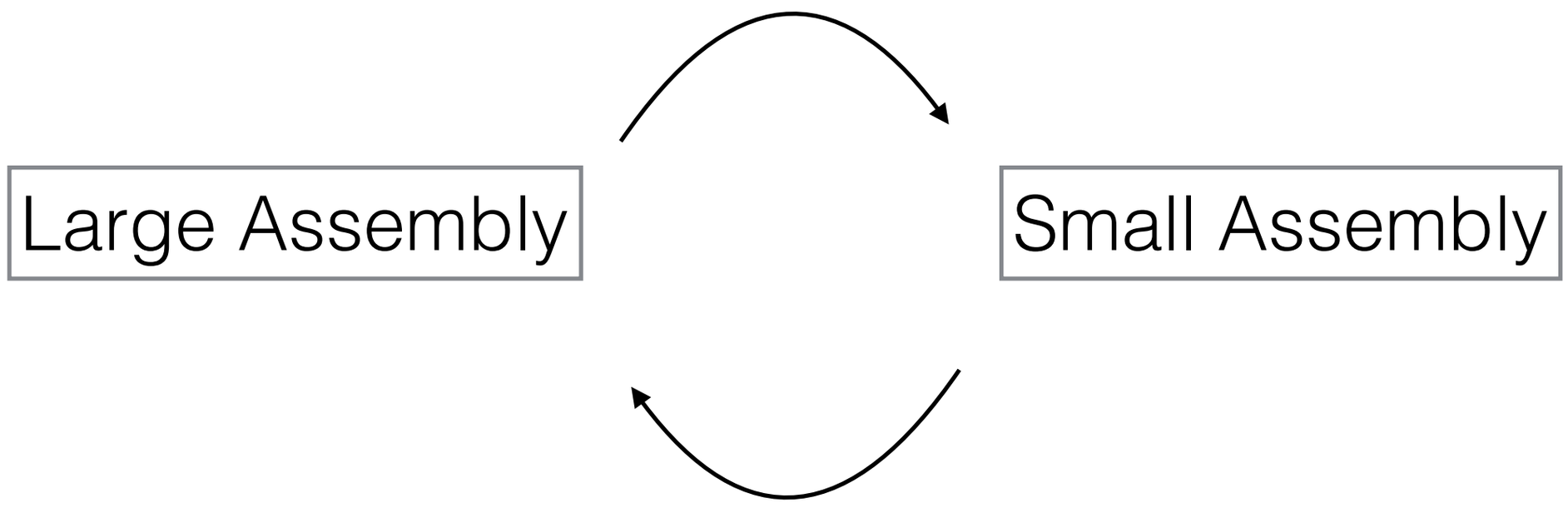
Hierarchical clustering

- Start with all fragments as singleton clusters and merge in priority order
- Fragment alignments are optimized in each iteration
- Process terminates when no good merges are possible



Challenge:
Catch - 22

Need larger assemblies to make decisions about correctness

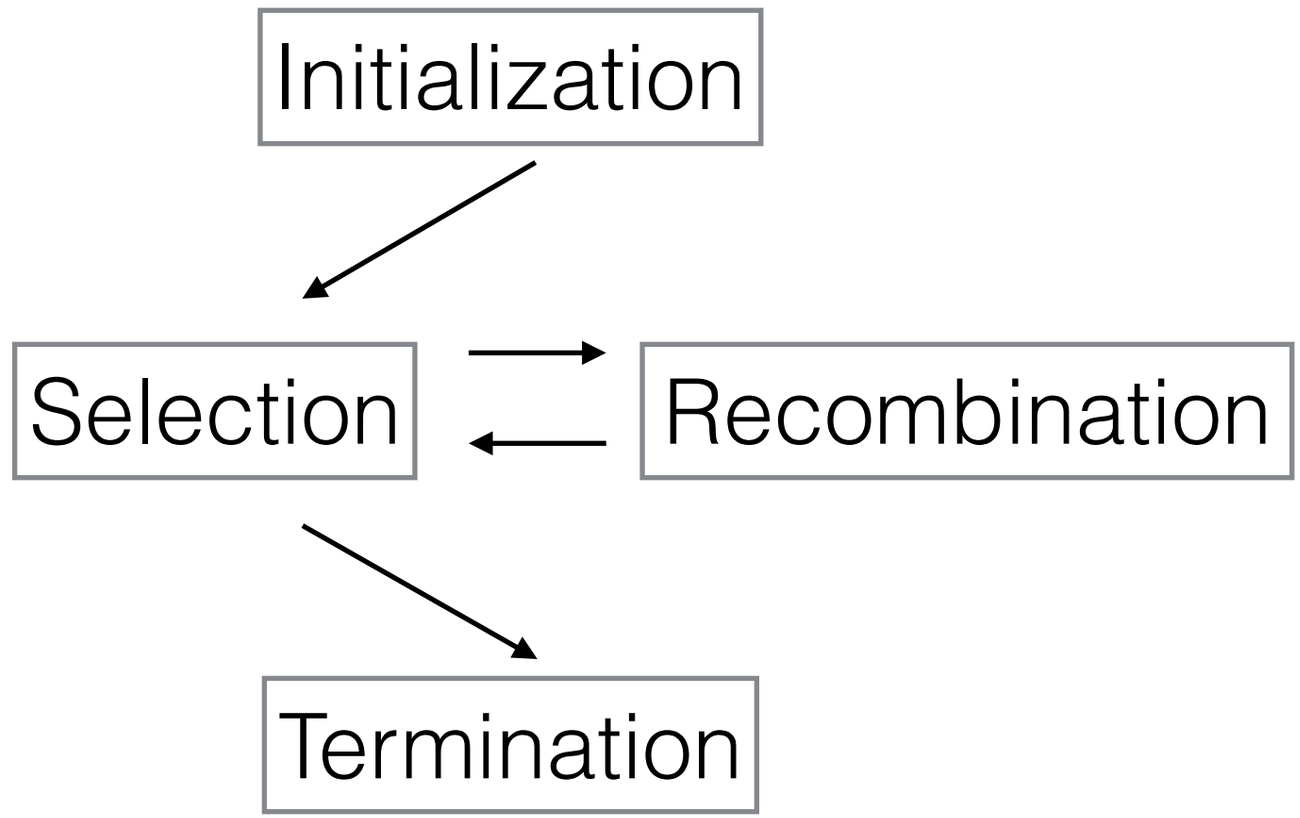


Need small assemblies to construct larger ones

Approach

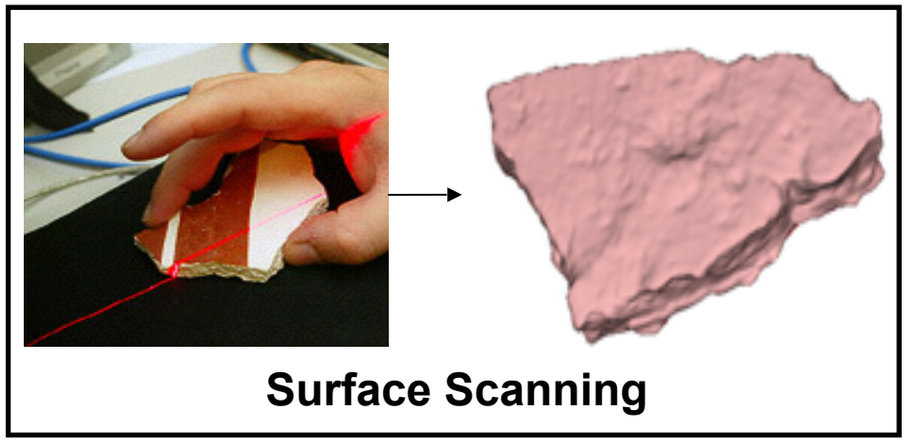
Genetic Algorithm

- Population of clusters
- Recombination
- Selection

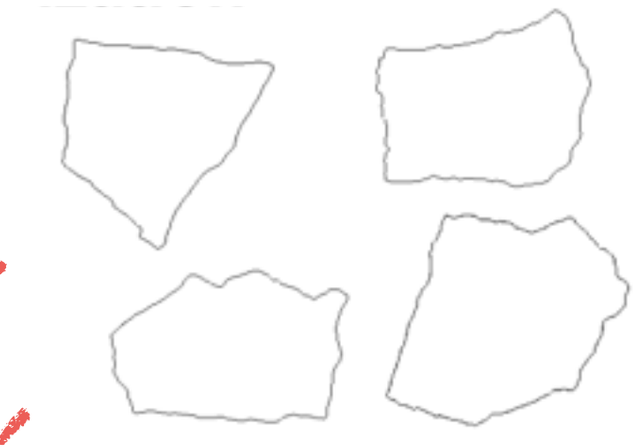


Initialization

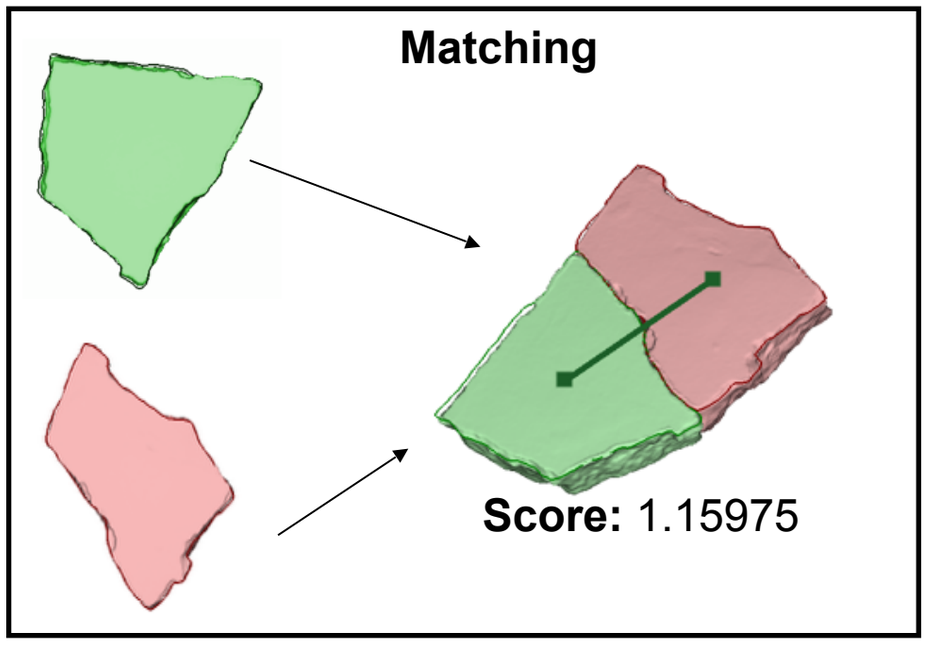
Fragments



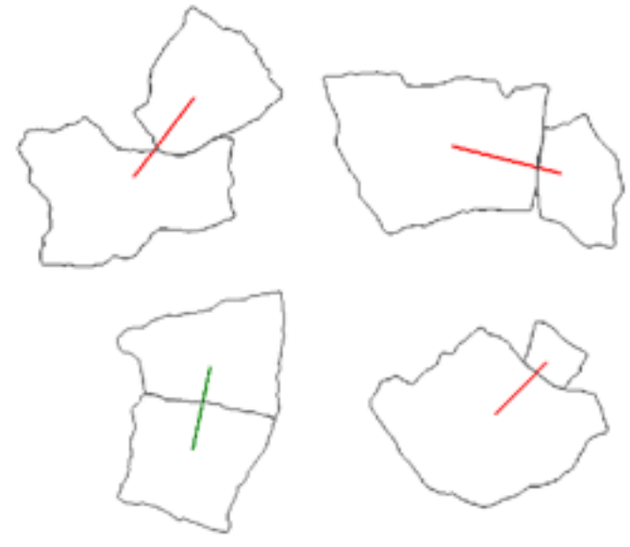
Single Fragment Clusters



Matches

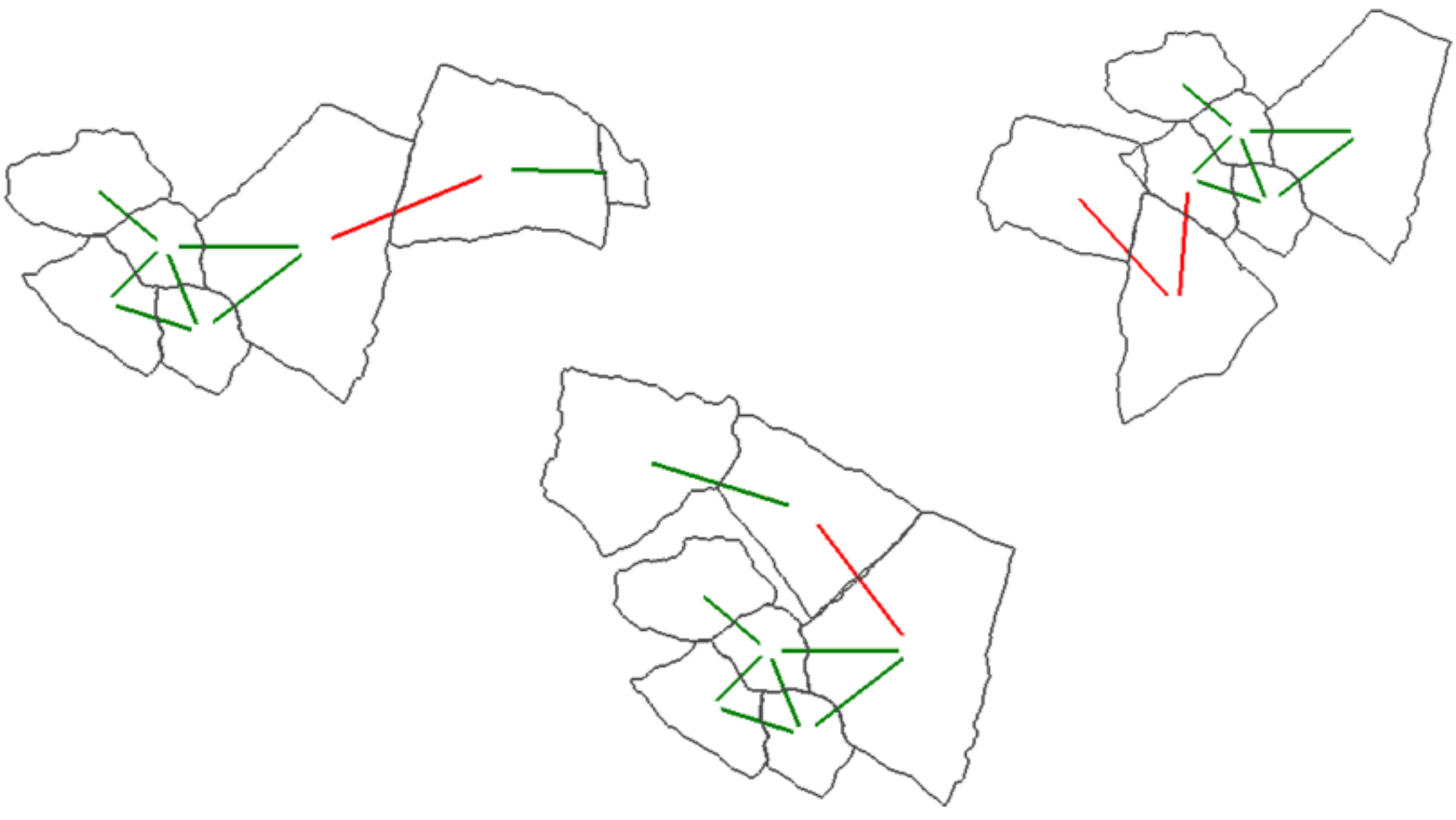


Match Clusters



Population

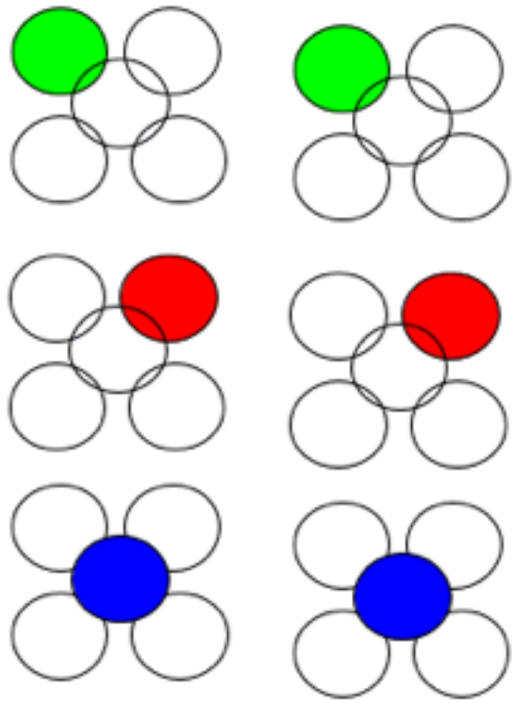
Clusters of fragments joined by matches



Recombination

Create a new cluster from two parent clusters

By Fragment



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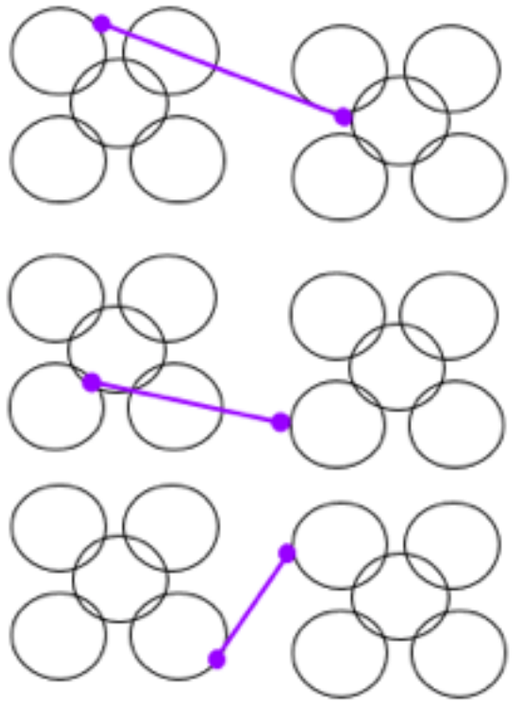


Cluster Optimization

Find rotation angles for each fragment with respect to the global coordinate system

- Find unknown angles

$$\theta_1, \theta_2, \ldots, \theta_n \in [0, 2\pi]$$

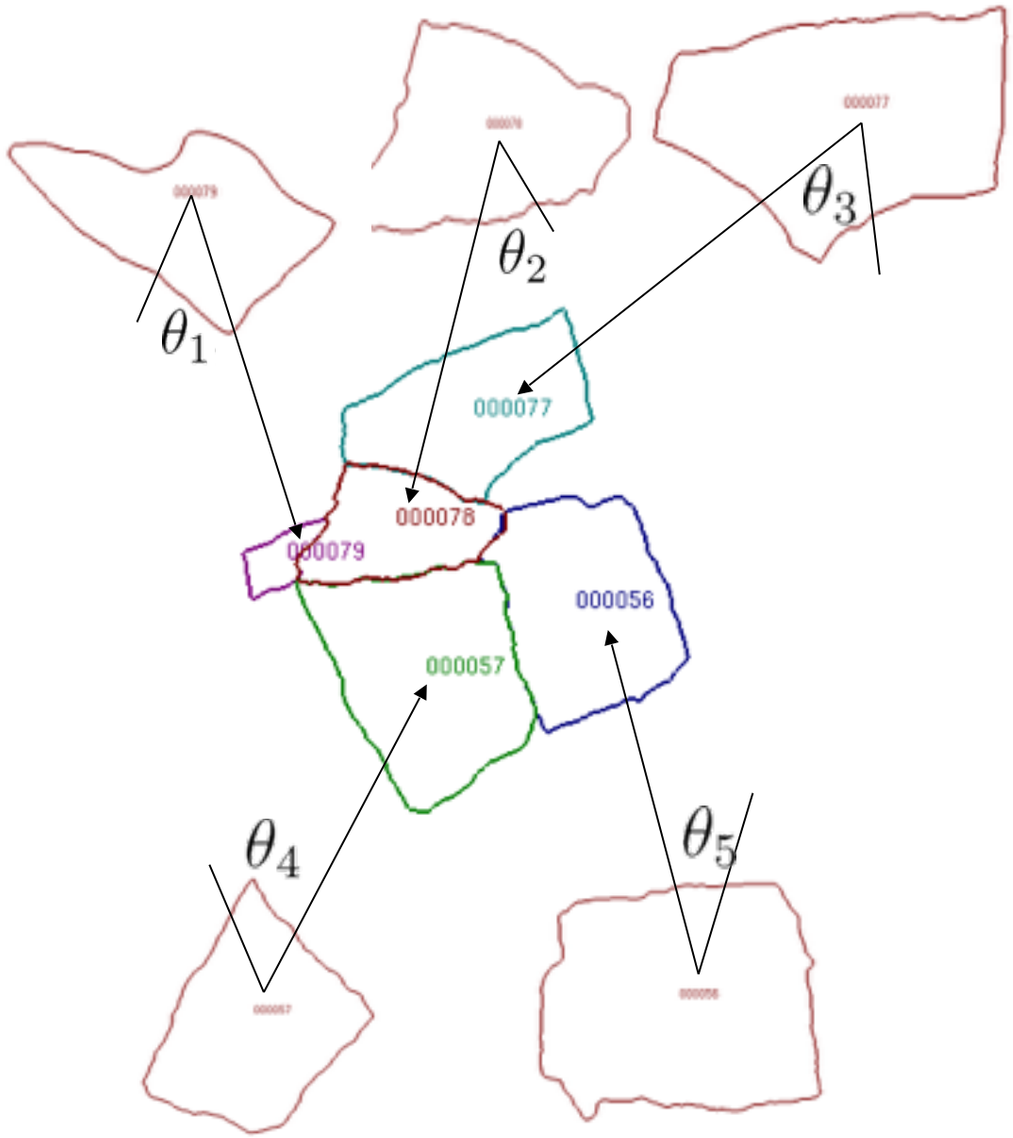
- from known pairwise matches

$$\delta_{ij} = \theta_i - \theta_j$$

Resulting set of equations:

$$\theta_i - \theta_j = \delta_{ij} \mod 2\pi$$

Solving the above is a non-linear problem



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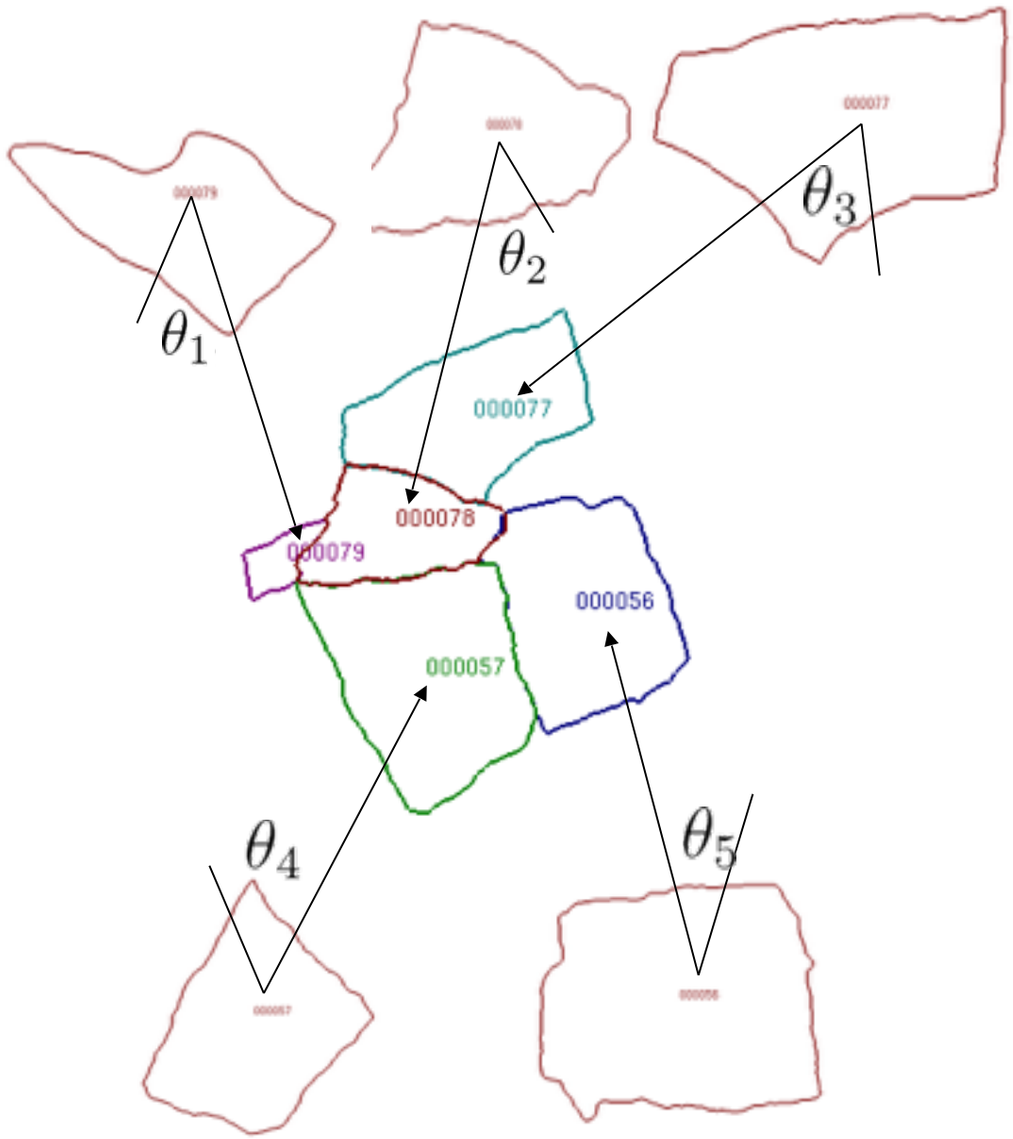
Optimize:

$$\min_{\theta_1,\theta_2,\ldots,\theta_n} \sum_{i,j} \left(z_i - e^{i\delta_{ij}} z_i\right)^2$$

- Least Squares (LS)
- Iterative Least Squares (LS)
- Normalized Eigenvector Method (NEVM) [Singer '11]
- Iterative Normalized Eigenvector Method (it. NEVM)



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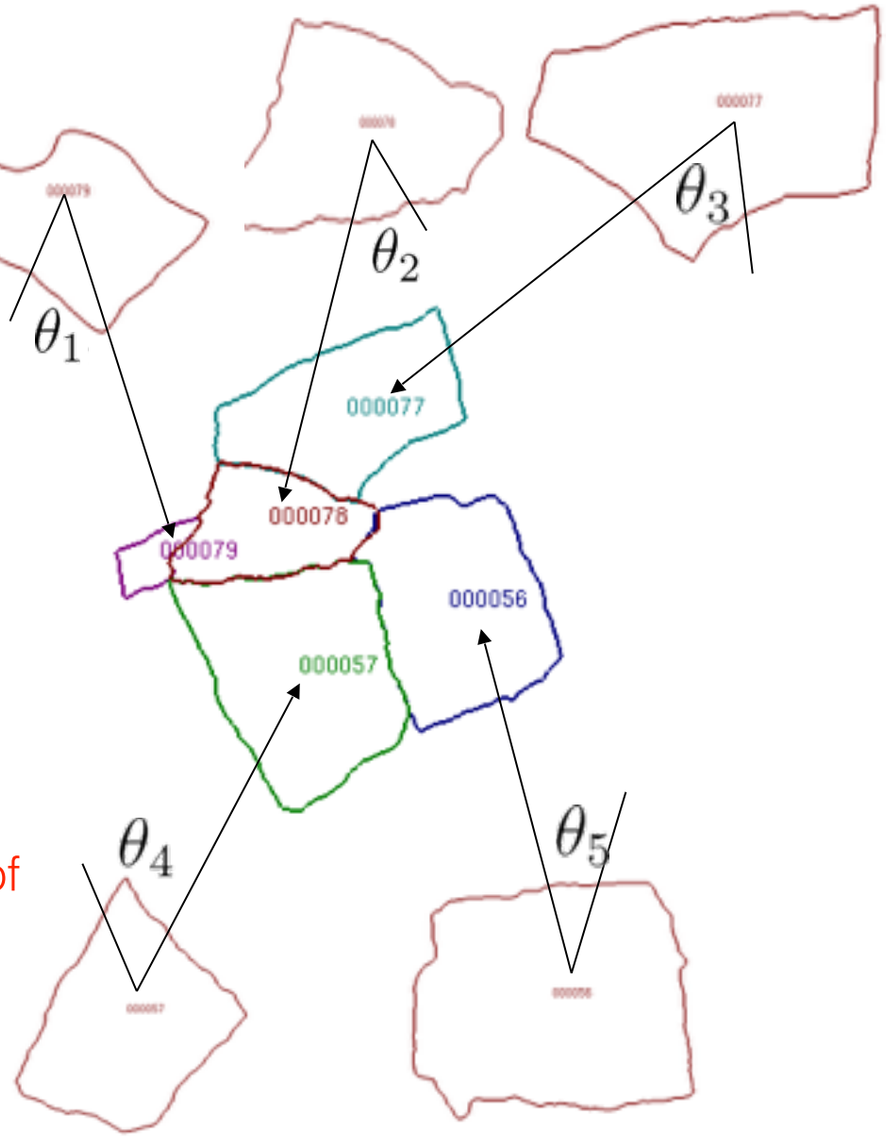
- **Normalized Eigenvector Method (NEVM) [Singer '11]**
- **Iterative Normalized Eigenvector Method (it. NEVM)**

Limit Contribution of Wrong Matches

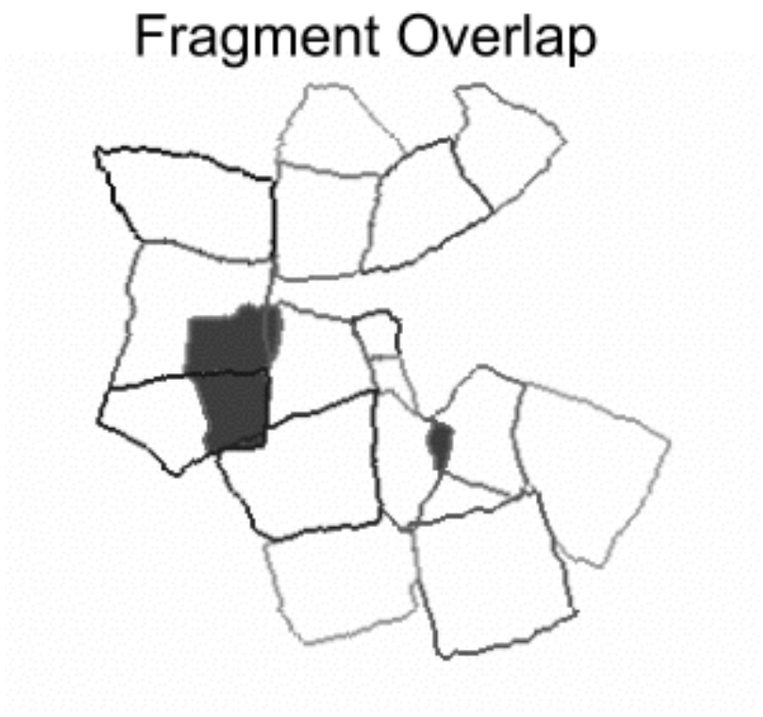


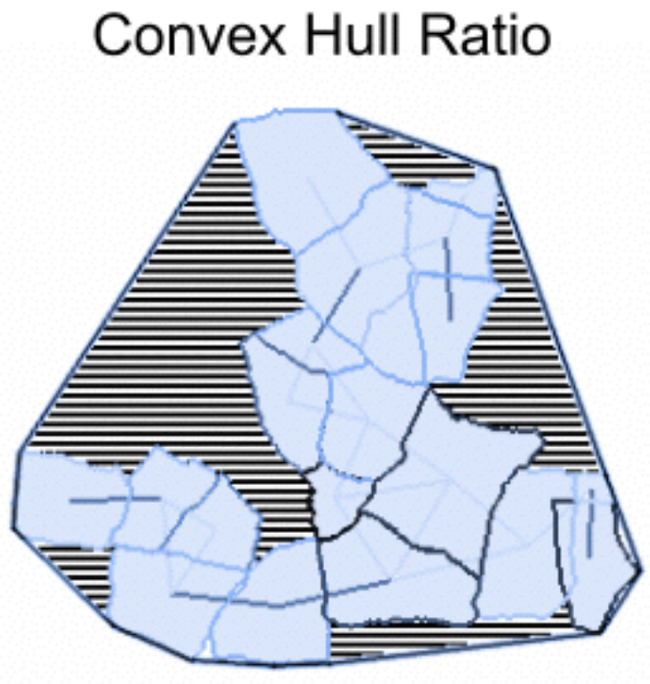
Selection

- Cluster Fitness
- Selection Algorithm
  - Round Robin
  - Diversification

Cluster Fitness

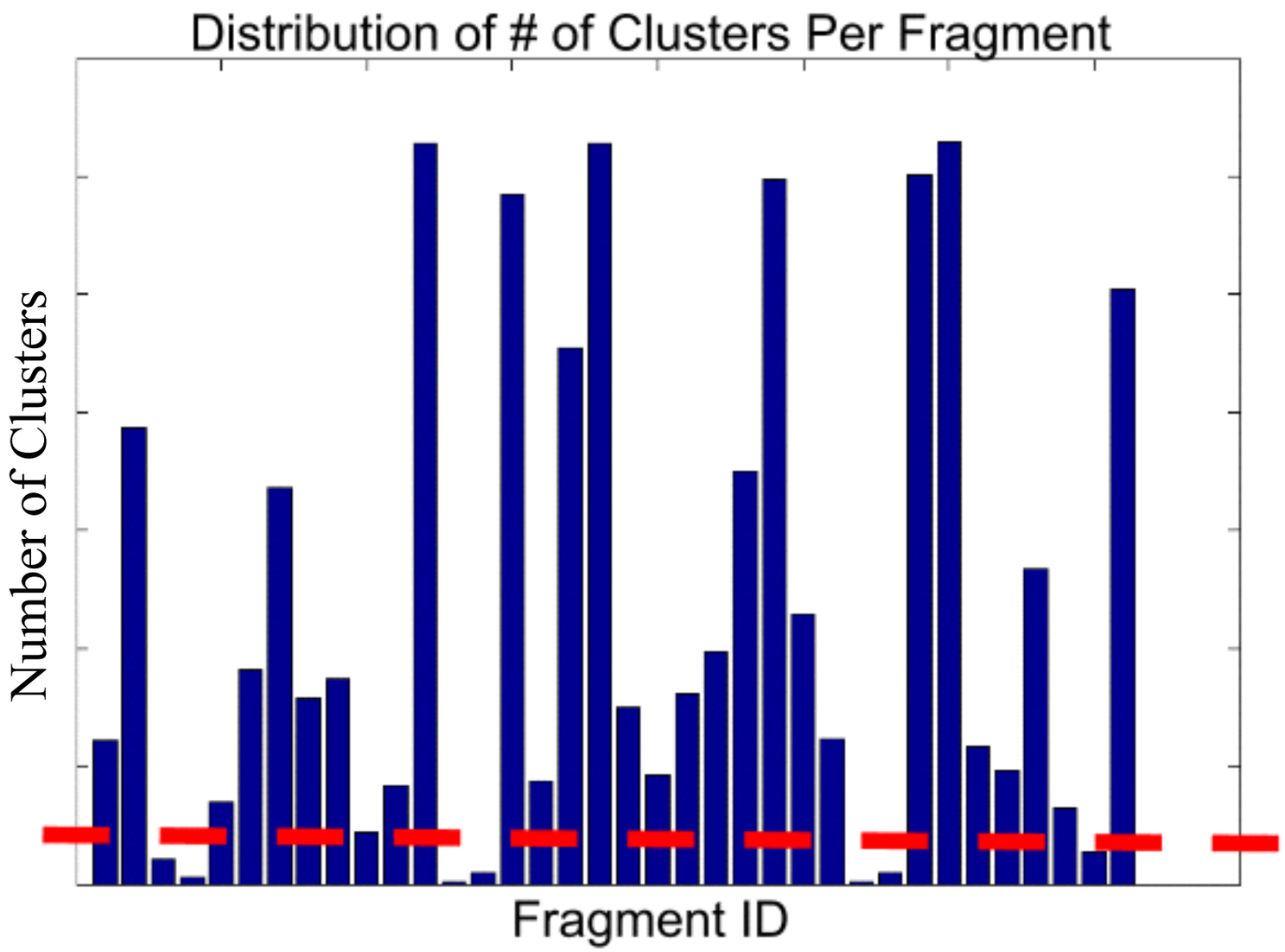
Assign clusters scores based on their intrinsic properties





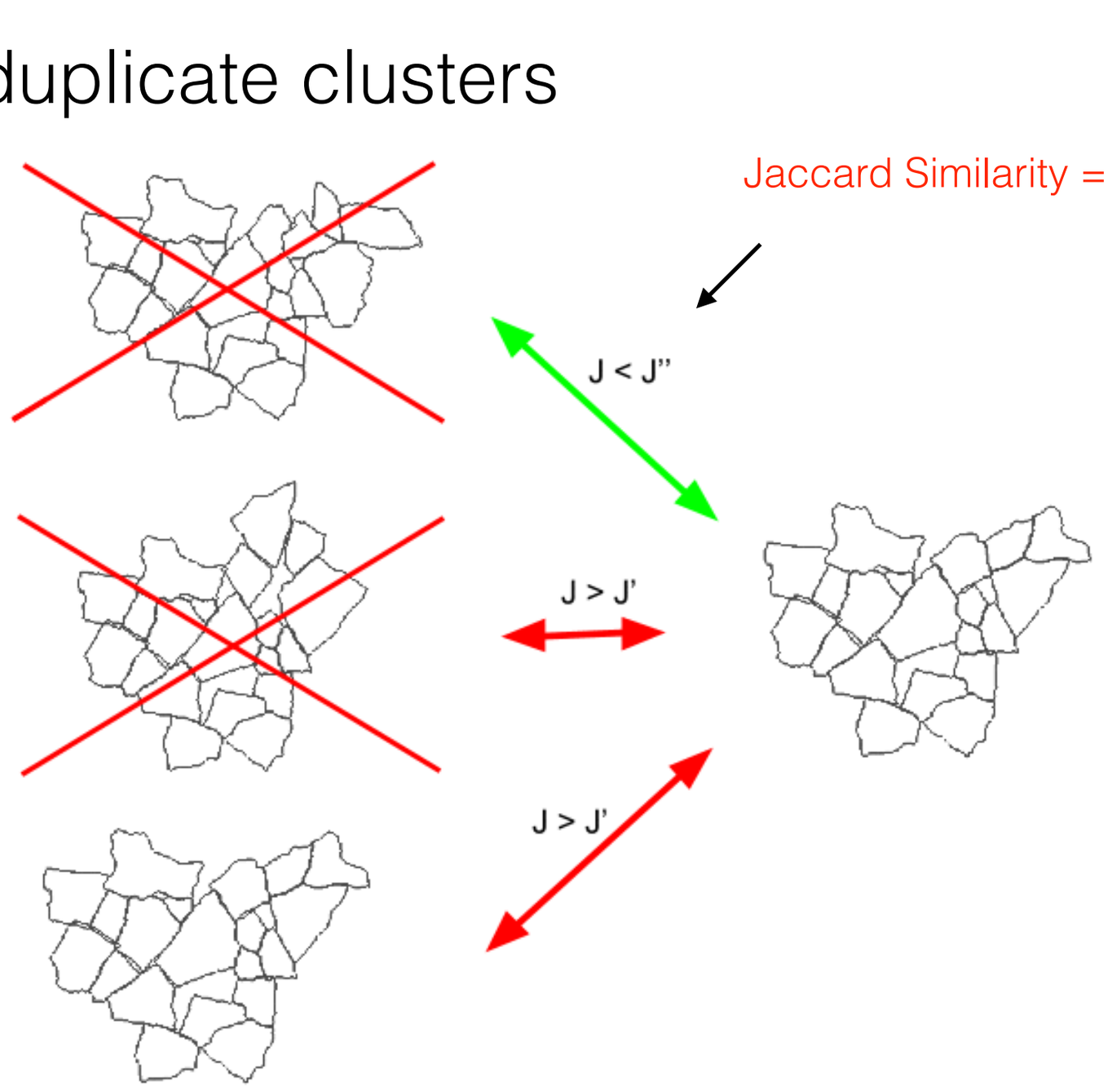
Round-Robin Selection

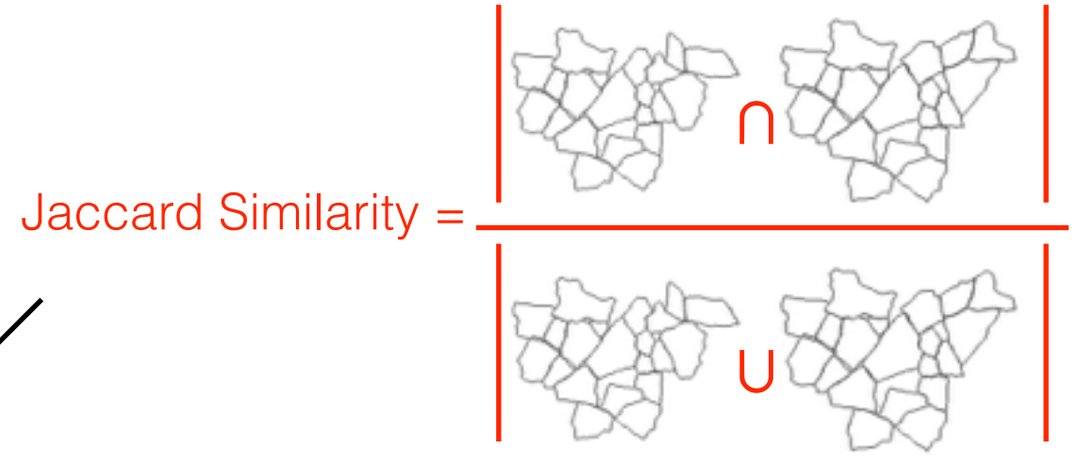
Limit number of clusters with the same fragment



Diversification

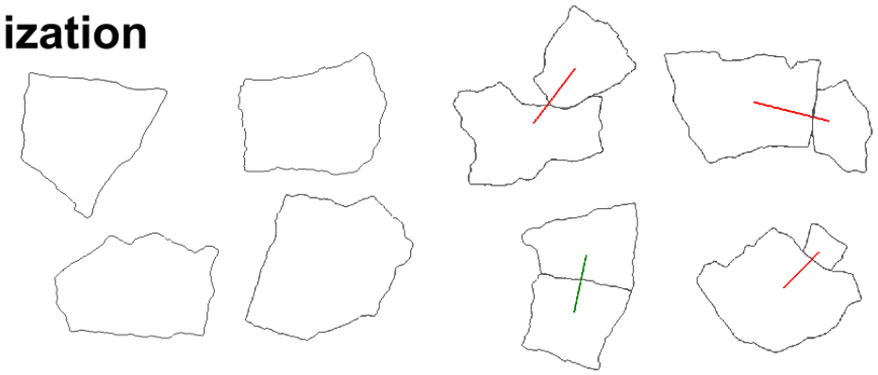
Remove duplicate clusters





Genetic Algorithm

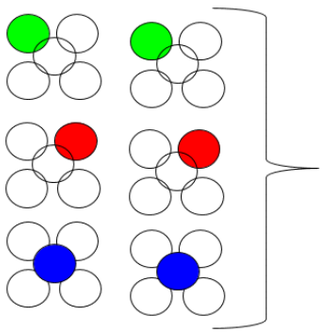
Initialization



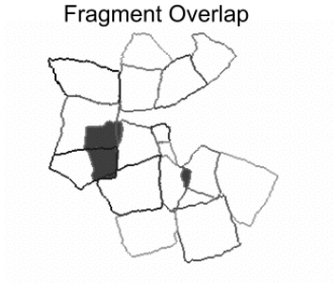
Recombination and Scoring

Merge Feasibility And Scoring

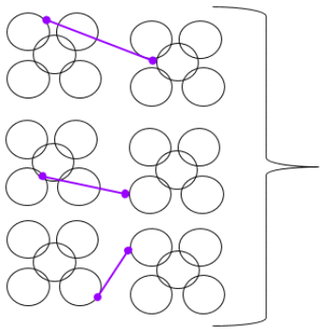
By Match



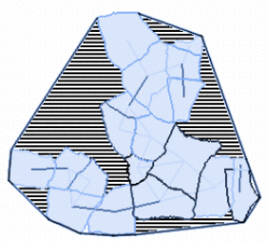
Fragment Overlap



By Fragment

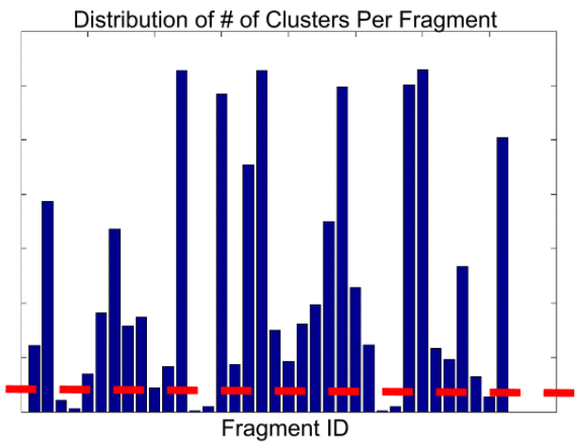


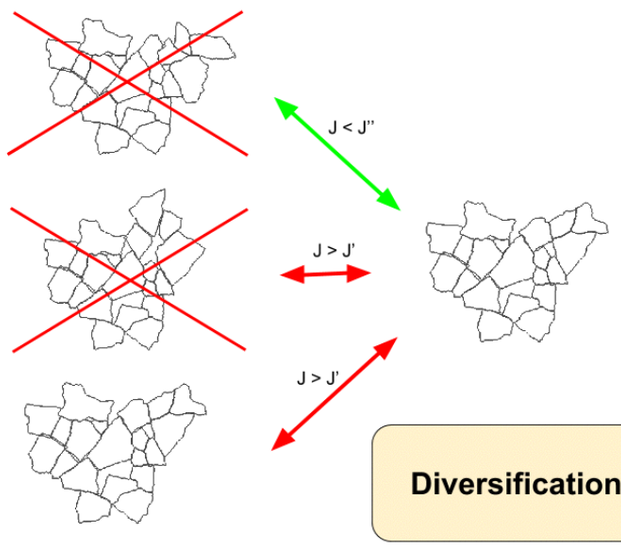
Convex Hull Ratio



Selection

Round robin selection





Diversification

Termination

Evaluation

- Reconstruction quality?
- Algorithmic contributions?

Evaluation:
Reconstruction Quality (Quantitative)

Method	# of Fragments	F-score
Our Full System (GA)	90	0.823
Hierarchical Clustering (HC)	42	0.411
Dense Cluster Growth (DCG)	7	0.082

Performance comparison of different wall painting reconstruction methods with our fitness and feasibility criteria.

$$\text{F-score} = 2 * \frac{\text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}}$$

of correct matches

Evaluation:
Reconstruction Quality (Qualitative)

[Dense Cluster Growth]

[Our Result]

[Ground Truth]

[Hierarchical Clustering]

[Castaneda et al. 2011]

Evaluation:
Reconstruction Quality (Qualitative)

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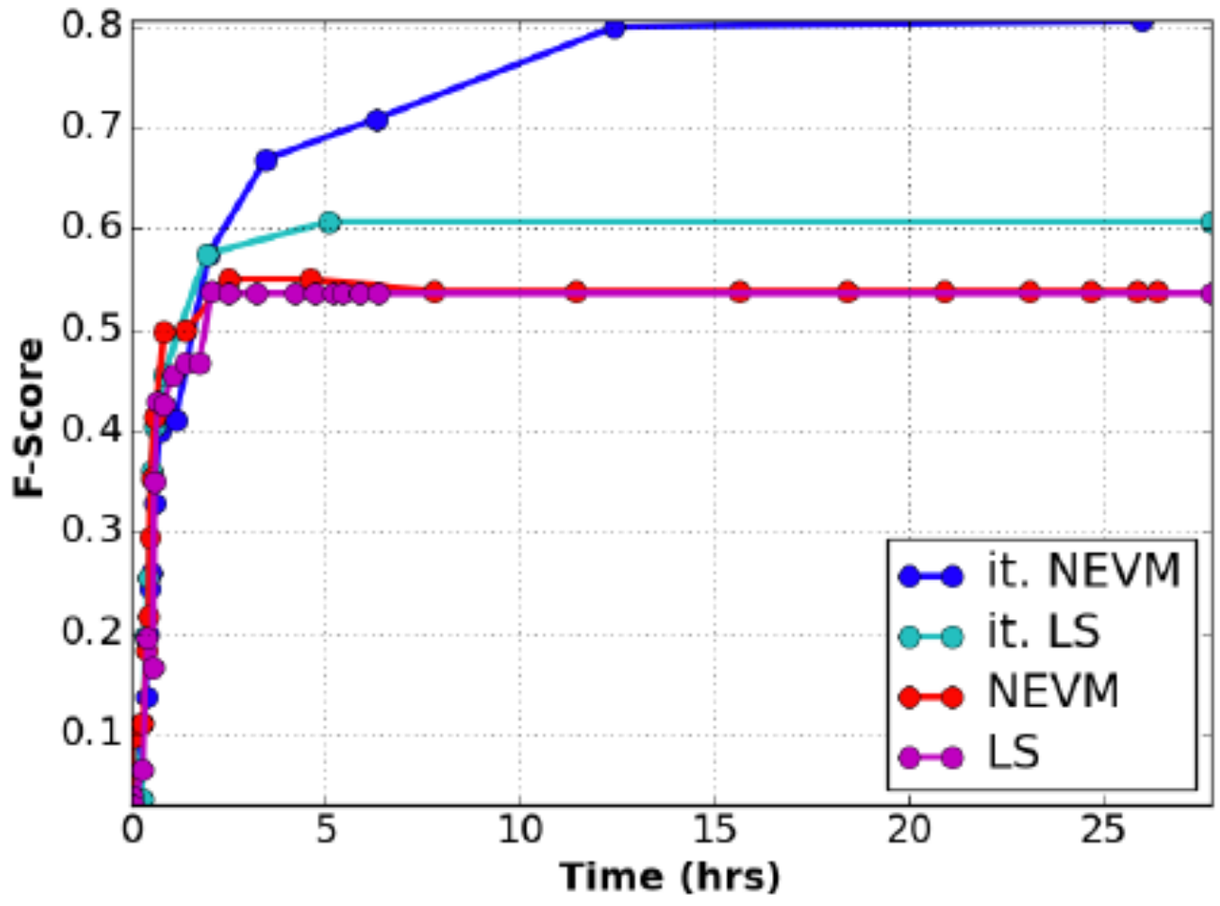
[Ground Truth]

[Hierarchical Clustering]

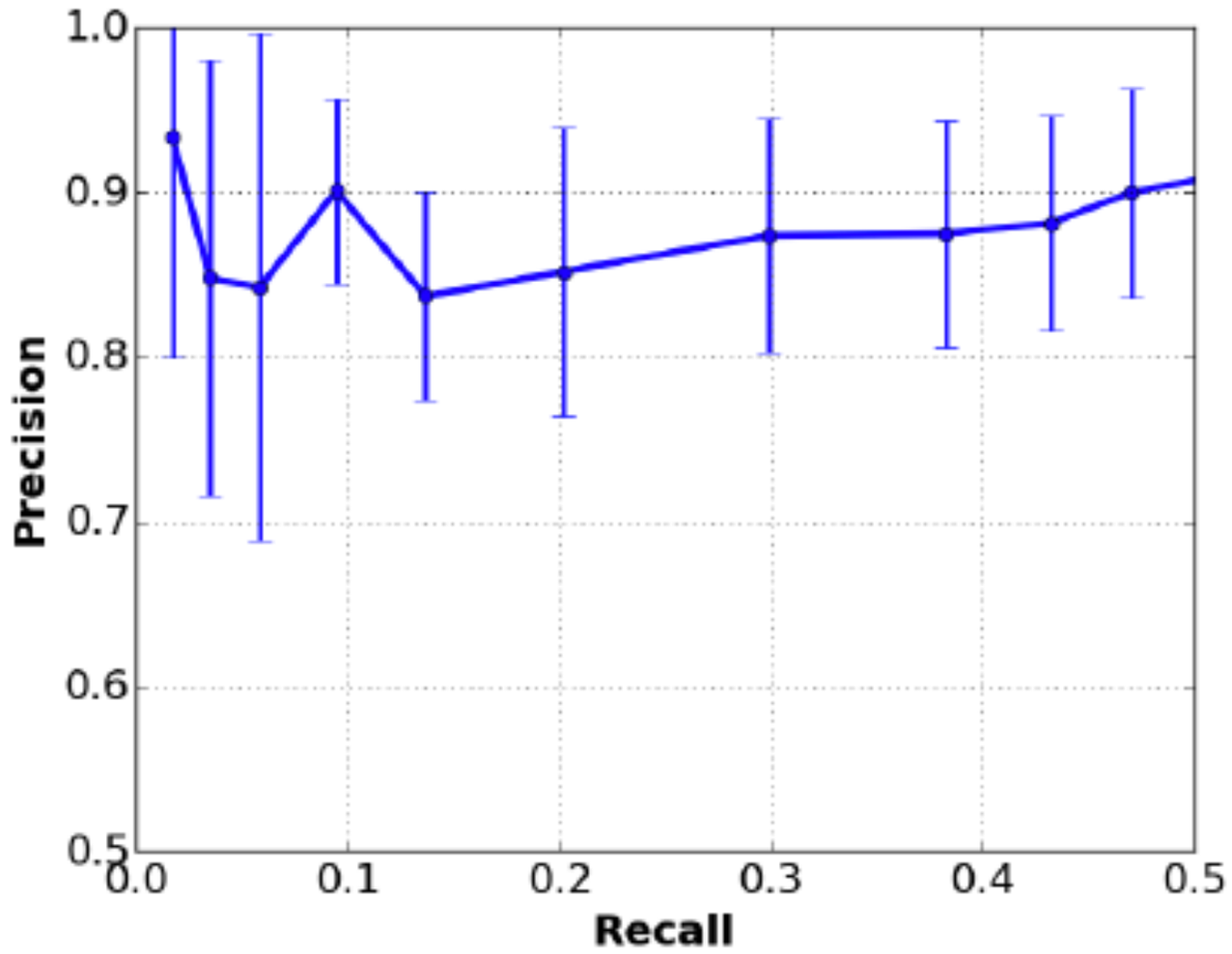
[Castaneda et al. 2011]

Evaluation:
Does Our Cluster Optimization Help?



Comparison of performance of our method with various cluster optimization routines.

Evaluation:
Do Larger Clusters Have Higher Precision?



Precision - Recall comparison of different iteration of our algorithm (aggregated over 10 runs)

Summary

- Genetic algorithms are not greedy - they defer selection of matches until large assemblies are formed

- Our genetic algorithm is able to find larger assemblies than previous methods

- More robust cluster optimization helps find larger assemblies

Limitations

- GA is very time consuming (tens of hours)
- Hand - tuned cluster scoring function

Acknowledgements

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