

A Memetic Algorithm for Searching Spatial Configurations with the Histograms of Forces



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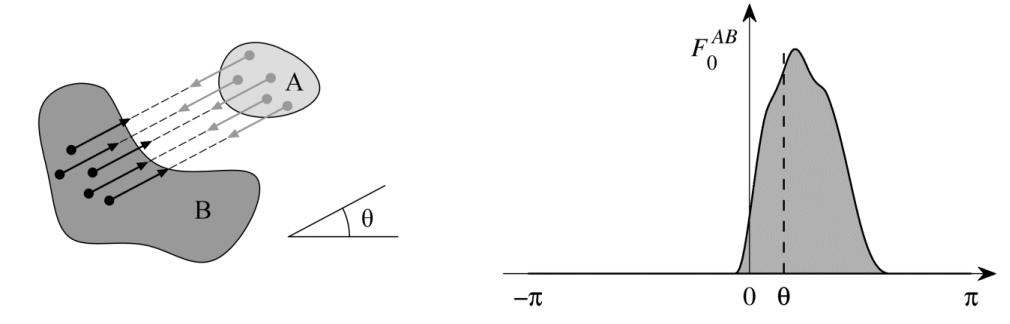


Abstract

We present an approach for searching a large spatial database for a small set of two-dimensional objects based on their spatial relationships. We focus here on the specific problem of matching a sketched map containing several 2D objects to actual satellite imagery. Spatial relationships between objects are captured by the histograms of forces and encoded as an attributed relational graph. The matching process is performed by a memetic algorithm which combines the global search strategy of an evolutionary algorithm with a problem-specific local search method. We investigate several different local search methods and compare the results on randomly generated test data.

Histograms of Forces

The histograms of forces [1] provides a framework for capturing the spatial relationship between a pair of objects. A force histogram $F_r^{AB}(\theta)$ represents the degree of support for the proposition, "A is in direction θ of B."



Attributed Relational Graphs

We are given a geospatial database of known object locations, and a sketch representing a general configuration of objects which is to be located within the reference database. The sketch can be machine or hand-drafted in any orientation and may contain significant simplifications to object shapes and positions. Both the reference database and the sketch are represented as attributed relational graphs (ARGs) in which object labels (e.g. building, parking lot) become node attributes and the force histogram relationships between objects become edge attributes.

A Memetic Algorithm

Create initial population of random chromosomes

While stopping criteria is not satisfied **Do**

For Each parent chromosome in the population **Do**

 Generate children using local search

 Add children to current population and increment the age of the parents

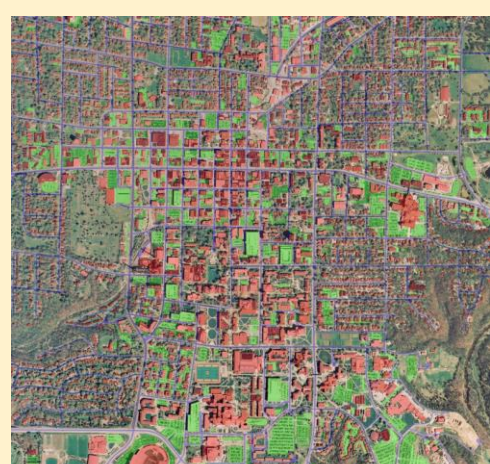
 Old parents are replaced with new random chromosomes

 Save the top chromosomes for the next generation (elitism)

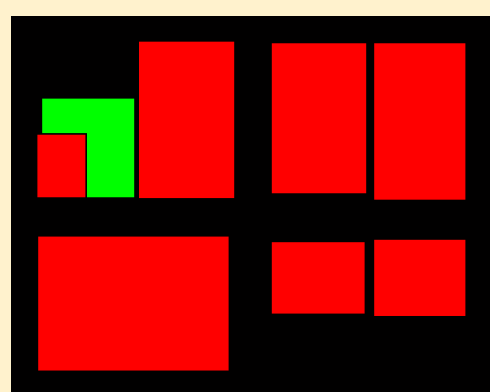
 Fill out the remainder of the population using proportional selection

Return top scoring individuals from the last generation

Input

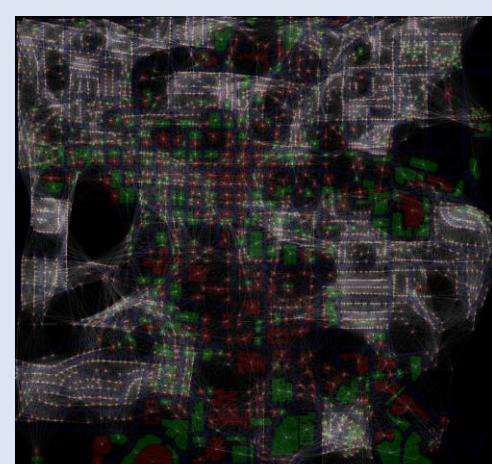


Reference Database

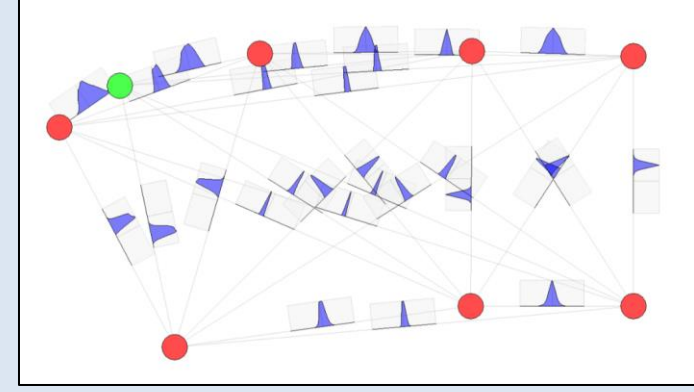


Sketch

ARGs



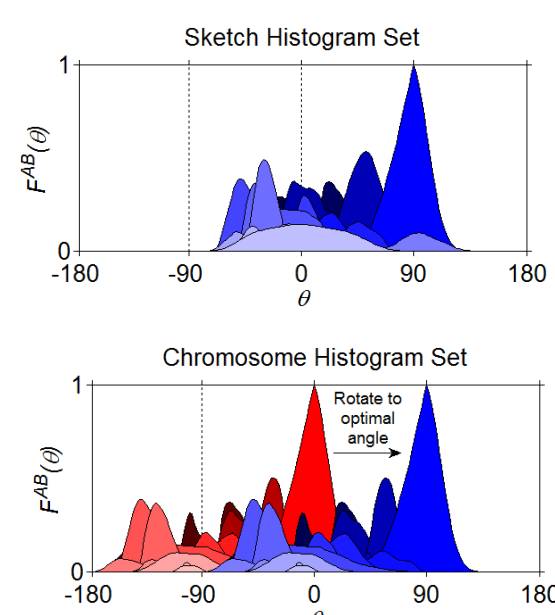
Reference ARG (G_R)



Sketch ARG (G_S)

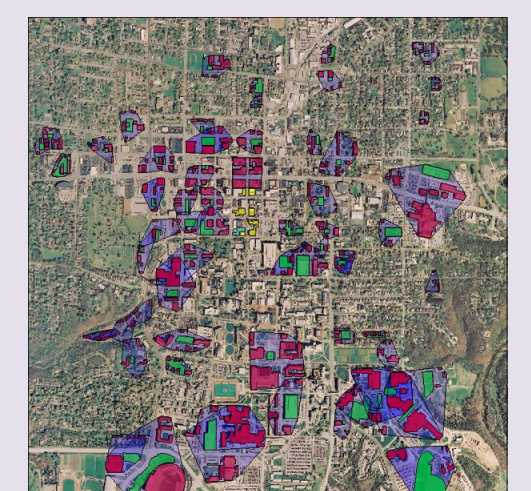
Fitness Evaluation

Chromosomes are compared to the sketch by computing the average cross-correlation between the force histograms of corresponding ARG edges.

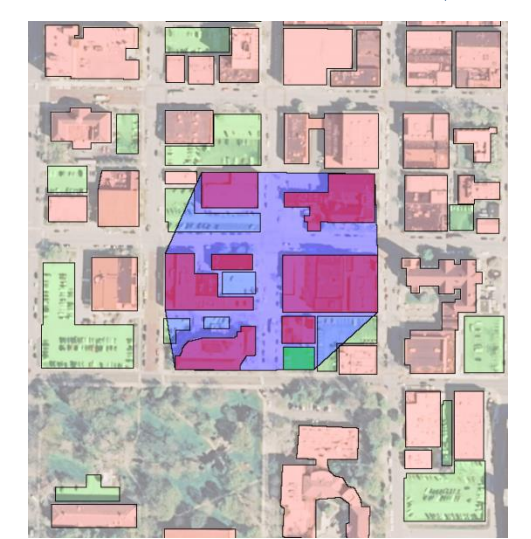


Global Search

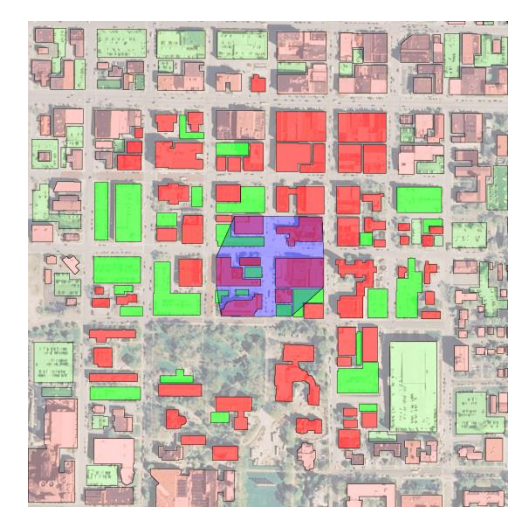
An evolutionary framework maintains a population of chromosomes which could match the sketch.



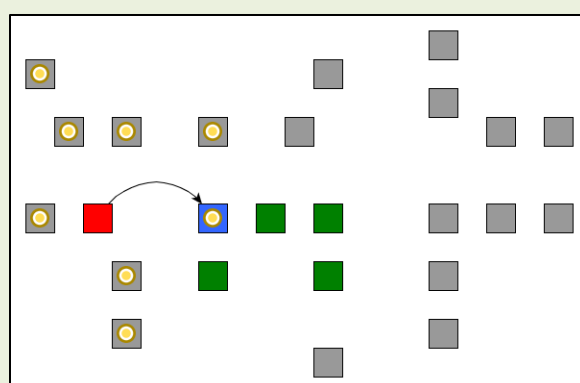
For each chromosome ...



... get nearest neighbors

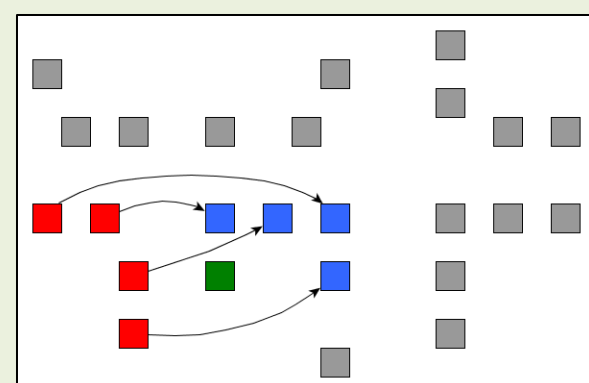


Local Search



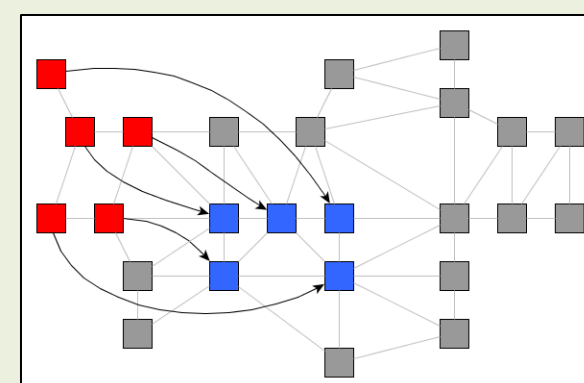
Single-Object Replacement (SOR)

A single object from the chromosome is replaced by one of its neighbors.



Set Reconstruction (1-Seed)

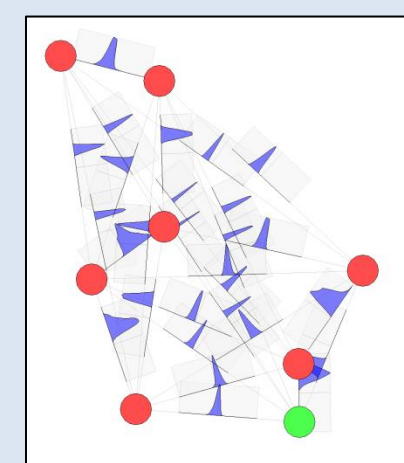
A single seed object is kept from the chromosome, and the remaining objects are chosen to give the best match with the sketch.



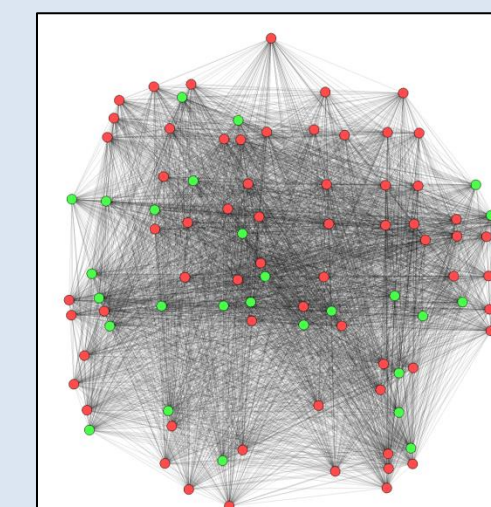
VF2 Subgraph Isomorphism

The VF2 matching algorithm [3] is used to find the subgraph which most closely matches the sketch.

ARGs



Chromosome ARG (G_C)



Neighborhood ARG (G_N)

Experimental Results

We tested our algorithm with resubstitution sketches taken directly from our database of 2814 objects, and simplified versions of these sketches with random orientations. We created 100 test sets for each type of experiment and averaged the search results of 10 trials for each test configuration. Details can be found in [2].

COMMON ALGORITHM PARAMETERS		TEST CONFIGURATIONS AND RESULTS								
Parameter	Value	Sketch Type	Local Search Operator	Min Stall Generations	Max Generations	% Found in Top 1	% Found in Top 5	% Found in Top 10	Average Evaluations	Average Time (seconds)
Population Size	50	Resubstitution	SOR	1000	1000	62.0%	62.0%	62.0%	$1.54 \times 10^8 \pm 3.89 \times 10^7$	3367 ± 849
Max Children per Parent	6	Resubstitution	1-Seed	1000	1000	99.8%	99.8%	99.8%	$2.18 \times 10^8 \pm 9.01 \times 10^7$	7814 ± 3196
Elite Size	5	Resubstitution	2-Seed	100	100	88.2%	88.2%	88.2%	$1.24 \times 10^8 \pm 6.90 \times 10^7$	4703 ± 2660
Max Chromosome Age	10	Simplified	SOR	100	1000	21.4%	23.0%	23.0%	$2.57 \times 10^7 \pm 1.15 \times 10^7$	556 ± 249
Number of Sketch Objects	5	Simplified	1-Seed	100	1000	59.1%	69.0%	69.0%	$2.84 \times 10^7 \pm 1.44 \times 10^7$	1008 ± 508
Nearest Neighbor Connectivity	50	Simplified	2-Seed	100	100	59.9%	72.8%	73.0%	$1.25 \times 10^8 \pm 6.74 \times 10^7$	4883 ± 2651
SOR Permutations	5									

Acknowledgments & References

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[1] P. Matsakis, J. M. Keller, O. Sjahputera, and J. Marjamaa, "The Use of Force Histograms for Affine-Invariant Relative Position Description," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 26, pp. 1-18, Jan. 2004.

[2] A. R. Buck, J. M. Keller, and M. Skubic, "A Memetic Algorithm for Matching Spatial Configurations with the Histograms of Forces," *IEEE Transactions on Evolutionary Computation*, 2012, (in review).

[3] L. P. Cordella, P. Foggia, C. Sansone, and M. Vento, "A (sub)graph Isomorphism Algorithm for Matching Large Graphs," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 26, pp. 1367-1372, Oct. 2004.