Discrete Optimization for Shape Matching

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Problem Statement

Goal: Find correspondence/map between a pair of isometric (or nearly isometric) shapes.
Goal: Find correspondences/maps between all pairs of a shape collection at once.

With a total distortion sum of $0.061 + 0.063 + 0.069 = 0.193$

VS.

With a total distortion sum of $0.061 + 0.065 + 0.060 = 0.186$

$0.186 < 0.196$ 😊
Problem Statement

Theme: Define a way to measure isometric distortion $D$ of a given map. Perform discrete optimization to get the optimal map that minimizes $D$. 
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• Greedy optimization, CVPR 2010.
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• Deformation (continuous), Medical Image Analysis, 2015.
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• Expectation-Maximization (EM), PAMI 2012.
• Deformation (continuous), Medical Image Analysis, 2015.
• Genetic optimization, Transactions on Graphics 2018.
A Genetic Isometric Shape Correspondence Algorithm with Adaptive Sampling

Yusuf Sahillioğlu

SIGGRAPH Asia 2018

Computer Eng. Dept. ORTA DOĞU TEKNİK ÜNİVERSİTESİ MIDDLE EAST TECHNICAL UNIVERSITY Turkey
Goal: Find one-to-one correspondence between a pair of isometric (or nearly isometric) shapes.
Goal: Find sparse one-to-one correspondence between a pair of isometric (or nearly isometric) shapes.
Goal: Find sparse one-to-one correspondence between a pair of isometric (or nearly isometric) shapes using GA.
Applications

✓ Correspondence information needed in many apps such as

✓ Shape interpolation: [Kilian et al. 2007]

✓ Deformation transfer: [Sumner & Popovic 2014]

✓ Attribute transfer: [Sahillioğlu & Kavan 2015]

✓ Shape registration: [Chang & Zwicker 2008]

✓ Shape matching: [Sahillioğlu & Kavan 2016]

✓ Statistical analysis: [Allen et al. 2003]
Contributions

✓ Natural connection established: GA and correspondence.

EvoLisa: Evolving color & geometry of semi-transparent polygons. [Alsing,Hua]
Contributions

✓ Existing maps improved: Adaptive Sampling scheme.
Contributions

✓ Auto-initialization provided: dense match.

Four landmark matches for [Aigerman and Lipman 2015].
Contributions

✓ Auto-initialization provided: real-world scan registration.

Six (left) or more (right) landmark matches for FAUST scans [Bogo et al. 2014].
Contributions

✓ Simple extension demonstrated: partial matching.

More challenging partial matching problem solved with a simple extension.
Method: Overview

✓ Permutation creation task carried out by genetic algorithm.
✓ Looking for the best/fittest permutation/chromosome of samples/genes that matches w/ the fixed samples: 1 2 .. N.
Method: Design Decisions

✓ Healthy parts of two bijections \textit{xovered} into a better one.
Method: Design Decisions

✓ Individual map mutated into a better one.
**Method: Design Decisions**

✓ **Fitness** of a given chromosome representing permutation \( \pi \)

\[
F(\pi) = 1 - D_{iso}(\phi_\pi)
\]

where \( \phi_\pi \) is the bijection that maps \( i^{th} \) sample to \( \pi[i]^{th} \) sample, and

\[
D_{iso}(\phi) = \frac{1}{|\phi|} \sum_{(s_i, t_j) \in \phi} \left( \frac{1}{|\phi'|} \sum_{(s_l, t_m) \in \phi'} |d_g(s_i, s_l) - d_g(t_j, t_m)| \right),
\]

which is a variant of the isometric distortion measures used in [Bronstein et al.’06, Huang et al.’08, Sahillioğlu & Yemez’11].
Method: Design Decisions

✓ **Fitness** of a given chromosome representing permutation $\pi$

\[ F(\pi) = 1 - D_{iso}(\phi_\pi) \]

\[
D_{iso}(\phi) = \frac{1}{|\phi|} \sum_{(s_i, t_j) \in \phi} \left( \frac{1}{|\phi'|} \sum_{(s_l, t_m) \in \phi'} |d_g(s_i, s_l) - d_g(t_j, t_m)| \right)
\]

A bad/high-distortion map.

\[ |.34 - .48| = .64 \]
Method: Initial Population

✓ Current population evolved to the next generation.
✓ Initial population based on geodesic consistency.

✓ $g^s_i$ and $g^t_j$: Vector of geodesic distances to a few special samples that are already accurately matched – see Initial Bijection.
✓ Initial match candidates for each sample $s_i$ are $\{t_j\}$ that satisfy

$$d_c(g^s_i, g^t_j) = \max_k |g^s_i[k] - g^t_j[k]| < .125 \text{ (toe to knee half geo)}$$

- Special sample matches.
- $s_i$ and its initial match candidates.
Method: Initial Population

✓ Current population evolved to the next generation.
✓ Initial population based on geodesic consistency.
   ✓ About 10 candidates per sample (for N=100 case).
   ✓ Each initial chromosome filled by picking a random candidate for its $i^\text{th}$ gene. Population size always $10N$, i.e. 1000 chromosomes.
✓ Duplicates prevented to preserve bijection.
✓ Some samples to random matches, not initial match candidates.

- $Si$: Special sample matches.
- $si$: $si$ and its initial match candidates.
Method: Initial Population

- Current population evolved to the next generation.
- Random initial population (left) also lead to a good final generation, but not as fast & accurate as our initialization.

Fittest members of initial (top) and final (bottom) populations shown.
Method: Evolution of Population

- Current population evolved to the next generation through genetic operators.
- Current population divided into good and bad parts based on chromosome fitnesses.
- Some chromosomes in the bad part replaced by the crossovered child of two good parents.
- Some chromosomes mutated for individual improvement.
- Elitism for free: best chromosome copied to the next gen.
Method: Evolution of Population

✓ Current population evolved to the next generation through genetic operators.

```plaintext
Input: S and T s.t. |S| = |T| = N, samples on two meshes
Output: φ : S → T, one-to-one correspondence
U = initPopulation() //U = {C₁, C₂, ..., Cₚ}, P is population size
For generation = 1 to max # generations
  Fₚ = getFittest(U) //Evaluates all {Cᵢ} via F(Cᵢ) made ready
  If (Fₚ is fixed for the last L₁ generations || //L₁ = 100
    no swap mutations in the last L₂ generations || //L₂ = 10
    Fₚ > 1 - ε) //ε = .001
    Break; //Converged!
  evolvePopulation()
  For i = 1 : N //N is # of genes (= samples on mesh)
    φ(sᵢ) = t₁[i] //fittest is maintained as the first chromosome C₁
  Return φ

evolvePopulation(Population U)
  Descending sort on U s.t. Cᵢ > Cⱼ ∀i < j, i.e., C₁ is the fittest
  G = {C₁, C₂, .., Cₙ}, B = {Cₙ₊₁, .., Cₚ} //Good and bad parts,
  For each Cᵢ ∈ B //where h = P/2
    If rand() < fₓover //rand() returns a number in [0, 1]
      Let Cⱼ and Cₖ be random chromosomes from G s.t. Cⱼ > Cₖ
      Cᵢ = xover(Cⱼ, Cₖ) //Cᵢ ∈ B updated by the newborn child of
                   //2 good parents. Elitism for free as Cᵢ can’t
                   //initially be C₁, the fittest chromosome
  For i = 2 : P
    If rand() < fmutation
      mutate(Cᵢ) //Cᵢ ∈ U is updated. Elitism for free as the fittest C₁
                   //is excluded from consideration (i ≥ 2)
```
Current population evolved to the next generation through genetic operators.

- **Crossover:** duplication-free (bijection), winner/loser-based.
- **Mutation:** duplication-free, geodesic vector compatibility.

```plaintext
mutate(Chromosome C)
For i = 1 : N - 1
If d_c(g^s_i, g^t_{C[i]}) > τ // for d_c (τ = .125)
  //Geodesic vectors g are incompatible; swap C[i] with a good C[j]
    Repeat j = rand(i + 1, N)
    Until d_c(g^t_{C[j]}, g^s_i) ≤ τ
    Swap C[i] and C[j]
```

Resulting child:
Current population evolved to the next generation through genetic operators, whose relative advantages visualized:

- (a) random initialization.
- (b) result w/ muts only.
- (c) result w/ xovs only.
- (d) result w/ both on.
Method: Initial Bijection

✓ While evaluating $F$, $\phi' = \phi$ to make this frequent op. fast.

✓ Few special samples by FPS w/ a special stopping condition.
✓ Initial population of chromosomes evolved through Slide19.
Adaptive Sampling

✓ Matched samples relocated in a local neighborhood by considering geodesic consistency & sampling regularization.

\[ \mathcal{E}(\hat{t}, \phi) = \sum_{(s_i, t_j) \in \phi} \sum_{(s_l, t_m) \in \phi} |d_g(s_i, s_l) - d_g(\hat{t}_j, \hat{t}_m)| + \alpha \|\hat{r} - r_s\| \]

✓ Given a map (bijection or not) \( \phi : S \rightarrow T = \{(s_i, t_j)\} \), new target sample locations computed such that \((s_i, \hat{t}_j)\) is a better match than \((s_i, t_j)\) was.

✓ New sampling radius on target \( \hat{r} \) (based on new \( \{\hat{t}_j\} \)) asked to look like the radius of the source samples \( r_s \).

✓ Coordinate descent idea: if moving from \( t_j \) to \( t_k \) in its 1-ring improves \( \mathcal{E} \), then \( t_j = \hat{t}_k \) performed. Process repeated.
Adaptive Sampling

✓ Matched samples relocated in a local neighborhood by considering geodesic consistency & sampling regularization.

Sole without AS.

Sole with AS.
Matched samples relocated in a local neighborhood by considering geodesic consistency & sampling regularization.

\[ D_{grd} = 0.0341 \]

\[ D_{grd} = 0.0303 \]
Results

✓ Genetic maps on isometric (top 2 rows), nearly-isometric (bottom left-middle) cases. **Limitation** on non-isometries (gorilla-human).
Results

- Fitness guaranteed to increase in new generations (elitism).
- Ground-truth distortion decreased in new generations.
- AS takes the final distortion of GA and decreases it further.
Results

✓ Comparisons with BIM [Kim et al.’11], PS [Tevs et al.’11], OTE [Aigerman & Lipman’15], GW [Solomon et al.’16].

BIM and OTE fail on non-sphere topology but we do not. Holes fail PS but not us.
Future Work

✓ Dense correspondence.
✓ Non-isometric correspondence.
✓ Partially-isometric correspondence.
✓ Collection-wise consistent correspondence.

✓ Partially-isometric matching already done by updating our fitness using the scale-invariant measure in [Sahillioğlu & Yemez’12] and introducing dummy entries that represent the unmatched samples on the full shape.
First genetic algorithm presented for isometric shape correspondence problem.

- Easy to implement, e.g., no algebra library.
- Fast as space of permutations explored wisely.
- Free of embedding errors, e.g., no parameterization.
- Requires no initial input matches, no genus restrictions.
- Robust against triangulation quality, mild geometric noise.

Adaptive Sampling algorithm presented for improvement of any sample-based correspondence method.
Thanks

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