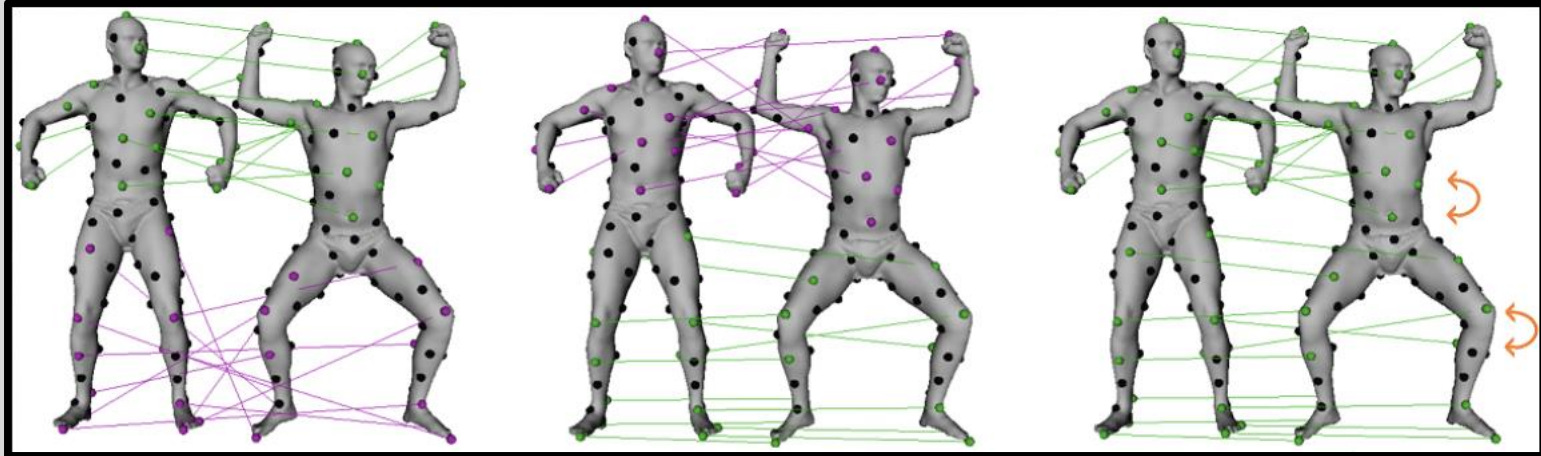# A Genetic Isometric Shape Correspondence Algorithm with Adaptive Sampling
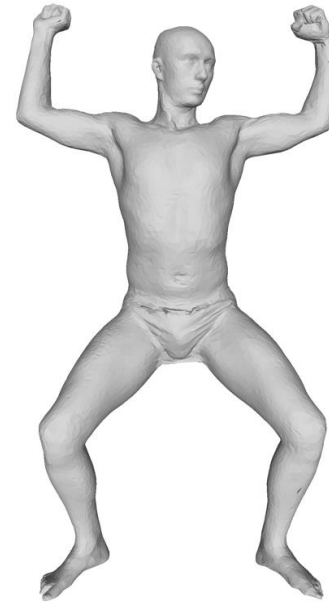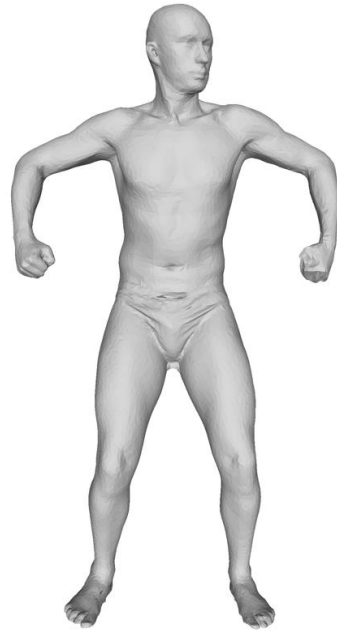

Yusuf Sahillioğlu

SIGGRAPH Asia 2018

Computer Eng. Dept. ORTA DOĞU TEKNİK ÜNİVERSİTESİ MIDDLE EAST TECHNICAL UNIVERSITY Turkey
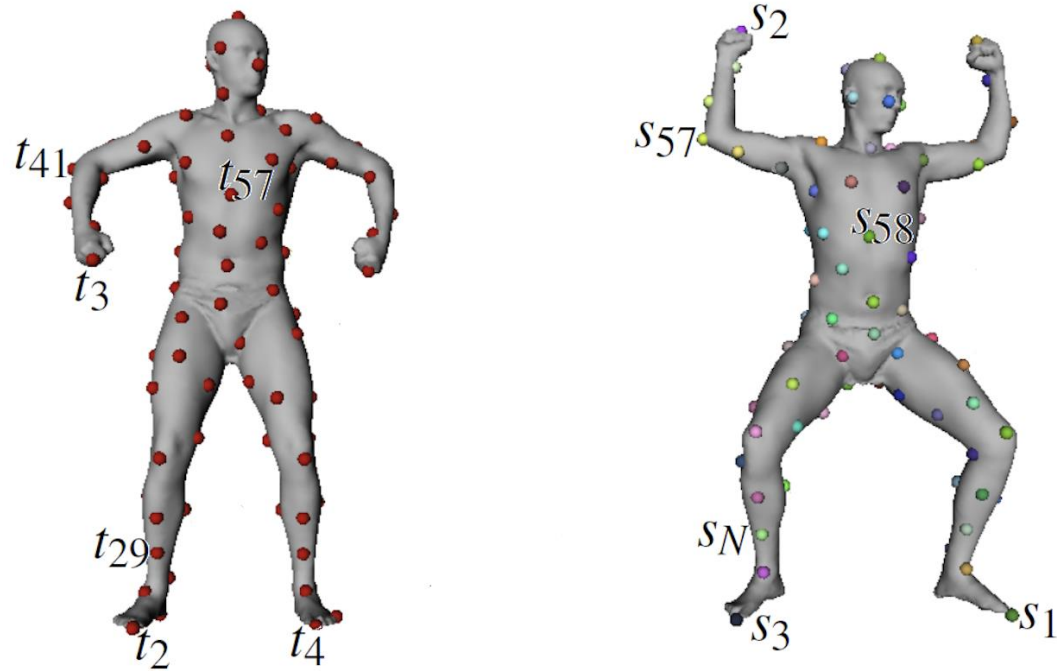
Problem Statement

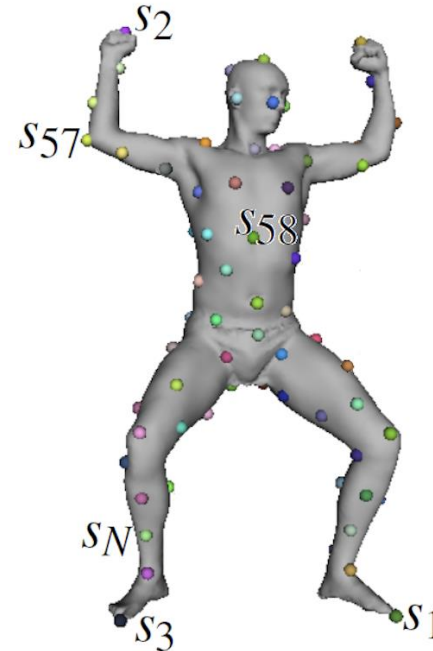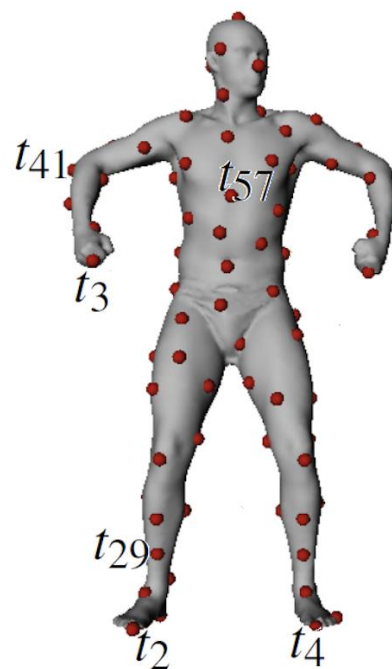Goal: Find one-to-one correspondence between a pair of isometric (or nearly isometric) shapes.

Problem Statement

Goal: Find sparse one-to-one correspondence between a pair of isometric (or nearly isometric) shapes.

Problem Statement

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:
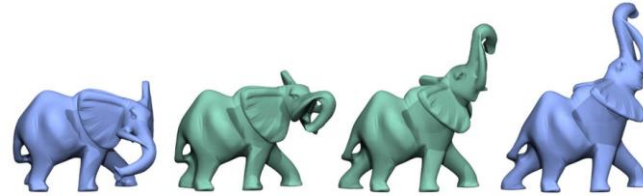
[Kilian et al. 2007]

✓ Deformation transfer:

[Sumner & Popovic 2014]

✓ Attribute transfer:
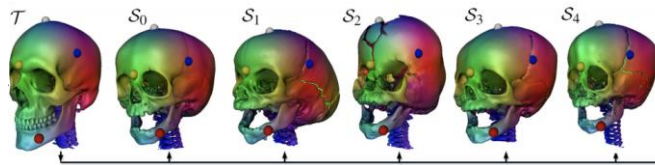
[Sahillioğlu & Kavan 2015]

✓ Shape registration:

[Chang & Zwicker 2008]

✓ Shape matching:
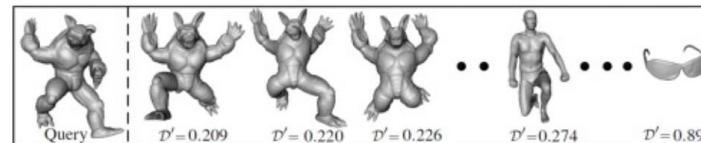
[Sahillioğlu & Kavan 2016]

✓ Statistical analysis:

[Allen et al. 2003]

Contributions

✓ Natural connection established: GA and correspondence.
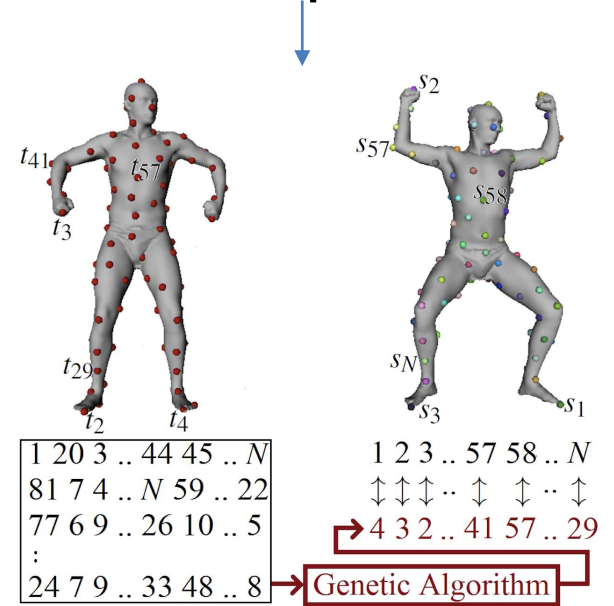
EvoLisa: Evolving color & geometry
of semi-transparent polygons. [Alsing,Hua]

Contributions

✓ Existing maps improved: Adaptive Sampling scheme.
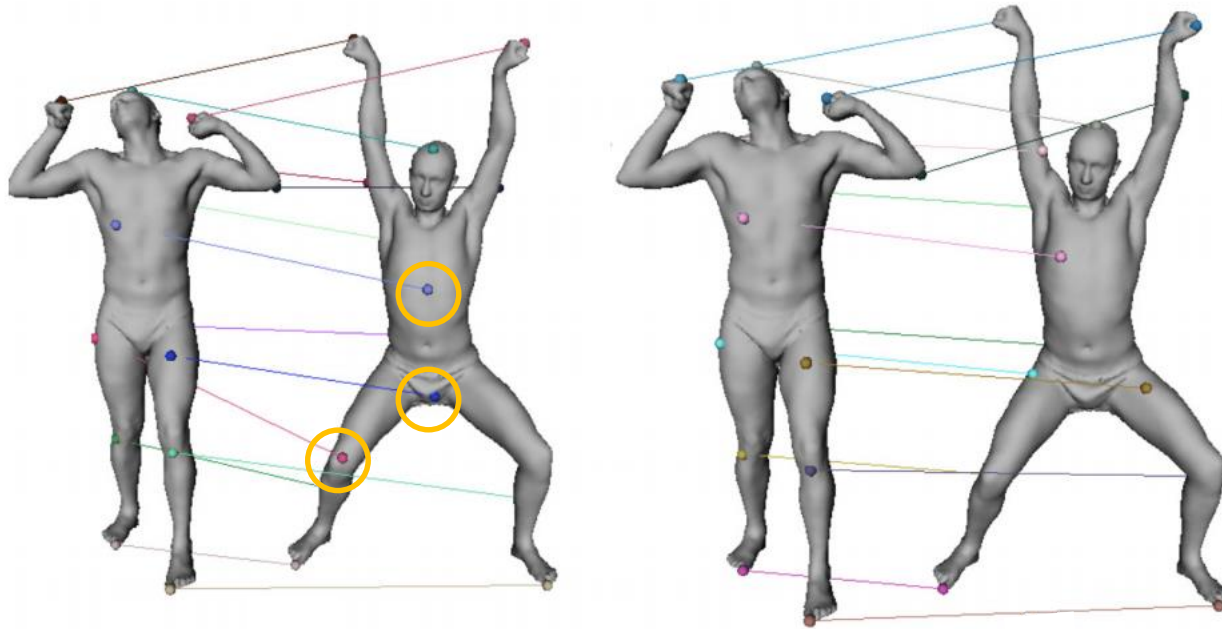
Contributions

✓ Auto-initialization provided: dense match.
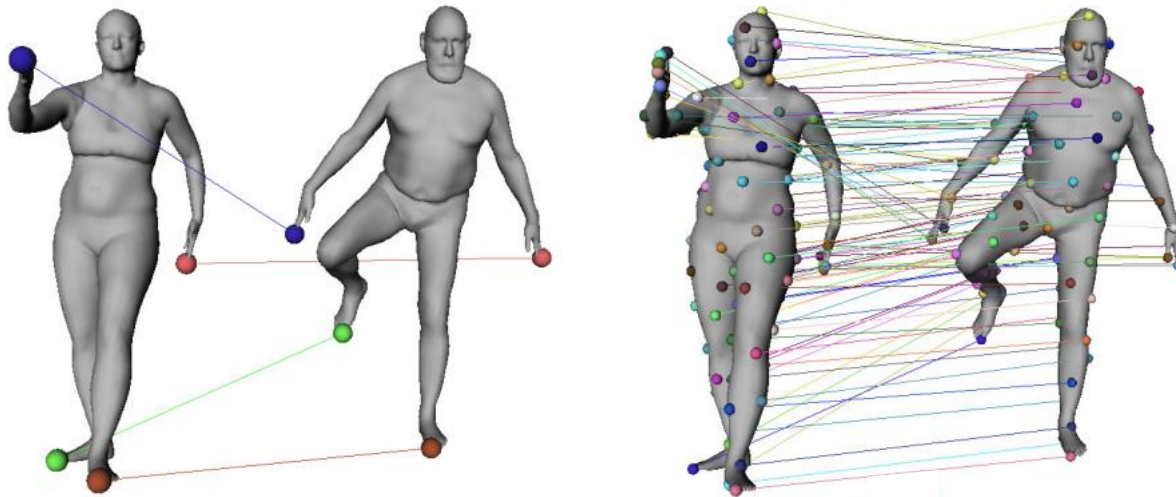
Four landmark matches for [Aigerman and Lipman 2015].

Contributions

✓ Auto-initialization provided: real-world scan registration.
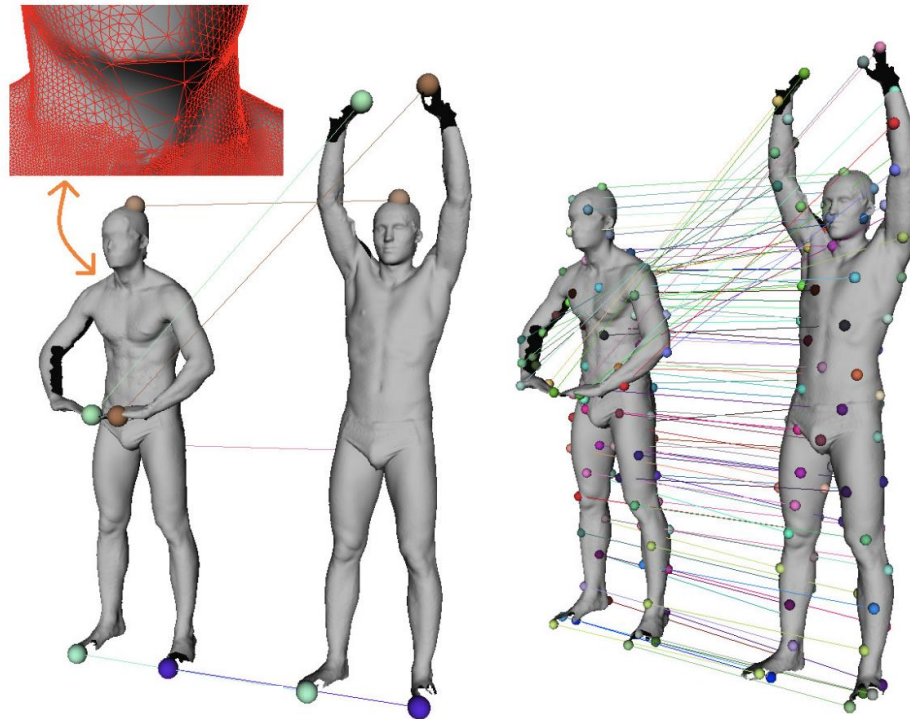
Six (left) or more (right) landmark matches for FAUST scans [Bogo et al. 2014].

Contributions

✓ Simple extension demonstrated: partial matching.
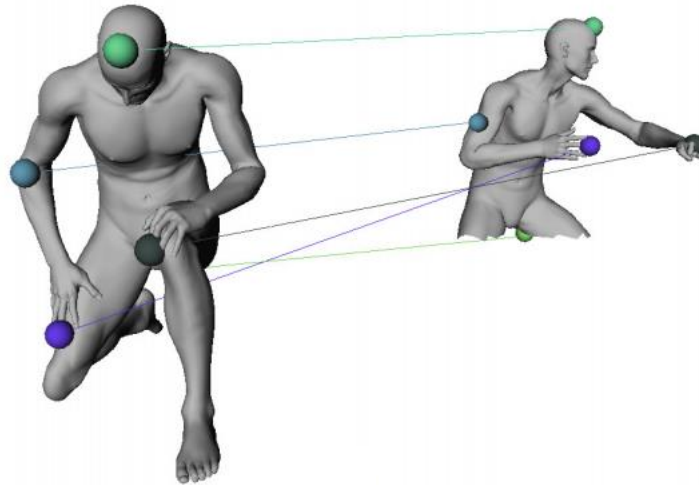
More challenging partial matching problem solved with a simple extension.

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.
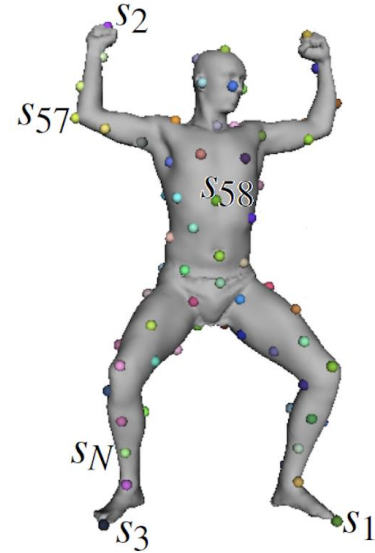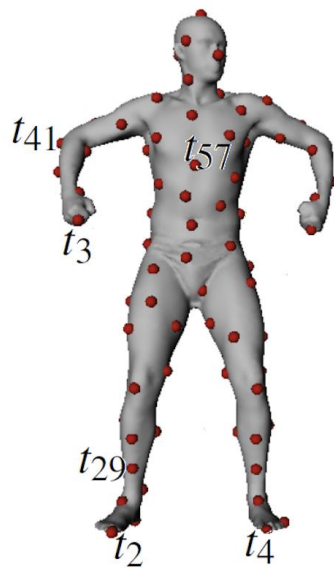
Method: Design Decisions

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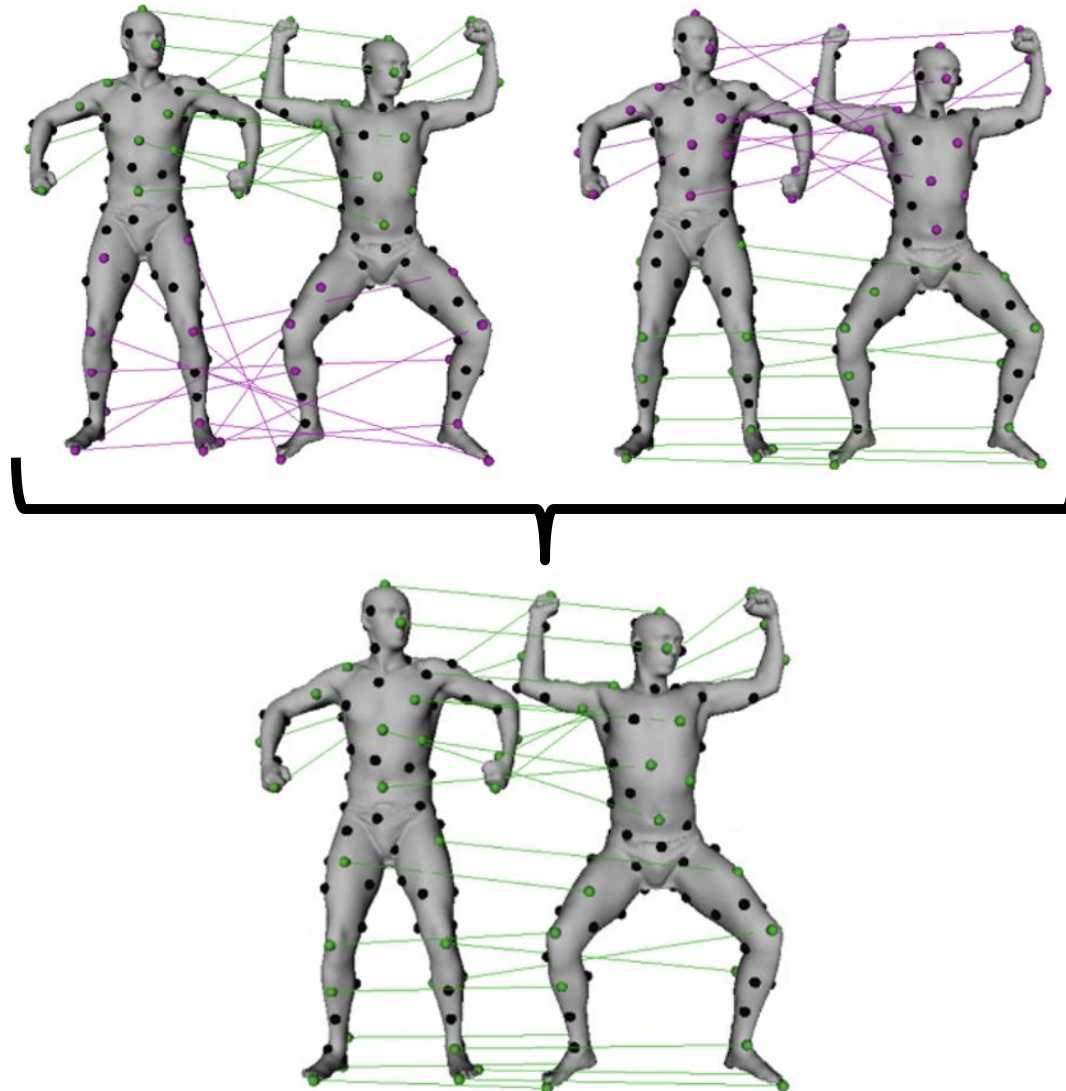
Method: Design Decisions

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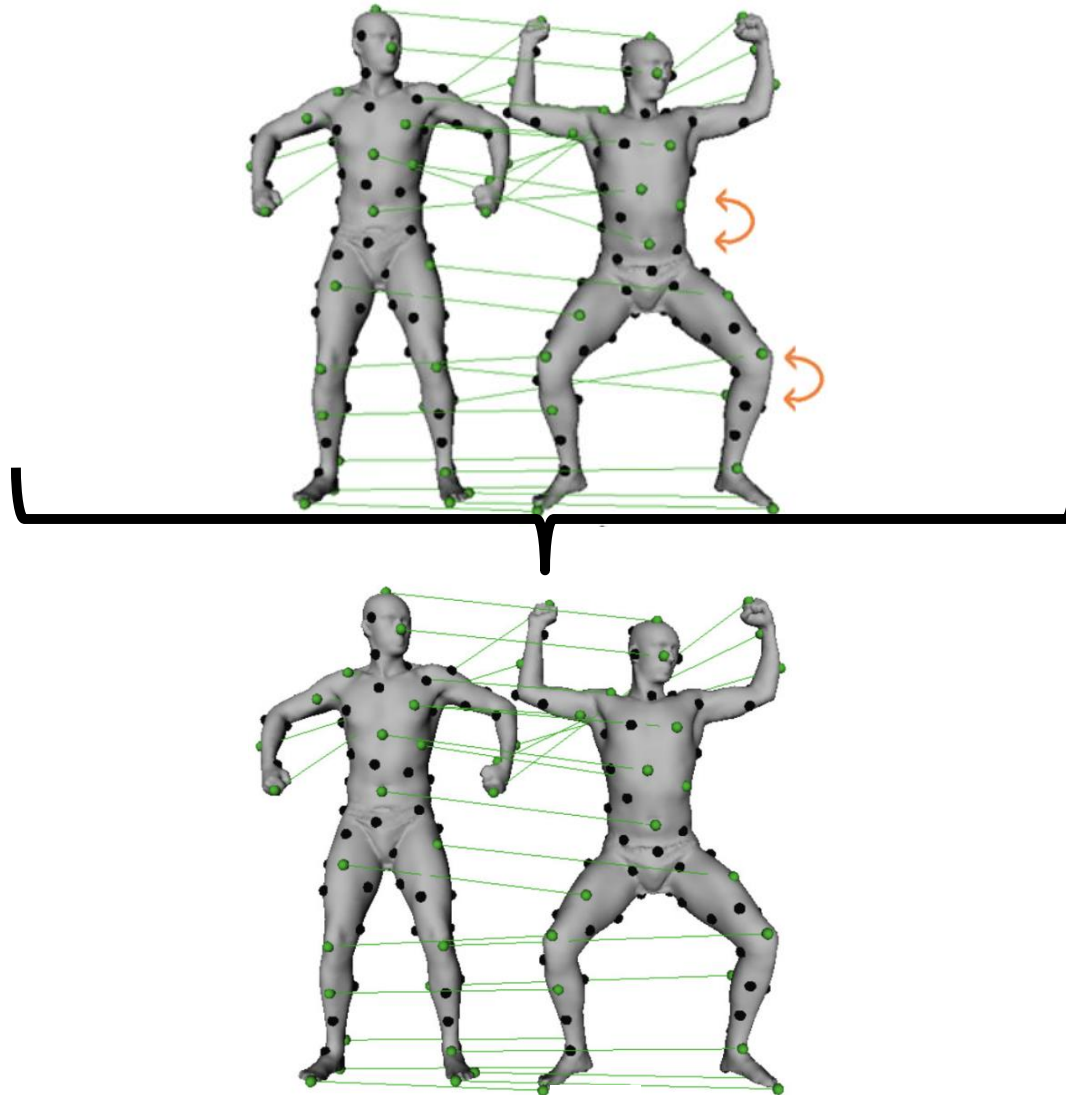
Method: Design Decisions

✓ Fitness of a given chromosome representing permutation π

$$\mathcal{F}(\pi) = 1 - \mathcal{D}_{\mathrm{iso}}(\phi_\pi)$$

where ϕ_π is the bijection that maps i^{th} sample to $\pi[i]^{\mathrm{th}}$ sample,

and $\quad \mathcal{D}_{\mathrm{iso}}(\phi) = \dfrac{1}{|\phi|} \displaystyle\sum_{(s_i, t_j) \in \phi} \left(\dfrac{1}{|\phi'|} \sum_{(s_l, t_m) \in \phi'} |d_{\mathrm{g}}(s_i, s_l) - d_{\mathrm{g}}(t_j, t_m)| \right)$,

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 π

$$\mathcal{F}(\pi) = 1 - \mathcal{D}_{\text{iso}}(\phi_\pi)$$

$$\mathcal{D}_{\text{iso}}(\phi) = \frac{1}{|\phi|} \sum_{(s_i, t_j) \in \phi} \left(\frac{1}{|\phi'|} \sum_{(s_l, t_m) \in \phi'} |d_{\text{g}}(s_i, s_l) - d_{\text{g}}(t_j, t_m)| \right)$$

s_i

t_j

t_m

s_l

s_l

$|.35 - .99| = .64$ ☹

t_{jm}
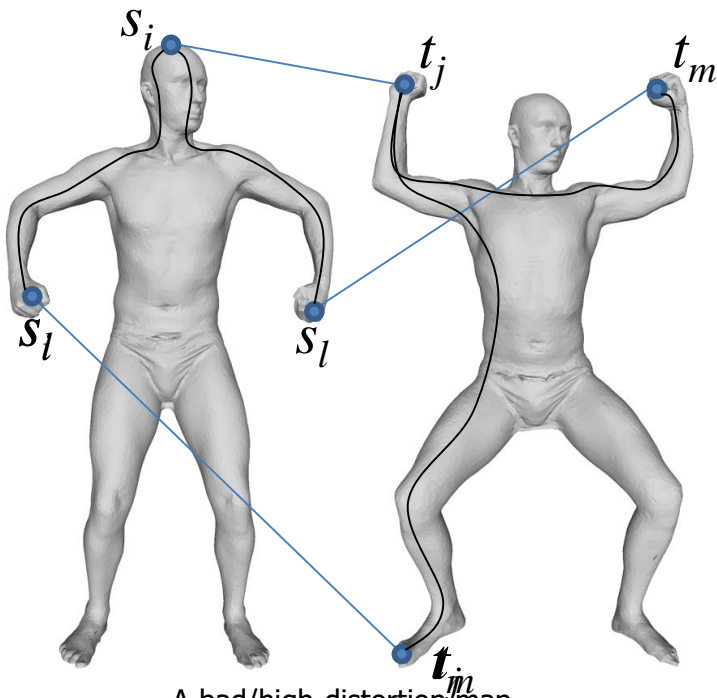
A bad/high-distortion map.

Method: Initial Population

✓ Current population evolved to the next generation.

✓ Initial population based on geodesic consistency.

  ✓ $\mathbf{g}_i^s$ and $\mathbf{g}_j^t$: 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

$$d_{\mathbf{c}}(\mathbf{g}_i^s, \mathbf{g}_j^t) = \max_{k} |\mathbf{g}_i^s[k] - \mathbf{g}_j^t[k]| < .125 \text{ (toe to knee half geo)}$$
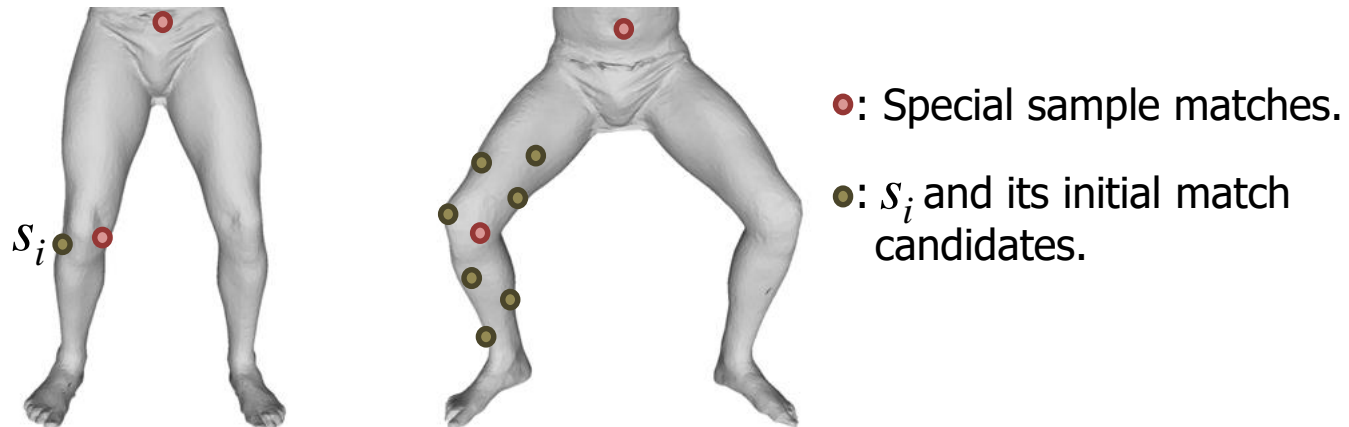
○ : Special sample matches.

○ : 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 ith gene. Population size always 10N, i.e. 1000 chromosomes.
  ✓ Duplicates prevented to preserve bijection.
  ✓ Some samples to random matches, not initial match candidates.

●: Special sample matches.

●: s_i and its initial match candidates.
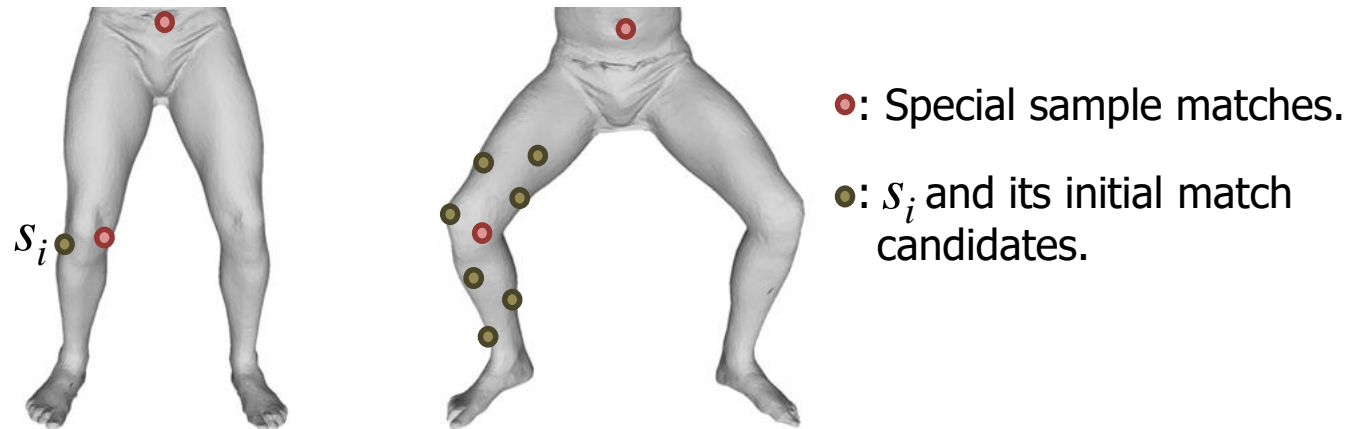
Method: Initial Population

✓ 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.
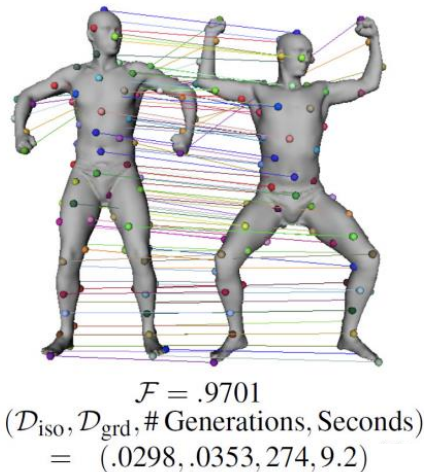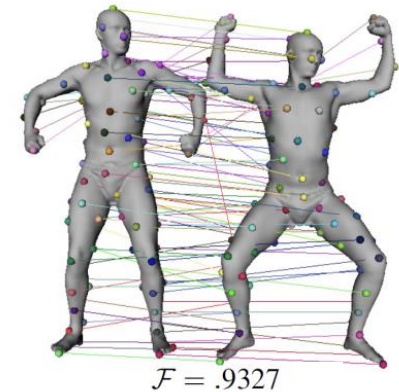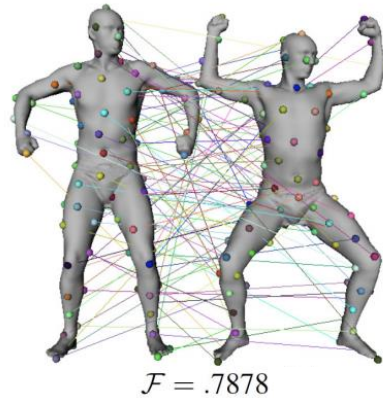
$\mathcal{F} = .7878$

$\mathcal{F} = .9327$

$\mathcal{F} = .9701$
$(\mathcal{D}_{\text{iso}}, \mathcal{D}_{\text{grd}}, \# \text{Generations}, \text{Seconds})$
$= \quad (.0298, .0353, 274, 9.2)$

$\mathcal{F} = .9710$

$(.0290, .0312, 164, 7.8)$

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.
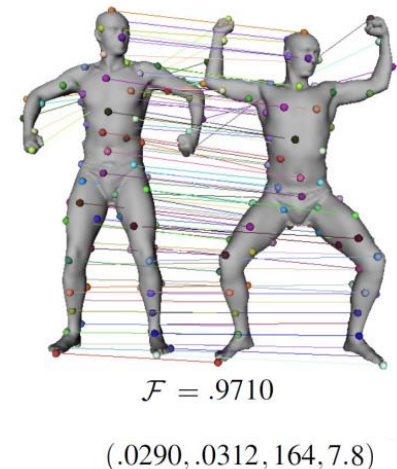- ✓ Elitism for free: best chromosome copied to the next gen.

Method: Evolution of Population

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

Input: S and T s.t. $|S| = |T| = N$, samples on two meshes
Output: $\phi : S \rightarrow T$, one-to-one correspondence
$U = \textbf{initPopulation}()$ //$U = \{C_1, C_2, .., C_P\}$, P is population size
For $generation$ = 1 to max # generations
  $\mathcal{F}^* = \textbf{getFittest}(U)$ //Evaluates all $\{C_i\}$ via $\mathcal{F}$ ($C_i^{\mathcal{F}}$ made ready)
  If ($\mathcal{F}^*$ is fixed for the last L_1 generations $||$ //L_1 = 100
      no swap mutations in the last L_2 generations $||$ //L_2 = 10
      $\mathcal{F}^* > 1 - \epsilon)$ //ϵ = .001
    Break; //Converged!
  $\textbf{evolvePopulation}()$
For $i = 1 : N$ //N is # of genes (= samples on mesh)
  $\phi(s_i) = t_{C_1[i]}$ //fittest is maintained as the first chromosome C_1
Return ϕ

$\textbf{evolvePopulation}(\text{Population } U)$
  Descending sort on U s.t. $C_i^{\mathcal{F}} > C_j^{\mathcal{F}}$ $\forall i < j$, i.e., C_1 is the fittest
  $G = \{C_1, C_2, .., C_h\}$, $B = \{C_{h+1}, .., C_{N_p}\}$ //Good and bad parts,
  For each $C_i \in B$ //where $h = P/2$
    If $\textbf{rand}() < f_{\text{xover}}$ //$\textbf{rand}()$ returns a number in $[0, 1]$
      Let C_j and C_k be random chromosomes from G s.t. $C_j^{\mathcal{F}} > C_k^{\mathcal{F}}$
      $C_i = \textbf{xover}(C_j, C_k)$ //$C_i \in B$ updated by the newborn child of
                                      //2 good parents. Elitism for free as C_i can't
                                      //initially be C_1, the fittest chromosome
  For $i = 2 : P$
    If $\textbf{rand}() < f_{\text{mutation}}$
      $\textbf{mutate}(C_i)$ //$C_i \in U$ is updated. Elitism for free as the fittest C_1
                //is excluded from consideration ($i \geq 2$)

Method: Evolution of Population

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

✓ Crossover: duplication-free (bijection), winner/loser-based.

W: 2 4 7 6 5 1 3 12 17 9 13 10 15 14 11 16 8

L: 5 3 1 2 4 7 6 10 9 16 11 15 12 17 13 14 8

Resulting child: 5 4 7 6 2 13 3 12 17 9 14 15 10 1 11 16 8

✓ Mutation: duplication-free, geodesic vector compatibility.

mutate(Chromosome C)
   For $i = 1 : N - 1$
   If $d_c(\mathbf{g}_i^s, \mathbf{g}_{C[i]}^t) > \tau$ // Slide 16 for d_c ($\tau = .125$)
     //Geodesic vectors $\mathbf{g}$ are incompatible; swap $C[i]$ with a good $C[j]$
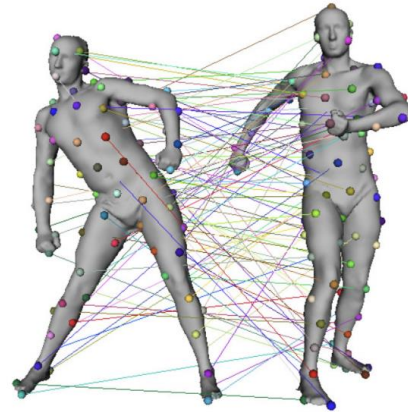   Repeat $j = \mathbf{rand}(i + 1, N)$
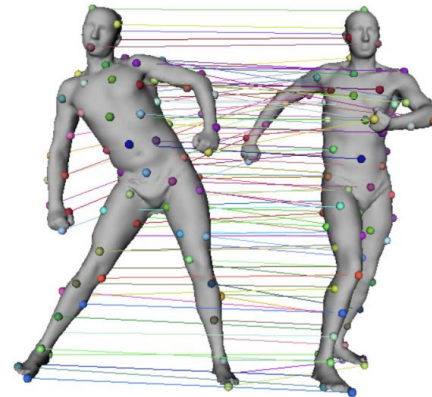   Until $d_c(\mathbf{g}_{C[j]}^t, \mathbf{g}_i^s) \leq \tau$
     Swap $C[i]$ and $C[j]$
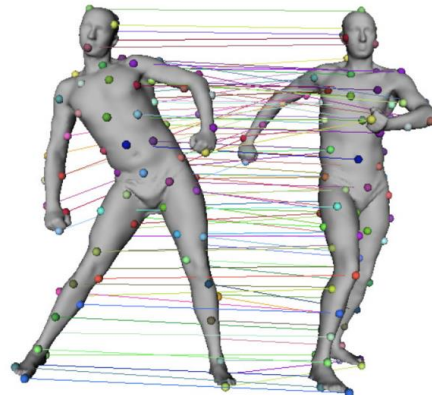
Method: Evolution of Population

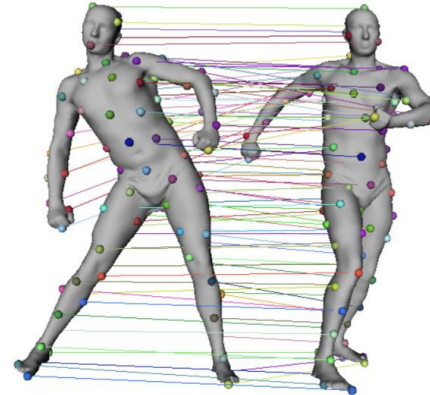✓ Current population evolved to the next generation through genetic operators, whose relative advantages visualized:
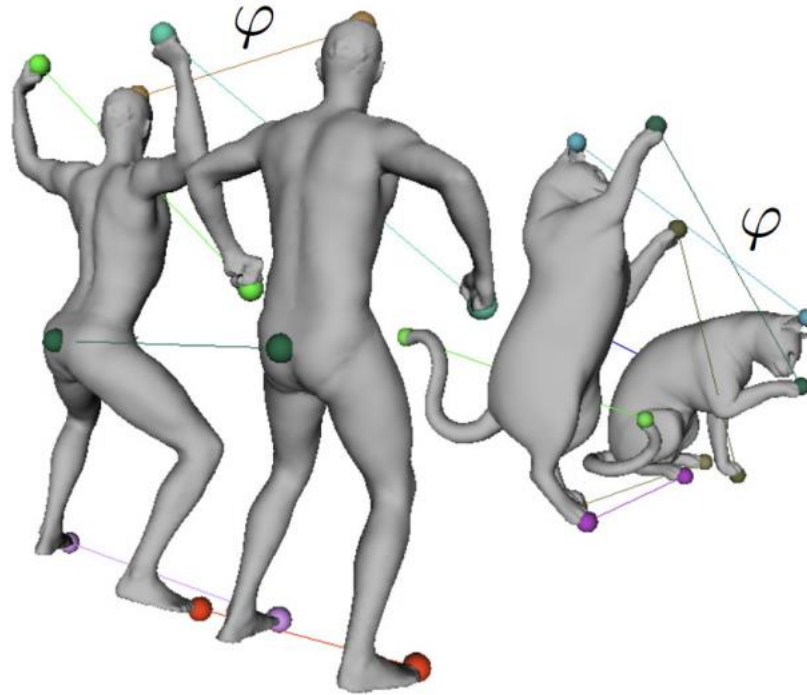
Fittest members shown.
(a) random initialization.
(b) result w/ muts only.
(c) result w/ xovs only.
(d) result w/ both on.

$(\mathcal{D}_{iso}, \mathcal{D}_{grd}, \text{\# Generations, Seconds})$
$= \quad (.2125, .3299, 1, 0)$ (a)

$(.0311, .0418, 170, 8.1)$
(d)

$(.0574, .0820, 45, 2.0)$
(b)

$(.0368, .0548, 375, 11.4)$
(c)

Method: Initial Bijection

✓ While evaluating $\mathcal{F}$, $\phi' = \varphi$ 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.

$$\mathcal{E}(\hat{t}, \phi) = \sum_{(s_i, t_j) \in \phi} \sum_{(s_l, t_m) \in \phi} |d_{\mathrm{g}}(s_i, s_l) - d_{\mathrm{g}}(\hat{t}_j, \hat{t}_m)| + \alpha ||\hat{r} - r_{\mathrm{s}}||$$

✓ 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.

Adaptive Sampling

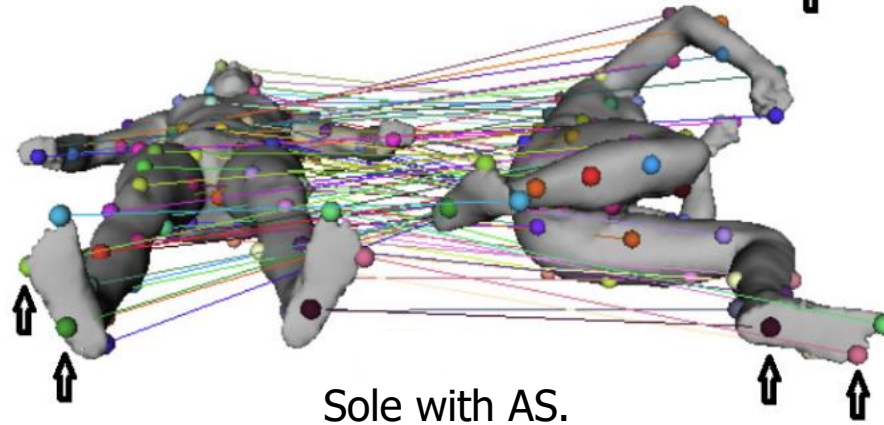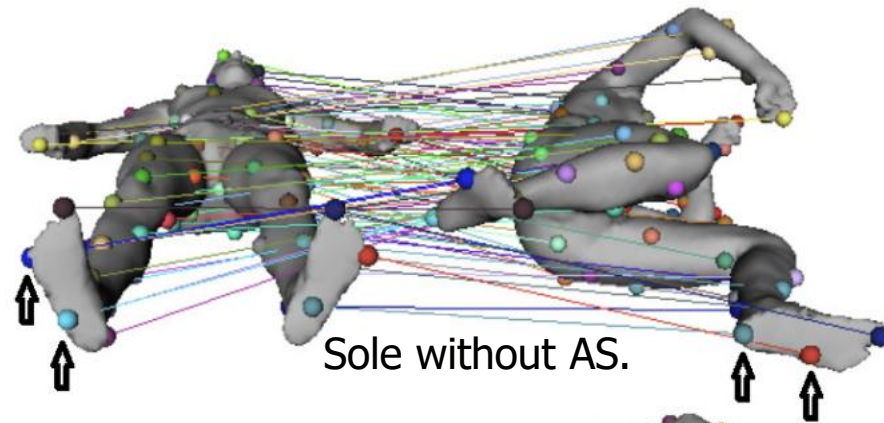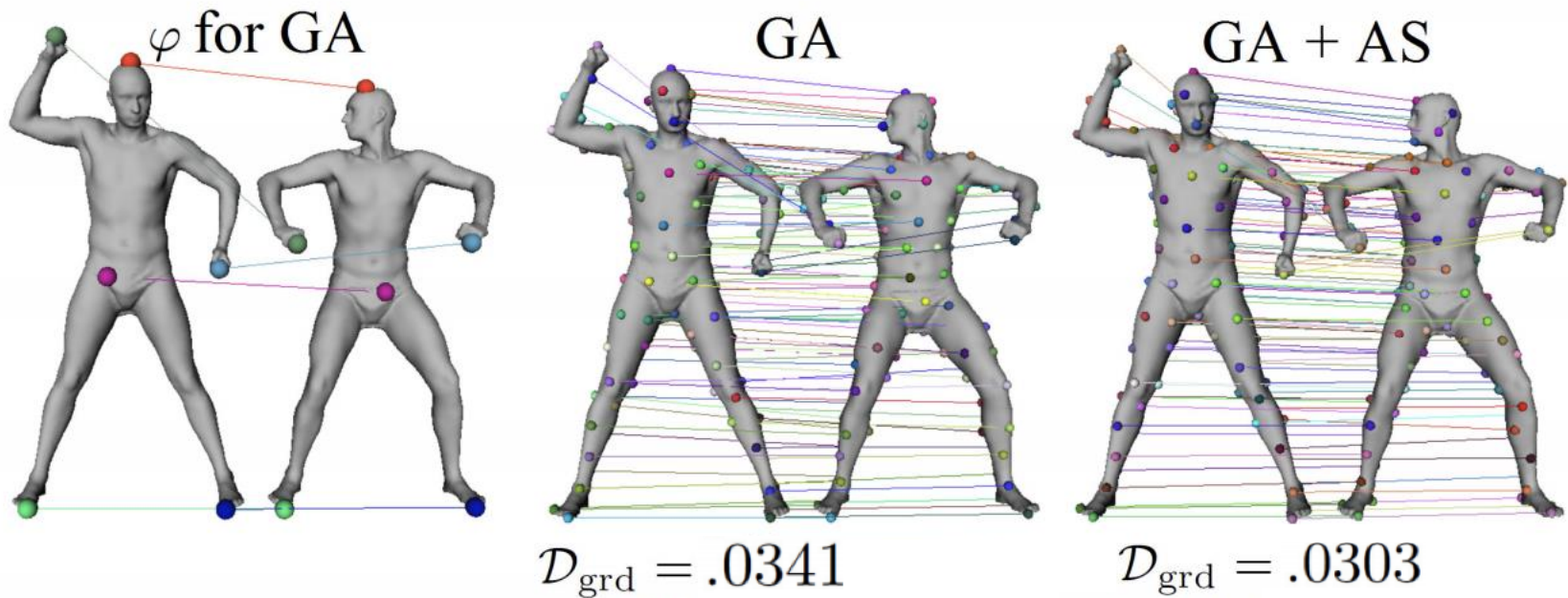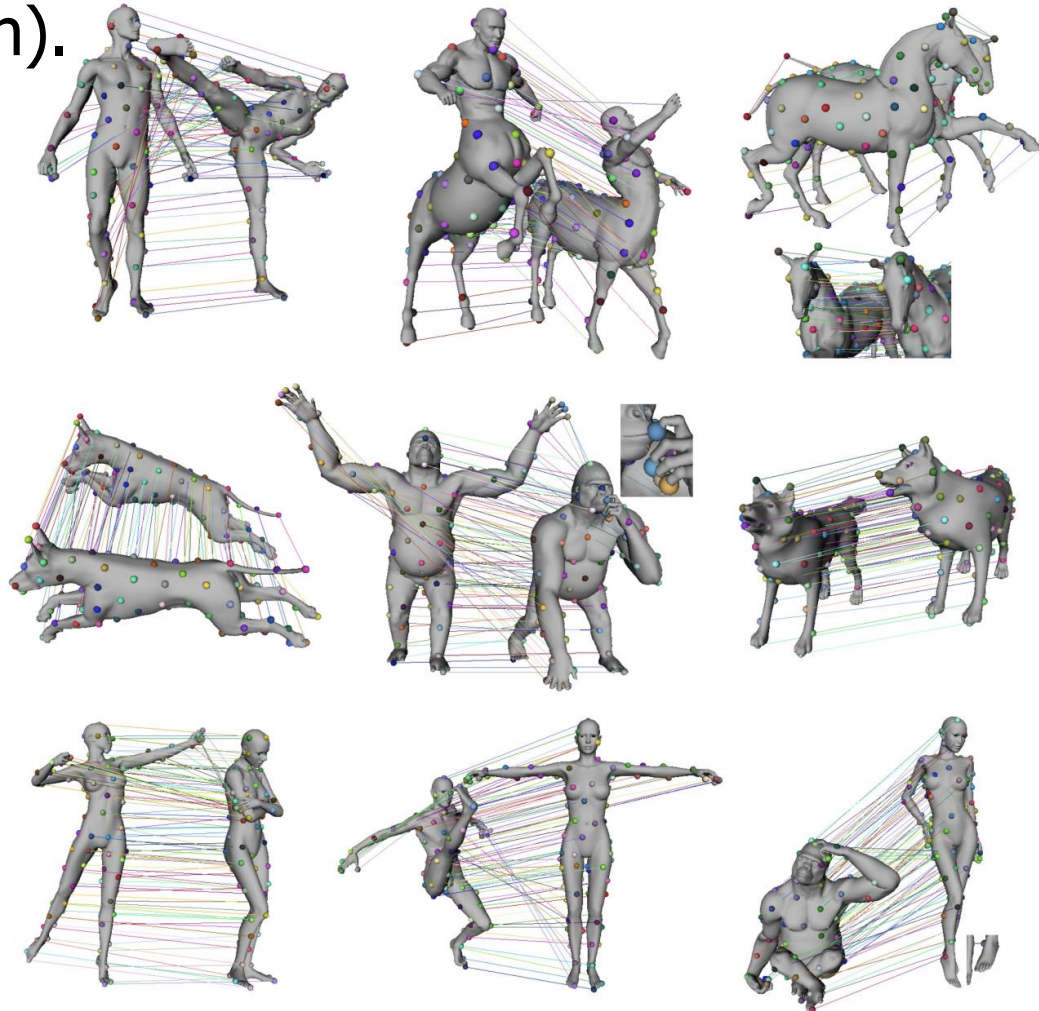✓ Matched samples relocated in a local neighborhood by considering geodesic consistency & sampling regularization.

φ for GA

GA

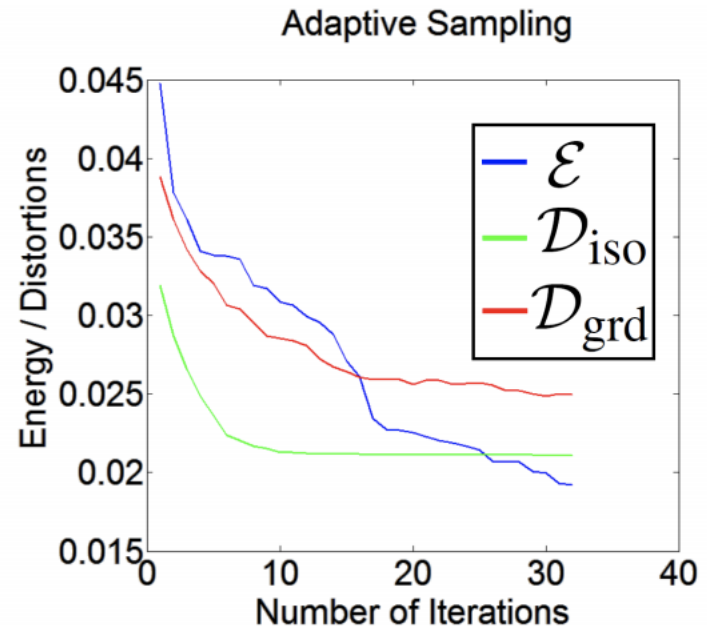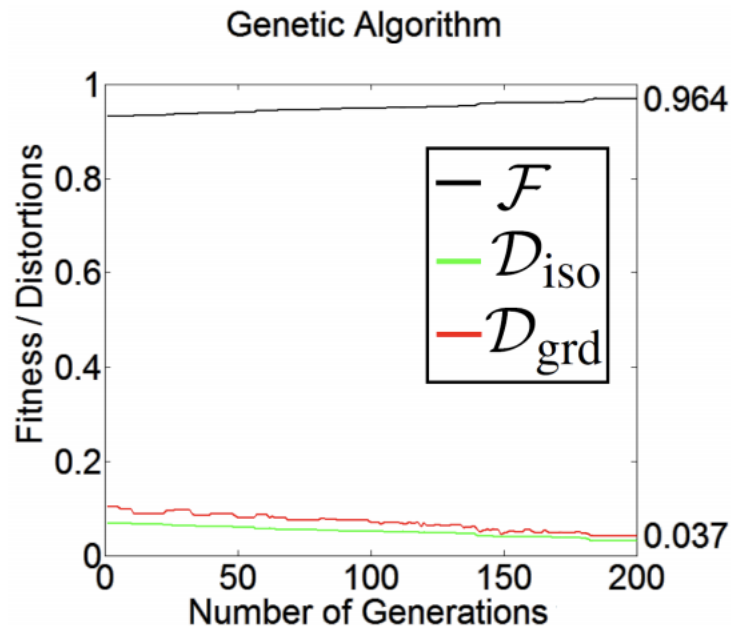$\mathcal{D}_{grd} = .0341$

GA + AS

$\mathcal{D}_{grd} = .0303$

Results

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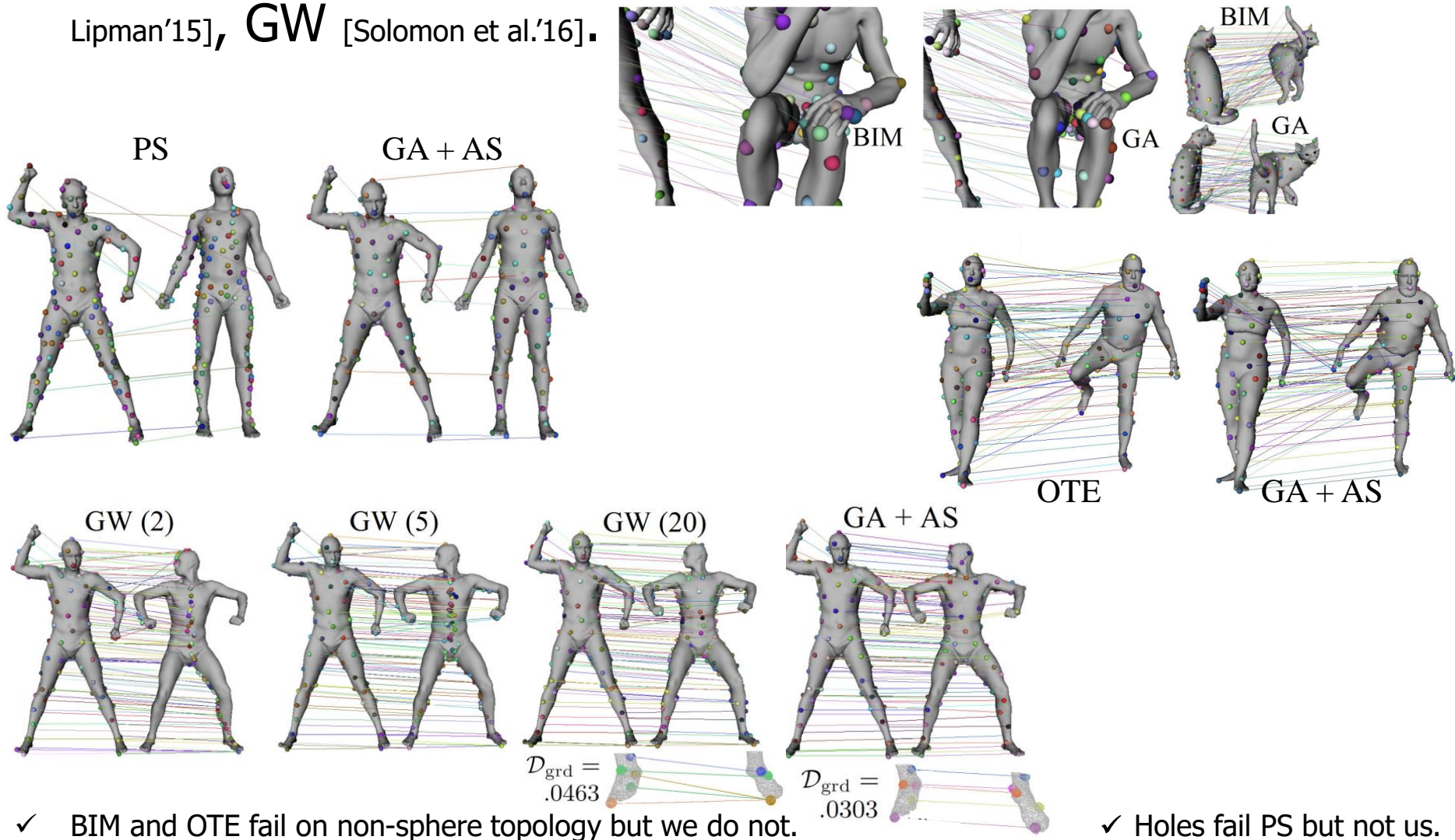
Results

✓ 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].

PS

GA + AS

BIM

GA

BIM

GA

OTE

GA + AS

GW (2)

GW (5)

GW (20)

GA + AS

$\mathcal{D}_{\mathrm{grd}} = .0463$

$\mathcal{D}_{\mathrm{grd}} = .0303$

✓ 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.

Full shape.

Partial shape.
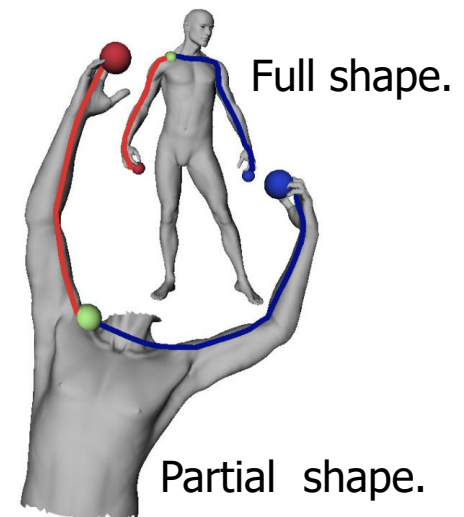
Conclusion

✓ 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

Yusuf, Assoc. Prof.