

Probabilistic Fingerprints for Partial Shape Similarity

Niloy J. Mitra[†]

[†]Stanford University

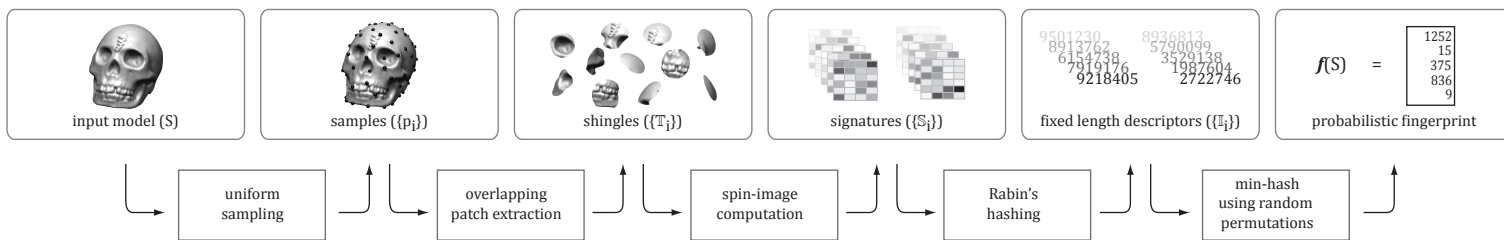
Leonidas J. Guibas[†]

Joachim Giesen[‡]

[‡]Max Planck Institut für Informatik

Mark Pauly[§]

[§]ETH Zurich



Shape Similarity

Given two shapes S_1 and S_2 , their *distance* $D(S_1, S_2)$ satisfies the following:

- (Identity) $D(S_1, S_1) = 0$
- (Symmetry) $D(S_1, S_2) = D(S_2, S_1)$
- (Rigid transform invariance) $D(S_1, S_2) = D(\alpha(S_1), S_2)$
- (Partiality) $S_1 \subseteq S_2 \Rightarrow D(S_1, S_2) = 0$

Compute a *compact fingerprint* f such that:

- $f(S_1) \neq f(S_2) \Rightarrow S_1$ and S_2 are dissimilar
- $f(S_1) = f(S_2) \Rightarrow S_1$ and S_2 are similar
- f is compact $\rightarrow |f(S)| \ll |S|$
- f is efficiently computable

with high probability

Motivation

scan alignment
shape retrieval
partial matching
shape clustering
recognition

are two shapes similar?

Shingles

partial shape matching \Rightarrow comparing two *unordered* high dimensional point sets (spatial relations lost) using *sketches*

robustness to mesh tessellation ensured using dense sampling $\delta \ll \rho$

Resemblance

DEFINITION **resemblance** computed from signatures

$$r(S_1, S_2) = \frac{|S_1 \cap S_2|}{|S_1 \cup S_2|} = \frac{\sum_{\sigma \in S_1 \cap S_2} \min(m_1(\sigma), m_2(\sigma))}{\sum_{\sigma \in S_1 \cup S_2} \max(m_1(\sigma), m_2(\sigma))}$$

APPROXIMATION **min-hash** [Broder '00]

π_1, \dots, π_m : m random permutations on \mathbb{U} , the universe of all possible symbols

probabilistic fingerprint

$$f(S) = (\min\{\pi_1(S)\}, \dots, \min\{\pi_m(S)\})$$

resemblance *estimate* using fingerprints

$$r'(S_1, S_2) = \sum_j \min(m_{1j}, m_{2j}) \chi(f(S_1)_j = f(S_2)_j) / \sum_j D_j$$

$D_j = \max(m_{1j}, m_{2j}) \chi(f(S_1)_j = f(S_2)_j) + m_{1j} \chi(f(S_1)_j < f(S_2)_j) + m_{2j} \chi(f(S_1)_j > f(S_2)_j)$

Estimation Error

Pipeline Stage	Source of Error	Analyzed using
Rabin's hashing	many-to-one mapping	counting argument
min-hashing	random sampling	Chernoff bound

For sets, in order to have probabilistic error bound

$$\Pr [(1-\delta)r(S_1, S_2) \leq r(S_1, S_2) \leq (1+\delta)r(S_1, S_2)] \geq 1-\eta$$

we have to choose,

$$m \geq 4 \ln(2/\eta) / (\delta^2 r(S_1, S_2))$$

For typical values of parameters, $m \approx 1000$ suffice.

Evaluation

Comparison with ground truth : cumulative error due to Rabin's hashing and min-hashing

Effect of shingle size on resemblance

Applications

MULTIPLE SCAN ALIGNMENT

multiple scans in arbitrary initial positions

alignment order

final alignment

PARTIAL SCAN ALIGNMENT

model

data

adaptive features

final alignment

SHAPE SPACE

COMPLEMENTARY SHAPE MATCHING

scan A

scan B

final alignment

PERFORMANCE (fingerprint size 10kB)

model	# vertices	pre-proc. (in secs)	query time (in msec)
skull	54k	13	15
Caesar	110k	18	15
bunny	1,210k	16	15
horse	8k	7	15
database (1,814 models)	average 7k	average 5	average < 1/2 sec

DATABASE RETRIEVAL

query

59% 33% 26%

24% 19% 15%

