Gaussian Process Landmarking on Manifolds

Tingran Gao

Department of Statistics, The University of Chicago

`tingrangao@galton.uchicago.edu`

As a means of improving analysis of biological shapes, we propose a greedy algorithm, termed *Gaussian process landmarking* [1], for sampling a Riemannian manifold based on the uncertainty of a Gaussian process. Closely related to *krigging* [2] and *Gaussian Process Active Learning* [3, 4], this sequential approach is known to produce a near optimal experimental design with the manifold as the domain. We adapt a feature matching algorithm for registering pairs of anatomical surfaces via matching the Gaussian process landmarks computed on each individual surface; such defined surface registration induces novel shape Procrustes distances with comparable power of taxonomic group separation as traditional methods based on the "ground truth" landmarks manually placed by professional comparative biologists. We establish the rate of decay (with respect to the number of landmarks) of the maximum conditional variance of the Gaussian process used, borrowing tools from scattered data approximation [5] and reduced basis methods [6, 7].

Joint work with: Shahar Z. Kovalsky, Doug M. Boyer, Ingrid Daubechies.

References

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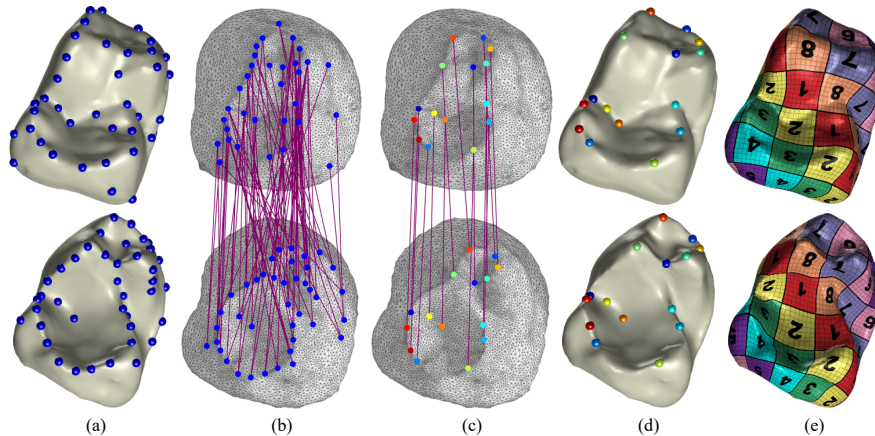
Figure 1: Outline of landmark matching and surface registration. (a) Gaussian process landmarks; (b) Planar parameterizations overlaid with putative landmark matches; (c) Bounded-distortion maps selecting a subset of geometrically-consistent matches; (d) Pairs of corresponding Gaussian process landmarks illustrated by spheres with matching colors; (e) Texture-map visualization of an inter-surface map interpolating the landmark correspondences.