

Thesis Literature Review

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1 Plane Extraction

2 Segmentation

Popularised by Comaniciu [4] for use in image segmentation, mean shift was first introduced by Fukunaga [5] in 1975, and rediscovered by Cheng [2] in 1995. The technique finds stationary points in a density estimate of the feature space, for example pixel RGB values, and uses those points to define regions in the space by allocating pixels to them. Pixels which follow the gradient of the density to the same stationary point are part of the same segment. An example can be seen in Figure 1.

3 Interest Points

Mikolajczyk and Schmid [10] introduce an interest point detector which is an improvement on SIFT [9] and the Laplacian of Gaussians [8] in the sense that it is able to deal with affine transformations. They do not, however, introduce a new type of descriptor to go with the point selection.

4 2D Descriptors

Different considerations must be made for 2D images because of affine transforms, rotation and so on

Van Gool [12] gives a description of how to use moment invariants to recognise planar patterns like labels and signs under affine deformations. The moments describe things like the size of the shape and its centre of mass, or statistics like the mean and variance of pixel intensities in the shape. These moments can be combined in such a way that they are invariant to deformations, which is useful to have in a descriptor.

5 3D Descriptors

The Ensemble of Shape Functions (ESF) descriptor introduced in [13] combines the Shape Distribution approach introduced by [11] along with some extensions proposed by [7]. Pairs or triples of points are sampled from segmented partial clouds of objects, and histograms are created by extracting information such as distance, angle, ratios, and whether points are inside or outside (or a mix) of the model. See Figure 2.

Work in protein-protein docking also uses 3D descriptors to help with simulations of an otherwise lengthy process. The Surface Histogram is introduced by Gu et al. [6], and uses the local geometry around two points with specific normals on the surface of a protein. A coordinate system is defined by the two points and the line between them, and a rectangular voxel grid is defined around the points. The grid is then marked in locations where the surface crosses the grid, and a 2D image is constructed by squashing the data onto one of the axes. The descriptor is designed to immediately give a potential pose for the docking.

6 Point Matching

In [3], Chui and Rangarajan introduce an extension to ICP which allows for non-rigid registration and improved robustness to outliers. In contrast to ICP, their approach does not use the nearest-neighbour approach to define correspondence. Instead, they use an alternating algorithm similar to expectation maximisation. Annealing is used to prevent binary correspondences when the algorithm is not yet close

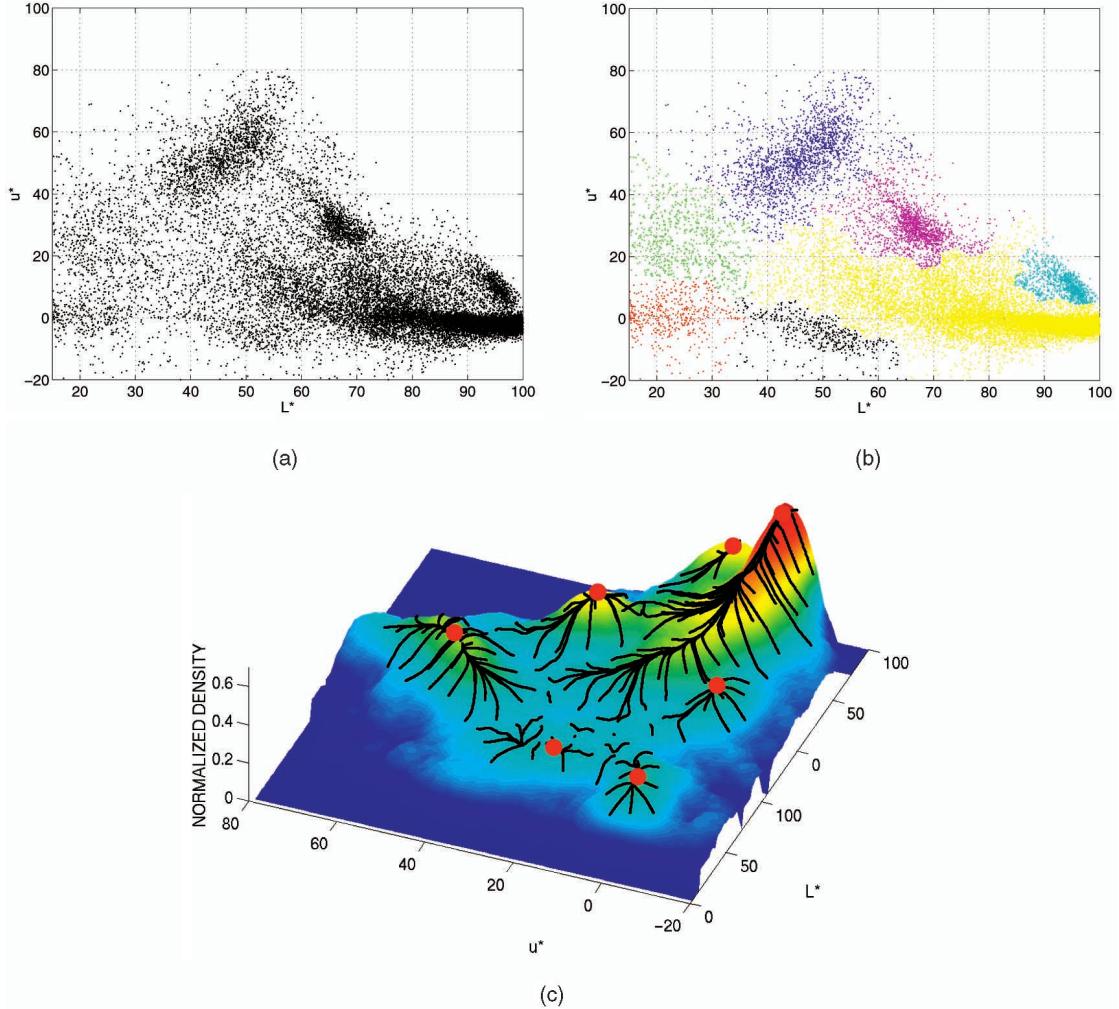


Figure 1: Visualisation of mean shift [4]. a) First two components of image pixels in LUV space. b) Decomposition found by running mean shift. c) Trajectories of mean shift over the density estimate.

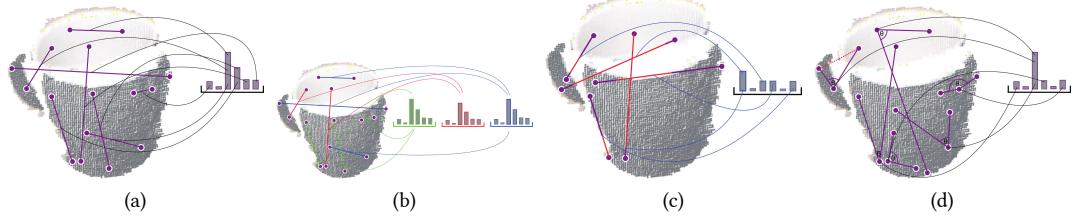


Figure 2: Examples of the measures used to construct the Ensemble of Shape Functions histograms of [13]. a) Distance between points. b) Whether the points are on or off the model, or mixed. c) Ratio of line segments on and off the surface of the model. d) Angle between pairs of lines.



(a) Conformal factors. High value indicates high required deformation to sphere [1].

Figure 3: Model matching approaches

to the solution — at the beginning there is a large search range for correspondences, which gradually shrinks as the temperature decreases.

7 Model Matching

In [1], Chen et al. describe another approach to model matching using conformal factors. This technique uses ideas from conformal geometry, transforming the mesh of an object such that it has a uniform Gaussian curvature. Information is stored about how much deformation is needed locally to globally transform the object into a sphere — this is the conformal factor. The factor is based on a global computation on the whole mesh, as opposed to per-vertex computations of the Gaussian curvature, which makes it much smoother and appropriate for use in histograms. The histogram of a sample of the factors is used as a descriptor, and is pose invariant, as seen in Figure 3a. The authors say that it should be possible to use the approach in partial model matching.

8 Storing and Querying Descriptors

References

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