Computing Match Functions for Curves in $\mathbb{R}^2$ and $\mathbb{R}^3$ by Refining Polyline Approximations

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1 Algorithm Summary

We believe geometry is particularly important in the medical domain because shape descriptions can help quantify diagnosis. Our work follows the geometric matching methods of [1] and [2] but is also related to [3] and [4].

Dynamic programming is used in [1] to find suboptimal matching with respect to the following bending and stretching energy function:

$$E(g) = \int_0^L [|\cos(\psi) - \sin(\psi)| + R|\kappa_1 \cos(\psi) - \kappa_2 \sin(\psi)|] d\eta. \quad (1)$$

Here, κ is curvature, L is the length of the match curve, and $\psi \in [0, \frac{\pi}{2}]$ is the angle of its tangent vector with the x -axis (some details are omitted.) The performance of the algorithm is very sensitive, in practice, to the value of R . Also, no global knowledge of the curve is incorporated. Iteration over polygonal curve approximations is used to restrict the problem in [2] while including global geometric information.

Our solution builds on both approaches. We aim to minimize equation (1) using polyline approximations to eliminate explicit choice of R . Therefore, our goal is to find a function, g , such that, $g: C^1 \mapsto C^2$ and $g^{-1}: C^2 \mapsto C^1$. We require that every point on C^1 maps optimally to a unique corresponding point on C^2 (or is deleted). The algorithm is summarized here:

1. Re-parameterize each curve with constant arc length.
2. Initialize g_1 as a minimum stretching energy match.
3. Compute the $g_2, \dots, g_n$ set of match functions, where each g_i corresponds to the match implied by pairing the vertices of the $i + 1$ sized best polygon fits with linear interpolation between vertices.
4. Evaluate the terms of the energy function for each g_i . Select the minimum.
5. Perform gradient descent to refine g_{min} .
6. Repeat the procedure between vertices of g_{min} until the distance between curves and approximations reaches a given tolerance $\epsilon \geq 0$.

Fig. 1. A correspondence of corpora callosa with the associated match curves g and g^{-1} (left). Average human corpus callosum and one standard deviation of its shape (right).

2 Results

We used dynamic programming to implement a version of the algorithm that is fast (seconds) enough to be of use in clinical situations. Here, we give results of its use on an instance of real patient data as well as on a large dataset. The coronal direction of the corpus callosum was automatically segmented from MRI for each of 87 human controls matched roughly for age and handedness. No adjustments for scale were necessary.

3 Conclusions and Further Work

We summarized a novel solution to the curve correspondence problem. The statement of the solution is flexible and general enough that it may be adapted to find constrained minima of a large range of energy functions. In addition, it can be shown that dependence on explicit values of R in (1) can be eliminated. Automatic generation of the average callosa from a large dataset indicates the reliability of the method. Similar work is under way on open contours in $\mathbb{R}^3$. Future work will explore the effect of the polygon approximation, choice of refinement technique and incorporation of probability.

References

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