1067-05-1043   **Maxim J. Goldberg** (`mgoldber@ramapo.edu`), Ramapo College of NJ, TAS, 505 Ramapo Valley Road, Mahwah, NJ 07430, and **Seonja Kim*** (`skim4@sunyrockland.edu`), SUNY Rockland Community College, 145 College Road, Suffern, NY 10901. *An efficient tree-based computation of a natural diffusion distance.*

Using diffusion to define distances between points on a manifold (or a sampled data set) has been successfully employed in various applications such as data organization and approximately isometric embedding of high dimensional data in low dimensional Euclidean space. Recently, P. Jones has proposed a diffusion distance (symmetric, but not satisfying the triangle inequality) which is both intuitively appealing and scales appropriately with increasing time. Roughly, his proposal is to define the distance between two points as the first *time* that the diffusion densities "spreading" from the points overlap sufficiently. We present an efficient tree-based approach to computing an approximation to Jones' diffusion distance. We also illustrate that our approximation is comparable to Jones' proposal.

One can then apply a general construction to obtain an "almost" metric from a general distance (we presented this construction at the Joint Meetings in San Francisco in 2010). (Received September 18, 2010)

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