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Thomas Wanner* (twanner@gmu.edu), Department of Mathematical Sciences, George Mason University, Fairfax, VA 22030. *Homology Computations for Random Nodal Domains.*

Stochastic evolution equations frequently generate complex time-evolving patterns which are hard to quantify due to the lack of any underlying regular structure. The influence of stochasticity leads to variations in the details of the patterns and forces one to concentrate on rougher common geometric features. In many of these instances, such as in phase-field type models, one is interested in the geometry of nodal domains of a function in terms of their homology. Recent computational advances make it possible to compute the homology of discrete structures efficiently and fast. Such methods can be applied to the above situation if the nodal domains of interest are approximated using an underlying discretization. Yet, this method immediately raises questions concerning the accuracy of the computed homology and the appropriate location of the discretization points. In this talk, I present a probabilistic approach which gives insight into the suitability of the above method in the context of random fields. We obtain explicit probability estimates for the correctness of the homology computations, which in turn yield a-priori bounds for the suitability of certain grid sizes as well as information on the optimal location of sampling points. (Received September 03, 2008)