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Progress in algorithmic computation of the homological Conley index map

Advancement in the development of algorithms and software for automatic analysis of global dynamics in multi-parameter dynamical systems, has recently made it possible to apply the method to a wide class of dynamical models with both discrete and continuous time (the latter through a time-1 map); for example, a disease spreading model in epidemiology (Knipl, Pilarczyk, Röst 2015). One of the most computationally challenging steps is the computation of the Conley index, especially the index map in homology. In this talk, a focus will be on an approach that uses a rectangular grid to construct an index pair and to approximate the map. Recent progress in the computation of the homomorphism induced in homology by a continuous map in this context will be introduced (Harker, Kokubu, Mischaikow, Pilarczyk 2016). This approach uses a combinatorial approximation of the map, and overcomes several constraints that were previously considerably limiting the applicability of this method.