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Capturing the complexity of earthquake sequences by different methods

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Earthquake clustering is an essential property of seismicity and the space-time patterns of the identified seismic clusters may provide important information about the structural and dynamic features of an area. Still, the application of different methods, relying on different physical and/or statistical assumptions, may lead to diverse identification earthquake clusters and of their internal structure. Moreover, the techniques used to formally describe the topological complexity of clusters' related structure, including quantitative metrics and graphical tools, may provide a different insight on the same process.
Hence we examine different declustering techniques, to investigate classification similarities and differences that might highlight their strengths/limits, and we explore the possible contribution to clusters characterization provided by some existing and new tools. In particular, two clustering approaches are applied:
- the "nearest-neighbor" method (NN), which is based on nearest-neighbor distances between events in space-time-energy domain,
- the stochastic declustering method (SD), which is based on the space-time ETAS (epidemic-type aftershock sequence) model, a branching point process defined by a hazard function conditional on the observation history.
Both methods are data-driven and can be satisfactorily applied to decompose the seismic catalog into background seismicity and individual sequences of earthquakes; in addition, they provide the links between events forming each cluster (or even several possible realizations of it, in the case of SD method), and thus allow studying the internal structure of the identified sequences.
In this study we investigate the spatio-temporal features of earthquake clustering in Northeastern Italy, based on a systematic analysis of robustly detected seismic sequences reported in the local bulletins, compiled at the National Institute of Oceanography and Experimental Geophysics (OGS) since 1977. We uniformly analyse the sequences identified by the two methods and we find that a comparable number of clusters is detected by both declustering methods: most of the events included in a SD-cluster are also included in the corresponding NN-cluster. Moreover, since both methods establish hierarchical relationships among events in a cluster, it is possible to represent each cluster as a tree graph in which the internal structure is displayed. Accordingly, we analyse in some detail the tree structure for a set of selected sequences. For this purpose we borrow some measures of centrality from network analysis, with the aim of characterizing the internal structure of the clusters in the study region, and to identify possible common features that emerge from both declustering methods.