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Aftershock prediction by the statistical absolute reaction rate model

A. Marcellini, R. Daminelli

Istituto per la Dinamica dei Processi Ambientali (CNR), Italy

alberto.marcellini@idpa.cnr.it

Static fatigue models have been applied by a number of researchers to predict time to fracture in brittle materials. Particularly relevant because of the good agreement with the experiments is the statistical absolute reaction rate model (SARR), that could be considered as an Arrhenius-type static fatigue model. In this model the time to break is a function of the applied stress, the absolute temperature, the internal energy and some material constant. Moreover it includes a quantitative formulation of the Damage through a dynamic definition of the fraction of integrity of the material, that is the fraction of unbroken elements. Therefore it is a good physical model for material characterized by the presence of cracks or by pre-existing fracture (the usual situation in seismic zones). SARR constitutes the backbone of the present aftershock model (AM) that could be summarized as follows: the aftershocks zone is composed by a patch of asperities, each one subjected to a specific stress that accounts also for the stress change induced by the mainshock (that acts as initial condition for aftershocks). Each asperity breaks (that is an aftershock occurs) once the conditions of stress and time are met. As a consequence there is a modification of the fraction of integrity that produces a change of the expected time of the subsequent aftershocks. To note that the prediction is not in terms of numbers of earthquakes versus time, as in ordinary Omori law, but in terms of energy released (or Magnitude) versus time. However, at the end, the validity of this approach (as of any physical model) stems from the agreement with the data. AM has been applied to several aftershock sequences of different seismogenic zones. In particular we focused on Southern California data as collected by SCEC. The results obtained show the effectiveness of the model. To note that a good fitting has been obtained also in cases of "anomalous sequences", i.e. sequences characterized by the maximum magnitude shock inside the sequence.