Modelling Paleoearthquake Slip Distributions using a Gentic Algorithm

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Along the Sunda trench, the annual growth rings of coral microatolls store long term records of tectonic deformation. Spread over large areas of an active megathrust fault, they offer the possibility of high resolution reconstructions of slip for a number of paleo-earthquakes. These data are complex with spatial and temporal variations in uncertainty. Rather than assuming that any one model will uniquely fit the data, Monte Carlo Slip Estimation (MCSE) modelling produces a catalogue of possible models for each event. From each earthquake's catalogue, a model is selected and a possible history of slip along the fault reconstructed. By generating multiple histories, then finding the average slip during each earthquake, a probabilistic history of slip along the fault can be generated and areas that may have a large slip deficit identified. However, the MCSE technique requires the production of many hundreds of billions of models to yield the few models that fit the observed coral data. In an attempt to accelerate this process, we have designed a Genetic Algorithm (GA). The GA uses evolutionary operators to recombine the information held by a population of possible slip models to produce a set of new models, based on how well they reproduce a set of coral deformation data. Repeated iterations of the algorithm produce populations of improved models, each generation better satisfying the coral data.
Preliminary results have shown the GA to be capable of recovering synthetically generated slip distributions based their displacements of sets of corals faster than the MCSE technique. The results of the systematic testing of the GA technique and its performance using both synthetic and observed coral displacement data will be presented.