Back-projection results of the 4 May 2018 Hawaii earthquake using a genetically optimized sub-array selection scheme
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The back-projection method uses the orientations of nonplanar wavefronts recorded at dense seismic arrays to image the sources of seismic energy in space and time (Ishii et al., 2005). Data from seismic stations at teleseismic distances (30°–90°) from the event of interest are typically used in this method. P-waves recorded within this distance window at different seismic stations usually have very similar waveforms, which enhances the imaging process. Outside of the teleseismic distance range, waveform similarity can degrade significantly due to interference between P-waves and other seismic phases. Though the incorporation of this data into back-projection analyses can theoretically improve resolution, the degradation of waveform similarity can cause artifacts in the back-projection results.

This study removes data that causes these artifacts using an approach to seismic array selection that focuses on the quality of the source image that the data produces, as opposed to the data itself. The key idea behind this approach is that small earthquakes should be imaged as point sources in back-projection results, and any additional imaged energy is likely an artifact caused by poor data quality. Using a genetic algorithm, an optimization method inspired by natural evolutionary processes such as selection, crossover, and mutation, an array of seismic stations is chosen that optimizes the point source nature of the back-projection results of small events within a region of interest. For this study, an optimal subarray for the source region of the 4 May 2018 Hawaii earthquake (M_W=6.9) is presented. This subarray is determined by optimizing the point source nature of foreshocks and aftershocks surrounding the mainshock event. The optimal subarray is used to image details of the rupture properties of the mainshock.
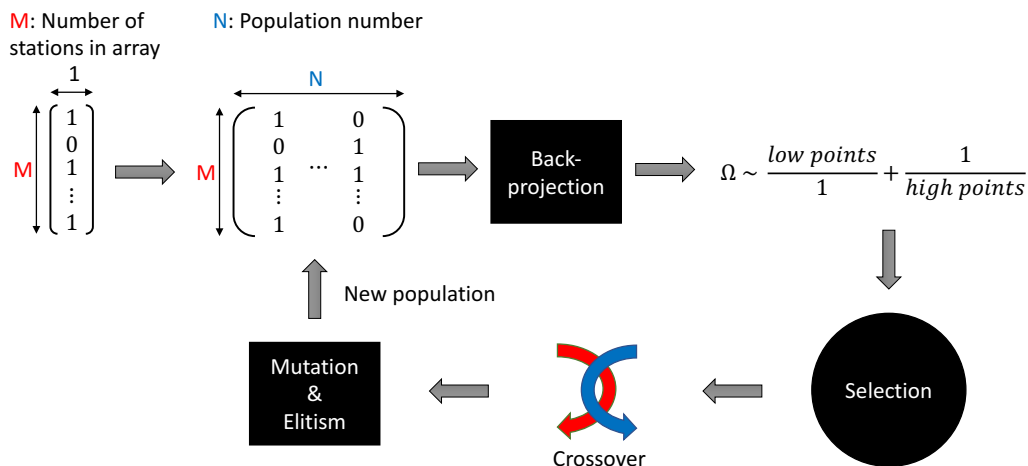
Figure 1: Generational cycle of the genetic algorithm. N potential solutions (population) of length M binary strings that represent a sub-array (individuals) are assigned a fitness value according to a cost function. Individuals are identified proportionally to their fitness (selection) and are used to form a new population of individuals that are, on average, better potential solutions to the problem (crossover). Random bits within a binary string flip to increase diversity and search more of the solution space (mutation).