

This package MDGD (the main program MDGD and the HelpMDGD program) searches Minimum Distance estimates for mutational parameter using Mutation Accumulation Data. It is a version improved by Aurora García-Dorado (2003) of a previous program by Aurora García-Dorado and Juan Miguel Marín (1995). The model and methods are described in:

García-Dorado, A. (1997). The rate and effects distribution of viability mutation in *Drosophila*: minimum distance estimation. *Evolution*, 1130-1139.

García-Dorado, A., & Marin, J. M. (1998). Minimum distance estimation of mutational parameters for quantitative traits. *Biometrics*, 1097-1114.

García-Dorado, A., & Gallego, A. (2003). Comparing analysis methods for mutation-accumulation data: a simulation study. *Genetics*, 164(2), 807-819.

#### **IF YOU USE THIS PROGRAM CITE:**

**García-Dorado, A., & Marin, J. M. (1998). Minimum distance estimation of mutational parameters for quantitative traits. *Biometrics*, 1097-1114.**

This program uses the means of the Mutation Accumulation lines at a given generation. The rate of increase in between line variance, as well as the rate of change of the mean if a reliable control is available, must be estimated previously.

First run the helpmdgd programme to learn how to use the main program and to generate a file (par1.dat) with information for the main run. Then run mdgd. Both programs are given in two versions, one for UNIX and the other one for a Windows PC. I also attach a mutation accumulation data set (ohnv.dat, with per generation rate of mutational increase in variance between MA lines=0.000246, 40 mutation accumulation generations) and a suggested par1.data file that can help you to get familiar with the process.

Aurora García-Dorado