
SPSA-molecules:

This program uses the Simultaneous Perturbation Stochastic Approximation (SPSA) algorithm to find the optimal conformer structure when the bond lengths are known and the angles are the independent variables being optimized.

FDSA-molecules:

This program uses the Finite Difference Stochastic Approximation (SPSA) algorithm to find the optimal conformer structure when the bond lengths are known and the angles are the independent variables being optimized.