Analysis of Polymer Characteristics through C++ Computational Methods

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Protein folding and computational origami are gradually becoming revolutionary fields. With our ability to computationally analyze minuscule biological structures, we are making significant progress toward understanding how life works. I aimed to contribute to the field by analyzing polymers through C++ programming. I created a random initial polymer structure, and I calculated the energy expended by moving a particular random bond. This change in energy was used to calculate whether a move could be accepted by a Monte Carlo method. The end-to-end distances and spring constants of the polymers analyzed were calculated.