Central to the biology of genetic material is the ability of DNA-bound proteins to communicate via long-range interactions. In broad terms these interactions can be defined as either passive (DNA sliding, hopping/jumping and looping) or active (DNA translocation and unwinding). In many cases, the relative orientation of the binding sites must also be communicated. For example, site-specific recombinases achieve this using passive DNA looping. Alternatively, mismatch repair proteins rely on ATP hydrolysis to bias the interactions. In cleaving DNA, Type I and Type III restriction modification (RM) enzymes must communicate the relative orientation of two asymmetric recognition sites over hundreds of base pairs. The basis of this long-range interaction, which requires ATP hydrolysis by helicase domains, is poorly understood. Conflicting models have been proposed, invoking both passive and active DNA loop formation. Using a combination of biochemical and single molecule assays, we find strong evidence that Type I enzymes translocate DNA loops by hydrolysing at least one ATP per bp. In contrast, we find no evidence for loop formation by Type III enzymes, which move tens of bp for each ATP. Instead we propose an alternative communication scheme based on 1D diffusion. Our data illustrates an important role for helicases, not in unwinding DNA, but in communicating over long distances on intact DNA. Moreover, it illustrates that this same biological role can be undertaken by either energy-efficient or energy-inefficient means.