

Reference Frame for Protein Structure Recognition

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ABSTRACT

Data representation is an initial important issue in any procedures. For any raw data being input to a procedure, the researcher will first extract the required features from the raw data. These features must be embodied into a meaningful representation to be inserted in the procedure. This paper will discuss the data representation called reference frame used in geometric hashing algorithm for protein structure matching. Matching 3D structure needs special care so that the important and unique information can be encapsulated and differentiated between one another. The reference frame is generated from backbone fragment i.e. N- α -C. This paper will first show the calculation of the reference frame RF1 and second, given a single coordinate for atom S (x, y, z), we want to find new coordinate for S ($\hat{x}, \hat{y}, \hat{z}$) in terms of the reference frame RF1. These new coordinates will be used as the matching features between two structures. Add result here.

Keywords: Reference frame, geometric hashing and tertiary structure recognition