# Related work

On the basis of the component library in the DPPSAA domain, this article has carried out the research on the algorithm design and program generation of multiple sequence alignment algorithms under the PAR framework

In [Shi and Zhou (2019)](#), we analyzed the characteristics of DPPSAA, extracted the common and variable features and the constraints and dependencies between them, established the DPPSAA domain model and its algorithm component interaction model, and further implemented the models using the abstract programming language Apla to form a highly abstract DPPSAA component library, in order to automatically or semiautomatically assemble components to generate sequence alignment algorithms for specific fields, thereby reducing the error rate and time cost of manual selection algorithms for sequence similarity analysis, improving the efficiency of algorithm execution, and even assembling a more efficient new sequence alignment algorithm based on dynamic programming.