Parallel: A High-Level Programming Language for Efficient Bioinformatics Scientific and Mathematical Built-In Functions With an Easy and Flexible Syntax

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In this project, we propose the design and implementation of a new programming language that is specifically tailored for bioinformatics and computational science. The language has a simple syntax and a flexible structure that allows scientists and mathematicians to develop complex biological data analysis systems without prior experience in programming. The language incorporates a large number of built-in functions and algorithms for bioinformatics and computational biology, as well as new datatypes such as the math set and the biological sequence. The language also supports parallelism and the sliding window algorithm to speed up computations, making it efficient and scalable for large datasets. To ensure safety and performance, the language is designed to avoid buffer overflows and is just-in-time (JIT) compiled. This new programming language is a valuable tool for researchers in many fields of science, including biology, mathematics, and computer science, and opens up new possibilities for data analysis and research.

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