Editors

*Bioinformatics*

**Application Note Submission**

Dear Editor

We are pleased to submit our manuscript entitled "PxBLAT: An Ergonomics and Efficient Python Binding Library for BLAT" for your kind consideration for publication in *Bioinformatics*. In this manuscript, we introduce the PxBLAT Python library, a tool designed to enhance the functionality and user experience of the widely-used sequence alignment tool, BLAT. As the volume of genomic data continues to grow, tools like BLAT have become indispensable in the analysis and manipulation of genetic sequences. However, the existing tools often present challenges due to language and interface limitations, hampering usability and efficiency. To address these issues, we developed PxBLAT, the first comprehensive Python library for BLAT, with the goal of bridging the gap between BLAT's high-performance capabilities and the flexibility of the Python environment.

Based on a dataset of 1,000 FASTA files sampled from the Human Genome, our benchmarks demonstrate that PxBLAT significantly improves execution speed by approximately 20% compared to BLAT. Beyond its performance improvement, PxBLAT seamlessly integrates with Biopython, eliminating the need for intermediate files and system calls. Moreover, PxBLAT includes features to manage server readiness, making it a valuable asset for the bioinformatics community. We firmly believe that PxBLAT will be of immense benefit to the bioinformatics community, given Python's widespread use in the field and the demand for faster, more efficient genome sequence alignment tools. Our team is dedicated to maintaining and further developing PxBLAT to ensure its continued relevance and usefulness.

In addition to the manuscript, we have included a supplementary document containing additional figures and tables that will aid in comprehending the features and capabilities of our tool. Furthermore, a preprint version of this work is available at [URL] for reference.

We hereby confirm that there are no conflicts of interest related to this submission.

Thank you for your careful consideration of our work. We eagerly anticipate your feedback.

On behalf of all authors, I remain with best regards,

A black text with a white background

Description automatically generated

Rendong Yang

Associate Professor

Department of Urology

Northwestern University Feinberg School of Medicine