PxBLAT: An Efficient and Ergonomics Python Binding Library for BLAT

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Abstract of the paper goes here.

Software Libraries | Sequence Analysis | BLAT
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Introduction

This is introduction.

Materials and Methods

This is materials and methods. Pybind11 (Jakob et al., 2016)

Design Philosophy of PxBLAT

Implementation

Results

PxBLAT has consistent result with BLAT

Benchmarking Performance

Ergonomics

Text is added like this This is a reference to a published paper (Watson and Crick, 1953). We can cite other things too (Tipton and Gorbsky, 2019; Zheng et al., 2011; Alberts, 2002)
This is a new paragraph. New sentences on a new line. New sentences on a new line.
This is a new result. As you can see (Figure 1).
It is possible to add a one-column Figure like this (Figure 2).

Discussion

This is the discussion section where you wax lyrical about your findings. You can put your work in the context of other published work (Brenner et al., 1967).

Acknowledgements

Conflict of interest

Funding

Data availability

Reference

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Figure 1. These are cells.
(**A**) This is a regular figure with a legend as a caption underneath. Inset: 3X zoom. Scale bar, 10 µm.

Figure 2. This is a nucleus.
(**A**) This is a one-column figure with a legend as a caption underneath.

Supplementary Information

Figure S1. This is an endosome.
(**A**) This is a supplementary figure shown as a two-column image with a legend underneath.