

KrATER: K-mer Analysis Tool Easy to Run

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K-mer based approaches are widely used in bioinformatics areas related to DNA/RNA sequences. Analysis of k-mer distribution is crucial step in quality control of raw reads, error correction and genome or transcriptome. Several tools were developed for drawing and analysis of k-mer distributions, however, all of them are very difficult and sometimes impossible even to install or fail to perform in complicated cases.

Here we present KrATER - K-mer Analysis Tool Easy to Run, which was developed to be simple and easy for both installation and run. This tool reports basic statistics of k-mer distributions regardless of its pattern. The only assumption about distribution is used for genome size estimation. Also KrATER draws useful and publication-ready plots in both logarithmic and linear scales.

KrATER is available at the Python Package Index (PyPI, <https://pypi.python.org>) and GitHub (<https://github.com/mahajrod/KrATER>).

We hope that KrATER will fill the lack of simple, working in all conditions and user-friendly tool in k-mer analysis area. KrATER can be used in quality control and initial analysis of reads, estimation of error correction efficiency, publication preparation and development of new k-mer based approaches.

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