**Abstract**

**Background**: Metagenomics is the genomic analysis of entire biological communities. This task analyzes species composition in metagenomic sequencing data. Previous popular algorithms need to utilize a large amount of information in the reference sequence. However, these algorithms only care about the existence of k-mers in the reference sequence and do not pay attention to its weight, which suffers from a large amount of information loss. In addition, prior Kraken2 algorithm cannot get the correct classification label from the complex hit tree when selecting the classification label. These problems lead to misjudgment of the algorithm.

**Results**: Here, we present KrakenWeight, precise and fast metagenomics classification using weighted k-mer. We divide k-mers into three categories: repeated k-mers, shared k-mers, and distincted k-mers. And we define the repetition value (R value) according to the repeated k-mer, defines the shared value (S value) according to the shared k-mer, and redistributes the weight of the k-mer according to S value and R value. Meanwhile, for the conflict in the matching process, this thesis defines a dynamic conflict value to resolve the conflict. The source code of KrakenWeight is publicly available at https://github.com/zhang570221322/kraken2.

**Keywords**: Metagenomics; Species taxonomy; Weight; Taxonomy

**Background**

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**Results**

To evaluate the performance of KrakenWeight,

**Simulated WGS data from reference database**

**Performance evaluation**

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**Discussion**

In this study,

**Conclusion**

False Positive.

**Methods**

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