

## Sequence analysis

# VisFeature: a stand-alone program for visualizing and analyzing statistical features of biological sequences

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## ***Abstract***

In this paper, we developed 'VisFeature', which aims to be a helpful software tool that allows the users to intuitively visualize and analyze statistical features of all types of biological sequence, including DNA, RNA and proteins. VisFeature also integrates sequence data retrieval, multiple sequence alignments and statistical feature generation functions.

VisFeature is a **desktop application** that is implemented using JavaScript/Electron and R. The source codes of VisFeature are freely accessible from the GitHub

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## ***Introduction***

Over the last two decades, the number of known **biological sequences** has been growing exponentially. Many efficient computational methods for generating statistical features from sequences have been developed. Several web servers and stand-alone programs have been released for **practical applications**, such as

1. PseAAC
2. PseAAC-General
3. PseKNC-General
4. Pse-in-One
5. UltraPse

These software tools provide efficient and convenient solutions to generate statistical features for biological sequences. However, a helpful software tool for visualizing **the statistical features is still lacking**. To the best of our knowledge, this is the first toolkit that is designed especially for this purpose. **VisFeature**

integrates sequence feature visualization and analysis, statistical feature visualization and comparison.

online database querying, multiple sequence alignment and color sequence visualization together.

All these functions are useful in the explorative stage of developing predictive algorithms for functional attributes.