

sefOri: selecting the best engineered sequence features to predict DNA replication origins

The software sefOri selects the subset of sequence features with the best prediction accuracies of the DNA replication origins for the four yeast genomes. The user may also export features extracted from the DNA sequences for further analysis.

Update

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Citation

Chenwei Lou, Jian Zhao, Ruoyao Shi, Wenyang Zhou, Yubo Wang, Guoqing Wang, Lan Huang, Xin Feng, Fengfeng Zhou. sefOri: selecting the best engineered sequence features to predict DNA replication origins. Submitted.

Running environment

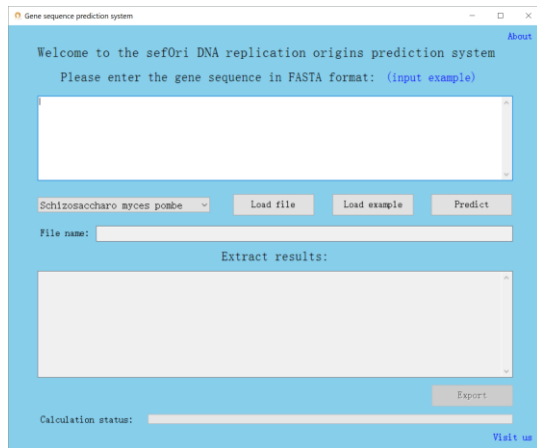
Compiler: Visual Studio 2017 , JetBrains PyCharm 2018.1.1 x64

Language: C++11, C++ clr, python3, openmp

Environment: .NET framework

Manual

The software sefOri is a GUI-based software, whose main interface is in the following figure.



The user may load the query sequences from a file by clicking the button “Load file”, or load the example sequences by clicking the button “Load example”.

The prediction results may be generated by clicking the button “Predict”. The user may choose one of the four models to predict the query sequences by clicking the dropbox listing the four species.

The features generated from the query sequences may be exported to a file for further analysis.

Maintainers and contact

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