

cBar: a computer program to distinguish plasmid-derived from chromosome-derived sequence fragments in metagenomics data

[Fengfeng Zhou](#), [Ying Xu](#)

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Prerequisite

cBar needs the following softwares:

- **BioPerl**: A perl library for bioinformatics computation.
URL: http://www.bioperl.org/wiki/Main_Page
- **Weka**: A data mining software. cBar has attached Weka 3.6.0
URL: <http://www.cs.waikato.ac.nz/~ml/weka/>

Download

cBar version 1.2: <http://csbl.bmb.uga.edu/~ffzhou/cBar/cBar.1.2.tar.gz>

Installation

Use this command to compile the c codes in your system:

```
make
```

Usage

You may use this command to process the example genome sequence of *Synechococcus elongatus* PCC 7942.

```
> ./cBar.pl Synechococcus_elongatus_PCC_7942.fna  
Synechococcus_elongatus_PCC_7942.cBar.txt  
Formatting the sequences ... [FormattedSeq:2] [done]  
Generating the K-mer profiles ... [KMer] [Profile] [done]  
Predicting ... [Predicted] [Saved] [Cleared] [done]
```

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