CRISPRdigger: detecting CRISPRs with better direct repeat annotations

Ruiquan Ge[1,2,*], Guoqin Mai[1,*], Pu Wang[1,2], Manli Zhou[1,2], Youxi Luo[3], Yunpeng Cai[1,#], Fengfeng Zhou[4,5,#].

[1] Shenzhen Institutes of Advanced Technology, and Key Lab for Health Informatics, Chinese Academy of Sciences, Shenzhen, Guangdong 518055, China.

[2] Shenzhen College of Advanced Technology, University of Chinese Academy of Sciences, Shenzhen, Guangdong, 518055, China.

[3] School of Science, Hubei University of Technology, Wuhan, Hubei, 430068, China.

[4] College of Computer Science and Technology, Changchun, Jilin, 130012, China.

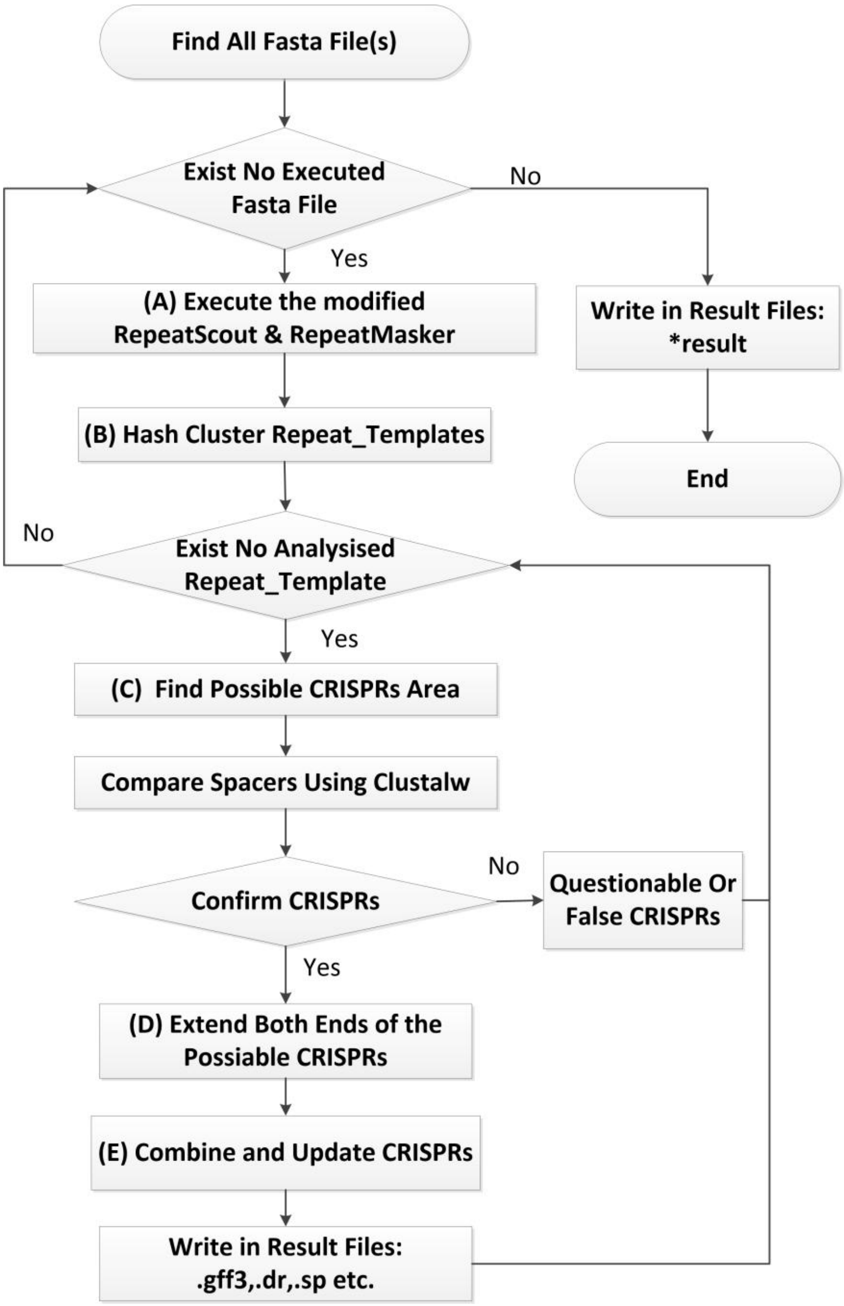
[5] Key Laboratory of Symbolic Computation and Knowledge Engineering of Ministry of Education, Jilin University, Changchun, Jilin 130012, China.

[*] These authors contribute equally to this work.

[#] Corresponding author: Fengfeng Zhou, e-mail: FengfengZhou@gmail.com or ffzhou@jlu.edu.cn .Web site: http://www.healthinformaticslab.org/ffzhou/.

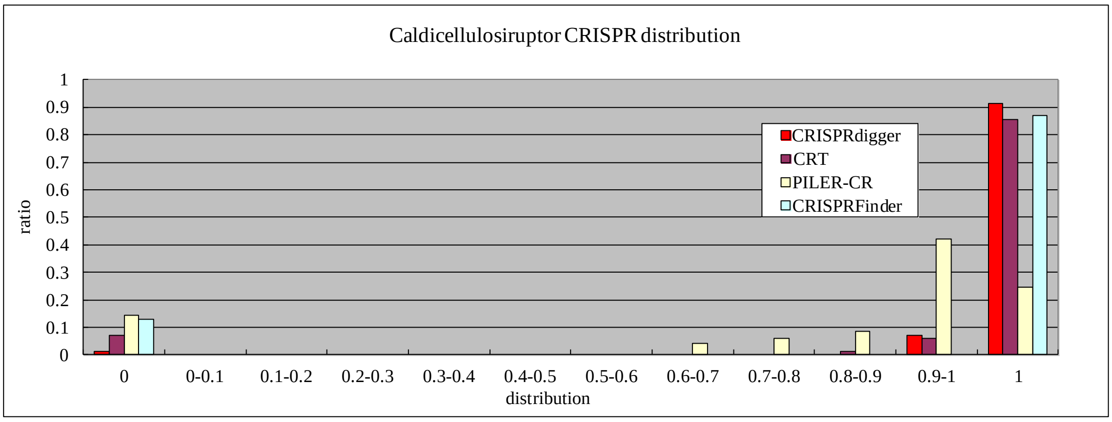
Supplementary Figure S1

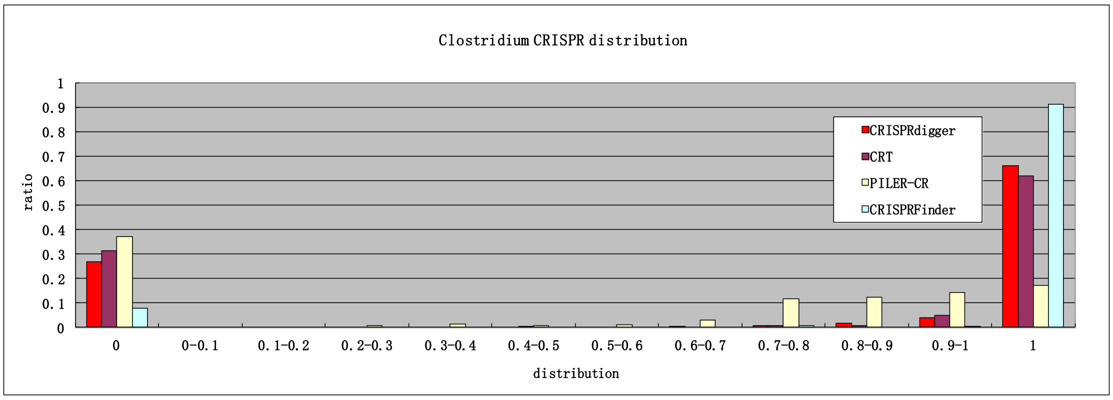
The work flow of the program CRISPRdigger. Below is the algorithmic flow of the program CRISPRdigger. Input files should be in the FASTA format. Direct Repeats (DRs) were mainly found by RepeatScout and RepeatMasker. According to the character and the restriction of the DRs and spacers, parts of the CRISPRs were identified. After extending the DRs, the CRISPRs were enlarged or combined. Result files included the detailed information of the CRISPRs.

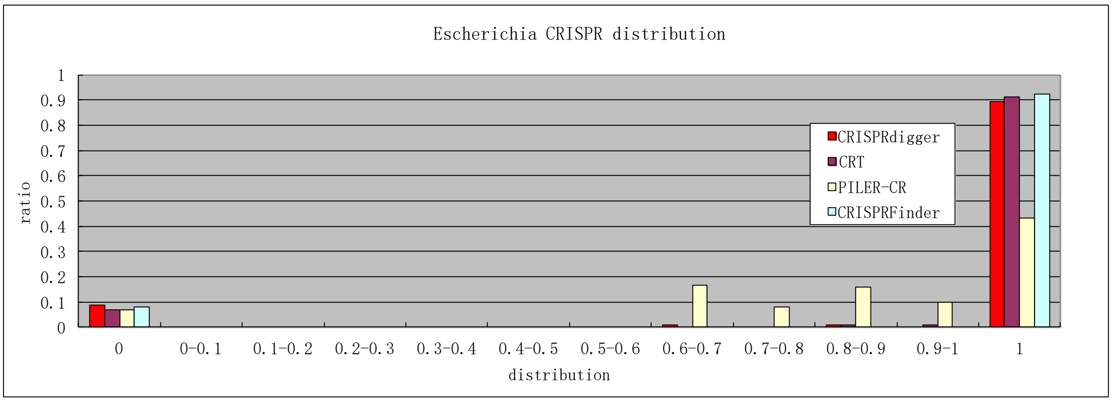


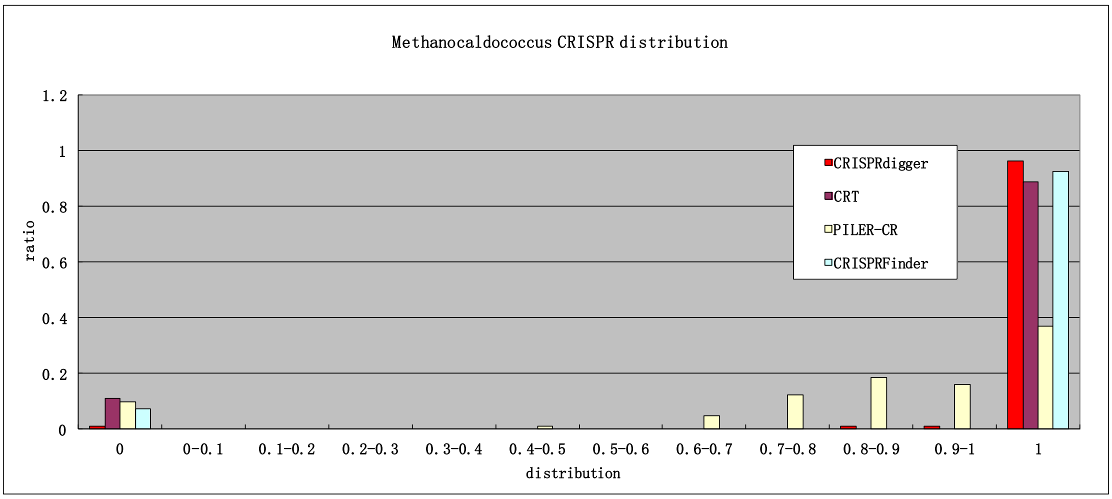
Supplementary Figure S2

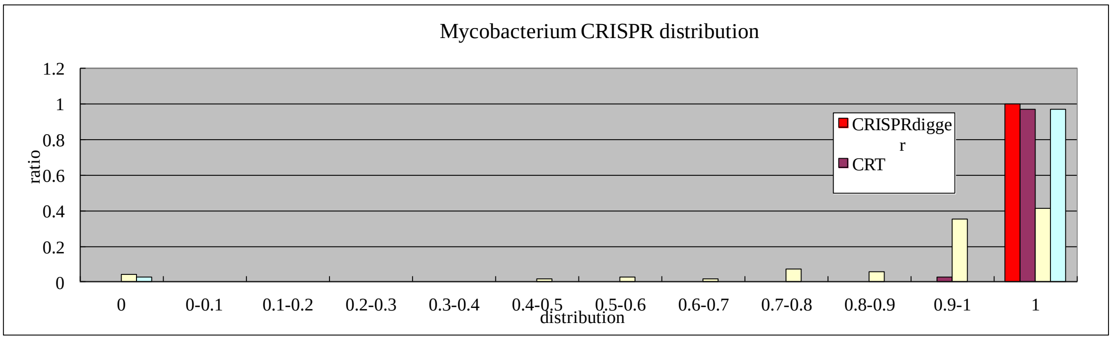
The comparison on the top 10 prokaryotic genus with the largest CRISPR numbers. The top 10 prokaryotic genus with the largest CRISPR numbers are used to analyze in dbCRISPR. The bottom figures show their CRISPRs statistical distributions in the four CRISPR detection programs: CRISPRdigger, CRT, PILER-CR and CRISPRFinder.

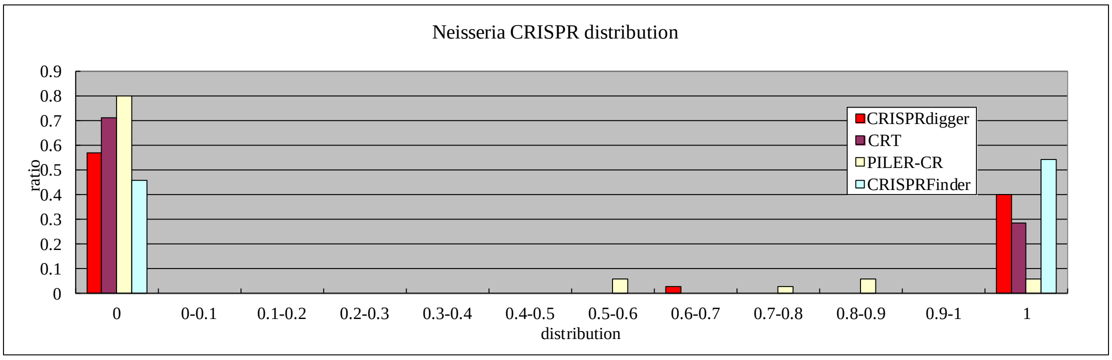


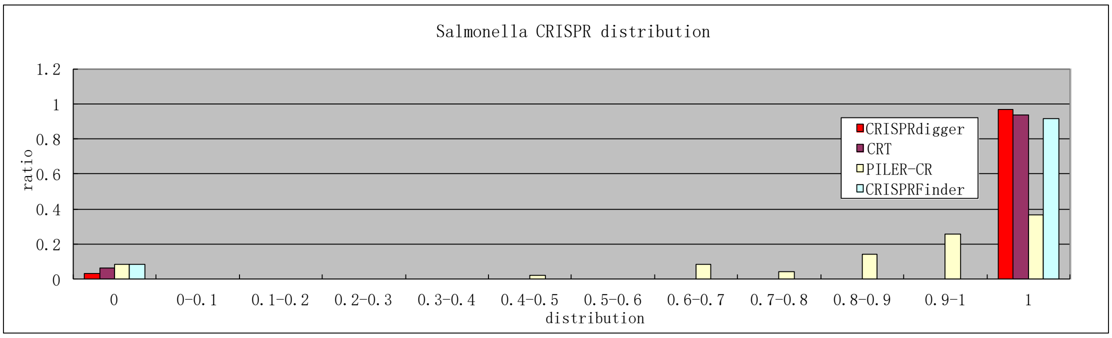


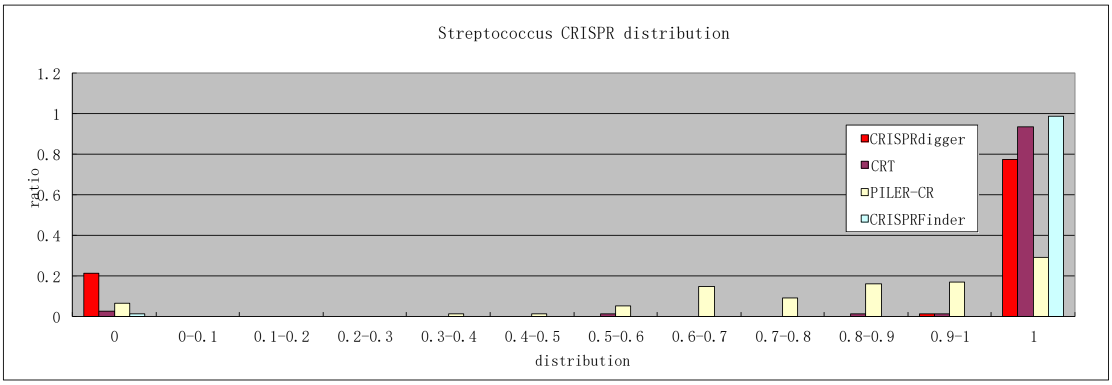


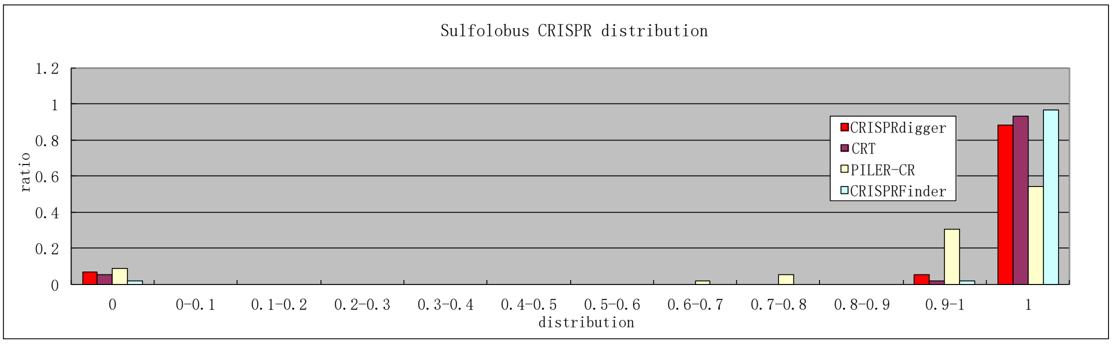

Methanocaldococcus CRISPR distribution
1.2
1
0.8
0.6
0.4
0.2
0
ratio
CRISPRdigger
CRT
PILER-CR
CRISPRFinder
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution

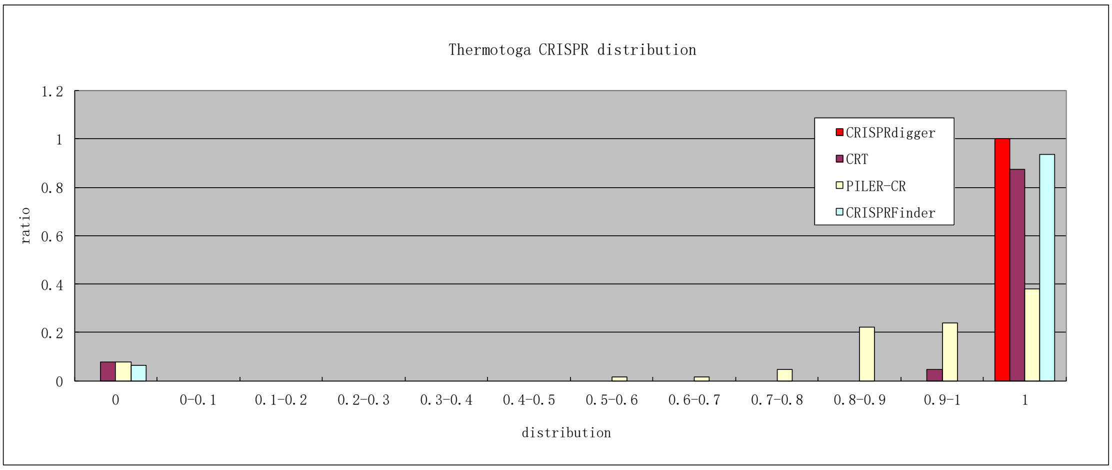

Mycobacterium CRISPR distribution
1.2
1
0.8
0.6
0.4
0.2
0
ratio
CRISPRdigger
CRT
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution


Neisseria CRISPR distribution
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
ratio
CRISPRdigger
CRT
PILER-CR
CRISPRFinder
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution


Salmonella CRISPR distribution
1.2
1
0.8
0.6
0.4
0.2
0
ratio
CRISPRdigger
CRT
PILER-CR
CRISPRFinder
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution


Streptococcus CRISPR distribution
ratio
1.2
1
0.8
0.6
0.4
0.2
0
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution
CRISPRdigger
CRT
PILER-CR
CRISPRFinder


Sulfolobus CRISPR distribution
ratio
1.2
1
0.8
0.6
0.4
0.2
0
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution
CRISPRdigger
CRT
PILER-CR
CRISPRFinder


Thermotoga CRISPR distribution
ratio
1.2
1
0.8
0.6
0.4
0.2
0
0
0-0.1
0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1
1
distribution
CRISPRdigger
CRT
PILER-CR
CRISPRFinder