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Mini Review

Collecting Bio Information against COVID-19 with Pse-in-One Software

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Abstract

A better understanding of the genetic codes of the Covid-19 virus, especially in vaccination studies, reaching 328 million cases worldwide and still being 40% of community immunity, requires the normalization of vaccine and drug treatments by 60% of community immunity and standardization of the outbreak. It is going to continue up to 40 months. The focus of our study, which we will describe the Pse-in-One software, is to ensure that the correct vaccine is produced in vaccine studies. In the review of Liu et al. published in a nucleic acid science journal in 2015 and Nature science journal in 2017, how this program became functional is summarized in this study. I hope this article helps scientists in vaccine and drug development. I wish you good days.

Introduction

On May 1, 2020, approved the number of cases in countries nominal 1.1 million united states, 215 thousand Spain, 205 thousand Italy, 177 thousand United Kingdoms, 163 thousand Germany, 130 thousand in France, 120 thousand Turkey, 114 thousand Russia, and 95 thousand It is listed as Iran. Improving the numbers 133 thousand united states of America, Spain 115 thousand, 76 thousand Italy, Iran, 76 thousand, 118 thousand Germany, France 50 thousand, 48 thousand Turkey, Russia is ranked as 13 thousand. If death rates of United States 64 thousand, 25 thousand Spain, Italy, 28 thousand, 27 thousand united kingdoms, Germany 7 thousand, 24 thousand France, Turkey 3174 1200 Russia, Iran, and six thousand [1]. Last Friday, India peaked with 2293 daily cases, and in Mumbai, a woman tried to reduce the potential virus load in her body by passing through the sterilization cabinet (Figure 1) [2].

Figure 1: A woman is passing through a sanitization tunnel in Mumbai, last week.

A private company in Calif produces 1.5 million vials sufficient for 150000 patients. And the company in La Verne declared that these bottles would be distributed free of charge (Figure 2) [2]. Beyond that, bus drivers in London began to refrain from driving because of the increasing number of deaths in the country (Figure 3) [2].

Figure 2: Gilead Sciences in La Verne, Calif.

Figure 3: 28 bus drivers in 37 transportation workers in London died.

In Manila, 9731 detainees were released between March 1 and April 29. Of these, 4600 were reported to have traveled to the Luzon region, which includes the capital. This week, 212 people were diagnosed with coronavirus in the Philippines, Cebu City (Figure 4) [2].Here, the determination of coronavirus in urban wastes can be a solution for taking precautions by knowing the onset of pandemics early (Figure 5) [2].

Figure 4: Prisoners released in Manila.

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Figure 5: In Brazil's National Institute of Science and Technology, the researcher collected sewage samples testing for coronavirus last month.

Introduction to Pse-in-One 2.0

The Pse-in-One version 2.0 was previously developed by Liu et al. From the Pse-in-One version of the Pse-in-One version. It is a web server and is more flexible than the first version. It contains many component modes [3].This model has emerged today in computational biology because of the difficulty of determining sequences such as RNA, DNA, or protein for a biology unit. This software is especially "Neural network," "NN algorithm," Supporting vector machine," and "SVM algorithm." It also enables faster resolution of difficulties encountered in existing machine learning algorithms such as "Nearest Neighbor" because it is tough to think of all these machine learning methods in a single learning method [3].

Table 1: 6 new modes lists for DNA sequences.

Category	Mode
Nucleic acid composition	1.Increment of diversity (IDKmer)[226,270,291]
	2.The occurrences of kmers, allowing at most m mismatches (Mismatch)[264,265,292]
	3.The occurrences of kmers, allowing non-contiguous matches(subsequence)[265,292,293]
Autocorrection	4.Moran autocorrelation (MAC)[268,294]
	5.Geary autocorrelation (MAC)[217,295]
	6.Normalized Moreau-Broto autocorrelation (NMBAC)[217,296]

Table 2: Eight new modes list for RNA sequences .

Category	Mode
Nucleic acid composition	1.The occurrences of kmers, allowing at most m mismatches (Mismatch)[264,265,292]
	2.The occurrences of kmers, allowing non-contiguous matches(subsequence)[265,292,293
Autocorrection	3. Moran autocorrelation (MAC)[217,294]
	4. Geary autocorrelation (GAC)[217,295]
	5. Normalized Moreau-Broto autocorrelation (NMBAC)[217,296]
Predicted structure composition	6.Local structure- sequence triplet element (Triplet)[266]
	7.Pseudo- structure status composition(PseSSC)[226]
	8. Pseudo- distance structure status pair composition (PseDPC)[10]

Table 3: Eight new modes list for protein sequences.

Category	Mode
Nucleic acid composition	1.Distance- based Residue(DR)
	2.PseAAC of Distance-Pairs and Reduced Alphabet (Distance-Pairs)[271]
	3.Physicochemical distance transformation (PDT)[270]
Autocorrection	4.Select and combine then most frequent amino acids according to their frequencies(Top-n-gram)[269]
	5.Profile-based physicochemical distance transformation (PDT-profile)[270]
	6.Distance-based Top-n-gram (DT)[271]
Predicted structure composition	7.Profile-based Auto covariance(AC-PSSM)[272]
	8.Profile-based Cross covariance(CC-PSSM)[272]
	9.Profile-based Auto-cross covariance(ACC-PSSM)[272]

The entries related to Pse-in-one 2.0 software can be seen in Tables 1-3. The algorithm of the program can be seen in Figure 4. The results obtained by running the program are automatically notified by e-mail [3].In the old version of the software, the sub server can be seen in Figure 7 [4].

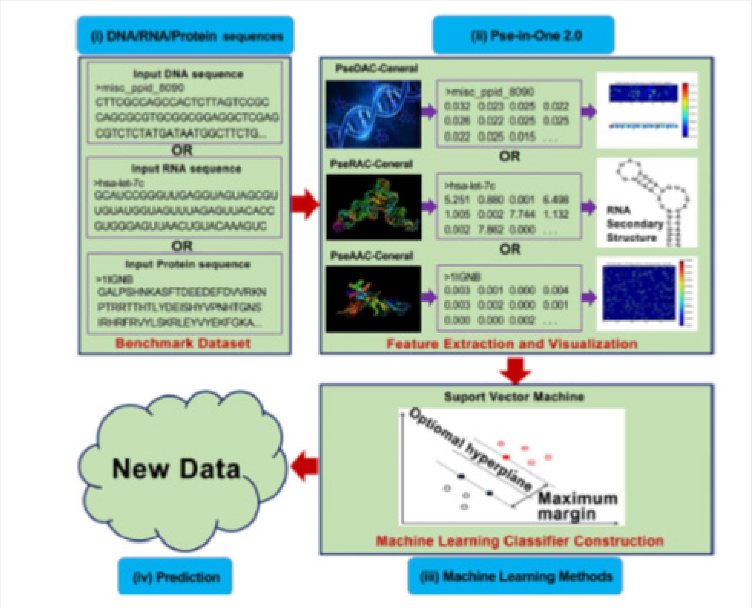
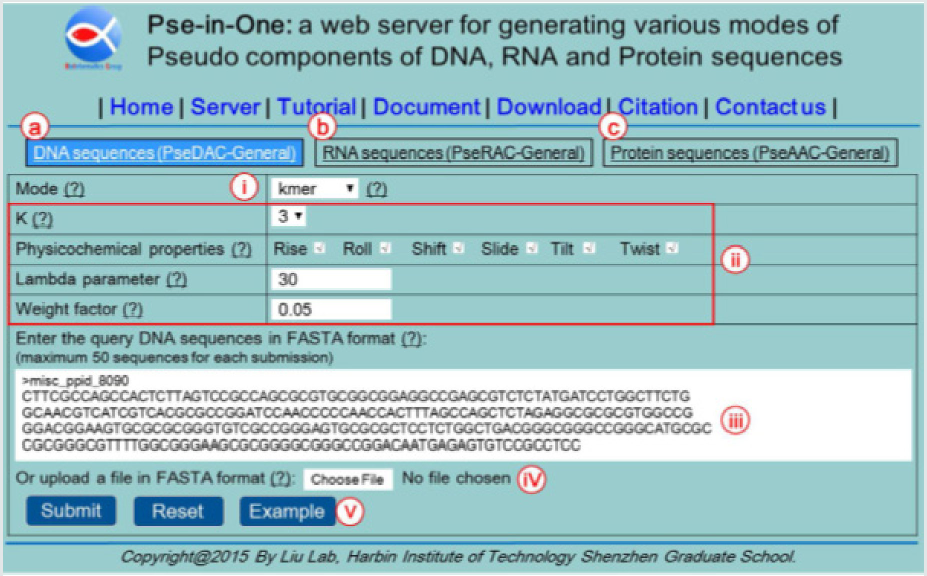


Figure 6: Flow chart of the Pse-in-One 2.0.



Mode (?) kmer (?)
K (?) 3
Physicochemical properties (?) Rise Roll Shift Slide Tilt Twist
Lambda parameter (?) 30
Weight factor (?) 0.05

Enter the query DNA sequences in FASTA format (?):
(maximum 50 sequences for each submission)

```
>misc_ppid_8090
CTTCGCCAGCCACTCTTAGTCCGCCAGCGCGTGCGGCGGAGGCCGAGCGTCTCTATGATCCTGGCTTCTG
GCAACGTCATCGTCACGCGCCGGATCCAACCCCCAACCACTTTAGCCAGCTCTAGAGGCGCGCGTGGCCG
GGACGGAAGTGCGCGCGGGTGTCGCCGGGAGTGCGCGCTCCTCTGGCTGACGGGCGGGCCGGGCATGCGC
CGCGGGCGTTTTGGCGGGAAGCGCGGGGCGGGCCGGACAATGAGAGTGTCCGCCTCC
```

Or upload a file in FASTA format (?): No file chosen

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Figure 7: A sub server of Pse-in-One.

Conclusion

To improve the knowledge and interest of medical science, the Pse-in-One 2.0 version presented in this article to obtain the data needed by the researchers quickly and effectively in vaccine development and drug discoveries.

References

1. Inc G COVID-19 map. 2020.
2. Magno D (2020) The Coronavirus Outbreak. The New York Times. The New York Times.
3. Liu B, Wu H, Chou K-C (2017) Pse-in-One 2.0: An Improved Package of Web Servers for Generating Various Modes of Pseudo Components of DNA, RNA, and Protein Sequences. Natural Science 09: 67-91.
4. Liu B, Liu F, Wang X, Chen J, Fang L, and et al., (2015) Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences. Nucleic Acids Res 43(W1): W65-W71.

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