

Showcase to Illustrate How the Web-Server pLoc_Deep-mHum Is Working

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Abstract

Recently, a very useful method called “pLoc_Deep-mHum” has been proposed for finding against the Pandemic COVID-19. Illustrated in this short report is a step-by-step guide for how to use its web-server.

Keywords

Coronavirus, Human Proteins, Multi-Label System, PseAAC, Five-Steps Rules

In 2020, a very powerful web-server predictor has been established for identifying the subcellular localization of human proteins based on the sequence information alone [1], in which a same protein may occur or move between two or more location sites and hence needs to be marked with the multi-label approach [2].

The web-server predictor is called “pLoc_Deep-mHum”, where “Deep” means the web-server has been further improved by the “Deep Learning” technique [3-6], and “m” means the capacity able to deal with the multi-label systems.

Moreover, its power has been further strengthened by using the “Pseudo Amino Acid Component” [7] or “PseAAC” [8] treatment widely used in computational biology (see, e.g., [9-136] and the “5-steps rules” [137] widely and increasingly used in system biology and biomedicine (see, e.g., [4, 138-160])).

To learn how the web-server is working, please do the following.

Step 1. Click the link at http://www.jci-bioinfo.cn/pLoc_Deep-mHum/, the top page of the pLoc_bal-mHumweb-server will appear on your computer screen, as shown in **Figure 1**. Click on the Read Me button to see a brief introduction about the predictor.

Step 2. Either type or copy/paste the sequences of query human proteins into

the input box at the center of **Figure 1**. The input sequence should be in the FASTA format. For the examples of sequences in FASTA format, click the [Example](#) button right above the input box.

Step 3. Click on the [Submit](#) button to see the predicted result. For instance, if you use the four protein sequences in the [Example](#) window as the input, after 10 seconds or so, you will see a new screen (**Figure 2**) occurring. On its upper part are listed the names of the subcellular locations numbered from (1) to (14) covered by the current predictor. On its lower part are the predicted results: the query protein O15382 of example-1 corresponds to “10,” meaning it belonging to “Mitochondrion” only; the query protein P08962 of example-2 corresponds to “8, 13” meaning it belonging to “Lysosome” and “Plasma membrane”; the query protein P12272 of example-3 corresponds to “2, 6, 11”, meaning it belonging to “Cytoplasm”, “Extracellular”, and “Nucleus”. All these results are perfectly consistent with experimental observations.

Figure 1. The top page of the web-server for pLoc_Deep-mHum.

Protein ID	Subcellular location or locations
>O15382	10
>P08962	8,13
>P12272	2,6,11

[Continue Test](#)

Figure 2. The new screen shown on your computer obtained by Step 2.

Step 4. As shown on the lower panel of **Figure 2**, you may also choose the batch prediction by entering your e-mail address and your desired batch input file (in FASTA format of course) via the **Browse** button. To see the sample of batch input file, click on the button **Batch-example**. After clicking the button **Batch-submit**, you will see “Your batch job is under computation; once the results are available, you will be notified by e-mail.”

Step 5. Click on the **Citation** button to find the papers that have played the key role in developing the current predictor of pLoc_Deep-mEuk.

Step 6. Click the Supporting Information button to download the Supporting Informations mentioned in this paper.

Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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