

KW2 Summary

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1 SSSIz Prediction

Checks whether the pipeline is still running anyway and whether the output is correct, i.e. no corrupt or incorrect files have been created. Unfortunately, several files with 0 bytes were created because I mistakenly worked on the wrong script and changed some code. I deleted all 0 bytes and restarted the pipeline.

2 RNAz Prediction

The pipeline is finished and has no false files.

3 Samples from SSSIz, Multiperm and aln-Shuffle

Checked the Data from the Samples and they are fine. I make a script to convert the CLUSTAL Files into FASTA Files because the Method SPOT-RNA needs a FASTA file to predict the RNA Structure. I installed Biopython on my PC and also on the Server.

Biopython with version 1.84.

```
pip install biopython
```

Tested the script (convertCluFasta.py) on my PC and it works fine.

```
python3 convertCluToFasta.py
```

The script is attached.

4 SPOT-RNA2

Try to install SPOT-RNA2 as described in the following.

<https://github.com/jaswindersingh2/SPOT-RNA2>.

I was able to install SPOT-RNA2 on my PC, but was unable to run the program due to the requirement of the entire NCBI database (400GB), which caused issues as there is insufficient memory available on the server (only 15-30GB in my virtual environment). Therefore this method will probably not work.

4.0.1 Idea

To create a link between the database and SPOT-RNA2 and simulate that the database is on the system.

5 SPOT-RNA

Since the SPOT-RNA2 could not be used, I tried to install the previous version SPOT-RNA as described in the description:

<https://github.com/jaswindersingh2/SPOT-RNA>

I was able to install it on my PC and it works perfectly.

6 RNA-MSM

<https://github.com/yikunpku/RNA-MSM?tab=readme-ov-file>

I'm just about to install it and try it out soon.

7 Questions

- Can I compare SPOT-RNA with SISSIZ? The output of a sample is attached.
- Should I use SPOT-RNA instead of SPOT-RNA2 or should I look for an alternative?