First version = single\_DNA\_seq.py

Second version = paper\_algo.py

1. Approach: The first version of `DLLSimpute` uses a dynamic local least squares approach, while the second version employs a method based on matrix operations using SVD and pseudoinverse.

2. Missing Value Handling:

- In the first version, missing values are handled within the function by dynamically expanding the local neighborhood until a suitable value is found.

- In the second version, missing values are replaced with `None` initially, and then the entire matrix is processed until all missing values are filled.

3. Implementation Details:

- The first version explicitly checks for the presence of suitable neighborhoods around missing values.

- The second version sorts rows based on the number of missing values and proceeds to handle missing values row by row.

4. Dependencies:

- The first version utilizes `numpy` for array manipulation and `scikit-learn` for NRMSE calculation.

- The second version relies solely on `numpy` and `scipy` for SVD and pseudoinverse computation.

5. NRMSE Calculation:

- Both versions calculate NRMSE, but the second version includes an additional step to handle cases where the difference between the original and imputed values is zero.

6. Usage:

- The usage of both versions involves passing the sequence to be imputed, but the second version additionally involves converting the sequence to numerical data and back.

Overall, both versions tackle missing value imputation differently, with the first version focusing on local neighborhood exploration and the second version utilizing matrix operations. Depending on the specific requirements and characteristics of the data, one approach may be more suitable than the other.