**A comparative case study of Multiple Sequence Alignment for analyzing its performance with different MSA tools**

**Team Members**

[1] Arnav Aima UFID:

[2] Sakshi Dubey UFID: 4813-1141

[3] Suhani Mehta UFID:

**Abstract**

Multiple Sequence Alignment(MSA) is a biological concept of aligning three or more sequences. It is of great importance for studying the genetic functions, structures and evolution process of the biological sequences. The aligning of multiple sequences is one of the most fundamental problem in Bioinformatics & it has been widely used for a lot of biological applications like predicting the shapes of proteins, constructing the phylogenetic trees, etc. MSAs demand extremely sensitive computational methodologies to come up with precise results. The objective of this project is to conduct a comparative study on different MSA tools on the basis of computation time, accuracy & other parameters to contrast the pros/cons of MSA tools for different objectives.

**Plan of Action**

**Phase 1 :** Researching the relevant research work & developing the understanding for MSA Algorithms

**Phase 2:** Look for the appropriate data sets & derive strategies to conduct the comparative study of different tools

**Phase3:** Testing the implemented algorithms on different parameters & debugging for improved results

**Phase 4:** Evaluating the results & preparing a detailed report on inferences

**Workload Distribution**

* All the members are initially responsible for developing a deep understanding of MSA Algorithms
* Arnav Aima: Responsible for testing the clustalw2 sample & analyze its data
* Sakshi Dubey: Responsible for testing the T-coffee sample & analyze its data
* Suhani Mehta: Responsible for testing the MAFFTs ample & analyze its data
* All members will contribute together on contrasting their results & for preparing a combined informative report

// We can change the exact names in today's meeting

**References**

1. Robert C. Edgar “MUSCLE: multiple sequence alignment with high accuracy and high throughput” Nucleic Acids Research, 2004

2. Jason S. Papadopoulos, Richa Agarwala “COBALT: constraint-based alignment tool for multiple protein sequences” Bioinformatics, 2007

3. Robert C Edgar, Serafim Batzoglou “Multiple sequence alignment” Current opinion in structural biology, 2006

4. Feng,D.F., Doolittle,R.F. “Progressive sequence alignment as a prerequisite to correct phylogenetic trees” J. Mol. Evol. 1987

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