**Milestones**

* Literature Research
* Compute the skew (Task 1)
* Develop algorithm for DnaA motif finding (Task 2)
* Apply algorithm to different bacterial genomes (Task 3+4)
* Write report

**Data Management Plan**

1. Data types and formats used in this project:
   * Journals, papers (PDF)
   * Genome and motif/oriC sequences (.fasta, .txt)
   * Code files
2. Access, Sharing and Re-use:

Data (especially code-, text-, and excel-files) are shared using the file hosting services “github” and “overleaf”.

Furthermore, all data is stored on personal storage devices by each group member individually.

OriC sequence data will be taken from the DoriC database.

1. Long-term storage:

Copies of the final project will be stored by each group member.

**Working Plan & Task Distribution**

|  |  |
| --- | --- |
| **Coding Tasks** | **Literature/Evaluation Tasks** |
| * Compute skew and draw diagram   (also include *Wigglesworthia glossinidia* from Task 6) | * How does the skew help with motif prediction? |
| * Develop motif finding algorithm * Download genome sequences and reference sequences for comparison | * Evaluate and compare the findings to references |
|  | * Find paper which shows that bacterial chomosomes do not just have one oriC (Task 5) * Evaluation of *Wigglesworthia glossinidia* data (Task 6) |