## CRC cards

## Fasta

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| **Class name** | **Superclass** | | **Subclass** |
| Fasta |  | |  |
| **Responsibility** | | **Collaboration** | |
| Loads FASTA file from a given path. | | Parser | |
| Processes and stores sequence data. | |  | |
| Counts number of sequences. | |  | |
| Converts parsed data into a Pandas DataFrame. | |  | |

## Parser

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| **Class name** | **Superclass** | | **Subclass** |
| Parser |  | | Fasta |
| **Responsibility** | | **Collaboration** | |
| Initializes with a file path. | |  | |
| Parses raw sequence data from file. | |  | |
| Stores and returns parsed content as a list. | |  | |
| Displays top records or summaries. | |  | |

## Analyzer

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| **Class name** | **Superclass** | | **Subclass** |
| Analyzer |  | |  |
| **Responsibility** | | **Collaboration** | |
| Initializes with a DNA sequence. | | Sequence\_motif | |
| Calculates GC content and reverse complements. | |  | |
| Aligns two sequences. | |  | |
| Performs motif analysis and generates summary DataFrame. | |  | |
| Provides transcription, length, and subsequence extraction tools. | |  | |

## Sequence\_motif

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| --- | --- | --- | --- |
| **Class name** | **Superclass** | | **Subclass** |
| Sequence\_motif |  | |  |
| **Responsibility** | | **Collaboration** | |
| Initializes with a DNA motif and its function. | | Analyzer | |
| Analyzes distribution of the motif across a DNA sequence. | |  | |