

## CRC Cards

<b>Class:</b> MitochondrialDNAParser	<b>Super Class:</b>	<b>Sub Class:</b>
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>• Parse a FASTA file and organise the data in the file into a Pandas Dataframe</li> <li>• Represent sequence identifiers, description and sequences</li> <li>• Abstract the parsing logic to make it reusable for other genomic data formats.</li> </ul>		<b>Collaborators:</b> <ul style="list-style-type: none"> <li>• MitochondrialDNA</li> <li>• ComparativeAnalysis</li> <li>• ConservedMotifs</li> </ul>

<b>Class:</b> MitochondrialDna	<b>Super Class:</b>	<b>Sub Class:</b> GenomicMotif
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>• Extract subsequences from genomic sequences</li> <li>• Calculate the GC content</li> <li>• Calculate the length of the sequence</li> </ul>		<b>Collaborators:</b> <ul style="list-style-type: none"> <li>• MitochondrialDNAParser</li> <li>• ComparativeAnalysis</li> <li>• ConservedMotifs</li> </ul>

<b>Class:</b> GenomicMotif	<b>Super Class:</b> MitochondrialDna	<b>Sub Class:</b>
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>• Represent sequence motifs</li> <li>• Search for motifs within mitochondrial DNA</li> <li>• Count motif occurrences and analyse their distribution across sequences</li> </ul>		<b>Collaborators:</b> <ul style="list-style-type: none"> <li>• ComparativeAnalysis</li> <li>• ConservedMotifs</li> <li>• AlignmentAnalysis</li> </ul>

<b>Class:</b> ComparativeAnalysis	<b>Super Class:</b>	<b>Sub Class:</b>
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>• Compare sequences of different species based on sequence length and GC</li> </ul>		<b>Collaborators:</b> <ul style="list-style-type: none"> <li>• MitochondrialDNAParser</li> <li>• MitochondrialDna</li> <li>• GenomicMotif</li> </ul>

<ul style="list-style-type: none"> <li>Summaries the statistics of sequences based on longest, shortest sequences and highest and lowest sequences.</li> </ul>	
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<b>Class:</b> ConservedMotifs	<b>Super Class:</b>	<b>Sub Class:</b>
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>Identifies conserved motifs across multiple sequences and species</li> </ul>	<b>Collaborators:</b> <ul style="list-style-type: none"> <li>MitochondrialDNAParser</li> <li>MitochondrialDna</li> <li>GenomicMotif</li> </ul>	

<b>Class:</b> AlignmentAnalysis	<b>Super Class:</b>	<b>Sub Class:</b>
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>Aligns sequences pairwise</li> <li>Provide alignment scores and visual representation of the alignments</li> </ul>	<b>Collaborators:</b> <ul style="list-style-type: none"> <li>MitochondrialDna</li> <li>GenomicMotif</li> </ul>	

<b>Class:</b> InputForm	<b>Super Class:</b>	<b>Sub Class:</b>
<b>Responsibilities:</b> <ul style="list-style-type: none"> <li>Upload a FASTA file to popularise the system with genomic data</li> <li>View statistical summaries of mitochondrial data</li> <li>View motif occurrence and alignment results through interactive visualisation</li> <li>Search specific motifs or sequence patterns and visualise their location on the mitochondrial DNA</li> </ul>	<b>Collaborators:</b> <ul style="list-style-type: none"> <li>MitochondrialDNAParser</li> <li>MitochondrialDna</li> <li>SequenceAligner</li> </ul>	