Class name:	Superclass:	Subclasses:	Class name:	Superclass:	Subclasses:	Class name:	Superclass:	Subclasses:
FileParser		FastaParser	FastaParser	FileParser		GenomicEntity		Mitochondriall
Responsibilites:	Collaborations:		Responsibilites:	Collaborations:		Responsibilites:	Collaborations:	
Analyzes files			Creates dataframe from a FASTA file			Returns its characteristics		
			Shows dataframe containing FASTA data			Specifies length		
			Summarizes data across dataframes					
			Gives the identifier, the descrpition and the sequence of the dataframe					
Class name:	Superclass:	Subclasses:	Class name:	Superclass:	Subclasses:	Class name:	Superclass:	Subclasses:
MitochondrialDNA	GenomicEntity		MotifAnalyser		SequenceMotif	SequenceAlignment		
Responsibilites:	Collaborations:		Responsibilites:	Collaborations:		Responsibilites:	Collaborations:	
Counts % of Gs and Cs			Finds motifs	MitochondrialDNA		Performs alignment	MitochondrialDNA	
Extracts subsequences						Prints N alignments		
						Returns % of identity		
			Class name:	Superclass:	Subclasses:			
			SequenceMotif	MotifAnalyser				
			Responsibilites:	Collaborations:				
			Extracts motifs and the positions where they are found at	MitochondrialDNA				
			Find in which sequence and how many times a given motif is found					