BAMseek is used to read and display the content of the BAM, SAM, VCF and SFF files. It was developed for people that want to analyze the content of a large file but have not much time to do it. BAMseek is distributed under the GNU GPL v3 license and is available for download at Copyright (C) 2015, www.dinsom.com.ar SequenceTools is a collection of tools for sequence manipulation, comparison, sequence assembly and visualization. It includes HMMer, HMM-based applications, blast, blast2seq, local blast, blastfast, blastp, blastn, blastx, clustalo, blastp, blastx, clustalo, clustalw, clustalo, EMu, EMuClust, ESTmatrix, est2genome, est2genome, est2genome