

DAMBE – Integrated software package for data analysis in molecular biology and evolution

What is DAMBE?

DAMBE is a Windows program featuring many powerful analytical functions for genomics and molecular evolution including:

1. Reading and writing all standard sequence files including trace files from automatic sequencers. In particular, it uses the FEATURES table in the GenBank file to allow the user to extract specific sequence fragments such as CDS, exon, intron, tRNA, rRNA and many others.
2. Contig assembly.
3. Implementation of all known genetic codes for codon-based sequence analysis.
4. Sequence manipulation including CDS→protein translation, extracting 1st, 2nd and 3rd codon positions from CDS sequences to facilitate separate analyses.
5. Sequence alignment and manual alignment editor as well as aligning protein-coding nucleotide sequences against aligned amino acid sequences.
6. Descriptive sequence analysis functions including various measures of codon usage indices such as relative synonymous codon usage (RSCU) and codon adaptation index (CAI), protein isoelectric point calculations, amino acid energetics analysis, extract tRNA sequence and identify the anticodon loop and anticodon, etc.
7. Comprehensive comparative sequence analysis including (1) the quantification of substitution patterns, (2) molecular phylogenetics with distance-based, maximum parsimony and maximum likelihood methods, (3) testing the molecular clock hypothesis with nucleotide-based or codon-based relative-rate tests or with tree-based tests for multiple OTUs, (4) evaluating the relative statistical support of alternative phylogenetic trees by bootstrapping and jackknifing or by the Kishino-Hasegawa test in the maximum likelihood framework, or by the Templeton test in the maximum parsimony framework, (5) fitting statistical distributions (Poisson, negative binomial and gamma) to substitution rates over sites, and (6) estimating the proportion of invariant sites for a given distribution. DAMBE also includes extensive tree-viewing and tree-manipulation functions and can export graphic images (BMP and encapsulated metafile) to other graphic software packages such as PowerPoint.
8. Extensive graphic functions for hydrophobicity plot (or for many other amino acid properties), dinucleotide stacking energy plot and twist angle plot, tetranucleotide flexibility plot and minimum energy plot, substitution saturation plot, and plots for visualizing varying substitution rates over sites.
9. Comprehensive on-line help.

Why use DAMBE?

1. DAMBE aims to become a one-stop software package so that you do not need to learn dozens of programs in order to analyze your data.
2. DAMBE is convenient. For example, to get bootstrapping support for a tree in PHYLIP by using the neighbor-joining method, one has to run DNADIST, NEIGHBOR, and CONSENSE in sequence, and finally use a tree-viewing program to view the consensus tree. In DAMBE, all is done with just a few clicks.

3. For a number (but not all) of analytical methods, DAMBE is faster than many other software packages by eliminating redundant calculations, simplifying data structures and minimizing disk reading and writing. One should try out those computation-intensive methods such as sequence alignment and maximum-likelihood-based phylogenetic reconstruction methods.
4. DAMBE has functions not available in other software packages. For example, DAMBE implements more nucleotide-based and codon-based genetic distances than most other packages. Because DAMBE implements all known genetic codes, codon-based analysis, such as the calculation of synonymous and nonsynonymous substitutions and codon-based relative-rate tests can be performed for aligned sequences from any taxonomic group.

Availability and Installation

DAMBE is freely available at <http://aix1.uottawa.ca/~xxia/software/software.htm>. Follow the installation link and click the [DAMBE.msi](#) link to initiate the automatic installation process.

Using DAMBE

Click the DAMBE icon after the installation to start the program. Click File|Open to read in a sequence file. Click one of many functions organized in 10 categories (File, Edit, Alignment, Sequences, Seq.Analysis, Graphics, Phylogenetics, SeqLab, Tools). Whenever in doubt, click Help or just press the F1 key.

References

1. Xia, X. 2001. Data analysis in molecular biology and evolution. Kluwer Academic Publishers, Boston.
2. Xia, X., AND Z. Xie. 2001. DAMBE: Software package for data analysis in molecular biology and evolution. J. Hered. 92:371-373.