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What DnaSP can do:

Abstracts: [DnaSP v. 1.0](#) [DnaSP v. 2.0](#) [DnaSP v. 3.0](#) [DnaSP v. 4.0](#)

DnaSP, DNA sequence polymorphism, is an interactive computer program for the analysis of DNA polymorphism from nucleotide sequence data. The program, addressed to molecular population geneticists, calculates several measures of DNA sequence variation within and between populations (with or without the sliding window method) in noncoding, synonymous or nonsynonymous sites; linkage disequilibrium, recombination, gene flow and gene conversion parameters; and some neutrality tests, Fu and Li's, Hudson, Kreitman and Aguadé's, McDonald and Kreitman, and Tajima's tests. DnaSP can also conduct computer simulations based on the coalescent process.

What DnaSP can not do:

DnaSP can not align sequences. There are some available programs that can do this. For example, you can perform the multiple alignment with CLUSTAL W ([Thompson et al. 1994](#)). This program produces an output (multiple aligned sequences in NBRF/PIR format) that can be read by DnaSP.

DnaSP can not make phylogenetic inferences or manipulate trees. There are many programs to do this, for example, MacClade ([Maddison and Maddison 1992](#)), MEGA ([Kumar et al. 1994](#)), PHYLIP ([Felsenstein 1993](#)), PAUP ([Swofford 1991](#)). Nevertheless, the input file formats used by DnaSP ([FASTA](#), [MEGA](#), [NBRF/PIR](#), [NEXUS](#) and [PHYLIP](#) format) are also recognized for some of them.

DNA sequences can not be edited or manipulated by DnaSP. You can do this by using, for example, MacClade ([Maddison and Maddison 1992](#)) or SeqApp / SeqPup programs ([Gilbert 1996](#)).

DnaSP can not directly analyze diploide genetic information (for instance, SNPs data from diploid genomic regions). If you are using diploid unphase data, you can reconstruct the phase using the [Open Unphase/Genotype Data](#) module.



Introduction

Abstracts: [DnaSP v. 1.0](#) [DnaSP v. 2.0](#) [DnaSP v. 3.0](#) [DnaSP v. 4.0](#)

Population genetics is a branch of the evolutionary biology that tries to determine the level and distribution of genetic polymorphism in natural populations and also to detect the evolutionary forces (mutation, migration, selection and drift) that could determine the pattern of genetic variation observed in natural populations. Ideally, the best way to quantify genetic variation in natural populations should be by comparison of DNA sequences ([Kreitman 1983](#)). However, although the methodology for DNA sequencing is available since 1977 ([Maxam and Gilbert 1977](#) [Sanger et al. 1977](#)), until 1990 the use of DNA sequence data had had little impact on population genetics. This is because the effort (in terms of both money and time) required to obtain DNA sequence data from a relative large number of alleles was substantial.

The introduction of the polymerase chain reaction (PCR) ([Saiki et al. 1985; 1988](#)) which allows direct sequencing of PCR products and avoids, therefore, their cloning, has changed the situation. Undoubtedly this has produced a revolutionary change in population genetics. Although, at present, population studies at the DNA sequence level are still scarce and primarily carried out in *Drosophila* (for example: [McDonald and Kreitman 1991](#) [Schaeffer and Miller 1993](#) [Rozas and Aguadé 1994](#)), they will certainly increase in the future.

The DnaSP (DNA Sequence Polymorphism) is a software addressed to molecular population geneticists and can compute several measures of DNA sequence variation within and between populations in noncoding, in synonymous or in nonsynonymous sites; gene flow, gene conversion ([Betrán et al. 1997](#)), recombination and linkage disequilibrium parameters. In addition, DnaSP performs some neutrality tests: the [Hudson, Kreitman and Aguadé \(1987\)](#), the [Tajima \(1989\)](#), [McDonald and Kreitman 1991](#); and the [Fu and Li \(1993\)](#) tests. DnaSP takes advantage of the Microsoft Windows capabilities, so that it can handle a large number of sequences of thousands of nucleotides each on a microcomputer. Furthermore, DnaSP can easily exchange data with other programs, for example, programs to perform multiple sequence alignments, phylogenetic tree analysis, or statistical analysis.



System requirements

See Also: [Limitations](#)

DnaSP is written in Visual Basic v. 6.0 (Microsoft), and it runs on an IBM-compatible PC under 32-bit Windows.

The minimum hardware requirements for the program are:

- a processor based on the Intel Pentium (or higher)
- 32 megabytes of RAM memory
- a mouse
- a hard disk.

DnaSP also requires:

- Microsoft Windows, versions 95/98/NT/ME/2000/XP

DnaSP can run in Macintosh (PowerMac) using SoftWindows or VirtualPC software emulators, or in Linux using WMWare or Wine emulators.

NOTE: Using emulators, the computation speed of the program will decrease.



Limitations

See Also: [System requirements](#)

Both the number and length of the sequences that can be handled by DnaSP mainly depend on the available memory. Nevertheless, DnaSP is able to use all RAM memory available in a computer, both the conventional and the extended memory. DnaSP can also use virtual memory (it can use the hard disk space as memory, although in this case the computation speed will be much lower than when using RAM). Thus, the program can handle large numbers of sequences of up to thousands nucleotides each.

Input data file limitations:

Maximum number of nucleotides per sequence: Depends on the available memory (> 3,000,000 nt).

Maximum number of sequences: 32767

Other limitations:

The grid control cannot display more than 16351 rows or 5448 columns. Therefore, for the sliding window option, the maximum number of rows of results is 16351. Hence, the maximum number of polymorphic sites (linkage disequilibrium module) or of sequences (synonymous and nonsynonymous module) that can be analyzed *and displayed on the screen* is 181 (the total number of pairwise comparisons is: $181 * 180 / 2 = 16290$). Although DnaSP will not display the results of these analyses on the screen, the results could be saved in a file.

NOTE: These upper limits will be increased (I hope) in following DnaSP versions.



Input Data Files

DnaSP can automatically read the following types of data file formats:

[FASTA](#),

[MEGA \(Kumar et al. 1994\)](#),

[NBRF/PIR \(Sidman et al. 1988\)](#),

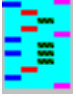
[NEXUS \(Maddison et al. 1997\)](#),

[PHYLIP \(Felsenstein 1993\)](#),

In all cases one or more homologous nucleotide sequences should be included in just one file (ASCII file). The sequences must be aligned (i. e. the sequences must have the same length).

Nucleotide sequences should be entered using the letters A, T (or U), C or G (in lower case, upper case, or any mixture of lower and upper case).

DnaSP allows you to analyze a subset of sites of the data file (this option is useful for the analysis of particular regions of the data file, for example, when analyzing exonic and intronic regions separately), or to carry out analyses in a subset of sequences of the data file (see the [Include / Exclude Sequences](#) command).



FASTA format

See Also: [Input Data Files FASTA Format Example](#)

DnaSP can recognize FASTA data file formats (also called Person format). FASTA file format must begin with the symbol '>' in the first line of the file; the sequence name is the first word after that symbol. Additional characters in this line are considered to be comments. The sequence data starts in the second line. Nucleotide data can be written in one or more lines.

DnaSP only recognize noninterleaved FASTA data files.

Special characters

Blank spaces, Tabs, and Carriage returns are ignored (i. e. they can be used to separate blocks of nucleotides). By default DnaSP uses the following symbols:

the hyphen character '-' to specify an alignment gap;

the dot character '.' to specify that the nucleotide in this site is identical to that in the same site of the first sequence (i.e. identical site or matching symbol);

the symbols '?', 'N', 'n' to designate missing data.

Sequence name

The sequence name can be up to 20 characters. Blank spaces and tabs are not allowed (underlines should be used to indicate a blank space).



Example of FASTA format

```
>seq_1 [comment -optional-]
ATATACGGGGTTA---TTAGA----AAAATGTGTGTGTGTTTTTTTTTTCATGTG
>seq_2 [comment -optional-]
ATATAC--GGATA---TTACA----AGAATCTATGTCTGCTTTCTTTTTCATGTG
>seq_3
ATATACGGGGATA---TTATA----AGAATGTGTGTGTGTTTTTTTTTTCATGTG
>seq_4
ATATACGGGGATA---GTAGT----AAAATGTGTGTGTGTTTTTTTTTTCATGTG
```




MEGA format (Kumar et al. 1994)

See Also: [Input Data Files Mega Format Example](#)

References: [Kumar et al. 1994](#)

DnaSP can recognize interleaved and noninterleaved MEGA formats (DnaSP v. 1.0 only recognized noninterleaved MEGA formats). MEGA formats must contain the identifier **#MEGA** in the first line of the file. The second line must start with the word **TITLE:** followed by some comments (if any) on the data (comments within the sequences must be contained by a pair of double quotation marks: "**comment**"). The sequence data starts in the third line. The sequence name is the text after the character '#' until the first Blank space, Tab or Carriage return. The nucleotide sequence is written in one or more lines after the sequence name, until the next sequence name that also starts with the symbol '#' (see the MEGA user manual).

Special characters

Blank spaces, Tabs, and Carriage returns are ignored (i. e. they can be used to separate blocks of nucleotides). By default DnaSP uses the following symbols: the hyphen character '-' to specify an alignment gap; the dot character '.' to specify that the nucleotide in this site is identical to that in the same site of the first sequence (i.e. identical site or matching symbol); the symbols '?', 'N', 'n' to designate missing data. Nevertheless, these symbols can be changed in the dialog box that appears when opening a data file.

Sequence name

The sequence name can be up to 20 characters. Blank spaces and tabs are not allowed (underlines should be used to indicate a blank space).



Example of MEGA format

```
#MEGA
TITLE: 4 sequences (55 nucleotides). File: EX##N1.MEG
#seq_1
ATATACGGGGTTA---TTAGA----AAAATGTGTGTGTGTTTTTTTTTCATGTG
#seq_2
.....--..A.....C.....G...C.A...C..C...C.....
#seq_3
.....A.....T.....G.....
#seq_4
.....A.....G...T.....
```



NBRF/PIR format (Sidman et al. 1988)

See Also: [Input Data Files](#) [NBRF/PIR Format Example](#)

References: [Sidman et al. 1988](#)

In the NBRF/PIR files, the sequence names are placed immediately after the identifier **>DL;** . The next line is used for comments. The nucleotide sequence is written in the next line (in one or more lines) and is ended with the symbol **'*'** . The file must contain nucleotide sequences in a noninterleaved form.

Sequence data

Blank spaces, Tabs, and Carriage returns are ignored (i. e. they can be used to separate blocks of nucleotides). The hyphen character '-' must be used to specify an alignment gap. The dot character '.' can be used to specify that the nucleotide in this site is identical to that in the same site of the first sequence. The symbols '?', 'N', 'n' could be used to designate missing data. No other symbols are allowed.

Sequence name

The sequence name can be up to 20 characters. Blank spaces and tabs are not allowed (underlines should be used to indicate a blank space).



Example of NBRF/PIR format

>DL;seq_1

Comment on seq 1 (example file: EX##N1.NBR).

ATATACGGGG TTA---TTAG A----AAAAT GTGTGTGTGT TTTTTTTTC ATGTG*

>DL;seq_2

Comment: seq 2

ATATAC--GG ATA---TTAC A----AGAAT CTATGTCTGC TTCCTTTTC ATGTG*

>DL;seq_3

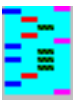
Comment: seq 3

ATATACGGGG ATA---TTAT A----AGAAT GTGTGTGTGT TTTTTTTTC ATGTG*

>DL;seq_4

Comment: seq 4

ATATACGGGG ATA---GTAG T----AAAAT GTGTGTGTGT TTTTTTTTC ATGTG*



See Also: [Input Data Files NEXUS Format Example 1](#) [NEXUS Format Example 2](#)

References: [Maddison et al. 1997](#)

DnaSP can read NEXUS file formats. These files are standard text files that have been designed (Maddison et al. 1997) to store systematic data. DnaSP can read NEXUS files (both old and new versions, Maddison et al. 1997) containing DNA or RNA sequence data. The file can contain one or more sequences; in the later case, the homologous nucleotide sequences must be aligned (i. e. the sequences must have the same length).

Nucleotide sequences should be entered using the letters A, T (or U), C or G (in lower case, upper case, or any mixture of lower and upper case). Blank spaces and Tabs are ignored (i. e. they can be used to separate blocks of nucleotides). Carriage returns are also ignored in non-interleaved file formats.

Alignment gap symbol

The symbol used to designate an alignment gap should be indicated by the subcommand **GAP**:

For example, **GAP=-** indicates that the hyphen character '-' should be used to specify an alignment gap.

Default symbol: -

Identical site (matching character) symbol

The symbol used to designate that the nucleotide in a site is identical to that in the same site of the first sequence should be indicated by the subcommand **MATCHCHAR**:

For example, **MATCHCHAR=.**

Default symbol: .

Missing data symbol

The symbol used to designate missing data should be indicated by the subcommand **MISSING**:

For example, **MISSING=?**

Default symbol: ?

Note: the following symbols are not allowed in the subcommands **GAP**, **MISSING**, and **MATCHCHAR**:

The white space, and **() [] { } / \ , ; : = * ' " ` < >**

(see Maddison et al. 1997).

Moreover, these subcommands cannot share the same symbol.

Sequence name

There is no limit for the sequence name length; nevertheless, DnaSP will only display the first 20 characters.

Blank spaces and tabs are not allowed (underlines should be used to indicate a blank space).

Interleaved format

NEXUS files can contain nucleotide sequences with interleaved and non-interleaved formats. The former format must be indicated by the subcommand **INTERLEAVE**

NEXUS blocks

NEXUS blocks must end with the command **END**; . DnaSP will read the following NEXUS blocks (see Maddison et al. 1997):

DATA, TAXA, CHARACTERS blocks. These blocks contain information about the taxa and the molecular sequence data.

SETS block. That block allows the user to store information of groups of sequences, characters, taxa, etc. DnaSP only uses the TaxSet command. This block contains information about groups of sequences.

NOTE: See also Define Sequence Sets.

CODONS block. This block contains information about the genetic code, and about the regions of the sequence that are noncoding, or protein coding regions.

NOTE: See also Assign Coding Regions.

CODONUSAGE block. This is a private NEXUS that contains information about the specific table of Preferred and Unpreferred codons that will be used in the [Preferred and Unpreferred Synonymous Substitutions](#) analysis. There are 8 predefined tables; nevertheless, the user can define their own table.

Subcommands:

Pref*: subcommand. Includes the preferred codons.

Unknown: subcommand. Includes codons of unknown preference nature.

NOTE: See also the [Data Menu](#). See also the NEXUS Format Example 1.

DNASP block. This is a private NEXUS block that contains information about:

i) the chromosomal location of the DNA region:

CHROMOSOMALLOCATION= command. There are 8 predefined chromosomal locations:

Autosome

Xchromosome

Ychromosome

Zchromosome

Wchromosome

prokaryotic

mitochondrial

chloroplast

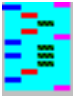
ii) or the organism's genomic type:

GENOME= command. There are 2 predefined genomic types:

Diploid

Haploid

NOTE: See also [Data Menu](#)



Example 1 of NEXUS file format

#NEXUS

[This is an example of the new NEXUS file format, NEXUS version 1. This is the version used by MacClade 3.05 or later. File: EX##new1.nex]

BEGIN TAXA;

DIMENSIONS NTAX=4;

TAXLABELS

seq_1

seq_2

seq_3

seq_4;

END;

BEGIN CHARACTERS;

DIMENSIONS NCHAR=55;

FORMAT DATATYPE=DNA MISSING=? GAP=- MATCHCHAR=. INTERLEAVE ;

MATRIX

seq_1 ATATACGGGGTTA---TTAGA----AAAATGTGTGTGTGT

seq_2--..A.---...C.----.G...C.A...C..C

seq_3A.---...T.----.G.....

seq_4A.---G...T----.....

seq_1 TTTTTTTTTCATGTG

seq_2 ...C.....

seq_3

seq_4

;

END;

BEGIN SETS;

TaxSet Barcelona = 1-2;

TaxSet Girona = 3;

TaxSet Catalunya = 1-3;

TaxSet Outgroup = 4;

END;

BEGIN CODONS;

CODONPOSSET * UNTITLED =

N: 1 2 6-26 51-55,

1: 3 27-48\3,

2: 4 28-49\3,

3: 5 29-50\3;

CODESET * UNTITLED = Universal: all ;

END;

BEGIN CODONUSAGE;

PREFUNPREFCODONS GENETICCODE=Universal Drosophila_melanogaster =

PREF*: UUC UCC UCG

UAC UGC CUC CUG

CCC CAC CAG CGC

AUC ACC AAC AAG

AGC GUC GUG GCC

GAC GAG GGC;

END;

BEGIN DNASP;

CHROMOSOMALLOCATION= Autosome;

GENOME= Diploid;

END;



Example 2 of NEXUS file format

#NEXUS

[This is an example of the Old NEXUS File Format used by MacClade 3.0 File: EX##old1.nex]

BEGIN DATA;

DIMENSIONS NTAX=4 NCHAR=55;

FORMAT MISSING=? GAP=- DATATYPE=DNA ;

MATRIX

seq_1 ATATACGGGGTTA---TTAGA----AAAATGTGTGTGTGTTTTTTTTTTCATGTG

seq_2 ATATAC--GGATA---TTACA----AGAATCTATGTCTGCTTTCTTTTTTCATGTG

seq_3 ATATACGGGGATA---TTATA----AGAATGTGTGTGTGTTTTTTTTTTCATGTG

seq_4 ATATACGGGGATA---GTAGT----AAAATGTGTGTGTGTTTTTTTTTTCATGTG

;

END;

BEGIN CODONS;

CODPOSSET UNTITLED =

1: 3 27 30 33 36 39 42 45 48,

2: 4 28 31 34 37 40 43 46 49,

3: 5 29 32 35 38 41 44 47 50;

GENCODE UNIVNUC

;

END;



PHYLIP format (Felsenstein 1993)

See Also: [Input Data Files](#) [PHYLIP Format Example](#)

References: [Felsenstein 1993](#)

DnaSP can recognize interleaved and noninterleaved PHYLIP formats. PHYLIP formats must contain two integers in the first line of the file: the first number indicates the number of sequences in the data file, while the second indicates the total number of sites. The sequence data starts in the second line. The sequence name can be up to 10 characters. The nucleotide sequence starts immediately (position 11). Nucleotide data can be written in one or more lines.

In PHYLIP interleaved formats, the sequence name must be indicate only in the first block.

Special characters

Blank spaces, Tabs, and Carriage returns are ignored (i. e. they can be used to separate blocks of nucleotides). By default DnaSP uses the following symbols:

the hyphen character '-' to specify an alignment gap;

the dot character '.' to specify that the nucleotide in this site is identical to that in the same site of the first sequence (i.e. identical site or matching symbol);

the symbols '?', 'N', 'n' to designate missing data.

Sequence name

The sequence name can be up to 10 characters. Blank spaces are allowed.



Example of PHYLIP format

4 55

seq_1 ATATACGGGGTTA---TTAGA-----AAAATGTGTGTGTGTTTTTTTTTTCATGTG

secuencia2ATATAC--GGATA---TTACA-----AGAATCTATGTCTGCTTTCTTTTTTCATGTG

DmelanogasATATACGGGGATA---TTATA-----AGAATGTGTGTGTGTTTTTTTTTTCATGTG

seq_4 ATATACGGGGATA---GTAGT-----AAAATGTGTGTGTGTTTTTTTTTTCATGTG



Open Multiple Data Files

DnaSP can automatically read several data file formats (see [Input Data Files](#)).

This module also allows you to analyse -at once- multiple files sequentially (as a Batch mode). These data files can contain different number of sequences, or different genomic regions.

Analysis

This command can analyse sequentially several data files. It can compute a number of measures of the extent of DNA polymorphism and can also perform some common neutrality tests.

Haplotype/Nucleotide Diversity

- The number of Segregating Sites, S
- The total number of mutations, Eta
- The number of haplotypes N_{Hap} , (Nei 1987, p. 259).
- Haplotype (gene) diversity and its sampling variance (Nei 1987).
- Nucleotide diversity, Pi (p), (Nei 1987), and its sampling variance (Nei 1987, equation 10.7).
- The average number of nucleotide differences, k (Tajima 1983).
- Theta (per gene or per site) from Eta (h) or from S , (Watterson 1975; Nei 1987).

Neutrality tests

- Tajima's D , (Tajima 1989), and its statistical significance.
- Fu and Li's D^* , (Fu and Li 1993), and its statistical significance.
- Fu and Li's F^* , (Fu and Li 1993), and its statistical significance.
- Fu's F_s , (Fu 1997).
- $G+C_n$, $G+C$ content at noncoding positions.
- $G+C_c$, $G+C$ content at coding positions.

More Information in the specific modules: [Codon Usage Bias](#) [DNA Polymorphism](#) [Fu and Li's \(and other\) Tests](#)

[Tajima's Test](#)



Open Unphase/Genotype Data Files

References: [Stephens 2001](#) [Stephens 2005](#) [Wang and Xu 2005](#)

DnaSP can automatically read Unphase (or Genotype) data files (diploid individuals) in FASTA format (see [FASTA](#)). This format is the standard FASTA format but including the [IUPAC nucleotide ambiguity codes](#) to represent heterozygous sites.

Suppose a data set containing 5 diploid individuals (therefore a total of 10 sequences) with 16 positions each.

```

      *   *   *
Ind1  TRCAAGACCGGAGGCG
Ind2  .A.C.--.....
Ind3  .A..M.....S...
Ind4  .A---.....C...
Ind5  .G..C....-----

```

For instance, as the second site of Ind1 is heterozygous (R = Purine; A and G), Ind1 includes the following two sequences:

```

Ind1-1  TACAAGACCGGAGGCG
Ind1-2  .G.....

```

As there are not heterozygous site in Ind2, then the two composing sequences are:

```

Ind2-1  TACCAG--CGGAGGCG
Ind2-2  .....--.....

```

This DnaSP module allows reconstructing the 10 sequences from the 5 individuals. DnaSP might handle and use the reconstructed data set (10 sequences of 16 nucleotides each) for further analysis.

Haplotype Reconstruction

DnaSP can reconstruct the haplotype phases from unphase data. This haplotype reconstruction is conducted using the algorithms provided by PHASE (Stephens et al. 2001), fastPHASE (Stephens et al. 2005) and HAPAR (Wang and Xu, 2005).

PHASE 2.1 uses a coalescent approximation method to estimate haplotype frequencies, under the assumption of Hardy-Weinberg equilibrium, random mating, the best solution for an individual is that with haplotypes at higher frequencies. It can also be used to estimate the recombination rate along the sequences.

fastPHASE 1.1, modifies the PHASE algorithm, and takes into account the locus spacing and the decay of linkage disequilibrium with the physical distance.

HAPAR uses a pure parsimony approach to estimate the haplotypes; the optimal solution is that which requires less haplotypes to resolve the genotypes. For positions not completely resolved, the user can choose between to replace unresolved positions as "N", or to assign randomly nucleotide variants.

Note:

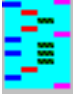
fastPHASE and HAPAR can not handle positions with more than two variants; in this case, therefore, these methods will not be able to be used.

Very important:

See the PHASE, fastPHASE or HAPAR documentation for more information and details.

IUPAC nucleotide ambiguity codes

Symbol	Meaning	Nucleic Acid
A	A	Adenine
C	C	Cytosine
G	G	Guanine
T	T	Thymine
U	U	Uracil
M	A or C	
R	A or G	
W	A or T	
S	C or G	
Y	C or T	
K	G or T	
V	A or C or G	
H	A or C or T	
D	A or G or T	
B	C or G or T	
X	G or A or T or C	
N	G or A or T or C	



Output

See Also: [Graph Window](#)

The output is displayed in three kinds of windows: text, table or grid (the output data are laid out in rows and columns like in a spreadsheet) and graphic (scatter graph and line chart).

All commands produce an output text window; moreover, some of them also produce a grid (table) window. Data in the grid can be used to create a graph (Graphs command in the [Display](#) menu). The data generated from DnaSP can be saved as an ASCII text file. The grid output data file can be easily used by other applications, such as spreadsheets, statistical or graphics applications, by simply removing the header.



UCSC Browser

References: [Kent 2002](#)

DnaSP allows you visualizing DNA sequence data and sliding window results, integrated with available genome annotations using the UCSC browser. To display the genome annotations DnaSP requires that the information of genomic position of the data (chromosome and physical position) was defined.

DnaSP allows searching available genomes in UCSC. To define the genomic position of your data, choose the appropriate genome, and specify the chromosome and the physical position of the reference sequence (the first one). If you don't know this information you can obtain it:

- Performing a BLAT search (Kent et al. 2002) against the appropriate UCSC genome.
- Searching the appropriate UCSC genome by key words, and import the output-information to DnaSP.

Genomic position assignments can be stored in NEXUS data files; for that, use the save/export or update commands.



Data Menu

Format

Use this command to indicate if the data file contains sequences of:

DNA or RNA

the chromosomal (genomic) type where the region is located:

Autosome

X chromosome

Y chromosome

Z chromosome

W chromosome

prokaryotic

mitochondrial

chloroplast

or the organism's genomic state:

Diploid or Haploid

Gaps in Sliding Window.

This command is used to exclude/include sites with alignment gaps in the length of the windows (Sliding Window method).

Gaps in Sequence Sets

Use this command to choose how to treat alignment gaps in sequence sets.

Segregating Sites/Mutations

Use this command to select between the number of segregating sites or the total number of mutations in computing some parameters of the [Fu and Li's \(and other\) Tests](#), [Fu and Li's \(and other\) Tests with an Outgroup](#), and [Tajima's Test](#).

Assign Coding Regions

Use this command to assign noncoding and coding protein regions to a particular data file.

Assign Genetic Code

Use this command to assign the Genetic Code used for translation. There are 9 pre-defined Genetic codes:

Nuclear universal (Table 1)

Mitochondrial of mammals (Table 2)

Mitochondrial of *Drosophila* (Table 5)

Mitochondrial of Yeast (Table 3)

Mitochondrial of Mold, Protozoan and Coelenterate (Table 4)

Mitochondrial of Echinoderm (Table 9)

Mitochondrial of Flatworm (Table 14)

Nuclear of Ciliate, Dasycladacean and Hexamita (Table 6)

Nuclear of some *Candida* species (Table 12)

In parenthesis is indicated the GenBank translation table number. More information on the Genetic Codes used by GenBank in:

<http://www.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c>

Assign Preferred / Unpreferred Codons Table

Define Sequence Sets

Filter / Remove Positions

Include / Exclude Sequences

Note:

This information will be stored if you save/export (or update) the data file as a NEXUS file format.



Define Sequence Sets

This command allows you to define sequence sets (groups of sequences). A sequence set is a group of related sequences that could represent, for example, a population, a species of an outgroup. That allows conducting analyses on a specific group of sequences.

Sequence sets assignments can be stored in NEXUS data files; for that use the `save/export` or `update` commands.



Define Domain Sets

This command allows you to define domain sets. A domain set is a partial fragment of the multiple alignment that could represent, for example, an exon, a gen, an intrón, etc. That definition allows DnaSP conducting analyses on specific functional regions using [MultiDomain Analysis](#) command.

Domain sets assignments can be stored in NEXUS data files; for that use the save/export or update commands.

Example: in the data file DmelOsRegions.nex (included in DnaSP package) there are defined two genes with three and four exons. Each gene would correspond to a domain and each exon to a subdomain.



Filter / Remove Positions

See Also: [Input Data Files](#) [Output](#)

This command allows the user to remove some positions. DnaSP module generates a NEXUS Data File including information about the polymorphic sites.

Selected Positions:

DnaSP can select the following sorts of positions:

Coding and Noncoding positions;

First, Second and Third codon positions;

Zero, Two and Four-Fold Degenerate positions;

Example (using the nuclear universal genetic code):

How DnaSP select the X-fold degenerate positions

```
  3   6   9
  *   *   *
ATA TTA ACT
ATA TTA GAT
ATA TTA -CT
```

Positions 1, 2, 5, 7 and 8, are zero-fold degenerate positions.

Position 3, is a three-fold degenerate position.

Position 4 and 6, are two-fold degenerate positions.

Position 9 could be i) four-fold degenerate (codon ACT) or ii) two fold-degenerate (codon GAT). DnaSP will no include that position neither for two-fold degenerate positions nor for four-fold degenerate positions.

Codons with missing information or alignment gaps are not considered.

Positions with Alignment Gaps option:

Excluded: These sites are removed.

Included: These sites are included.

Included if there is a polymorphism: These sites are included if there is a polymorphism.

Positions option:

Remove Non-Selected Positions: Non-Selected positions will be definitively removed from the active data.

Generate a NEXUS File with selected: Selected positions will be included in a NEXUS data file. The active data file will maintain all the positions.



Include / Exclude Sequences

DnaSP allows you the analysis in a subset of sequences of the original data file. This command allows you to include (or exclude) sequences from the analysis. *All analyses* will be performed with the information of *only* the included sequences. Consequently, if you use the Save/Export Data As command, the saved/exported data file will not contain excluded sequences.

Note: DnaSP also allows you the analysis in a subset of sequences by using the Define Sequence Sets command.

Options

There are two options that deal with alignment gaps. Suppose the following original data file:

```
          10          20          30
          *          *          *
Seq1 ATCTCTTAGGGTCGATTTGTTGTTTGTATTTAAT
Seq2 AT-TCTTATTTTCGA-TTGTTGTTTGTATTTAAT
Seq3 ATCGCTTA---TCGATTTGT----TGTATTTAAT
Seq4 ATCTCTTA---TCGATTTGTTGTTTGTATTTAAT
Seq5 ATCTCTTA---TCGATTTGTTGTTTGTATTTAAT
```

DnaSP will not use any site with alignment gaps or missing data. Thus, if you are using the complete data file, DnaSP will not use sites 3, 9, 10, 11, 16, 21, 22, 23, 24 for further analysis.

If you exclude 2 sequences (for example, Seq2 and Seq4) from the previous original data file, the active data will be composed of:

```
          10          20          30
          *          *          *
Seq1 ATCTCTTAGGGTCGATTTGTTGTTTGTATTTAAT
Seq3 ATCGCTTA---TCGATTTGT----TGTATTTAAT
Seq5 ATCTCTTA---TCGATTTGTTGTTTGTATTTAAT
```

With the **Sites with alignment gaps are excluded if they are present in the active subset** option (default option), DnaSP will not use information of sites 9, 10, 11, 21, 22, 23, 24.

With the option **Sites with alignment gaps in the original data file are excluded in all subsets** DnaSP will not use information of sites 3, 9, 10, 11, 16, 21, 22, 23, 24 (i.e., all sites with alignment gaps in the original data file). This option is appropriate to analyze exactly the same sites in different subsets of sequences.

Note

Both options generate the same estimates of the nucleotide distance (see the [Linkage Disequilibrium](#) command).



Include / Exclude Populations

Use this command to include or exclude a particular population (a group of sequences; i.e. a sequence set) from the analysis. In any case, populations with a single included sequence will not be used.

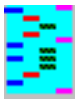


Polymorphic Sites

See Also: [Input Data Files](#) [Output](#)

This command displays some general information about the polymorphisms on the data file: the number of sites with alignment gaps (or missing data), the number of monomorphic sites, the number of polymorphic sites segregating for two, three, or four nucleotides. DnaSP also indicates the total number of parsimony-informative sites (sites that have a minimum of two nucleotides that are present at least twice), and non-informative sites (singleton sites).

This command also displays information about the genetic code used for these data, and the regions that are protein coding and noncoding (if this information was included in the NEXUS file, or has been defined using the Assign Coding Regions command in the [Coding Region](#) Menu). In this case, for the coding region, DnaSP also displays the number of synonymous and nonsynonymous (replacement) substitutions (see [how DnaSP estimates the number of Synonymous and Nonsynonymous changes in a codon](#))



How DnaSP estimates Synonymous and Nonsynonymous changes in a codon:

In general DnaSP uses a conservative criterion to decide if a particular change in a nucleotide site is synonymous or nonsynonymous (replacement); see the following examples. Nevertheless, the user should check the complex cases (those triplets of sites segregating for several codons; i.e. in highly variable regions).

Example using the Nuclear Universal Genetic Code

```

3   6   9   12  15  18  21  24  27
*   *   *   *   *   *   *   *   *
AGT TCT ATT CCC AAT ATA AGT UAU UAU
AGC TCT ATT CCC AGG TTA AGT UAU UAU
AGA TCT CTG CAG ACT TTG AGA CUG CUG
AGG TCT CTG CAG ACT ATG AGA CUG CUG

```

Codon (1,2,3):

3 mutations in site#3: 1 replacement, 2 synonymous.

Codon (4,5,6):

Monomorphic.

Codon (7,8,9):

Site#7 is replacement; Site#9 is synonymous.

When there are two possible evolutionary paths:

Path#1: ATT (Ile) -> CTT (Leu) -> CTG (Leu) Site#7 Replacement; Site#9 Synonymous

Path#2: ATT (Ile) -> ATG (Met) -> CTG (Leu) Site#7 Replacement; Site#9 Replacement

DnaSP will choose path#1, **the path that requires the minor number of replacements.**

Codon (13,14,15):

Site#14 (2 replacements); Site#15 is Synonymous.

Here there are four possible paths:

Path#1: ACT (Thr) -> AAT (Asp) -> AGT (Ser) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Replacement).

Path#2: ACT (Thr) -> AAT (Asp) -> AAG (Lys) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Replacement).

Path#3: AAT (Asn) -> ACT (Thr) -> AGT (Ser) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Replacement).

Path#4: AAT (Asn) -> ACT (Thr) -> ACG (Thr) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Synonymous).

DnaSP will choose path#4, **the path that requires the minor number of replacements.**

Codon (16,17,18):

Site#16 (1 replacement); Site#18 (1 synonymous).

Here there is a circular path:

```

ATA (Ile) -> TTA (Leu)
      |
      !
ATG (Met) <- TTG (Leu)

```

Let us suppose that the number of mutations were *only* two (one in site 16, and another in site 18), **DnaSP must assume one recombination event, the recombination event that requires the lower number of replacement substitutions:**

```

      | TTG (Leu)
TTA (Leu) -> | recomb: ATG (Met)
      | ATA (Ile)

```

Note: This kind of codons will be analyzed only for Nuclear Genetic Codes.

Codon (19,20,21):

- 1. replacement (site#21).

Codon (22,23,24):

There are 3 changes among codons. So that there are 6 putative evolutionary paths (in this particular example there are only 4 because we exclude paths that go through stop codons). **DnaSP will choose randomly between:**

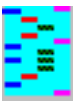
- 2. replacements (Site#22 and Site 23), and 1 synonymous (Site#24) and

2 replacements (Site#23 and Site 24), and 1 synonymous (Site#22).

Codons not analyzed:

DnaSP does not estimate synonymous and replacement changes in some complex cases (ambiguous/complex codons; those sites segregating for several codons; i.e. in highly variable regions). The user should do manually. DnaSP does not estimate synonymous and replacement changes in codons with alignment gaps.

NOTE: Estimates of the number of synonymous and nonsynonymous substitutions might be different than the number of the synonymous and nonsynonymous differences (see the [Synonymous and Nonsynonymous Substitutions](#) module).



DNA Polymorphism

See Also: [Coalescent Simulations](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Jukes and Cantor 1969](#) [Lynch and Crease 1990](#) [Nei 1987](#) [Nei and Miller 1990](#) [Tajima 1983](#) [Tajima 1989](#) [Tajima 1993](#) [Tajima 1996](#) [Watterson 1975](#)

This command computes several measures of the extent of DNA polymorphism and their variances.

Alignment gaps and missing data:

Sites with alignment gaps (or missing data) are not used (these sites are completely excluded).

Analysis:

DnaSP computes the following measures:

- Haplotype (gene) diversity and its sampling variance (Nei 1987, equations 8.4 and 8.12 but replacing $2n$ by n). The standard deviation (or standard error) is the square root of the variance.
- Nucleotide diversity, π (π), the average number of nucleotide differences per site between two sequences (Nei 1987, equations 10.5 or 10.6; see also Nei and Miller 1990), and its sampling variance (Nei 1987, equation 10.7). The standard deviation (or standard error) is the square root of the variance.
- Nucleotide diversity (Jukes and Cantor), π (JC), the average number of nucleotide substitutions per site between two sequences (Lynch and Crease 1990, equations 1-2). Unlike the previous estimates (Nei 1987, equations 10.5 or 10.6), this one has been obtained using the Jukes and Cantor (1969) correction. The correction has been performed *in each pairwise comparison*; the π (π) estimates were obtained as the average of the values for all comparisons. Note that DnaSP does not use the simplification indicated in Nei and Miller 1990 (equation 25); i. e. to perform the Jukes and Cantor (1969) correction directly on π (π) (Nei 1987, equations 10.5). Nevertheless, for low levels of polymorphism both methods give similar estimates.
- Theta (per site) from Eta (η) or from S, i.e. the Watterson estimator (Watterson 1975, equation 1.4a, but on base pair basis; Nei 1987, equation 10.3). Theta (θ) = $4N\mu$ for an autosomal gene of a diploid organism (N and μ are the effective population size and the mutation rate per nucleotide site per generation, respectively), Eta (η) is the total number of mutations, and S is the number of segregating (polymorphic) sites. The variance of this estimator depends on the recombination between sites. The variances for no recombination and for free recombination are estimated from equations 4 and 8 of Tajima 1993, respectively. These variances are computed on a per nucleotide site basis:

$$\text{Variance(per nucleotide site)} = \text{Variance(per DNA sequence)} / m * m$$

where m is the total number of nucleotides studied. The standard deviation (or standard error) is the square root of the variance.

Note: for no recombination, estimates of the variance of theta can be different from those obtained from equation 10.2 of Nei 1987 (see Tajima 1989 equations 33 and 34, Tajima 1993 equations 4 and 8).

- Finite Sites Model (four possible nucleotides per site). The total number of mutations Eta (η) (Fu and Li 1993) also referred as the minimum number of mutations (Tajima 1996). Estimates of theta (θ) per site. $\theta = 4N\mu$ for an autosomal gene of a diploid organism (N and μ are the effective population size and the mutation rate per nucleotide site per generation, respectively).

Theta (θ) per site from π (π) (Tajima 1996, equation 9)

Theta (θ) per site from S (Tajima 1996, equation 10)

Theta (θ) per site from Eta (η) (Tajima 1996, equation 16)

- The average number of nucleotide differences, k (Tajima 1983, equation A3).
 - Stochastic variance of k (no recombination), $V_{st}(k)$ (Tajima 1993, equation 14).
 - Sampling variance of k (no recombination), $V_s(k)$ (Tajima 1993, equation 15).
 - Total variance of k (no recombination), $V(k)$ (Tajima 1993, equation 13).
 - Stochastic variance of k (free recombination), $V_{st}(k)$ (Tajima 1993, equation 17).
 - Sampling variance of k (free recombination), $V_s(k)$ (Tajima 1993, equation 18).
 - Total variance of k (free recombination), $V(k)$ (Tajima 1993, equation 16).
- Theta (per DNA sequence) from S (Watterson estimator). Theta (θ) = $4Nu$ for an autosomal gene of a diploid organism (N and u are the effective population size and the mutation rate per DNA sequence per generation, respectively) (Tajima 1993, equation 3).

Variance of θ (no recombination) (Tajima 1993, equation 4).

Variance of θ (free recombination) (Tajima 1993, equation 8).

Note: Tajima (1993) uses M to indicate θ (per DNA sequence), and v to indicate the mutation rate per DNA sequence per generation.

Effective Population size

Sliding window option:

This option allows you to calculate the nucleotide diversity, theta (per site), and S (the number of segregating sites), by the [Sliding Window](#) method.

The output of the sliding window analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph the nucleotide diversity, theta or S (Y axis) is plotted against the nucleotide position (X axis).

Pairwise-Deletion option:

The average number of nucleotide differences, k (Tajima 1983, equation A3), and nucleotide diversity π (π) (Nei 1987, equations 10.5 or 10.6) can also be calculated by the Pairwise-Deletion option (DnaSP will not compute their variances). Using this option, only those gaps present in a particular pairwise comparison are ignored.

Note: Pairwise sequence comparisons with 0 sites (after excluding the gaps) are ignored.

Statistical significance by the coalescent:

DnaSP can provide the confidence intervals of the number of haplotypes, the haplotype diversity and the nucleotide diversity by computer simulations using the coalescent algorithm (see [Coalescent Simulations](#)).

Note:

n.a., not applicable. When the proportion of differences is equal or higher than 0.75, the Jukes and Cantor correction can not be computed.



Gaps in Pairwise Deletion; Gaps as the Fifth Character

DnaSP allows you the analysis of the nucleotide diversity using the pairwise-deletion option ([DNA Polymorphism](#) commands), and of the gene flow and genetic differentiation among populations using the pairwise-deletion and also using the gap as the fifth character ([Gene Flow and Genetic Differentiation](#) commands). The results of these analyses could differ in function of how the alignment gaps are dealt; (see: [Data Menu|Gaps in Sequence Sets](#) or [Include / Exclude Sequences](#) commands).

Suppose the following complete data file:

```
          10          20          30
          *          *          *
Seq1 ATCTCTTAGGGTCGATTTGTTGTTTGTATTTAAT
Seq2 AT---TTATTTTCGA-TTGTTGTTTGTATTTAAT
Seq3 ATCGCTTA---TCGATTTGT----TGTATTTAAT
Seq4 AT-TCTTA---TCGATTTGTTGTTTGT---TAAT
Seq5 AT-TCTTA---TCGATTTGTTGTTTGTATTTAAT
```

Assume that the active sequence set is constituted by sequences [Seq1](#), [Seq2](#) and [Seq3](#). [Sequences [Seq4](#) and [Seq5](#) would be excluded ([Include / Exclude Sequences](#) command), or alternatively, [Seq4](#) and [Seq5](#) would be part of a different (non active) sequence set ([Define Sequence Sets](#) command)]

With option **Sites with alignment gaps are excluded if they are present in the active subset**, the analysis of [Seq1](#), [Seq2](#) and [Seq3](#) sequences will be conducted using information of all sites with gaps.

However, with option **Sites with alignment gaps in the original data file are excluded in all subsets**, DnaSP will not use information of sites with gaps (or missing data) present in excluded sequences. Therefore, sites 3, 9, 10, 11, 28, 29, 30 (i.e., all sites with alignment gaps in the original data file) will not be used. On the contrary, sites with gaps in included sequences (sites 4, 5, 16, 21, 22, 23 and 24) will be used.



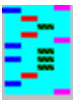
Effective Population Sizes

The mutation parameter θ (theta) is defined as $4N\mu$ for autosomal loci of diploid organisms, where N is the effective population size (diploid individuals) and μ is the neutral mutation rate (per gene or per base pair) per generation.

Assuming equal population sizes of males and females, the parameter θ is $3N\mu$ for X-linked (or Z-linked) loci of diploid organisms. In the same way, the parameter θ is $N\mu$ for Y-linked (or W-linked) loci of diploid organisms. In both cases, N is the effective population size considering both males and females (diploid individuals). For Y-linked loci the parameter θ would be $2N_m\mu$, where N_m is the *male* effective population size.

For mitochondrial DNA (or haploid individuals) θ is $2N\mu$, where N is the effective population size of females.

Likewise, the recombination parameter C (or R) is $4Nc$ for autosomal loci of diploid organisms, where N is the effective population size and c is the recombination rate per generation. $C = 3Nc$ and $C = Nc$ for X-linked and Y-linked loci, respectively.



Graphs Window

This window displays graphs from results given in a grid (table). The are the following commands:

Select Graph.

Use this command to select the kind of graph. There are the following:

DNA Polymorphism command. Graph: Line chart

- X axis: Nucleotide position; Y axis: $\Pi(\pi)$
- X axis: Nucleotide position; Y axis: Theta (per site)
- X axis: Nucleotide position; Y axis: S

DNA Divergence between Populations. command. Graph: Line chart

- X axis: Nucleotide position; Y axis: $\Pi(1)$ (pop 1)
- X axis: Nucleotide position; Y axis: $\Pi(2)$ (pop 2)
- X axis: Nucleotide position; Y axis: Dxy
- X axis: Nucleotide position; Y axis: Da
- X axis: Nucleotide position; Y axis: $\Pi(1)$ and $\Pi(2)$
- X axis: Nucleotide position; Y axis: Dxy and Da
- X axis: Nucleotide position; Y axis: $\Pi(1)$, $\Pi(2)$ and Dxy
- X axis: Nucleotide position; Y axis: $\Pi(1)$, $\Pi(2)$ and Da

Polymorphism and Divergence command. Graph: Line chart

- X axis: Nucleotide position; Y axis: $\Pi(\pi)$ and K

Gene Conversion command. Graph: Line chart

- X axis: Nucleotide distance; Y axis: $\Psi(\psi)$

Linkage Disequilibrium command. Graph: Scatter graph

- X axis: Nucleotide distance; Y axis: D
- X axis: Nucleotide distance; Y axis: $|D|$
- X axis: Nucleotide distance; Y axis: D'
- X axis: Nucleotide distance; Y axis: $|D'|$
- X axis: Nucleotide distance; Y axis: R
- X axis: Nucleotide distance; Y axis: R^2

Population Size Change command.

Pairwise Number of Differences. Graph: Line chart

- X axis: Pairwise differences; Y axis: Frequency

Segregating sites. Graph: Line and Bar chart:

- X axis: Number of nucleotide variants in a site; Y axis: Frequency
- X axis: Sample size; Y axis: Segregating sites

Fu and Li's tests command. Graph: Line chart

- X axis: Nucleotide distance; Y axis: D^*
- X axis: Nucleotide distance; Y axis: F^*
- X axis: Nucleotide distance; Y axis: D
- X axis: Nucleotide distance; Y axis: F

Tajima's test command. Graph: Line chart

- X axis: Nucleotide distance; Y axis: D

Print Graph (Black/White).

Use this command to print in black and white the contents of the window (the graph) at the default printer.

Print Graph (color).

Use this command to print the graph in color at the default printer.

Save Graph (*.bmp).

Use this command to save the graph in a file (bmp format).

Copy Graph (clipboard).

Use this command to copy the graph to the clipboard (i.e. you can paste it to other applications).

Show Significant.

This command displays the significant values in Linkage Disequilibrium analysis.

Display in Black/White.

Use this command to display the graph in black and white.

Display Default Color.

Use this command to display the graph in the default colors.

Colors.

You can use this command to change the default colors of the graph.



Sliding Window

The sliding window method allows you to calculate some measures or parameters (for example the nucleotide diversity) across a DNA region. In this method a window (segment of DNA) is moved along the sequences in steps. The parameter is calculated in each window, and the value is assigned to the nucleotide at the midpoint of the window. Both the window length and the step size default values can be changed by the user. DnaSP allows you to perform sliding window analyses in non-overlapping windows; for that analysis you must assign the same values to both the window length and the step size.

The output of the sliding window analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph the parameter (Y axis) is plotted against the nucleotide position (X axis).

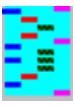
Gaps in Sliding Window

Sites with alignment gaps are not considered in the length of the windows (i.e. all windows have the same number of net nucleotides).

Windows with a fixed number of *net* nucleotides. All windows will have the same number of net nucleotides (i.e. the number of nucleotides excluding sites with alignment gaps). In the same way, the step size will also have the same number of net nucleotides.

Sites with alignment gaps are considered.

Windows with a fixed number of *total* nucleotides. All windows will have exactly the same number of nucleotides. For example, if we choose a window length of 50 nucleotides, and in a particular window the DNA region contains 4 sites with gaps the analysis will be performed in only 46 sites. Likewise, the step size will also have the same total number of nucleotides.



InDel (Insertion-Deletion) Polymorphism

This module allows estimating several measures of the level of Insertion/Deletion (InDel) polymorphism (DIPs). In particular, DnaSP will infer the number of InDel events from the data.

Let me suppose the following example data file (13 sequences with 18 positions each).

```

          *   *   *
Seq1  AAAAAAGGGGGGGGGGGG
Seq2  .....
Seq3  ...C..--.....
Seq4  .....
Seq5  ..---.....
Seq6  .....-----
Seq7  ..-----
Seq8  .....-----
Seq9  .C.....-
Seq10 .....-----
Seq11 .....-----
Seq12 .....
Seq13 .....

```

In this data file we can identify 4 InDel events:

- Event#1 (Seq5 and Seq7); InDel length = 3 nucleotides.
- Event#2 (Seq3); InDel length = 2 nucleotides.
- Event#3 (Seq6, Seq7, Seq8, Seq10 and Seq11); InDel length = 7 nucleotides.
- Event#4 (Seq9); InDel length = 3 nucleotides.

Option#1: Diallelic

Only InDel diallelic states (gap event/not gap) will be considered. That is, positions 10-16 will be excluded from the analysis since InDel event#3 and event#4 overlap at positions 14-16.

Output

- Total number of InDel events analysed: 2 (event#1 and event#2)
- Average InDel length per event: 2.5 (the average length of event#1 and event#2)
- Average deletion length: 2.667 (2 sequences with 3 nucleotides deleted plus 1 sequence with 2 deleted nucleotides, divided by 3 -the number of analysed sequences with gaps-).

DnaSP also computes:

- The number of InDel Haplotypes: 3
- InDel Haplotype Diversity: 0.410
- InDel Diversity, $k(i)$: 0.436 (this is the analogue of k , the average number of nuc. differences)
- InDel Diversity per site, $\Pi(i)$: 0.03963 (this is the analogue of Π , the nucleotide diversity). $\Pi(i)$ is computed as $k(i)/m$, where m is the net number of positions analysed, 11 (18 minus the 7 positions with overlapping InDels)
- Theta (per sequence) from the number of InDel events: 0.644
- Tajima's D: -0.9092

Additionally, DnaSP allows generating a NEXUS file with ONLY InDel events information. The data file will be recoded as:

```

Seq1  AA
Seq2  ..
Seq3  .G
Seq4  ..
Seq5  G.
Seq6  ..
Seq7  G.
Seq8  ..
Seq9  ..
Seq10 ..
Seq11 ..
Seq12 ..
Seq13 ..

```

where, A and G represents the two InDel states (no InDel/InDel).

Option#2: Triallelic

Only Diallelic and Triallelic InDel states will be considered. In the example, all positions will be used.

- Total number of InDel events analysed: 4
- Average InDel length per event: 3.75
- Average deletion length: 5.111
- Number of InDel haplotypes: 6
- ...

DnaSP will generate the following recoded NEXUS file:

```

Seq1  AAAA
Seq2  ....
Seq3  .G..
Seq4  ....
Seq5  G...
Seq6  ..G.
Seq7  G.G.
Seq8  ..G.
Seq9  ...G
Seq10 ..G.
Seq11 ..G.
Seq12 ....
Seq13 ....

```

Option#3: Tetrallelic

Only Diallelic, Triallelic and Tetrallelic InDel states will be considered.

Option#4: Multiallelic

All InDel events will be considered.

Option#5: "As Is"

DnaSP will no infer events from InDel information. DnaSP will generate the following recoded NEXUS file:

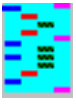
```

          *   *
Seq1  AAAAAAAAAA
Seq2  .....
Seq3  ...GG.....
Seq4  .....
Seq5  GGG.....
Seq6  .....GGGGGG
Seq7  GGG..GGGGGG
Seq8  .....GGGGGG
Seq9  .....GGG
Seq10 .....GGGGGG
Seq11 .....GGGGGG
Seq12 .....
Seq13 .....

```

Note:

Throughout this module, nucleotide substitution polymorphism is not considered; either in non-InDel sites (such as the nucleotide polymorphism at site#2 in the example data file), or in InDel positions (such as the nucleotide polymorphism at site#4).



DNA Divergence Between Populations

See Also: [Gene Flow and Genetic Differentiation](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Hey 1991](#) [Jukes and Cantor 1969](#) [Nei 1987](#) [Tajima 1983](#) [Wakeley and Hey 1997](#)

This command computes some measures of the extent of DNA divergence between populations taking into account the effect of the DNA polymorphism.

Data Files:

For the present analysis, at least two sets of sequences (one for each population) must be defined (see: [Data | Define Sequence Sets](#) command).

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) in any population are not used (these sites are completely excluded).

Analysis:

The program estimates the following measures:

For each individual population:

- The average number of nucleotide differences (Tajima 1983, equation A3).
- The nucleotide diversity, π (Nei 1987 equation 10.5).
- Nucleotide diversity with Jukes and Cantor, π (JC) (Nei 1987, equations 10.19 and 5.3; Lynch and Crease 1990, equations 1-2).

Variance of π (JC) (Nei 1987, equation 10.7). The standard deviation (or standard error) is the square root of the variance.

These estimates may be different from those obtained by the [DNA Polymorphism](#) command. This is because in the present analysis all sites with alignment gaps in population 1 or in population 2 are not considered. That is, the total number of analyzed sites considered in this command can be equal or lower than those taken into account in the DNA polymorphism command.

For the total data:

- The average number of nucleotide differences (Tajima 1983, equation A3).
- The nucleotide diversity, π (total) (Nei 1987, equation 10.5).

Between populations:

- #The number of fixed differences between populations, nucleotide sites at which all of the sequences in one population are different from all of the sequences in the second population (Hey 1991).
- #Mutations that are polymorphic in population 1, but monomorphic in population 2.
- #Mutations that are polymorphic in population 2, but monomorphic in population 1.
- #The total number of shared mutations.
- The average number of nucleotide differences between populations.
- The average number of nucleotide substitutions per site between populations, D_{xy} (Nei 1987, equation 10.20).
- D_{xy} with Jukes and Cantor (Nei 1987, equation 10.20 using the Jukes and Cantor correction).
- The number of net nucleotide substitutions per site between populations, D_a (Nei 1987, equation 10.21).
- D_a with Jukes and Cantor (Nei 1987, equation 10.21 using the Jukes and Cantor correction).

Variance of D_{xy} (JC) (Nei 1987, equation 10.24). The standard deviation (or standard error) is the square root of the variance.

Variance of D_a (JC) (Nei 1987, equation 10.23). The standard deviation (or standard error) is the square root of the variance.

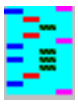
#, This information can be used to estimate the 4 parameters (θ_A , θ_1 , θ_2 and τ) that describes the isolation model (see Wakeley and Hey 1997, equations 1-3).

Sliding window option:

This option computes the nucleotide diversity for populations 1 and 2, D_{xy} , and D_a by the [Sliding Window](#) method. The output of the analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph the nucleotide diversity, D_{xy} , or D_a (Y axis) can be plotted against the nucleotide position (X axis).

DNA Divergence among Populations:

You can perform some analyses of the DNA divergence among populations by using the [Gene Flow and Genetic Differentiation](#) command.



Polymorphism and Divergence

See Also: [Graphs Window Input Data Files Output](#)

References: [Jukes and Cantor 1969](#) [Lynch and Crease 1990](#) [Nei 1987](#) [Nei and Gojobori 1986](#) [Nei and Miller 1990](#) [Watterson 1975](#)

This command computes some measures of the extent of DNA polymorphism and divergence in synonymous, nonsynonymous, silent and in all sites.

Data Files:

For the present analysis, at least one set of sequences must be defined (see: [Data | Define Sequence Sets](#) command).

Analysis using one sequence set. The sequence set must include intraspecific data information. DnaSP will estimate some measures of the extent of DNA polymorphism.

Analysis using two sequence sets. One Sequence Set must contain the intraspecific data, while the other must contain sequences (one or more) from a different species (or from a different population). DnaSP will estimate some measures of the extent of DNA polymorphism and of divergence.

Alignment gaps and missing data:

Sites (or codons) with alignment gaps or missing data in any data file are not used, i.e. these sites (or codons) are completely excluded.

Output:

The program estimates the following measures:

From the intraspecific data file:

- Nucleotide diversity π (π) (Nei 1987 equation 10.5).

Nucleotide diversity with Jukes and Cantor correction, π (JC) (Lynch and Crease 1990, equations 1-2).

- Theta (per site) from Eta (η), the total number of mutations (Watterson 1975, equation 1.4a, but on base pair basis; Nei 1987, equation 10.3). Theta values will not be reported in some cases where codons might differ by multiple changes (this feature will indicated by n.a.).

From both data files:

- Nucleotide divergence, (average proportion of nucleotide differences between populations or species), K (or D_{xy}) (Nei 1987, equation 10.20).
- $K(JC)$, average number of nucleotide substitutions per site between populations or between species with Jukes and Cantor correction (Between populations, D_{xy} ; Nei 1987, equation 10.20), (Between species, K ; Nei 1987, equation 5.3, but computing as the average of all comparisons between sequences of data file 1 and 2).

Estimation of nucleotide diversity and divergence separately for synonymous and nonsynonymous sites is performed using Nei and Gojobori (1986), equations 1-3.

Implementation:

Estimation of nucleotide diversity (and of divergence) by the Jukes and Cantor (1969) correction is performed using the simplification indicated in Nei and Miller 1990 (equation 25). That is, the correction of π (and of K) is performed directly on the uncorrected value, and not *in each pairwise comparison* of two sequences. Nevertheless, for low levels of polymorphism (and of divergence) both methods give similar estimates. For high polymorphism and divergence levels the use of the [DNA Polymorphism](#) and [Synonymous and Nonsynonymous Substitutions](#) commands might be desirable.

The total number of synonymous and nonsynonymous sites for a set of sequences is estimated as the average of the number of synonymous and nonsynonymous sites of all sequences; these values are used for all sequences. Note that in the [Synonymous and Nonsynonymous Substitutions](#) command, the total number of synonymous and nonsynonymous sites is performed in every pairwise comparison. So that, nucleotide diversity estimates (in synonymous, nonsynonymous, and silent sites) based on the present and on the [Synonymous and Nonsynonymous Substitutions](#) command could be slightly different.

Sites Considered:

Silent (synonymous sites and noncoding positions): Only silent (both synonymous sites and noncoding positions) are used.

Noncoding Positions: Only noncoding positions are used.

Only synonymous sites: Only synonymous sites are used (substitutions in the coding region that cause no amino acid changes). This option works only if the data file contains sequences with assigned coding regions (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

Only Nonsynonymous sites: Only nonsynonymous sites are used (substitutions in the coding region that cause amino acid changes). This option works only if the data file contains sequences with assigned coding regions (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

$\pi(a)/\pi(s)$ and Ka/Ks ratios: DnaSP will compute ω ratios ($\omega = Ka/Ks$; also known as $\omega = dN/dS$) for the intraspecific and interspecific (if available) data sets. This option works only if the data file contains sequences with assigned coding regions (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

All sites: All sites are used (excluding substitutions in sites with gaps or missing data).

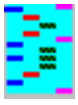
Note: See [how DnaSP estimates the number of Synonymous and Nonsynonymous changes in a codon](#).

Sliding window option:

This option computes the nucleotide diversity (intraspecific data file) and divergence (between both data files) by the [Sliding Window](#) method. The output of the analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph π , the nucleotide diversity, and K , divergence, (Y axis) can be plotted against the nucleotide position (X axis).

Abbreviations:

n.a. not available.



Polymorphism and Divergence in Functional Regions

[See Also: Input Data Files Output](#)

[References: Jukes and Cantor 1969 Lynch and Crease 1990 Nei 1987 Nei and Gojobori 1986 Nei and Miller 1990 Watterson 1975](#)

This command computes some measures of the extent of DNA polymorphism and divergence in synonymous, nonsynonymous, silent and in all sites. Unlike the [Polymorphism and Divergence](#) command, this command provides estimates of nucleotide diversity, divergence, and the number of mutations in functional regions; i.e. separately for noncoding regions, exons, introns, etc.

Data Files:

For the present analysis, at least one set of sequences must be defined (see: [Data | Define Sequence Sets](#) command).

Analysis using one sequence set. The sequence set must include intraspecific data information. DnaSP will estimate some measures of the extent of DNA polymorphism.

Analysis using two sequence sets. One Sequence Set must contain the intraspecific data, while the other must contain sequences (one or more) from a different species (or from a different population). DnaSP will estimate some measures of the extent of DNA polymorphism and of divergence.

Alignment gaps and missing data:

Sites (or codons) with alignment gaps or missing data in any data file are not used, i.e. these sites (or codons) are completely excluded.

Output:

The program estimates the following measures:

From the intraspecific data file:

- Nucleotide diversity π (Nei 1987 equation 10.5).

Nucleotide diversity with Jukes and Cantor correction, π (JC) (Lynch and Crease 1990, equations 1-2).

- Theta (per site) from Eta (η), the total number of mutations (Watterson 1975, equation 1.4a, but on base pair basis; Nei 1987, equation 10.3). Theta values will not be reported in some cases where codons might differ by multiple changes (this feature will be indicated by n.a.).

From both data files:

- Nucleotide divergence, (average proportion of nucleotide differences between populations or species), K (or D_{xy}) (Nei 1987, equation 10.20).
- $K(JC)$, average number of nucleotide substitutions per site between populations or between species with Jukes and Cantor correction (Between populations, D_{xy} ; Nei 1987, equation 10.20), (Between species, K ; Nei 1987, equation 5.3, but computing as the average of all comparisons between sequences of data file 1 and 2).

Estimation of nucleotide diversity and divergence separately for synonymous and nonsynonymous sites is performed using Nei and Gojobori (1986), equations 1-3.

Implementation:

Estimation of nucleotide diversity (and of divergence) by the Jukes and Cantor (1969) correction is performed using the simplification indicated in Nei and Miller 1990 (equation 25). That is, the correction of π (and of K) is performed directly on the uncorrected value, and not **in each pairwise comparison** of two sequences. Nevertheless, for low levels of polymorphism (and of divergence) both methods give similar estimates. For high polymorphism and divergence levels the use of the [DNA Polymorphism](#) and [Synonymous and Nonsynonymous Substitutions](#) commands might be desirable.

The total number of synonymous and nonsynonymous sites for a set of sequences is estimated as the average of the number of synonymous and nonsynonymous sites of all sequences; these values are used for all sequences. Note that in the [Synonymous and Nonsynonymous Substitutions](#) command, the total number of synonymous and nonsynonymous sites is performed in every pairwise comparison. So that, nucleotide diversity estimates (in synonymous, nonsynonymous, and silent sites) based on the present and on the [Synonymous and Nonsynonymous Substitutions](#) command could be slightly different.

Sites Considered:

Silent (Synonymous and Noncoding): The analysis is limited to both synonymous sites and noncoding positions.

Only Synonymous Sites: The analysis is restricted to synonymous sites.

Only Nonsynonymous Sites: The analysis is restricted to nonsynonymous sites.

All (total) sites: All sites will be used (excluding those sites with gaps or missing data).

The synonymous and nonsynonymous sites (and changes) will be computed if the data file contains sequences with assigned coding regions (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

Note: See [how DnaSP estimates the number of Synonymous and Nonsynonymous changes in a codon](#).

Sites:

Silent (Synonymous and Noncoding): Indicates both synonymous sites (in coding region) and noncoding positions.

Synonymous Sites: Indicates sites in **the coding region** where all mutations result in synonymous substitutions (no amino acid changes).

Nonsynonymous Sites: Indicates sites in **the coding region** where all mutations cause amino acid changes. The analysis is restricted to nonsynonymous sites.

Abbreviations:

Tot, Total, analysis in total (all) sites.

Sil, analysis in silent (synonymous and noncoding) sites.

Syn, analysis in synonymous (coding region only) sites.

NoSyn, analysis in nonsynonymous sites.

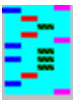
SilSites, the total number of silent sites.

NSynSites, the total number of nonsynonymous sites.

SilMut, the total number of silent mutations (intraspecific data file).

NSynMut, the total number of nonsynonymous mutations (intraspecific data file).

n.a. not available.



Synonymous and Nonsynonymous Substitutions

See Also: [Assign Coding Regions](#) [Input Data Files](#) [Output](#)

References: [Jukes and Cantor 1969](#) [Lynch and Crease 1990](#) [Nei 1987](#) [Nei and Gojobori 1986](#) [Nei and Miller 1990](#) [Osawa et al. 1992](#) [Watterson 1975](#)

This command estimates K_a (the number of nonsynonymous substitutions per nonsynonymous site), and K_s (the number of synonymous substitutions per synonymous site) for any pair of sequences (Nei and Gojobori 1986, equations 1-3); it also computes several measures of the extent of DNA polymorphism in protein coding regions, noncoding regions, or in regions with both protein coding and noncoding regions (i.e. regions with both exons and introns, or exons and flanking regions). One interesting feature of DnaSP is that both coding and noncoding protein regions can be included in the data file; DnaSP can thus estimate the nucleotide diversity for synonymous, nonsynonymous and silent (both synonymous and noncoding positions) sites. Four pre-defined genetic codes can be used: the universal nuclear code, and the mitochondrial code of *Drosophila*, mammals and yeast.

Alignment gaps and missing data:

Sites (or codons) with alignment gaps or missing data are not used, i.e. these sites (or codons) are completely excluded.

Implementation:

DnaSP can compute the nucleotide diversity in synonymous, nonsynonymous, and silent sites. The total number of synonymous and nonsynonymous sites is computed as Nei and Gojobori 1986. By **silent sites** we refer **both** to the **synonymous sites** and the **noncoding positions**. Synonymous sites are those sites in a codon where nucleotide changes result in synonymous substitutions. For computing synonymous and nonsynonymous sites, DnaSP will exclude all pathways that go through stop codons.

No stop codons should be found in the middle of coding regions, however, if DnaSP finds stop codons (in the middle of coding regions) they will be considered as if they would code for a new amino acid (the amino acid 21; for example Selenocysteine, Secys (Osawa et al. 1992).

DnaSP computes the synonymous and nonsynonymous differences between a pair of sequences as Nei and Gojobori 1986. When there are two or three nucleotide differences between the two codons compared, two or six putative pathways exist. DnaSP considers all pathways with equal probability, but it excludes those pathways that go through stop codons. Obviously, all nucleotide differences in noncoding positions are considered silent. Silent differences will include, therefore, both the synonymous differences (in coding regions) and all differences in noncoding positions.

Silent Substitutions Considered:

Substitutions in Coding Regions: Only synonymous substitutions (coding region) will be considered.

In Coding and Noncoding Regions: All silent substitutions will be considered (synonymous substitutions and changes in noncoding positions). If the data file does not contain assigned coding regions all sites will be considered as noncoding positions; i.e. all substitutions will be considered as silent.

Analysis:

- The average number of nucleotide differences per site between two sequences, or nucleotide diversity, P_i (π) (Nei 1987, equations 10.5 or 10.6).
- The average number of nucleotide substitutions per site between two sequences or nucleotide diversity, P_i (π), using the Jukes and Cantor (1969) correction (Lynch and Crease 1990, equations 1-2). The correction has been performed **in each pairwise comparison** of two sequences (Nei and Gojobori 1986, equations 1-3); the P_i (π) estimates was obtained as the average of the values of all comparisons (of K_s and K_a values); (see also the [DNA Polymorphism](#) command).

Note that DnaSP has not used the simplification indicated in Nei and Miller 1990 (equation 25); i. e. to perform the Jukes and Cantor (1969) correction directly on P_i (π) (Nei 1987, equations 10.5). Nevertheless, for low levels of polymorphism similar estimates are given by both methods.

- Theta values (per site) from Eta (η), i.e. the Watterson estimator (Watterson 1975, equation 1.4a, but on base pair basis; Nei 1987, equation 10.3). See [how DnaSP estimates Synonymous and Nonsynonymous changes in a codon](#). Note that the number of mutations might be different than the number of Synonymous and Nonsynonymous differences obtained in each pairwise comparison (see below). Theta values will not be reported in some cases where codons might differ by multiple changes.

The DnaSP output shows also the following:

For each sequence:

- The total number of Synonymous (SS) and Nonsynonymous (NSS) sites.

For each pair of sequences:

- The total number of Synonymous, Nonsynonymous and silent sites,
- The total number of Synonymous, Nonsynonymous and silent differences,
- The estimates of K_a (the number of nonsynonymous substitutions per nonsynonymous site),

and K_s (the number of synonymous -or silent- substitutions per synonymous -or silent- site) (Nei and Gojobori 1986, equations 1-3).

Assign codons:

To assign noncoding and coding protein regions in a particular DNA sequence you should use the [Assign Coding Regions](#) command.

Genetic Code:

To compute synonymous and nonsynonymous substitutions DnaSP will use the defined [Assign Genetic Code](#) assigned (the default is the Nuclear Universal).

Notes and abbreviations:

n.a., not applicable. When the proportion of differences is equal or higher than 0.75, the Jukes and Cantor correction can not be computed.

Seq 1 and **Seq 2**, the two sequences compared.

SynDif, the total number of synonymous differences.

SynPos, the total number of synonymous sites.

SilentDif, the total number of silent differences.

SilentPos, the total number of silent sites.

Ks, the number of synonymous (or silent) substitutions per synonymous (or silent) site

NSynDif, the total number of nonsynonymous differences.

NSynPos, the total number of nonsynonymous sites.

Ka, the number of nonsynonymous substitutions per nonsynonymous site



Codon Usage Bias

See Also: [Input Data Files](#) [Output Window Menu](#)

References: [Morton 1993](#) [Sharp et al. 1986](#) [Shields et al. 1988](#) [Wright 1990](#)

This command computes some measures of the extent of the nonrandom usage of synonymous codons.

Data Files:

The present analysis requires only one data file. This command works only if the coding regions and the genetic code have been previously defined (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

Codon Bias Measures

RSCU, Relative Synonymous Codon Usage (Sharp et al. 1986)

For a given DNA sequence DnaSP shows the RSCU value at each codon (Codon Usage Table). The RSCU value of a codon is the observed frequency of that codon in the gene divided by that expected under the assumption of equal usage of synonymous codons. A RSCU value of 1 indicates that the frequency of that codon is the expected for an equal codon usage; values less than 1 (or more than 1) indicates that the codons are used less often (or more often) than the expected.

Codon Usage Table

DnaSP shows, for a given codon, the observed frequency and its RSCU value (in parenthesis). For a given DNA sequence, the Codon Usage Table also shows the "Scaled" chi square value.

ENC, Effective Number of Codons (Wright 1990)

That measure quantifies the "effective" number of codons that are used in a gene. For the nuclear universal genetic code, the value of ENC ranges from 20 (only one codon is used for each amino acid; i.e., the codon bias is maximum) to 61 (all synonymous codons for each amino acid are equally used; i.e., no codon bias).

CBI, Codon Bias Index (Morton 1993)

CBI is a measure of the deviation from the equal use of synonymous codons. CBI values range from 0 (uniform use of synonymous codons) to 1 (maximum codon bias).

SChi2, Scaled Chi Square (Shields et al. 1988)

The "scaled" χ^2 (chi square) is a measure based on the chi square statistics; i.e., based on the difference between the observed number of codons and those expected from equal usage of codons. The sum of the chi square values is divided by the total number of codons in the gene excluding those codons coding for a unique amino acid; i.e. all codons excluding the Trp and Met codons (nuclear universal genetic code).

DnaSP can compute the "scaled" chi square with Yates' correction, and also assuming a given G+C content (by default the G+C content is 50%).

G+C content

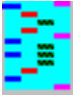
G+C_n, G+C content at noncoding positions.

G+C₂, G+C content at second coding positions.

G+C_{3s}, G+C content at (synonymous) third coding positions; i.e. the G+C content in the third codon positions excluding the Trp and Met codons (nuclear universal genetic code) (Wright 1990).

G+C_c, G+C content at coding positions.

G+C, G+C content in the genomic (whole) region.



Assign Coding Regions

This command allows you to assign noncoding and coding protein regions to the data file. This information might be needed for several analyses. The meaning of a specific codon will depend on the [Genetic Code](#) assigned. There is no maximum number of coding protein regions (exons).

You can assign a specific region as a noncoding region, or as a coding region. In the later case, you have to indicate what is the codon position of the first site selected (First, second, third); from this site DnaSP will assign codons to the remainder sites following the reading frame.

Example: Assume that you have a data file including DNA sequences 34 nucleotides long, and you would like to indicate (assign):

- exon 1, from site 6 to site 16,
- exon 2, from site 24 to site 30,
- noncoding, the rest of the sites.

Assuming a Universal Nuclear Genetic Code:

```

      10      20      30
      *      *      *
ATCTCTTATCGTCGATTTGTTGTTTGTATTTAAT
      LeuSerSerIleCysIle

```

You have to do two codon assignments:

- i) In the dialog box, indicate as selected region: 6 - 16
Set the codon position of the first site as: 1 (First position)
- ii) In the dialog box, indicate as selected region: 24 - 30
Set the codon position of the first site as: 3 (Third position)

You can see the current assignation using the [View Data](#) command. You will see the following:

```

NNNNNLeuSerSerIleNNNNNNNeCysIleNNNN
ATCTCTTATCGTCGATTTGTTGTTTGTATTTAAT

```

N, noncoding.

Examples:

DnaSP assigns codons in the following way (assuming the Universal Nuclear Genetic Code). Examples 3 and 4, show how DnaSP assigns codons in case of misassignments or alignment gaps.

Example#1

```

NNNNNLeuSerSerIleNNNNNNCysIleNNNN
ATCTCTTATCGTCGATTTGTTGTTTGTATTTAAT

```

Example#2

```

NNNNNLeuSerSerIleNNNNNNNeCysIleNNNN
ATCTCTTATCGTCGATTTGTTGTTTGTATTTAAT

```

Example#3

```

      123123112312      3123123
NNNNNLeuSerS#erIleNNNNNNNeCysIleNNNN
ATCTCTTATCGTGCATTTGTTGTTTGTATTTAAT
(#, wrong assignation)

```

Example#4

```

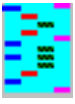
      12312312312      3123123
NNNNNLeu???SerIleNNNNNNNeCysIleNNNN
ATCTCTTA---TCGATTTGTTGTTTGTATTTAAT
      Leu  SerIle  eCysIle
(?, alignment gaps in nucleotide sequence)

```

Note:

The amino acid assignation corresponds to the first nucleotide sequence.

This information will be stored if you save/export the data file as a NEXUS file format.



Preferred and Unpreferred Synonymous Substitutions

See Also: [Codon Preference Table](#) [Input Data Files](#) [Output](#)

References: [Akashi 1995](#) [Akashi 1999](#)

This command determines the polarity status (ancestral -> derived) of the polymorphic (or fixed) substitutions, and it also estimates the number of preferred and unpreferred substitutions.

Data Files:

For the present analysis, at least two sets of sequences (one with the intraspecific data, and other with the outgroup sequences) must be defined (see: [Data | Define Sequence Sets](#) command).

Alignment gaps and missing data:

Sites (or codons) with alignment gaps or missing data in any group of sequences (sequence sets) are not used, i. e. these sites (or codons) are completely excluded.

Analyze:

One Species with an Outgroup: Analysis of the polarity status (ancestral -> derived) of the polymorphic substitutions. The outgroup allows inferring that information.

One Species with two Outgroups: Analysis of the polarity status (ancestral -> derived) of the polymorphic substitutions (intraspecific Data) and also of the fixed differences (between the MRCA of the intraspecific data and the common ancestor of the close outgroup). The distant outgroup allows inferring that information.

Pref / Unpref Tables:

Use this command to assign the specific [codon preference table](#) to the data.

Options:

Non Coding Positions: This option allows analyzing the polarity of changes in noncoding positions.

Statistical significance:

DnaSP conducts the Mann-Whitney test to determine if the frequency distribution of preferred and unpreferred substitutions are significantly different. DnaSP can carry out the fdMWU test (that uses information of only polymorphism data; Akashi 1999), or the fddMWU test (that uses information of both polymorphic substitutions and fixed differences; Akashi 1999).

Ambiguous information:

In some cases, the polarity of some substitutions could not be unambiguously determined (see below). There are several sources of ambiguity (ancestral polymorphism; multiple substitutions; alignment gaps/missing data, etc). In that cases, DnaSP will list the ambiguous sites (or codons).

How DnaSP polarizes the nucleotide changes and assigns the preferred and unpreferred status (coding region):

DnaSP uses a conservative (parsimony) criterion to infer the ancestral nucleotide state: only unambiguous cases are used for the analysis (see the following examples). Once the polarity has been established, DnaSP will use the [codon preference table](#) to assign codons (or changes) as preferred or unpreferred.

Some examples using the Nuclear Universal Genetic Code with the *D. melanogaster* (Akashi 1995) codon preference table:

Intraspecific Data

3	6	9	12	15	18	21	24	27	30	33
*	*	*	*	*	*	*	*	*	*	*
CTT	AAC	CTT	CTA	AAT	TTA	CCC	CTT	CTT	GGT	GGT
CTT	AAC	CTT	CTA	AAT	TTA	CCA	CTA	CTA	AGT	GGT
CTA	AAC	CTA	CTT	AAC	TTN	CCT	CTA	CTT	GGA	GGT

Close Outgroup

CTT AAT GTC GTT A-T TTT CCT CTT CTT GGA AGT

Distant Outgroup

CTT AAT GTT GTT AAT TTT CCT CTG CTA GGA TGT

One Species with an Outgroup (Close Outgroup)

Codon (1,2,3). CTT -> CTA. Polymorphic synonymous change: U -> U
 Codon (4,5,6). AAC. Monomorphic codon.
 Codon (7,8,9). CTT <-> CTA. Ambiguous Change.
 Codon (10,11,12). CTT -> CTA. Polymorphic synonymous change: U -> U
 Codon (13,14,15). AAT -> AAC. Polymorphic synonymous change: U -> P
 Codon (16,17,18). Not analyzed: Codon with missing data.
 Codon (19,20,21). Not analyzed: Multiple substitutions.
 Codon (22,23,24). CTT -> CTA. Polymorphic synonymous change: U -> U
 Codon (25,26,27). CTT -> CTA. Polymorphic synonymous change: U -> U
 Codon (28,29,30). Not analyzed: Multiple substitutions.
 Codon (31,32,33). GGT. Monomorphic codon.

One Species with two Outgroups

Codon (1,2,3). CTT -> CTA. Polymorphic synonymous change: U -> U
 Codon (4,5,6). AAT -> AAC. Fixed synonymous change: U -> P
 Codon (7,8,9). There are two changes:
 CTT -> CTA. Polymorphic synonymous change: U -> U
 GTT -> CTT. Fixed nonsynonymous change: Val -> Leu
 Codon (10,11,12). There are two changes:
 CTT -> CTA. Polymorphic synonymous change: U -> U
 GTT -> CTT. Fixed nonsynonymous change: Val -> Leu
 Codon (13,14,15). Not analyzed: Codon with alignment gaps.
 Codon (19,20,21). Not analyzed: Multiple substitutions.
 Codon (22,23,24). CTT -> CTA. Polymorphic synonymous change: U -> U
 Codon (25,26,27). CTT <-> CTA. Ambiguous polymorphic change (ancestral polymorphism ?).
 Codon (28,29,30). Not analyzed: Multiple substitutions.
 Codon (31,32,33). Not analyzed: Ambiguous fixed change.

Abbreviations:

- MRCA**, Most recent common ancestor.
- U -> U**, Unpreferred to unpreferred change
- U -> P**, Unpreferred to preferred change
- P -> U**, Preferred to Unpreferred change
- P -> P**, Preferred to Preferred change
- Syn**, Synonymous change
- NonSyn**, Nonsynonymous change



Table for Preferred and Unpreferred Codons

See Also: [Preferred and Unpreferred Synonymous Substitutions analysis](#)

References: [Akashi 1995](#) [Akashi and Schaeffer 1997](#) [Duret and Mouchiroud 1999](#) [Kanaya et al. 1999](#)

Use this command to assign the specific table of preferred/unpreferred synonymous codons for the [Preferred and Unpreferred Synonymous Substitutions](#) analysis. There are 8 predefined tables. Nevertheless, the user can define its own table. That information could be included in the NEXUS data file; for that use the save/export or update commands.

Create New Table:

This button allows the user to define a new preference synonymous codons table. The table will be linked to a particular Genetic code.

Codes:

P, preferred codon.

?, unknown preference.

none, unpreferred.



Gene Conversion

See Also: [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Betrán et al. 1997](#) [Rozas and Aguadé 1994](#)

Abstracts: [Betrán et al. 1997](#) [Rozas and Aguadé 1994](#)

DnaSP incorporates the algorithm developed by Betrán et al. (1997) to detect gene conversion tracts from two differentiated populations (referred to as subpopulations). These subpopulations could be, for example, two different chromosomal gene arrangements (Rozas and Aguadé 1994), or two sets of paralogous sequences.

Data Files:

For the present analysis, at least two sets of sequences (one for each population) must be defined (see: [Data | Define Sequence Sets](#) command).

Minimum number of sequences in each set:

One sequence set must contain at least three sequences, and the other a minimum of five.

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) in any population are not used (these sites are completely excluded).

Implementation:

DnaSP estimates the observed tract length in nucleotides as:

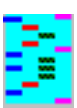
$$L = TR - TL + 1 - G$$

where TL (left) and TR (right) are the site positions of the outermost informative nucleotide sites of a congruent tract, and G is the number of alignment gaps (if any) between TL and TR in the particular sequence where the gene conversion tract is detected (see Betrán et al. 1997 equation A1).

DnaSP also estimates the parameter ψ (Betrán et al. 1997, equation A4), which measures the probability per site of detecting a conversion event between two subpopulations. From this information it is possible to estimate the true number and length of the gene conversion tracts.

Sliding window option:

This option computes the parameter ψ by the [Sliding Window](#) method. The output of the analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph the parameter ψ (Y axis) can be plotted against the nucleotide position (X axis).



See Also: [Define Sequence Sets \(Define Populations\)](#) [Input Data Files](#) [Output](#)

References: [Hudson et al. 1992a](#) [Hudson et al. 1992b](#) [Hudson 2000](#) [Lynch and Crease 1990](#) [Nei 1973](#) [Nei 1982](#) [Nei 1987](#) [Tajima 1983](#) [Wright 1951](#)

This command computes some measures of the extent of DNA divergence among populations, and from these measures it computes the average level of gene flow. Additionally, DnaSP allows testing for population subdivision.

Data Files:

For the present analysis, at least two sets of sequences (one set for each population) must be previously defined (see: [Data | Define Sequence Sets](#) command).

Missing data:

Sites containing missing data in any population are not used (these sites are completely excluded).

Include / Exclude Populations (set of sequences):

Use this command to include or exclude a particular population from the analysis. In any case, populations with a unique included sequence will not be used.

Sites with Alignment Gaps option:

- Excluded:** Sites with gaps (in any population) will be completely excluded from the analysis.
- Considered (Gap as the fifth state):** Gaps will be used. They will be considered as a different nucleotide variant.
- Excluded only in pairwise comparisons:** Using this option, gaps will be ignored only if they are present in a particular pairwise comparison. Note, this option does not work for estimating haplotype-based statistics; in that case, DnaSP will consider the gap as a fifth state.

Genetic Diversity Analysis:

The program estimates the following measures:

For each individual population:

- The number of haplotypes, h .
- The haplotype diversity, H_d (Nei 1987, equations 8.4).
- The average number of nucleotide differences, K (Tajima 1983, equation A3).
- The nucleotide diversity, π (π , Nei 1987, equation 10.5).
- Nucleotide diversity with the Jukes and Cantor correction, $\pi(JC)$ (Lynch and Crease 1990, equations 1-2).

Present estimates may differ from those obtained by the [DNA Polymorphism](#) command. This is because in the present analysis all sites with alignment gaps (in any population) are excluded (if you are using the **excluded** option in the **sites with alignment gaps**). That is, the total number of analyzed sites considered in this command can be equal or lower than those taken into account in the DNA polymorphism command.

For the total data:

- The average number of nucleotide differences, k (Tajima 1983, equation A3).
- The nucleotide diversity, π (π , Nei 1987 equation 10.5).
- The average number of nucleotide substitutions per site between populations, D_{xy} (Nei 1987, equation 10.20).
- The number of net nucleotide substitutions per site between populations, D_a (Nei 1987, equation 10.21).

Genetic Differentiation Analysis:

DnaSP conducts the following analyses:

Haplotype-based statistics:

H_s (Hudson et al. 1992a eq. 3a); H_{st} (Hudson et al. 1992a eq. 2).

Nucleotide Sequence-based statistics:

K_s (Hudson et al. 1992a eq. 10); K_{st} (Hudson et al. 1992a eq. 9).

K_s^* and K_{st}^* (Hudson et al. 1992a eq. 11).

Z (Hudson et al. 1992a).

Z^* (Hudson et al. 1992a).

S_{nn} (Hudson 2000).

Statistical tests:

Chi-square test (haplotype data) (Nei 1987; Hudson et al. 1992a, eq. 1).

PM, Permutation (randomization) test (Hudson et al. 1992a).

Population Size Weighting factor (see Hudson et al. 1992a, p. 144):

DnaSP uses the weighting factors recommended in Hudson et al. (1992a).

Export Genetic Distances:

Use this command to export genetic distances into MEGA or PHYLIP format files. These files will allow performing subsequent phylogenetic analyses using the MEGA or PHYLIP softwares.

Gene Flow Analysis:

The gene flow estimates are computed using information about the organism's genomic type (haploid, diploid) indicated in the [Data Menu](#). DnaSP computes the following measures:

From haplotype data information

- Nei 1973:

G_{st} (Nei 1973; equation 9) and N_m . DnaSP calculates G_{st} as equations 5 and 6 in Hudson et al. (1992a).

From nucleotide sequence data information:

- Hudson et al. 1992b:

F_{st} (equation 3) and N_m (equation 4).

- Lynch and Crease1990:

N_{st} (equation 36) and N_m .

N_{st} estimator is almost the same as F_{st} (Hudson et al. 1992b). The difference is that N_{st} uses the Jukes and Cantor (1969) correction.

- Nei 1982:

DeltaST (δ_{st}), equation 4; GammaST (γ_{st}), equation 5; N_m .

Note: DnaSP calculates π_s (π_s), the average of the π (π) for over populations, using Nei (1982) equation 2; i.e. making use of the relative size of any population.

Wright (1951)

The estimates of N_m are based on the island model of population structure:

Haploids: F_{st} , γ_{st} , $N_{st} = 1 / (1 + 2N_m)$

Diploids (autosome): F_{st} , γ_{st} , $N_{st} = 1 / (1 + 4N_m)$

Diploids (X-chromosome): F_{st} , γ_{st} , $N_{st} = 1 / (1 + 3N_m)$

Diploids (Y-chromosome): F_{st} , γ_{st} , $N_{st} = 1 / (1 + N_m)$

Effective Population size

Note:

n.a., not applicable. When the proportion of differences is equal or higher than 0.75, the Jukes and Cantor correction can not be computed.



Select Statistic

Use this command to choose the statistic to be included in the Genetic Distance MEGA or PHYLIP data files. That file will allow performing subsequent phylogenetic analyses using the MEGA or PHYLIP softwares.

Precision Value:

Number of decimal included in the distance data files.

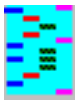
Note:

DnaSP can not read MEGA / PHYLIP data files with genetic distance information. These files can be read by the MEGA or PHYLIP softwares which allows performing some phylogenetic analysis.

Any Word Processor could also be used to read/edit MEGA or PHYLIP files (these files are just text files).

MEGA v.2 (Molecular Evolutionary Genetics Analysis) Software

The MEGA software is distributed by free from: <http://www.megasoftware.net/>



Linkage Disequilibrium

See Also: [Coalescent Simulations](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Hill and Robertson 1968](#) [Kelly 1997](#) [Langley et al. 1974](#) [Lewontin 1964](#) [Lewontin and Kojima 1964](#) [Rozas et al. 2001](#) [Sokal and Rohlf 1981](#) [Wall 1999](#) [Weir 1996](#)

Abstracts: [Rozas et al. 2001](#)

This command calculates the degree of linkage disequilibrium (LD), or nonrandom association between nucleotide variants at different polymorphic sites. Sites containing alignment gaps, or polymorphic sites segregating for three or four nucleotides, are completely excluded from the analysis. The analysis can be performed with all polymorphic sites in the data, or only with parsimony-informative sites (sites that segregate for only two nucleotides that are present at least twice).

Linkage disequilibrium between nucleotide variants:

The degree of LD is estimated by the following parameters:

D (Lewontin and Kojima 1964),

D' (Lewontin 1964),

R and R² (Hill and Robertson 1968).

DnaSP considers as coupling gametes those with the most or the least common variants (Langley et al. 1974).

Linkage disequilibrium for the whole data:

For the whole data DnaSP computes:

ZnS statistic (Kelly 1997, equation 3). ZnS is the average of R² (Hill and Robertson 1968) over all pairwise comparisons.

Za and ZZ statistics (Rozas et al. 2001). Za is the average of R² (Hill and Robertson 1968) over all pairwise comparisons between adjacent polymorphic sites; ZZ = Za - ZnS. ZZ statistic could be used for detecting intragenic recombination (see [Recombination](#)).

DnaSP can compute the Confidence Intervals of ZnS, Za, ZZ by coalescent-based simulations (see: [Coalescent Simulations](#)).

Association among nucleotide variants:

DnaSP also computes the B and Q statistics (Wall 1999).

Statistical significance of LD:

Both the two-tailed Fisher's exact test, and the chi-square test are computed to determine whether the associations between polymorphic sites are, or are not, significant (see Sokal and Rohlf 1981).

(* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).

DnaSP also performs the Bonferroni correction for multiple tests (see Weir 1996). The Bonferroni procedure tries to avoid spurious rejections of the null hypothesis in multiple tests (assuming that all tests are independent). For an overall α' (α' is the probability that *at least* one test causes the rejection of a true null hypothesis), α (α is the probability that *an individual* test causes the rejection of a true null hypothesis; i.e., type I error of an individual test) is obtained from:

$$\alpha = 1 - (1 - \alpha')^{1/L}$$

where L is the number of tests performed. DnaSP obtain the probability associated with a particular chi-square value (with 1 degree of freedom) by the trapezoidal method of numeric integration. Significant disequilibrium by the Bonferroni procedure for an $\alpha' = 0.05$ is indicated by the letter **B**.

NOTE: The Bonferroni correction applied to non-independent tests (as in the LD tests) would be highly conservative.

Statistical significance by the coalescent:

DnaSP can also provide the confidence intervals of B, Q, ZnS, Za and ZZ statistics by computer simulations using the coalescent algorithm (see [Coalescent Simulations](#)).

LINKAGE DISEQUILIBRIUM AND PHYSICAL DISTANCE

DnaSP estimates the relationship of linkage disequilibrium with physical distance by the regression analysis (Sokal and Rohlf 1981).

DnaSP estimates the linear regression equation: $Y = a + bX$,

where Y is the LD value, and X is the nucleotide distance (measured in kilobases; kb).

The regression equation is performed for |D| (absolute value of D), |D'| (absolute value of D') and R² values.

For |D'| values, DnaSP gives two regression equations:

i) for all |D'| values (blue line in the graph -default colour-);

ii) for all |D'| values excluding values of |D'| = 1 (+1 and -1); (black line in the graph -default colour-).

Statistical significance:

The statistical significance of the regression coefficient could be conducted by the Student's t-test with n-2 degrees of freedom (n is the total number of values -pairwise comparisons-) (this test is not included in DnaSP). But, be careful! This test requires independent sample values, and certainly, it is not the case for LD.

Alternative. You could determine the confidence intervals of the ZZ test statistic by coalescent-based simulations (see: [Coalescent Simulations](#)).

Another alternatives (not included in present version of DnaSP): you might test the decay of LD with physical distance by the randomization (permutation) test (i.e., by random permutation of the polymorphic sites).

Nucleotide distance:

The nucleotide distance (**Dist** in the output), i. e. the distance in nucleotides between a given pair of polymorphic sites, is calculated as the average number of nucleotides that separate two particular polymorphic sites.

For example, the nucleotide distance between polymorphic sites 1 and 18 (marked with asterisks) in the following four sequences is 13:

```

      *                *
seq_1 ATATACGGGGTTA---TTAGA
seq_2 CGATAC--GG-TA---TAACA
seq_3 AGATACGG-GATA---TAATA
seq_4 ATAAACGGGGATA---GTAGT
```

Output:

The output of the analysis is given in a grid (table). The columns **Site1** and **Site2** refer to the polymorphic sites analyzed (compared); **Dist** to the nucleotide distance between them; **Fisher** to the probability obtained by Fisher's exact test; and **Chi-sq** to the value of X². The results are also presented graphically (by a scatter graph). In the graph D, D', R, R² can be plotted against the nucleotide distance (X axis).



Recombination

See Also: [Coalescent Simulations Input Data Files Output](#)

References: [Hudson 1987](#) [Hudson and Kaplan 1985](#) [Rozas et al. 2001](#)

This command computes some estimates of the Recombination parameter $R = 4Nr$ (for autosomal loci of diploid organisms), where N is the population size and r is the recombination rate per sequence (per gene). In the literature, the recombination parameter is also indicated as $C = 4Nc$.

For the present analysis sites containing alignment gaps (or missing data) in the data files are not used (these sites are completely excluded). The program estimates the following measures:

Recombination parameter $R = 4Nr$ (Hudson 1987)

The estimator is based on the variance of the average number of nucleotide differences between pairs of sequences, $S2k$ (Hudson 1987, equation 1).

The estimator R is obtained after solving equation 4 (Hudson 1987). The solution of the function $g(C,n)$ of equation 4 is obtained numerically (see the Appendix in Hudson 1987).

The output DnaSP shows the estimate of $R (=4Nr)$, per gene (r , is the recombination rate per generation between the most distant sites) (Hudson 1987, from equation 4). DnaSP also calculates the estimate of R between adjacent sites:

$$R \text{ (between adjacent sites)} = R \text{ (per gene)} / D$$

where D , is the average nucleotide distance (in base pairs) of the analyzed region (the average nucleotide distance after removing the alignment gaps; i.e., nucleotide distance); (see Nucleotide Distance in [Linkage Disequilibrium](#) command). Note that the average *length* is equal to the average *nucleotide distance* + 1.

The minimum number of recombination events RM (Hudson and Kaplan 1985)

The parameter indicates the minimum number of recombination events in the history of the sample (note that RM underestimates the total number of recombination events). RM is obtained using the four-gamete test (see Figure 1 and Appendix 2 in Hudson and Kaplan 1985). From RM it is possible to estimate R by computer simulations [Coalescent Simulations](#).

The output shown by DnaSP is:

The RM value.

The list of all the pairs of sites with the four-gametic types.

The list of all RM pairs of sites where it is possible to assign at least one recombination event.

Note: for the present analysis sites segregating for three or four nucleotides are completely excluded from the analysis.

ZZ test statistic (Rozas et al. 2001)

This test statistic could be useful in detecting intragenic recombination (see [Linkage Disequilibrium](#)).

Statistical significance by the coalescent:

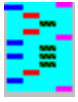
DnaSP can provide the confidence intervals of the RM statistic by computer simulations using the coalescent algorithm (see [Computer Simulations](#)).

Effective Population size

Other methods

The recombination parameter can also be estimated by the method described in [Hey and Wakeley 1997](#) this method, however, is not included in the DnaSP software. That method is implemented in the SITES computer program, distributed by Jody Hey.

Jody Hey Web Page: <http://heylab.rutgers.edu/>



Population Size Changes

See Also: [Coalescent Simulations](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Harpending 1994](#) [Ramos-Onsins and Rozas 2002](#) [Rogers 1995](#) [Rogers and Harpending 1992](#) [Rogers et al. 1996](#) [Slatkin and Hudson 1991](#) [Tajima 1989a](#) [Tajima 1989b](#) [Watterson 1975](#)

Abstracts: [Ramos-Onsins and Rozas 2002](#)

This command analyzes the frequency spectrum (for segregating sites) and the pairwise number of differences. DnaSP performs these analyses for constant size, and for growing size populations.

[Rozas et al. 2001](#)

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) in the data file are not used (these sites are completely excluded).

1. Pairwise Number of Differences:

1.1 Constant Population Size

DnaSP shows (in tabular and graphic form) the distribution of the observed pairwise nucleotide site differences (also called mismatch distribution), and the expected values (at equilibrium for no recombination) in a stable population, i.e. population with constant population size (Watterson 1975; Slatkin and Hudson 1991, equation 1; Rogers and Harpending 1992, equation 3).

1.2 Population Growth-Decline

DnaSP shows (in tabular and graphic form) the distribution of the observed pairwise nucleotide site differences (also called mismatch distribution), and the expected values (for no recombination) in growing and declining populations (Rogers and Harpending 1992, equation 4). The model is based on three parameters: Theta Initial (theta before the population Growth or Decline), Theta Final (theta after the population Growth or Decline), and τ (Tau) is the date of the Growth or Decline measured in units of mutational time ($\tau = 2ut$; t is the time in generations, and u is the mutation rate per sequence and per generation) (Rogers and Harpending 1992). By letting Theta Final as infinite it is possible to estimate Theta Initial and Tau ($2ut$) from the data (Rogers 1995). DnaSP gives these estimates that can be used to obtain the expected values.

DnaSP also estimates the raggedness statistic, r (Harpending 1994, equation 1). This statistic quantifies the smoothness of the observed pairwise differences distribution. DnaSP can provide the confidence intervals of this statistic by computer simulations using the coalescent algorithm (see: [Computer Simulations](#)).

Nevertheless, the raggedness statistic has low statistical power for detecting population expansion. Therefore, it is better to use more powerful statistics as the F_u 's F_s (see: [Fu and Li's \(and other\) Tests](#)) and the Ramos-Onsins and Rozas's R_2 ; DnaSP can also provide (by computer simulations using the coalescent; see: [Coalescent Simulations](#)) the confidence intervals of the F_s and R_2 statistics.

C.V., Coefficient of variation (see: [Rogers and Harpending 1992](#) p. 554)

MAE, Mean Absolute Error (see: [Rogers et al. 1996](#), p. 896).

2. Segregating Sites:

2.1 Constant Population Size

DnaSP shows (in tabular and graphic form) the distribution of the observed frequency spectrum (distribution of the allelic frequency in a site) (see Tajima 1989a, figure 6), and the expected values in a stable population, i.e. population with constant population size (Tajima 1989a, equation 50).

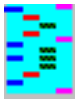
2.2 Population Growth-Decline

DnaSP shows (in tabular and graphic form) the distribution, at different times and for several sample sizes, of $S_n(t)$, the expected number of segregating sites among n DNA sequences in generation t , and $S_n(t) / a_1$ (at equilibrium this value is equal to theta) after a population growth or decline (Tajima 1989b, equation 9). The time is measured in N generations units, where N is the effective population size.

$$a_1 = \sum (1 / i) \text{ from } i = 1 \text{ to } n - 1$$

(n is the sample size, i.e., the number of nucleotide sequences)

[Effective Population size](#)



Fu and Li's (and other) Tests

See Also: [Coalescent Simulations](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Ewens 1972](#) [Fu and Li 1993](#) [Fu 1995](#) [Fu 1997](#) [Kimura 1983](#) [Simonsen et al. 1995](#) [Strobeck 1987](#) [Tajima 1983](#)

This command calculates the statistical tests D^* and F^* proposed by Fu and Li (1993) for testing the hypothesis that all mutations are selectively neutral (Kimura 1983). In this command DnaSP also computes the Fu's F_s and the Strobeck's S statistics. These tests require data only on molecular polymorphism.

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) are not used (these sites are completely excluded).

Minimum number of sequences in data files:

The data file must contain at least four sequences.

Analysis:

D^* and F^* tests are based on the neutral model prediction that estimates of η / a_1 , $(n-1)\eta_s / n$, and of k , are unbiased estimates of θ ,

where,

h , is the total number of mutations

$a_1 = S(1/i)$ from $i=1$ to $n-1$

n , the number of nucleotide sequences

h_s , is the total number of singletons (mutations appearing only once among the sequences).

k , is the average number of nucleotide differences between pairs of sequences (Tajima 1983, equation A3). (Note that Fu and Li use P_n to indicate k).

$q = 4Nu$ (for diploid-autosomal; N and u are the effective population size, and the mutation rate per DNA sequence per generation, respectively).

D^* test statistic

The D^* test statistic is based on the differences between η_s , the number of singletons (mutations appearing only once among the sequences), and η , the total number of mutations (Fu and Li 1993, p. 700 bottom).

F^* test statistic

The F^* test statistic is based on the differences between η_s , the number of singletons (mutations appearing only once among the sequences), and k , the average number of nucleotide differences between pairs of sequences (Fu and Li 1993, p. 702; see also Simonsen et al. 1995, equation 10).

Fu's F_s statistic

The F_s test statistic (Fu 1997, equation 1) is based on the haplotype (gene) frequency distribution conditional the value of θ (Ewens 1972, equations 19-21).

Strobeck's S statistic

The Strobeck's S test statistic (Strobeck 1987; see also Fu 1997) is also based on the haplotype (gene) frequency distribution conditional the value of θ (Ewens 1972, equations 19-21). The S statistic gives the probability of obtaining a sample with equal or less number of haplotypes than the observed. DnaSP also provides the probability of obtaining a sample with a number of haplotypes equal to the observed. See also the Discrete Distributions command in the [Tools](#) Menu.

Total number of mutations vs. number of segregating sites:

The D^* and F^* test statistics can also be computed using S , the number of segregating sites instead of η , the total number of mutations (Simonsen et al. 1995, equations 9 -10). Under the infinite site model (with two different nucleotides per site) both D^* and F^* values should be the same (S and η have the same value). However, if there are sites segregating for more than two nucleotides, values of S will be lower than those of η .

Effective Population size

Statistical significance:

DnaSP uses the critical values obtained by Fu and Li 1993 (two tailed test, Tables 2 and 4) to determine the statistical significance of D^* and F^* test statistics. Note that these values were obtained by computer simulations considering that the true value of θ falls into the interval $[2, 20]$; so that the critical values are not applicable when the true value of θ is not in that interval.

DnaSP will not determine the critical values for sample sizes larger than 300. For sample sizes 100-300 DnaSP uses the same critical values than for $n=100$; the reason is that the critical values increases (or decreases) with $\ln(n)$, so that when n is large the curve of critical values becomes flat (Fu, personal communication).

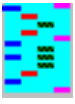
(**n.d.**, not determined; # $P < 0.10$; * $P < 0.05$; ** $P < 0.02$).

Statistical significance by the coalescent:

DnaSP can also provide the confidence intervals of the Fu and Li's D^* and F^* and the Fu's F_s by computer simulations using the coalescent algorithm (see: [Coalescent Simulations](#)).

Sliding window option:

This option computes both D^* and F^* values, and their statistical significance, by the [Sliding Window](#) method. The output of the analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph D^* and F^* values (Y axis) can be plotted against the nucleotide position (X axis).



Fu and Li's (and other) Tests with an Outgroup

See Also: [Coalescent Simulations](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Fay and Wu 2000](#) [Fu and Li 1993](#) [Fu 1995](#) [Kimura 1983](#) [Simonsen et al. 1995](#) [Tajima 1983](#)

This command calculates the statistical tests D and F proposed by Fu and Li (1993) for testing the hypothesis that all mutations are selectively neutral (Kimura 1983). These tests require data of the intraspecific variation (polymorphism) and data from an outgroup (one or more sequences from a related species).

Data Files:

For the present analysis, at least two sets of sequences (one with the intraspecific data, and other with the outgroup sequences) must be defined (see: [Data | Define Sequence Sets](#) command).

Minimum number of sequences in data files:

The intraspecific data file must contain at least four sequences.

The outgroup can contain more than one sequence, but the analysis will be performed in the first sequence one. Nevertheless, if there are more than one sequence in the outgroup, sites with alignment gaps (or with missing data) in any of the outgroup sequences will not be used (see below).

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) in any data file are not used (these sites are completely excluded).

Ambiguous information:

In some cases, the polarity of some substitutions could not be unambiguously determined; for example:

Intraspecific Data

```

      10
      *
seq1 CTTAACCTTC
seq2 CATTATTAC
seq3 CTATATTCCC
seq4 A-AAACCTAC

```

Outgroup

```

Seq5 CT-AAGGGAC
Seq6 CTA-AGCTAC

```

- Site 1. The "A" in seq 4 is an external mutation (and derived substitution)
- Site 2. Not used (alignment gaps in intraspecific data)
- Site 3. Not used (alignment gaps in the used outgroup)
- Site 4. Not used (alignment gaps in one sequence of the outgroup data file)
- Sites 6-8. Not used (ambiguous information in outgroup)
- Site 9. The "T" and the "C" on the intraspecific data file are singleton and also external mutations.

Ambiguous positions will not be used; DnaSP will list them.

Analysis:

These tests are based on the neutral model prediction that estimates of η / a_1 , η_e , and of k , are unbiased estimates of θ , where,

- h , is the total number of mutations
- $a_1 = \sum_{i=1}^{n-1} (1/i)$
- n , the number of nucleotide sequences
- h_e , is the total number of mutations in external branches of the genealogy.
- k , is the average number of nucleotide differences between pairs of sequences (Tajima 1983, equation A3). (Note that Fu and Li use P_n to indicate k).
- $q = 4Nu$ (for diploid-autosomal; N and u are the effective population size, and the mutation rate per DNA sequence per generation, respectively).

D test statistic

The D test statistic is based on the differences between h_e , the total number of mutations in external branches of the genealogy, and h , the total number of mutations (Fu and Li 1993, equation 32).

F test statistic

The F test statistic is based on the differences between η_e , the total number of mutations in external branches of the genealogy, and k , the average number of nucleotide differences between pairs of sequences (Fu and Li 1993, p. 702, top).

Fay and Wu H test statistic

The H test statistic (Fay and Wu 2000, equations 1-3) is based on the differences between two estimators of θ : θ_{π} (or k), the average number of nucleotide differences between pairs of sequences, and θ_H (Fay and Wu 2000, equation 3), an estimator based on the frequency of the derived variants.

The number of mutations in external branches

Assuming the infinite sites model DnaSP calculates the total number of mutations in the external branches of the genealogy as follows: at a given particular polymorphic site, the number of mutations in external branches is counted as the number of distinct singleton nucleotide variants (in the intraspecific data file) that are not shared with the outgroup (a singleton mutation is a nucleotide variant that appears only once among the sequences). The total number of mutations in external branches of the genealogy is then computed as the sum of the number of mutations in external branches of every polymorphic site.

Total number of mutations vs. number of segregating sites:

The D and F test statistics can also be computed using S , the number of segregating sites instead of η , the total number of mutations (see Simonsen et al. 1995). Under the infinite sites model (with two different nucleotides per site) both D and F values should be the same (S and η have the same value). However, if there are sites segregating for more than two nucleotides, values of S will be lower than those of η .

Effective Population size

Statistical significance:

DnaSP uses the critical values obtained by Fu and Li 1993 (two tailed test, Tables 2 and 4) to determine the statistical significance of D and F test statistics. Note that these values were obtained by computer simulations considering that the true value of θ falls into the interval $[2, 20]$; so that, the critical values are not applicable when the true value of θ is not in that interval. DnaSP will not determine the critical values for sample sizes larger than 300. For sample sizes 100-300 DnaSP uses the same critical values than for $n=100$; the reason is that the critical values increases (or decreases) with $\ln(n)$, so that when n is large the curve of critical values becomes flat (Fu, personal communication).

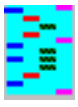
(n.d., not determined; # $P < 0.10$; * $P < 0.05$; ** $P < 0.02$).

Statistical significance by the coalescent:

DnaSP can also provide the confidence intervals of the Fu and Li's D and F, and the Fay and Wu's H by computer simulations using the coalescent algorithm (see [Coalescent Simulations](#)).

Sliding window option:

This option computes both D and F values, and their statistical significance, by the [Sliding Window](#) method. The output of the analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph D and F values (Y axis) can be plotted against the nucleotide position (X axis).



Hudson, Kreitman and Aguadé's Test (HKA Test)

See Also: [Input Data Files](#) [Output](#)

References: [Hudson et al. 1987](#) [Kimura 1983](#) [Nei 1987](#)

This command performs the Hudson, Kreitman and Aguadé's (1987) test (HKA test). The test is based on the Neutral Theory of Molecular Evolution (Kimura 1983) prediction that regions of the genome that evolve at high rates will also present high levels of polymorphism within species. The test requires data from one interspecific comparison of at least two regions of the genome, and also data of the intraspecific polymorphism in the same regions of at least one species.

Data Files:

For the present analysis, at least two sets of sequences (one with the intraspecific data, and other with the outgroup sequences) must be defined (see: [Data | Define Sequence Sets](#) command).

Minimum number of sequences in data files:

The intraspecific data file must contain at least two sequences, while the interspecific data file can contain one or more sequences.

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) in any data file are not used (these sites are completely excluded).

Implementation:

The test is performed considering intraspecific data from only one species (Hudson et al. equation 6). If there is more than one sequence in the interspecific data file, the intraspecific polymorphism will be ignored; however this information will be considered in computing the interspecific divergence. The estimate of D , the between species divergence, is obtained as the average number of differences between DNA sequences from species 1 and 2; that is, D is estimated in the same way as the D_{xy} (Nei 1987, equation 10.20) but per sequence.

Regions (loci):

DnaSP performs the HKA test of only two regions. These regions could be any two non-overlapping segments of sites of the data file.

Chromosomal location:

DnaSP assumes that the two regions (loci) are located in the same chromosome (the two compared regions are from the same data file); i.e., both are in autosomal chromosomes or in sex chromosomes. Even though, the statistical significance of the HKA test will be the same in both cases, different estimates of the divergence time or theta are expected; so that, it is convenient to indicate the chromosome where the region is located. DnaSP has considered that the expectation of π is $4N\mu$ for autosomal, $3N\mu$ for X-linked genes, and $N\mu$ for Y-linked genes [we have slightly modified the equations of Begun and Aquadro 1991 for comparisons involving autosomal (or X-linked) with Y-linked genes].

You can compare regions located in autosomes with regions in sex chromosomes using the module [HKA test - Direct Mode](#).

Substitutions Considered:

All substitutions: All substitutions are used (excluding substitutions in sites with gaps or missing data).

Silent substitutions: Only silent substitutions are used (synonymous substitutions and changes in noncoding positions). If the data file does not contain assigned coding regions all sites will be considered as noncoding positions; i.e. all substitutions will be considered as silent.

Synonymous substitutions: Only synonymous substitutions are used (substitutions in the coding region that not result in amino acid changes). This option works only if the data file contain sequences with assigned coding regions (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

Note: see [how DnaSP estimates Synonymous and Nonsynonymous changes in a codon](#).

Effective Population size

Output:

The present module displays the following output:

- Estimates of the Time of divergence (measured in $2N$ generations, where N is the effective population size),
- Estimates of theta (θ) per nucleotide in region (locus) 1,
- Estimates of theta (θ) per nucleotide in region (locus) 2,
- The X-square value, and the statistical significance.

Statistical significance:

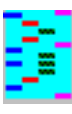
The statistical significance is obtained assuming a χ -square distribution with one degree of freedom.

DnaSP obtains the probability associated with a particular chi-square value (with 1 degree of freedom) by the trapezoidal method of numerical integration.

(# $P < 0.10$; * $P < 0.05$; * * $P < 0.01$; * * * $P, < 0.001$).

See also:

To compare autosomal and sex-linked regions, or to perform the HKA test with polymorphism data with different number of sequences in the two regions, or with different number of sites for the intraspecific and interspecific comparison the module [HKA test -Direct Mode-](#) should be used.



McDonald and Kreitman's Test

[See Also: Input Data Files Output](#)

[References: Fay et al. 2001 Kimura 1983 McDonald and Kreitman 1991 Rand and Kann 1996](#)

This command conducts the test of the neutral hypothesis (Kimura 1983) proposed by McDonald and Kreitman (1991). The test is based on a comparison of synonymous and nonsynonymous (replacement) variation within and between species. Under neutrality, the ratio of replacement to synonymous fixed substitutions (differences) between species should be the same as the ratio of replacement to synonymous polymorphisms within species.

Alignment gaps and missing data:

Codons containing alignment gaps (or codons with missing data) in any species are not used (these codons are completely excluded).

Data Files:

For the present analysis, at least two sets of sequences (one for each species) must be defined (see: [Data | Define Sequence Sets](#) command).

DnaSP performs the McDonald and Kreitman test from sequence information included in data files. DnaSP calculates:

- Number of (polymorphic) synonymous substitutions within species,
 - Number of (polymorphic) nonsynonymous (replacement) changes within species,
 - Number of synonymous substitutions fixed between species,
 - Number of nonsynonymous (replacement) differences fixed between species,
- and for these information computes the 2 x 2 contingency table.

A fixed nucleotide site between species is a site at which all sequences in one species contain nucleotide variants that are not in the second species.

Silent Substitutions Considered:

Substitutions in Coding Regions: Only synonymous substitutions (coding region) will be considered.

In Coding and Noncoding Regions: All silent substitutions will be considered (synonymous substitutions and changes in noncoding positions). If the data file does not contain assigned coding regions all sites will be considered as noncoding positions; i.e. all substitutions will be considered as silent.

How DnaSP estimates Synonymous and Nonsynonymous changes in a codon:

In general DnaSP uses a conservative criterion to decide if a particular change in a nucleotide site is synonymous or replacement (see the following examples). Nevertheless, the user should check the complex cases (those triplets of sites segregating for several codons; i.e. in highly variable regions).

Example using the Nuclear Universal Genetic Code

Species#1

```

  3   6   9  12  15  18  21  24  27
  *   *   *   *   *   *   *   *   *
AGT TCT ATT CCC AAT ATA AGT UAU UAU
AGC TCT ATT CCC AGG TTA AGT UAU UAU
AGA TCT CTG CAG ACT TTG AGA CUG CUG
AGG TCT CTG CAG ACT ATG AGA CUG CUG

```

Species#2

```

AGG CCT ATT CCC GGA TTT GGA CUG CUG
AGG CCT ATT CCC GGA TTT GGA CUG CUG
AGG CCT ATT CAC GGA TTT GGT CUG CUU
AGG CCT ATT CAC GGA TTT GGT CUG CUU

```

Codon (1,2,3):

species#1: 3 mutations in site#3: 1 replacement, 2 synonymous.

species#2: Monomorphic.

within species: 1 replacement and 2 synonymous (site#3).

fixed differences: 0

Codon (4,5,6):

species#1: Monomorphic.

species#2: Monomorphic.

within species: 0.

fixed differences: 1 replacement (site 4).

Codon (7,8,9):

species#1: Site#7 is replacement; Site#9 is synonymous.

If there are two possible paths:

```

Path#1: ATT (Ile) -> CTT (Leu) -> CTG (Leu) Site#7 Replacement; Site#9 Synonymous
Path#2: ATT (Ile) -> ATG (Met) -> CTG (Leu) Site#7 Replacement; Site#9 Replacement

```

DnaSP will choose path#1, **the path that requires the minor number of replacements** (however, see the next codon).

species#2: Monomorphic.

within species: 1 replacement, 1 synonymous.

fixed differences: 0.

Codon (10,11,12):

species#1: Site#11 is replacement; Site#12 is replacement.

Here there are also two possible paths:

```

Path#1: CCC (Pro) -> CCG (Pro) -> CAG (Gln) Site#11 Replacement; Site#12 Synonymous
Path#2: CCC (Pro) -> CAC (His) -> CAG (Gln) Site#11 Replacement; Site#12 Replacement

```

However, DnaSP will choose path#2. **If there are two possible paths, and one of the non-extant codons (e.g. CAC in this case) is found in the other species, DnaSP assume that the true evolutionary path is the path with that codon** (i.e. path#2 in the present example).

species#2: Site#11 is replacement.

within species: 2 replacements (site#11 and site#12)

fixed differences: 0

Codon (13,14,15):

species#1: Site#14 (2 replacements); Site#15 is Synonymous.

Here there are four possible paths:

```

Path#1: ACT (Thr) -> AAT (Asp) -> AGT (Ser) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Replacement).
Path#2: ACT (Thr) -> AAT (Asp) -> AAG (Lys) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Replacement).
Path#3: AAT (Asn) -> ACT (Thr) -> AGT (Ser) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Replacement).
Path#4: AAT (Asn) -> ACT (Thr) -> ACG (Thr) -> AGG (Arg) Site#14 (2 Replacements); Site#15 (1 Synonymous).

```

DnaSP will choose path#4, **the path that requires the minor number of replacements**.

species#2: Monomorphic.

within species: 2 replacements (site#14), and 1 synonymous (Site#15)

fixed differences: 2, Site#13 is replacement; Site#15 is synonymous.

For computing fixed differences, DnaSP will check all paths between codons of the two species, and it will choose the path with the minor number of changes. If there are several paths with the same number of differences, DnaSP will choose the path with the lower number of replacement changes.

Codon (16,17,18):

species#1: Site#16 (1 replacement); Site#18 (1 synonymous).

Here there is a circular path:

```

ATA (Ile) -> TTA (Leu)
  |
  i !
ATG (Met) <- TTG (Leu)

```

Let us suppose that the number of mutations were *only* two (one in site 16, and another in site 18), **DnaSP must assume one recombination event, the recombination event that requires the lower number of replacement substitutions:**

```

  | TTG (Leu)
TTA (Leu) ->| recomb: ATG (Met)
  | ATA (Ile)

```

species#2: Monomorphic.

within species: Site#16 (1 replacement); Site#18 (1 synonymous).

fixed differences: 1, Site#18 is replacement.

Note: This kind of codons will be analyzed only for Nuclear Genetic Codes.

Codon (19,20,21):

species#1: 1 replacement (site#21).

species#2: 1 synonymous (site#21).

within species: 1 replacement (site#21).

If there is discordance between replacement and synonymous changes within species (for the same nucleotide variants), DnaSP will choose the case with more replacement substitutions.

fixed differences: 1 replacement (site#19).

Codon (22,23,24):

species#1: There are 3 changes between codons. So that there are 6 putative evolutionary paths (in this particular example there are only 4 because we exclude paths that go through stop codons). **DnaSP will choose one of following paths:**

```

2 replacements (Site#22 and Site 23), and 1 synonymous (Site#24) and
2 replacements (Site#23 and Site 24), and 1 synonymous (Site#22).

```

(however, see also the next codon).

species#2: Monomorphic.

within species: the same than for species#1.

fixed differences: 0.

Codon (25,26,27):

The present example is similar to the previous codon (22,23,24) example. Here, however, there is variation in species#2. In this case **DnaSP will check the codons in species#2 to decide the assignation of species#1**.

species#1: 2 replacements (Site#22 and Site 23), and 1 synonymous (Site#24).

species#2: 1 synonymous (Site#24).

within species: 2 replacements (Site#22 and Site 23), and 1 synonymous (Site#24).

fixed differences: 0.

Output:

Codons not analyzed:

DnaSP does not estimate synonymous and replacement changes in some complex cases (ambiguous/complex codons; those sites segregating for several codons; i.e. in highly variable regions). The user should do manually.

DnaSP does not estimate synonymous and replacement changes in codons with alignment gaps.

Neutrality Index: Indicates the extent to which the levels of amino acid polymorphism depart from the expected in the neutral model (Rand and Kann, 1996).

Alfa value (α): Indicates the proportion of amino acid substitutions driven by positive selection (Fay et al. 2001).

Statistical significance:

Both the two-tailed Fisher's exact test, and G-test of independence are computed to determine whether the deviations on the ratio of replacement to synonymous (fixed substitutions between species vs. polymorphisms within species) are or not significant. DnaSP obtains the probability associated with the G value (with 1 degree of freedom) by the trapezoidal method of numerical integration.



Tajima's Test

See Also: [Coalescent Simulations](#) [Graphs Window](#) [Input Data Files](#) [Output](#)

References: [Kimura 1983](#) [Tajima 1983](#) [Tajima 1989](#)

This command calculates the D test statistic proposed by Tajima (1989), equation 38, for testing the hypothesis that all mutations are selectively neutral (Kimura 1983). The D test is based on the differences between the number of segregating sites and the average number of nucleotide differences.

Minimum number of sequences in data files:

The data file must contain at least four sequences.

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) are not used (these sites are completely excluded).

Analysis:

Tajima's test is based on the neutral model prediction that estimates of S / a_1 , and of k , are unbiased estimates of θ ,

where,

S , is the total number of segregating sites.

$a_1 = S (1 / i)$ from $i = 1$ to $n-1$

n , the number of nucleotide sequences

k , is the average number of nucleotide differences between pairs of sequences (Tajima 1983, equation A3).

$q = 4Nu$ (for diploid-autosomal; N and u are the effective population size, and the mutation rate per DNA sequence per generation, respectively).

Total number of mutations vs. number of segregating sites:

The D test statistic can also be computed using η , the total number of mutations (see [Fu and Li's test](#)), instead of S , the total number of segregating sites. Under the infinite sites model (with two different nucleotides per site) estimates of the D test statistic based on S and on η should be the same (S and η have the same value).

However, if there are sites segregating for more than two nucleotides, values of S will be lower than those of η .

Effective Population size

Statistical significance:

The confidence limits of D (two tailed test) is obtained assuming that D follows the beta distribution (Tajima 1989, equation 47), i.e. the confidence limits given in Table 2 of Tajima (1989). Note that the critical values will not be determined for sample sizes larger than 1000.

(**n.d.**, not determined; #, $P, < 0.10$; * $P, < 0.05$; * * $P, < 0.01$; * * * $P, < 0.001$).

Statistical significance by the coalescent:

DnaSP can also provide the confidence intervals of the Tajima's D by computer simulations using the coalescent algorithm (see: [Coalescent Simulations](#)).

Sliding window option:

This option computes the D test statistic and the confidence limits of D by the [Sliding Window](#) method. The output of the analysis is given in a grid (table). The results can also be presented graphically (by a line chart). In the graph the D value, can be plotted against the nucleotide position (X axis).



Intraspecific Data

See Also: [Input Data Files](#) [Output Window Menu](#)

References: [Ewens 1972](#) [Fu and Li 1993](#) [Fu 1997](#) [Nei 1987](#) [Strobeck 1987](#) [Tajima 1993](#) [Tajima 1989](#) [Watterson 1975](#)

This command computes a number of measures of the extent of DNA polymorphism and also performs some common neutrality tests. Use this command to obtain a summary of the data analysis.

Data Files:

The present analysis requires only one data file.

Analysis:

DnaSP computes the following measures:

G+C Content

- G+C_n, G+C content at noncoding positions.
- G+C_c, G+C content at coding positions.
- G+C, G+C content in the genomic region.

Haplotype/Nucleotide Diversity

- The number of haplotypes NHap, (Nei 1987, p. 259).
- Haplotype (gene) diversity and its sampling variance (Nei 1987, equations 8.4 and 8.12 but replacing 2n by n).
- Nucleotide diversity, Pi (π), the average number of nucleotide differences per site between two sequences (Nei 1987, equations 10.5 or 10.6), and its sampling variance (Nei 1987, equation 10.7).
- The average number of nucleotide differences, k (Tajima 1983, equation A3).
- Theta (per gene or per site) from Eta (η) or from S, (Watterson 1975, equation 1.4a; Nei 1987, equation 10.3). Theta (θ) = $4N\mu$ for an autosomal gene of a diploid organism (N and μ are the effective population size and the mutation rate -per gene or per site- per generation, respectively), Eta (η) is the total number of mutations, and S is the number of segregating (polymorphic) sites.

Neutrality tests

- Tajima's D, (Tajima 1989, equation 38).
- Fu and Li's D*, (Fu and Li 1993, p. 700 bottom).
- Fu and Li's F*, (Fu and Li 1993, p. 702; see also Simonsen et al. 1995, equation 10).
- Fu's Fs, (Fu 1997, equation 1).
- The Strobeck's S (Strobeck 1987; see also Fu 1997).
- DnaSP also provides the probability of obtaining a sample with a number of haplotypes equal to the number observed.

More Information in the specific modules: [Codon Usage Bias](#) [DNA Polymorphism](#) [Fu and Li's \(and other\) Tests](#)
[Fu and Li's \(and other\) Tests with an Outgroup](#) [Tajima's Test](#)



MultiDomain Analysis

See also: [Define Domain Sets](#)

DnaSP allows analysing polymorphism data in specific functional regions (see [Define Domain Sets](#)), for example; exons, introns, etc. It can compute a number of measures of the extent of DNA polymorphism and can also perform some common neutrality tests.

Haplotype/Nucleotide Diversity

- The number of Segregating Sites, S
- The total number of mutations, Eta
- The number of haplotypes NHap , (Nei 1987, p. 259).
- Haplotype (gene) diversity and its sampling variance (Nei 1987).
- Nucleotide diversity, Pi (p), (Nei 1987), and its sampling variance (Nei 1987, equation 10.7).
- The average number of nucleotide differences, k (Tajima 1983).
- Theta (per gene or per site) from Eta (h) or from S , (Watterson 1975; Nei 1987).

Neutrality tests

- Tajima's D , (Tajima 1989), and its statistical significance.
- Fu and Li's D^* , (Fu and Li 1993), and its statistical significance.
- Fu and Li's F^* , (Fu and Li 1993), and its statistical significance.
- Fu's F_s , (Fu 1997).
- $G+C_n$, $G+C$ content at noncoding positions.
- $G+C_c$, $G+C$ content at coding positions.



Concatenated Data File

See Also: [Input Data Files](#)

DnaSP allows you to create a concatenated data file (NEXUS format), that is, a big data file containing DNA sequence information from a number of single data files.

Assumptions

All files must have the same number of sequences **and in the same order**.

DnaSP generates the concatenated data file by consecutive adding single data files to the right.

Individual Data Files Option

Real length: For a single data file, DnaSP will use the DNA sequence information selected in the Region to Analyse box.

Fixed length: All data files will contribute with a fixed (X nucs) number of sites. If the current (single) data file has less than X sites, DnaSP will complement with missing information. On the contrary, if the current data file has more than X sites, DnaSP will use only the firsts X sites.

Notes

Any codon assignation present in single data files will be saved on the concatenated file. The concatenated file will also save the population set information present in only the first single data file.



Shuttle to: DNA Slider

See Also: [Input Data Files Output](#)

References: [Kimura 1983](#) [McDonald 1996](#) [McDonald 1998](#)

The neutral theory of molecular evolution predicts that the levels of polymorphism will be correlated with levels of divergence between species (Kimura 1983; see also [HKA test](#)). McDonald (1996, 1998) has proposed some tests to detect heterogeneity in the polymorphism to divergence ratio across a region of DNA. These tests are based on the distribution of polymorphic sites and fixed differences across a DNA region. DnaSP searches for polymorphic sites and fixed differences and can generate a Data File that can be read by the DNA Slider program (McDonald 1998). The DNA Slider program will perform the tests described in McDonald (1996, 1998).

Data Files:

For the present analysis, at least two sets of sequences (one with the intraspecific data, and other with the outgroup sequences) must be defined (see: [Data | Define Sequence Sets](#) command).

Alignment gaps and missing data:

Sites containing alignment gaps (or sites with missing data) in any population are not used (these sites are completely excluded).

Implementation:

If there are more than one sequence in the interspecific data file, DnaSP will assign one substitution as a fixed difference if (in a particular site) all nucleotide variants from file 1, differ from those of file 2.

Sites with three of four nucleotide variants are treated as if they were at adjacent sites, and polymorphism - fixed differences are put in the order that maximizes the number of runs (see McDonald 1996).

Substitutions Considered:

All substitutions: All substitutions are used (excluding substitutions in sites with gaps or missing data).

Silent substitutions: Only silent substitutions are used (synonymous substitutions and changes in noncoding positions). If the data file does not contain assigned coding regions all sites will be considered as noncoding positions; i.e. all substitutions will be considered as silent.

Synonymous substitutions: Only synonymous substitutions are used (substitutions in the coding region that not result in amino acid changes). This option works only if the data file contains sequences with assigned coding regions (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

Note: See [how DnaSP estimates the number of Synonymous and Nonsynonymous changes in a codon](#).

Note:

DnaSP does not perform the tests described in McDonald (1996, 1998); but it can create the data file with the relevant information for the test. This data file can be read by the DNA Slider program.

DNA Slider program:

It is a Macintosh program that performs the heterogeneity tests described in McDonald (1996, 1998). You can download the program from the John McDonald Web Page:

<http://udel.edu/~mcdonald>

<http://udel.edu/~mcdonald/aboutdnaslider.html>



ms (Dick Hudson) Data File Format

See Also: [Input Data Files](#) [Output](#)

References: [Hudson 2002](#)

This command allows exporting the data (intraspecific data) on the ms file format (Hudson 2002). This format can be read (among others) by some of Hudson (see Hudson 2002) and Kim programs:

Kim, Y. & Stephan, W. (2003): Selective sweeps in the presence of interference among partially linked loci. *Genetics*, 164: 389-398.

Kim, Y. & Stephan, W. (2002): Detecting a local signature of genetic hitchhiking along a recombining chromosome. *Genetics* 160: 765-777.

Data Files:

For the present analysis, at least one set of sequences must be defined (see: [Data | Define Sequence Sets](#) command).

Analysis using one sequence set. The sequence set must include intraspecific data information. DnaSP will estimate some measures of the extent of DNA polymorphism.

Analysis using two sequence sets (interspecific data). One Sequence Set must contain the intraspecific data, while the other must contain sequences (one or more) from an outgroup (DNA data from a different species or a different population); in this case DnaSP will use the first sequence to polarize substitutions.

Alignment gaps and missing data:

Sites with alignment gaps or missing data in any data file are not used, i.e. these sites are completely excluded.

Implementation:

Sites with three of four nucleotide variants will not be used. Sites with ambiguous information in the outgroup (if this option is chosen) will also not be used.



Polymorphic Sites File

See Also: [Input Data Files](#) [Output](#)

This module generates a NEXUS Data File including polymorphic sites information.

Sites with Alignment Gaps option:

Excluded: These sites are removed.

Included: These sites are included in the file.

Included if there is a polymorphism: These sites are included if there is a polymorphism.

Substitutions Considered:

All Substitutions: All polymorphic sites will be included.

Silent (Synonymous -coding region- and non coding region): Only silent (i.e. noncoding positions plus synonymous sites in the coding region) polymorphic sites will be included.

Only Synonymous: Only synonymous polymorphic sites (at the coding region) will be included.

Only Nonsynonymous: Only nonsynonymous polymorphic sites will be included.



Haplotype Data File

See Also: [Input Data Files](#) [Output](#)

References: [Bandelt et al. 1999](#) [Hudson et al. 1992](#) [Schneider et al. 2000](#)

This module generates Data Files with information on haplotype data. Results can be saved on a NEXUS or Roehl Data Files.

Sites with Alignment Gaps option:

Not considered: These sites are ignored (complete deletion).

Considered: Gaps are considered just like another nucleotide variant (fifth state).

Only gaps are considered: Only gaps information is considered to built haplotypes.

Invariable Sites option:

Removed: Invariable (monomorphic) sites will not be included in the output file.

Included: Invariable (monomorphic) sites will be included in the output file.

Generate option:

NEXUS Data File: Haplotype information will be stored on a NEXUS data file. Later, this file could be opened by DnaSP and might be exported in another data file format.

Arlequin Project File: DnaSP will create an Arlequin project file (*.arp) with haplotype information. This file format is the format accepted by the Arlequin software.

Roehl Data File: Haplotype information will be stored on a Roehl (Röhl) Data File (multistate data). This file format is the format accepted by the Network software. That program allows reconstructing intraspecific phylogenies (network analysis).

Arlequin software ([Schneider et al. 2000](#))

Arlequin is a software for population genetics analysis, and it is distributed from:

<http://lgb.unige.ch/arlequin/>

Network software ([Bandelt et al. 1999](#))

The Phylogenetic Network Analysis software was written by Arne Röhl, and it is distributed for free from:

<http://www.fluxus-engineering.com>



Translate to Protein Data File

See Also: [Input Data Files](#)

In this module DnaSP will translate the nucleotide sequence into an amino acid sequence, and generates a NEXUS Data File with that information. This command works only if the coding regions and the genetic code have been previously defined (more help in [Assign Coding Regions](#) and [Assign Genetic Code](#)).

Data File:

The present analysis requires only one data file.

Note:

DnaSP can not read NEXUS data files with Protein information. You can read that information with MacClade or with any Word Processor.



Reverse Complement Data File

See Also: [Input Data Files](#)

This module generates a NEXUS Data File including the sequence data in the reverse complement direction. This option would be interesting for the analysis of synonymous and nonsynonymous substitutions in data files with coding regions transcribed in both directions. DnaSP can only analyze nucleotide variation in synonymous and nonsynonymous sites if the coding regions (in data file) are in the 5' -> 3' direction. If the coding regions are transcribed in the opposite direction:

- i) you should generate the reverse complement data file;
- ii) define the coding regions;
- iii) perform the appropriate analysis.



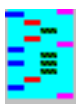
Prepare Submission for EMBL / GenBank Databases

See Also: [Input Data Files](#)

This command generates a text file with the relevant information for a submission of DNA sequence information to the nucleotide sequence database (EMBL / GenBank / DDBJ). This command is appropriated for researchers wishing to submit multiple related sequences (see the Bulk Submissions in the EMBL Nucleotide Sequence Database Information). If the coding regions have been previously defined (see [Assign Coding Regions](#) command), DnaSP will include information on the exonic/intronic regions.

More Information on the EMBL / GenBank Databases:

<http://www.ebi.ac.uk/embl/index.html>



Coalescent Simulations

See Also: [DNA Polymorphism](#) [Linkage Disequilibrium](#) [Population Size Changes](#) [Recombination](#) [Fu and Li's \(and other\) Tests](#) [Fu and Li's \(and other\) Tests with an Outgroup](#) [Tajima's Test](#)

References: [Depaulis and Veuille 1998](#) [Fay and Wu 2000](#) [Fu and Li 1993](#) [Fu 1997](#) [Harpending 1994](#) [Hudson 1983](#) [Hudson 1990](#) [Hudson and Kaplan 1985](#) [Kelly 1997](#) [Nei 1987](#) [Press 1992](#) [Ramos-Onsins and Rozas 2002](#) [Rozas et al. 2001](#) [Simonsen et al. 1995](#) [Tajima 1989](#) [Wall 1999](#) [Watterson 1975](#)

DnaSP can generate the empirical distributions of some test-statistics. From that distributions DnaSP can provide the confidence limits for a given interval. Both one-sided and two-sided tests can be conducted.

Statistics analysed (on per gene basis)

DnaSP can generate the empirical distribution of the following statistics:

Haplotype diversity, Hd (Nei 1987, equation 8.4 but replacing $2n$ by n). (See also Depaulis and Veuille 1998, eq. 1). By careful; the H test defined in Depaulis and Veuille 1998 eq. 1, corresponds to: $H = Hd * (n-1) / n$

Number of haplotypes, h, (Nei 1987, p. 259). (see also Deapulis and Veuille 1998).

Nucleotide diversity Pi (π) (Nei 1987, equations 10.5 or 10.6) but on per gene basis (that is, the average number of nucleotide differences).

Theta (θ), (Watterson 1975, equation 1.4a).

Linkage disequilibrium, ZnS statistic (Kelly 1997, equation 3).

Linkage disequilibrium, Za statistic (Rozas et al. 2001; equation 2).

Linkage disequilibrium, ZZ (Za - ZnS) statistic (Rozas et al. 2001; equation 1).

Recombination, Rm, the minimum number of recombination events (Hudson and Kaplan 1985, Appendix 2).

Tajima's D, (Tajima 1989, equation 38).

Fu and Li's D*, (Fu and Li 1993, p. 700 bottom).

Fu and Li's F*, (Fu and Li 1993, p. 702; see also Simonsen et al. 1995, equation 10).

Fu and Li's D, (Fu and Li 1993, equation 32).

Fu and Li's F, (Fu and Li 1993, p. 702, top).

Fay and Wu's H, (Fay and Wu 2000, equations 1-3).

Fu's Fs, (Fu 1997, equation 1).

Wall's B (Wall 1999)

Wall's Q (Wall 1999)

Raggedness, r (Harpending 1994, equation 1).

Ramos-Onsins and Rozas R2 (Ramos-Onsins and Rozas 2002, equation 1).

The Coalescent process

The computer simulations are based on the coalescent process for a neutral infinite-sites model and assuming a large constant population size (Hudson 1990). DnaSP uses the *ran1* routine (Press et al. 1992) as a source of uniform random deviates (i.e. random numbers uniformly distributed within a specified range).

No recombination. For no recombination DnaSP generates the genealogy of the alleles using a modification of the routine *make_tree* (Hudson 1990).

Intermediate level. For intermediate levels of recombination the genealogy is generated as described in Hudson (1983; 1990).

Free Recombination. For free recombination, DnaSP generates an independent genealogy for each segregating site. At each variable site, the number of sequences having one particular nucleotide variant (only two nucleotide variants per segregating site) is randomly obtained with probability proportional to their expected frequency (Tajima 1989, equation 50).

Simulations Given...

Theta (per gene). Mutations along the lineages are Poisson distributed using the *poidev* routine (Press et al. 1992).

Segregating Sites. The number of mutations (segregating sites) is fixed. Mutations are uniformly distributed (at random) along lineages.

Recombination option

No Recombination. It is assumed that there is no intragenic recombination ($R = 0$); e.g. mitochondrial DNA data.

Intermediate level (of Recombination). This is the case for most nuclear genes. You must indicate the value of the per gene recombination parameter (R).

Free Recombination. Maximum theoretical value of the Recombination parameter ($R = \infty$).

Recombination parameter, R

R , is the recombination parameter. $R = 4Nr$ (for autosomal loci of diploid organisms), where N is the effective population size and r is the recombination rate per gene -sequence- (i.e., r is the recombination rate per generation between the most distant sites of the DNA sequence); see also: the [Recombination](#) module and [Effective Population size](#) information.

Theta value (per gene)

Usually the theta value is unknown, in this case that value can be estimated from the data (see: [DNA Polymorphism](#) and [Tajima's Test](#) modules). Theta (per gene) can be estimated from:

- i) k , the average number of nucleotide differences
- ii) $S / a1$, where S is the total number of segregating sites
 - $a1 = \sum (1 / i)$ from $i = 1$ to $n-1$
 - n , the number of nucleotide sequences

Observed values

If the observed value is provided, DnaSP will estimate the probability of obtaining lower values than the ones observed.

For example, for the Tajima's D test statistic: $P[D \leq D(\text{obs})] = 0.01$

means that the probability of obtaining D values (under the neutral coalescent process) equal or lower than the observed is 0.01

Note:

You can perform computer simulations fixing the number of segregating sites. In this case the estimated values of theta (in different replicates) will be also fixed (because theta is estimated from the number of segregating sites).

Abbreviations:

(obs), observed value.



Hudson, Kreitman and Aguadé's Test (HKA Test). Direct Mode

See Also: [Input Data Files Output](#)

References: [Begun and Aquadro 1991](#) [Hudson et al. 1987](#) [Kimura 1983](#)

This command performs the Hudson, Kreitman and Aguadé's (1987) test (HKA test). The test is based on the Neutral Theory of Molecular Evolution (Kimura 1983) prediction that regions of the genome that evolve at high rates will also present high levels of polymorphism within species. The test requires data from an interspecific comparison of at least two regions of the genome, and also data of the intraspecific polymorphism in the same regions of at least one species.

In the present module DnaSP allows you to perform the HKA test when comparing autosomal and sex-linked regions (Begun and Aquadro 1991), or to perform the HKA test with polymorphism data with different number of sequences in the two regions, or with different number of sites for the intraspecific and interspecific comparisons. DnaSP has considered that the expectation of π is $4N\mu$ for autosomal, $3N\mu$ for X-linked genes, and $N\mu$ for Y-linked genes (so that, we have slightly modified the equations of Begun and Aquadro 1991 for comparisons involving autosomal (or X-linked) with Y-linked genes).

Effective Population size

Data:

The present module *does not* perform the HKA test from information of the DNA sequences included in the data file. Data from interspecific divergence and data on levels of intraspecific polymorphism must be entered in the dialog box. If you want that DnaSP obtains the information necessary to perform the HKA test directly from your sequences, you must use the [HKA test](#) module.

Output:

- Estimates of the Time of divergence (measured in $2N$ generations, where N is the effective population size),
- Estimates of theta (θ) per nucleotide in region (locus) 1,
- Estimates of theta (θ) per nucleotide in region (locus) 2,
- The X-square value, and the statistical significance.

Statistical significance:

The statistical significance is obtained assuming a χ -square distribution with one degree of freedom. DnaSP obtains the probability associated with a particular chi-square value (with 1 degree of freedom) by the trapezoidal method of numerical integration.

(# $P < 0.10$; * $P < 0.05$; * * $P < 0.01$; * * * $P, < 0.001$).



Tools Menu

References: [Ewens 1972](#) [Fu 1997](#) [Jukes and Cantor 1969](#) [Sokal and Rohlf 1981](#) [Strobeck 1987](#) [Tajima 1989](#) [Watterson 1975](#)

This menu has the following commands:

[Coalescent Simulations](#)

[HKA Test. Direct Mode](#)

[Discrete Distributions](#)

Use this command to calculate probabilities, the expected value and the variance of some distributions: Binomial, Hypergeometric and Poisson.

The Ewens option allows computing the Strobeck's S statistic (Strobeck 1987; see also Fu 1997), the Fu's Fs statistic (Fu 1997), and the probability (and the expected value) of obtaining a particular number of haplotypes (Ewens 1972, equations 19-21, 24). See also the [Fu and Li's Tests](#) command.

[Tests of Independence: 2 x 2 table](#)

This command allows testing independence in a 2 x 2 tables (contingency tables). DnaSP performs three types of Independence tests: Fisher's exact test, Chi-square test (standard, and using Yates' correction) and G test (standard, and using Williams' or Yates' corrections); (see Sokal and Rohlf 1981). The probability associated with a particular chi-square or G value (with 1 degree of freedom) is obtained by the trapezoidal method of numerical integration.

[Evolutionary Calculator](#)

This command displays a calculator that allows computing some commonly used molecular evolutionary parameters:

$$a1 = \sum (1 / i) \text{ from } i = 1 \text{ to } n-1$$

where, n is the number of nucleotide sequences (Watterson 1975; Tajima 1989, equation 3)

$$a2 = \sum (1 / i^2) \text{ from } i = 1 \text{ to } n-1$$

where, n is the number of nucleotide sequences (Watterson 1975; Tajima 1989, equation 4)

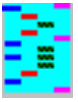
$K = (-3/4) \ln [1 - (4p/3)]$ is the Jukes and Cantor (1969) correction.

where, p is the proportion of different nucleotides between two sequences



DnaSP user interface

DnaSP has a standard Microsoft Windows user interface including the menu bar, pull-down menus, dialog boxes, and windows with scroll bars. The DnaSP menu bar displays the following pull-down menu titles: [File](#), [Data](#), [Display](#), [Analysis](#), [Overview](#), [Generate](#), [Tools](#), [Window](#), [Help](#). Each menu contains a set of related commands, which are displayed when the menu is pulled down.



File Menu

See Also: [Shortcut Keys](#) [Input Data Files](#) [Output](#)

This menu has the following commands:

Open Data File

This command allows you to open the data file. The command displays the standard Windows directory dialog box in which you may locate files.

Close Data File.

Use this command if you wish to close the active data file.

Save/Export Data As.

Use this command to save the changes made in the active data file or to export (translate) the active data file from one file format to another (note: the data file exported will not contain the excluded sequences; see the [Include / Exclude Sequences](#) command). The command displays the standard Windows directory dialog box where you may choose where to place the file.

This command also allows you to generate an Arlequin project file or a Roehl Data File (see the [Haplotype Data File](#) command).

Update NEXUS Data File

Use this command to update the information of the opened NEXUS Data File. The command is enabled for non NEXUS Data Files or if there are some excluded sequences.

Options for Saving (NEXUS format)

You can use this command to specify some options about saving or exporting NEXUS files:

Saving in an interleaved format. The number of nucleotides of each interleaved block.

To indicate the type of nucleotide sequences (DNA or RNA).

To indicate the type of line delimiter:

IBM-PC or compatible: CR + LF (ASCII 13 & ASCII 10).

Macintosh: CR (ASCII 13).

Unix systems: LF (ASCII 10).

To indicate the version of NEXUS file format:

Old version (used by MacClade 3.04 or older)

New version, NEXUS version 1 (used by MacClade 3.05 or later)

To indicate the symbol used for:

missing data, alignment gap, and identical site (matching character).

Send All Output to File.

Use this command to send all generated output (except graphs) in a file. The command displays the standard Windows directory dialog box where you may choose where to place the file.

Close Output File.

Use this command if you wish to close the output file.

Save Current Output.

Use this command to save the output (of the last analysis) in a file. The command displays the standard Windows directory dialog box where you may choose where to place the file.

Page Setup.

The command displays the standard Windows Page Setup dialog box where you may change various printer settings, for example, the default printer, paper size, orientation, etc.

Print Output.

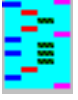
Use this command to print the output on the default printer.

File 1, 2, 3, 4

Lists the four most recently used Data Files.

Exit.

This command ends the current DnaSP session.



File Menu Shortcut Keys

To choose Press

Open Data File CTRL+O

Close File CTRL+W

Save Output CTRL+S

Print Output CTRL+P

Exit CTRL+X



Display Menu

This menu has four commands:

Graphs.

This command opens the [Graphs Window](#) where graphs from results given in the grid (table) can be displayed.

Data Info.

This command displays a summary of the data file:

The number of sequences; the number of sites; the data file format; the Genetic Code assigned; the organism's genomic type (diploid / haploid); the chromosome type where the nucleotide region is located (autosomal / X-chromosome, etc.).

View Data.

This command displays a window with the sequence data of the active data file. In this window you can get information about:

Coding and noncoding regions.

The status of a selected site (monomorphic, polymorphic, informative, synonymous, nonsynonymous, etc.).

View Data Options.

You can use this command to specify some options about displaying the nucleotide sequences:

To indicate by the dot symbol a nucleotide with identical nucleotide variant to the one in the first sequence.

To show polymorphic sites in Lower Case.



Analysis Menu

This menu is provided with the following commands. Each command starts with a dialog box that allows you to choose different options for the analysis.

[Polymorphic Sites](#)

[DNA Polymorphism](#)

[DNA Divergence Between Populations](#)

[Polymorphism and Divergence](#)

[Polymorphism and Divergence in Functional Regions](#)

[Synonymous and Nonsynonymous Substitutions](#)

[Codon Usage Bias](#)

[Preferred and Unpreferred Synonymous Substitutions](#)

[Gene Conversion](#)

[Gene Flow and Genetic Differentiation](#)

[Linkage Disequilibrium](#)

[Recombination](#)

[Population Size Changes](#)

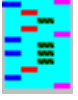
[Fu and Li's \(and other\) Tests](#)

[Fu and Li's \(and other\) Tests with an Outgroup](#)

[HKA; Hudson, Kreitman and Aguadé's Test](#)

[McDonald and Kreitman's Test](#)

[Tajima's Test](#)



Overview Menu

This menu has the following command. The command allows you to choose different options for the analysis.

[Intraspecific Data](#)



Generate Menu

This menu has the following commands:

[Shuttle to: DNA Slider](#)

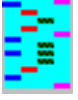
[Polymorphic Sites File](#)

[Haplotype Data File](#)

[Translate to Protein Data File](#)

[Reverse Complement Data File](#)

[Prepare Submission for EMBL / GenBank Databases](#)



Window Menu

Use this command to change the *active window* (windows with results, calculator, sequence data). The active window is the window that appears in the foreground.



Help Menu

This menu is provided with the following four commands:

Contents

This command provides information for using DnaSP (the commands open the present help file).

Search For Help on

This command displays Help's Search dialog box, where you can quickly find the information that you need by keywords.

DnaSP Bug Reports

This command displays DnaSP Bug Reports Web page.

Citation

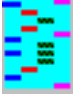
This command displays a dialog box with the suggested citation for DnaSP.

DnaSP Home Page

This command displays DnaSP Web page.

About DnaSP

This command displays a dialog box with information about authors, and the DnaSP version number.



Citation

Abstracts: [DnaSP v. 1.0](#) [DnaSP v. 2.0](#) [DnaSP v. 3.0](#) [DnaSP v. 4.0](#)

The suggested citation for the current DnaSP version is:

ROZAS, J., SÁNCHEZ-DELBARRIO, J. C., MESSEGUER, X. AND ROZAS, R. 2003. DnaSP, DNA polymorphism analyses by the coalescent and other methods. *Bioinformatics* **19**: 2496-2497.



Distribution Policy

Copies of DnaSP can be freely distributed **to academic users for research**. This software is provided as is, without of any kind of warranty.

For other uses, please get into contact with Julio Rozas:

E-mail: jrozas@ub.edu

Queries, comments and suggestions may be addressed via E-mail to Julio Rozas.

Availability

The program, the help file and some examples of the different data files are available from:

<http://www.ub.es/dnasp>

DnaSP updates and Bug reports will be advertised in the:

DnaSP Web in the Departament de Genètica, Universitat de Barcelona Web:

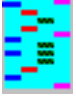
<http://www.ub.es/dnasp>

and in:

The Software Biocatalog (Molecular Evolution / Population Genetics):

<http://www.ebi.ac.uk/biocat/>

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Genetics **146**: 89-99. (1997).

Ester Betrán, Julio Rozas, Arcadi Navarro and Antonio Barbadilla

The estimation of the number and the length distribution of gene conversion tracts from population DNA sequence data.

Abstract

A growing number of DNA sequence data studies report the transfer of small continuous segments of DNA among different sequences within and among populations. This has been attributed to meiotic gene conversion events. Here, we provide (a) an algorithm to detect gene conversion tracts, and (b) a statistical model to estimate the number and the length distribution of conversion tracts for population DNA sequence data. Two length distributions are defined in the model: (1) that of the observed tract lengths; and (2) that of the true tract lengths. Assuming that the latter follows a geometric distribution, we obtain the relationship between both distributions, which depends on two basic parameters: ψ , that measures the probability of detecting a converted site, and ϕ , the parameter of the geometric distribution, from which the average true tract length, $1 / (1 - \phi)$, can be estimated. Expressions are provided for estimating ϕ by the method of the moments and that of the maximum likelihood. The robustness of the model to different types of sequence variation is examined by computer simulation. We also derive the expression for the probability of detecting a given conversion event, which allows the estimation of the rate of conversion events per generation. We show that, for a wide range of ψ and ϕ values, only a small percentage of extant conversion events is detected. The present methods have been applied to the published *rp49* sequences of *Drosophila subobscura*. Maximum likelihood estimate of ϕ for this data set is 0.9918, which represents an average conversion tract length of 122 bp.



Computer Applications in the Biosciences **11**: 621-625. (1995).

Julio Rozas and Ricardo Rozas

DnaSP, DNA sequence polymorphism: an interactive program for estimating population genetics parameters from DNA sequence data.

Abstract

DnaSP, DNA sequence polymorphism, is an interactive computer program for the analysis of DNA polymorphism from nucleotide sequence data. The program addressed to molecular population geneticists, calculates several measures of DNA sequence variation within and between populations, linkage disequilibrium parameters and Tajima's D statistic. The program, which is written in Visual Basic v. 3.0 and runs on an IBM-compatible PC under Windows, can handle a large number of sequences of up to thousands of nucleotides each.



Computer Applications in the Biosciences **13**: 307-311. (1997).

Julio Rozas and Ricardo Rozas

DnaSP version 2.0: a novel software package for extensive molecular population genetics analysis.

Abstract

Motivation: Several methods in molecular population genetics have recently been described to estimate the amount and pattern of the DNA polymorphism in natural populations, and also to test the neutral theory of molecular evolution. These methods are essential for understanding the molecular evolutionary process. However, a comprehensive computer program for the analysis is not currently available.

Results: Here we present DnaSP version 2.0, a software package for Windows that performs extensive population genetics analyses on DNA sequence data. DnaSP estimates several measures of DNA sequence variation within and between populations, linkage disequilibrium, recombination, gene flow and gene conversion (a new algorithm to detect gene conversion tracts has been included). DnaSP can also carry out several tests of neutrality: those of Fu and Li; Hudson, Kreitman and Aguadé; and Tajima. The results of the analyses are displayed in tabular and graphic form.

Availability: For academic uses, DnaSP is available via anonymous ftp: <ftp://ftp.ebi.ac.uk/pub/software/dos>.

Contact: E-mail: julio@porthos.bio.ub.es



DnaSP version 3.0

Bioinformatics **15**: 174-175. (1999).

Julio Rozas and Ricardo Rozas

DnaSP version 3: an integrated program for molecular population genetics and molecular evolution analysis

Summary: DnaSP, is a Windows integrated software for the analysis of the DNA polymorphism from nucleotide sequence data. DnaSP version 3 incorporates several methods for estimating the amount and pattern of DNA polymorphism and divergence, and for conducting neutrality tests.

Availability: For academic uses, DnaSP is available free of charge from: <http://www.ub.es/dnasp>



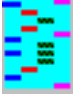
Bioinformatics **19**: 2496-2497. (2003).

Julio Rozas, Juan Carlos Sánchez-DelBarrio, Xavier Messeguer and Ricardo Rozas

DnaSP, DNA polymorphism analyses by the coalescent and other methods

Summary: DnaSP is a software package for the analysis of DNA polymorphism data. Present version introduces several new modules and features which, among other options allows, 1) handling big data sets (~5 Mbp per sequence); 2) conducting a large number of coalescent-based tests by Monte Carlo computer simulations; 3) extensive analyses of the genetic differentiation and gene flow among populations; 4) analysing the evolutionary pattern of preferred and unpreferred codons; 5) generating graphical outputs for an easy visualization of results.

Availability: The software package, including complete documentation and examples, is freely available to academic users from: <http://www.ub.es/dnasp>



Mol. Biol. Evol. **19**: 2092-2100. (2002).

Statistical Properties of New Neutrality Tests Against Population Growth

Sebastian E. Ramos-Onsins and Julio Rozas

Abstract

A number of statistical tests for detecting population growth are described. We compared the statistical power of these tests with that of others available in the literature. The tests evaluated fall into three categories: those tests based on the distribution of the mutation frequencies, on the haplotype distribution, and on the mismatch distribution. We found that, for an extensive variety of cases, the most powerful tests for detecting population growth are Fu's FS test and the newly developed R2 test. The behavior of the R2 test is superior for small sample sizes, whereas FS is better for large sample sizes. We also show that some popular statistics based on the mismatch distribution are very conservative.



Proc. Natl. Acad. Sci. USA **91**: 11517-11521. (1994).

Julio Rozas and Montserrat Aguadé

Gene conversion is involved in the transfer of genetic information between naturally occurring inversions of *Drosophila*.

Abstract

The DNA sequences of the ribosomal protein 49 (*rp49*) region were determined for 34 isochromosomal strains of *Drosophila subobscura* representing two chromosomal arrangements, the OST and the O3+4 gene arrangements, which differ by two overlapping inversions. The data reveal that gene conversion is a mechanism responsible for the transfer of genetic information between naturally occurring inversions of *Drosophila*. The estimated rate of gene transfer by gene conversion at this region, which is close to an inversion breakpoint, is lower than previous estimates obtained experimentally at the *rosy* (*ry*) gene in *Drosophila melanogaster*. Our data indicate that gene arrangements OST and O3+4 are monophyletic and rather old (0.58 and 0.73 million years old, respectively).



Genetics **158**: 1147-1155. (2001).

Julio Rozas, Myriam Gullaud, Gaelle Blandin and Montserrat Aguadé

DNA variation at the *rp49* gene region of *Drosophila simulans*: evolutionary inferences from an unusual haplotype structure.

Abstract

An approximately 1.3-kb region including the *rp49* gene plus its 5' and 3' flanking regions was sequenced in 24 lines of *Drosophila simulans* (10 from Spain and 14 from Mozambique). Fifty-four nucleotide and 8 length polymorphisms were detected. All nucleotide polymorphisms were silent: 52 in noncoding regions and 2 at synonymous sites in the coding region. Estimated silent nucleotide diversity was similar in both populations ($\pi = 0.016$, for the total sample). Nucleotide variation revealed an unusual haplotype structure showing a subset of 11 sequences with a single polymorphism. This haplotype was present at intermediate frequencies in both the European and the African samples. The presence of such a major haplotype in a highly recombining region is incompatible with the neutral equilibrium model. This haplotype structure in both a derived and a putatively ancestral population can be most parsimoniously explained by positive selection. As the rate of recombination in the *rp49* region is high, the target of selection should be close to or within the region studied.



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