

Nexus Files:

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Total files errors:	62
Possible parser errors:	9
Server issues*	1

*Not reproducible

Error type 1. File type errors:

Example 1. Fasta file: 10 times

Message: Nexus error in *<filename>* at line1:Expecting BEGIN and then a block name, but found > instead

Solution: Fasta files are not valid input.

Example 2. .ss file : 3 times; .jpg one time

Message: Nexus error in *file.ss* at line1:Expecting BEGIN and then a block name, but found xread instead

Solution: We don't handle Hennig86 yet. Please submit Phylip or Nexus files for now.

Error type 2. Parser problems:

Parser problems are errors in legal nexus that we can't handle yet.

All examples so far are below.

Example 1.

Message: Nexus error in <yourfile.nex> at line x:Expecting <someterm> name, but found <something else> instead

Here is the file that causes the message:

```
#NEXUS
```

```
log start filename=logfile;
```

```
Begin data;
```

```
Dimensions ntax=144 nchar=1159;
```

```
Format datatype=dna missing=? gap=-;
```

```
Matrix
```

```
Taxonname
```

```
GCCATGCATGTAGTACTGCCGATGGCTCATTAAATCAGTTATAGTTTATTTGACTTGGATAAC  
CGTGGTAATTCTAGAGCTAATACATGCCGATTCATTCAAATTTCTGCCCTATCAATCGTAACG  
GGACGGAGAATTAGGGTTTCGATTCCGGAGAGGGAGCCTGAGAAATGGCTACCACTTCTAAG  
GAAGGCAGCAGGCCGCGCAAATTACCAATGAGGTAGTGACAATAAATAACAATACAATTGGA  
ATGAGTACGAGTAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGTAATTCCAGCTC  
CAATAGCGTATATTAAGTTGTTGCAGTTAAAAGCTCGTAGTTGCGTTTACCGTGA  ;
```

```
End;
```

```
begin mrbayes;
```

```
set autoclose=yes;
```

```
lset nst=6 rates=gamma covarion=no;
```

```
mcmc ngen=10000000 printfreq=100 samplefreq=100 nchains=4 savebrlens=yes;
```

```
end;
```

```
log stop filename=logfile;
```

You must remove the lines in red to make it work.

Example 1b.

Message: Nexus error in <yourfile.nex> at line90:Expecting BEGIN and then a block name, but found exclude instead.

Comment [mam11]: What is the status of this issue

```
NNNNNNNNNNNNNNNNNNNN;
```

```
End;
```

```
exclude 161-164;
```

```
[charset 12S = 1-11 1-354;]
```

```
[charset COIall = 355-1760;]
```

```
[charset COIpos1 = 355-1760\3;]
```

```
[charset COIpos2 = 356-1760\3;]
```

```
[charset COIpos3 = 357-1760\3;]
```

[begin mrbayes;]

Solution: we cant handle the exclude statement. You can remove the line shown in red from the file. **but note that will change the results.**

Example 1c.

Message: Nexus error in **<yourfile.nex>** at line2236:Expecting BEGIN and then a block name, but found pset instead.

Comment [mam12]: Status of this issue?

```
ti97026?????????????????????????????????????????.....?????????????????????????????????????
??
;
end;
pset gapmode=newstate;
```

Solution: remove the line shown in red from the file, but that will change the results.

Example 2.

Message: Nexus error in **<yourfile.nex>** at line10:Could not read the value specified because NewTaxa = true was not specified before NTax (error in the NTax setting of the Dimensions command).Command Aborted.

The file has multiple character blocks in it. We do not support this at this time.

Error type 3. Misspellings, misplaced semi colons, etc

Example 1.

Message: Nexus error in test.nex at line984:Expecting BEGIN and then a block name, but found ; instead

At the end of the matrix the file looks like:

```
IARTSNEVEN QILTR--  
;  
end;  
  
;
```

Solution: end; signifies the end of the file, but if there is another character, the program expects

```
begin <blockname>;
```

to fix this remove the extraneous semicolon ; shown in red, after end;

Example 2.

A related problem produced this message:

Nexus error in <yourfile.nex> at line179:Expecting BEGIN and then a block name, but found #NEXUS instead

the extraneous word #Nexus was included, just remove it.

```
YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  
YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  
YYYYYYYYYYYYYYYYYYYY  
;  
End;  
End;
```

#NEXUS

```
Begin trees; [Treefile saved Thursday, June 14, 2007 9:34 PM]  
tree PAUP_2 = [&U]
```

Example 3.

Message: Nexus error in <yourfile.nex> at line1:Expecting BEGIN and then a block name, but found #NE instead

Misspelled first word of the file causes this error:

Just replace

#NE_US

With

#NEXUS

Example 4.

Message: Nexus error in <yourfile.nex> at line78;; is not a legal taxon name.

Solution: The taxon number supplied in the Nexus file is incorrect. In this case, ntax=70 was given, but the correct value is 69, hence the final semicolon is read as a taxa name.

To fix this, correct the number in the Dimensions block:

```
#NEXUS
```

```
Begin DATA;  
  Dimensions ntax=70 nchar=1402;  
  Format datatype=PROTEIN gap=-;
```

If instead, one ntax has fewer taxa than are present, this message will appear:

Nexus error in <yourfile.nex> at line24;; was expected, but Osh15 was entered.

Example 5.

Message: Nexus error in <yourfile.nex> at line7:Unexpected c in Dimensions command.
Command Aborted.

Issue: extraneous character in the command block.

```
BEGIN DATA; DIMENSIONS c NCHAR=1482; FORMAT DATA
```

Remove the character **c** in the dimension block.

Example 6.

Message: Nexus error in <yourfile.nex> at line7:Unexpected c in Dimensions command.
Command Aborted.

```
Taxon1  AATTTCTCAACTCTGA-GCTC---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon2  AATTTCTCAACTCTGAAGCTT---GGATGAGGGGCTTCCCTTGAAATAT  
Taxon3  AATTTCTCAACTCTGAAGCTT---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon4  AATTTCTCAACTCTGAAGCTT---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon5  AATTTCTCAACTCTGAAGCTT---GG-ATGAGGGGCTTCCC (CT) TTGAAATAT  
Taxon6  AATTTCTCAACTCTGA-GCTT---GG-ATGAGGGGCTTCCCTTGAAATAT
```

Solution: The line showed in bold caused the error. The (CT) character means this is either C or T. This is legal, but it masks that fact that an extra nucleotide has been inserted. You can see that by removing the character.

```
Taxon1  AATTTCTCAACTCTGA-GCTC---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon2  AATTTCTCAACTCTGAAGCTT---GGATGAGGGGCTTCCCTTGAAATAT  
Taxon3  AATTTCTCAACTCTGAAGCTT---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon4  AATTTCTCAACTCTGAAGCTT---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon5  AATTTCTCAACTCTGAAGCTT---GG-ATGAGGGGCTTCCCTTGAAATAT  
Taxon6  AATTTCTCAACTCTGA-GCTT---GG-ATGAGGGGCTTCCCTTGAAATAT
```

Example 7.

Message: Nexus error in **<yourfile.nex>** at line251:State specified (1) for taxon 245, character 1, not found in list of valid symbols.

```
Taxon1      GCAGGATTAAGTGCATTTTATATGTTTCGAATCTACTTACTTGTTTTT
Taxon2_2    GCAGGATTAAGTGCATTTTATATGTTTCGAATCTACTTACTTGTTTTT
Taxon3 1    GCAGGATTAAGTGCATTTTATATGTTTCGAATCTACTTACTTGTTTTT
Taxon4      GCAGGATTAAGTGCATTTTATATGTTTCGAATCTACTTACTTGTTTTT
```

Solution: The stored label. **Taxon3 1** is illegal, because there is a white space, so the one is taken as the first character.

Error Type 4. Taxon naming errors: 8 examples

Example 1.

Message: Nexus error in <yourfile.nex> at line5455:Could not find taxon named Acharagma aguirreana among stored taxon labels

Solution: This is simply a typing error on the part of the user. The stored label **Acharagma aguirreana** was spelled as **Acharagma aquirreana**. Just check your spelling and do a global replacement in your editor.

Example 2.

Message: Nexus error in <yourfile.nex> at line105:Data for this taxon (subpictus) has already been saved

In this example, the Taxons defined were genusA and genusB, but in the matix, the A and B labels were lost, making the taxons appear identical.

Error Type 5. Errors in GAP settings: 2 examples

Example 1.

Message: Nexus error in <yourfile.nex> at line7:the GAP character and MISSING character cannot be identical.

Solution: These two flags cannot be represented by the same symbol.
Find this flag;

```
FORMAT DATATYPE=DNA MISSING=? GAP=?
```

Then replace the character that represents one character state or the other. You must make this change relevant within the data set when you change the flags or the results will be meaningless.

Example 2. Illegal Gap characters

Message: Nexus error in <yourfile.nex> at line7:GAP character cannot be whitespace (including _) or any of the following: ()[]{}^&;:=*"'^

Error Type 6. Errors in state labels: 2 examples

Example 1.

Message: Nexus error in <yourfile.nex> at line42:- is an illegal CharLabels for character number 13.

Solution: Don't use the hyphen, use the underscore for Charlabels;

Example 2.

Message: Nexus error <yourfile.nex> at line752:The StateLabels for a character must be unique ((was repeated).

Solution: Don't use parens when creating state labels;

Error Type 7. Symbol Issues: 20 examples

Example 1.

Message: Nexus error in <yourfile.nex> at line6:the SYMBOL A is already in the symbols list;
Nexus error in ITS <yourfile.nex> at line6:the SYMBOL B is already a default equate code for
this DATATYPE

```
#NEXUS
BEGIN DATA;
dimensions ntax=28 nchar=1183;
format missing=?
symbols="ABCDEFGHIJKLMNPQRSTUVWXYZ"
interleave datatype=DNA gap= -;
```

matrix

Solution: Datatypes such as DNA have an implicit symbol list. Re-specification of these symbols is not permitted.

Example 2.

Message: Nexus error in <yourfile.nex> at line36:State specified (X) for taxon 28, character
164, not found in list of valid symbols

This file fails because the character X, found in the Matrix, is not defined, and is not among the explicitly defined characters for protein.

```
#NEXUS
```

```
Begin DATA;
  Dimensions ntax=92 nchar=1293;
  Format datatype=PROTEIN gap=-;
  Matrix
```

Solution: If the character X happens to stand for missing data, you can fix the problem by adding a definition for X.

```
#NEXUS
```

```
Begin DATA;
  Dimensions ntax=92 nchar=1293;
  Format datatype=PROTEIN missing=X gap=-;
  Matrix
```

Example 3.

Message: Nexus error in <yourfile.nex> x at line336:State specified (E) for taxon 1, character
1, not found in list of valid symbols

```
begin characters;
  dimensions nchar= 137;
  Matrix
```

Solution: This file lacked a format statement/datatype definition, so all character states were undefined. Insert the line in red below; taking care to define all symbols (see Example 2).

```
begin characters;  
  dimensions nchar= 137;  
  Format datatype=PROTEIN missing=. gap=-;  
  Matrix
```

Example 4.

Message: Nexus error in **<yourfile.nex>** at line6:State specified (1) for taxon 1, character 12, not found in list of valid symbols

```
#NEXUS  
begin data;  
dimensions ntax=13 nchar=44;  
format missing=? symbols="0-3";  
matrix
```

Solution: This file fails because the symbols statement is invalid. Nexus expects the symbols statement to be of the format " followed by the symbol values, separated by a white space, followed by a ". The correct statement is shown below in red:

```
#NEXUS  
begin data;  
dimensions ntax=13 nchar=44;  
format missing=? symbols="0 1 2 3 ";  
matrix
```

Example 5.

Message: The tree infer service encountered an error and was unable to obtain a starting tree.

These files load, but return the error message above. The issue in each case is the declaration of symbols that are not of the data type submitted, or the presence of a symbol not recognized by the parser. New symbols are not tolerated well by any of the programs, and even a declaration of symbols that aren't there causes a failure.

This file has no new symbols in the matrix, although it declares them (legally):

```
#NEXUS  
  
BEGIN DATA;  
  DIMENSIONS NTAX=71 NCHAR=1152;  
  FORMAT DATATYPE=PROTEIN SYMBOLS = " 1 2 3 4" MISSING=? GAP=- ;  
MATRIX
```

This file is corrected by striking out the section highlighted in red, which will not affect the results.

Error Type 8. Just plain illegal NEXUS

Example 1.

Message: Nexus error in ITS <yourfile.nex> at line735:Expecting BEGIN and then a block name, but found charpartition instead

```
;
end;
charpartition genes=ITS:1-617, LSU:618-.;
hompart partition=genes nreps=1000 seed=123
search=bandb;
```

Example 2.

Message: Nexus error in <yourfile.nex> at line22:Expecting BEGIN and then a block name, but found ctype instead

```
Congosaurus 11????1?1????1????1???110111????1100??21?110??
CNRSTSUNY278 ??1?1????00?0????1????????100?????0???1?????
;
end;

ctype ord: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31
32 33 34 35 36 37 38 39 40 41 42 43 44 ;

begin trees ;
tree tnt_1 = [&U]
(1,(3,(2,(4,(9,((13,(8,(5,(7,(6,12))))),(10,11))))));
tree tnt_2 = [&U]
```

Example 3.

Message: Nexus error in <yourfile.nex> at line9:State specified (o) for taxon 1, character 54, not found in list of valid symbols

For some reason, the parser sees taxon2 line 2 (Taxon 4) as a continuation of line 1 (Taxon2).

```
#NEXUS
BEGIN DATA;
dimensions ntax=4 nchar=121;
format missing=?
datatype=DNA gap= -;

matrix
Taxon2      GACGGTT-TTGTAGTACC-GAAATGCTGTTTTGACGGTCTTATCAGTGCG
Taxon4      -TTGGTCCTTTTTGAGCC-GCAAGGCTCTATTGAGAGCCTTAGCGGTGAG
Taxon3      -GCAGTCCCTCCATCGTC-ACCGCTGTTTAGCGGGCCCTTCGTGGCTTC
```

This problem is usually caused when the nchar value is incorrect.

Example 4.

Message: Nexus error in **<yourfile.nex>** DNA sequences at line331:Could not read the value specified because NewTaxa = true was not specified before NTax (error in the NTax setting of the Dimensions command).Command Aborted

This file has a taxa block, but the characters block also has an ntax statement in the Dimensions command. This implies that the characters block is introducing new taxa. In NEXUS, new taxa must be introduced explicitly:

```
dimensions newtaxa ntax= 322 nchar= 411;
```

instead of

```
dimensions ntax= 322 nchar= 411;
```

In this particular case, the taxa agree with the taxa that are in the taxa block, so new taxa should need not be introduced at this point. Instead, the character block should not contain an ntax statement:

```
#NEXUS  
[ Title : <yourfile.nex>]  
begin taxa;  
  dimensions ntax= 322;  
  taxlabels  
    E_histolytica2.1.  
    E_histolytica2.2....etc
```

subsequently, the character line

```
  X_tropicalis4.4.  
;  
end;  
begin characters;  
  dimensions ntax= 322 nchar= 411;  
  format missing=? gap=- matchchar=. datatype=DNA;  
  matrix
```

```
[!Domain=Data property=Coding CodonStart=1;]
```

You can just leave out the ntax statement; so the dimensions command of the characters block can simply be:

```
dimensions nchar= 411;  
  E_histolytica2.1.  
  E_histolytica2.2....etc
```

Error Type 10. Problems executing: 2 examples

Example1.

Message: RAxML:Server-side Exception: connection timeout of 1000 milliseconds expired

These errors are related to traffic levels, and were not repeatable.