```
#NEXUS

BEGIN DATA;


DIMENSIONS  NTAX=19 NCHAR=4938;

[NOTE: THE FORMAT COMMAND DATATYPE=MIXED IS A UNIQUE MRBAYES COMMAND FOR
MORPH+MOLEC DATASETS]

FORMAT DATATYPE=MIXED (DNA:1-4919, standard:4920-4938)   MISSING=? GAP=-
INTERLEAVE=yes;

MATRIX
```

[DATA MATRIX HERE!!!]

```
;


END;

BEGIN MRBAYES;

[BEWARE!  FILENAMES CAN BE CASE-SENSITIVE!!! ]

[log all output to the named file]
LOG START filename=PygoOrdGamma.screenoutput;

[automatically move onto next commands]
SET autoclose=yes;

[Define various character sets, which can be used later]

CHARSET nuc = 1-2736;
CHARSET nuc1 = 1-2734\3; [1st Codons - include every third character in set
starting from character 1]
CHARSET nuc2 = 2-2735\3; [2nd Codons - include every third character in set
starting from character 2]
CHARSET nuc3 = 3-2736\3;

CHARSET RAG = 1-1938;
CHARSET RAG1 = 1-1936\3;
CHARSET RAG2 = 2-1937\3;
CHARSET RAG3 = 3-1938\3;
```

```
CHARSET Cmos = 1939-2736;
CHARSET Cmos1 = 1939-2734\3;
CHARSET Cmos2 = 1940-2735\3;
CHARSET Cmos3 = 1941-2736\3;

CHARSET ND = 2737-3973;
CHARSET ND1 = 2737-3787\3;
CHARSET ND2 = 2738-3788\3;
CHARSET ND3 = 2739-3789\3;
CHARSET ND2tRNA =3790-3973;

CHARSET 16S = 3974-4919;

CHARSET Morph = 4920-4938;

CHARSET nucexcluded = 1-164 1887-1949 2731-2736;
CHARSET ND2excluded = 3796-3805 3839-3845;
CHARSET 16sexcluded = 3986-4028 4580-4602 4612-4629 4780-4919;
CHARSET Excluded = 1-164 1887-1949 2731-2736 3796-3805 3839-3845 3986-4028 4580-
4602 4612-4629 4780-4919;

[Exclude the unalignable characters -  the last charset defined above]
EXCLUDE Excluded;

[Define two possible partitioning schemes and call them 8Mol and 11Mol.  Note: 8
Mol = 8 molec partitions + morph = 9 partitions in all]
PARTITION 8Mol = 9: nuc1, nuc2, nuc3, ND1, ND2, ND3, ND2tRNA, 16s, morph;
PARTITION 11Mol = 12: RAG1, RAG2, RAG3, Cmos1, Cmos2, Cmos3, ND1, ND2, ND3,
ND2tRNA, 16s, morph;

[Implement the 8Mol partitioning scheme]
SET partition = 8Mol;

[The following lines to set up separate ML models for each partition]

LSET applyto=(1)  nst=6 rate=propinv; [Implement GTRi model for muc1]
LSET applyto=(2,4,5,6,7,8) nst=6 rates=invgamma; [Implement GTRig model for nuc2
ND1 ND2 ND3 ND2tRNA 16s]
LSET applyto=(3) nst=2  rates=gamma;  [Implement HKYg model nuc3]
LSET applyto=(9) coding=variable rates=gamma; [Implement morph model with gamma
rate variability and correction for inclusion of only variable characters]

[Set some morphological characters to unordered and others to ordered - default
is all unordered. If you only have binary characters it makes no difference]
CTYPE unordered:  4920 4924-4927 4930 4933-4936 4938;
CTYPE ordered:  4921 4922 4923 4928 4929 4931 4932 4937;
```

[The unlink command is used to unlink the parameters across partitions, so each partition can have, for example, a different value for the shape ie gamma parameter. Unless the parameters are explicitly unlinked, they will be shared across partitions.]

```
UNLINK tratio=(all) pinvar=(all) shape=(all) statefreq=(all) revmat=(all);
```

[These 2 commands set up separate morphological and molecular branch lengths, with all genes - partitions 1-8 - forced to have the same branch lengths. The RATE SCALER command allows them different rates]

```
UNLINK brlens=(all);
LINK brlens=(1,2,3,4,5,6,7,8);
```

[Rate Scalar - This scales rates among the molecular data sets which have linked branch lengths, so the genes can have different overall branch lengths as long as relative branch lengths are the same across all genes]

```
PRSET ratepr=variable;
```

[Start the mcmc chain - run for 10000 generations, printing to screen every 200 generations but sampling every 100 generations. Do two separate MCMC runs to make sure results are . Make each run have 4 chains of trees,
and save branch lengths as well as topology to file. Save results to filenames beginning with root PygoOrdGamma]

[Mr Bayes writes the file containing sampled parameters to XXXX.p, treefiles XXX.t. If there is more than one tree due to partitioning and linking scheme, treefiles will be automatically called XXXX.tree1.t, XXXX.tree2.t, etc]

```
MCMC ngen=1000 printfreq=100 samplefreq=100 nruns=2 nchains=4 savebrlens=yes
filename=PygoOrdGamma;
```

[Because you unlinked the morph and molec branch lengths, but linked all the molec branch lengths, you will get two trees at each generation - a molec and a morph tree. These trees will have the same topology but different branch lengths.]

[Get a majority rule consensus tree of all the molecular tree samples in file XXXX.tree1.t, discarding the first 5 as burn-in. MrBayes automatically adds .t to the file you specify in a SUMT command]

```
SUMT filename=PygoOrdGamma.tree1 burnin=5 contype=allcompat;
```

[Get a majority rule consensus tree of all the morph tree samples in file XXXX.tree2.t, discarding the first 5 as burn-in]

```
SUMT filename=PygoOrdGamma.tree2 burnin=5 contype=allcompat;
```

```
[Get a summary of all the parameters in file PygoOrdGamma.p, discarding the
first 5 as burn-in.  MrBayes automatically adds .p to the file you specify in a
SUMT command]
SUMP filename=PygoOrdGamma burnin=5;

END;
```