

Stec D., Vecchi M., Maciejowski W., Michalczyk L. - Resolving the systematics of Richtersiidae by multilocus phylogeny and integrative redescription of the nominal species for the genus Crenubiotus (Tardigrada)

Model selection for MrBayes

Settings used

alignment : ./infile.phy
branchlengths : linked
models : JC, K80, SYM, F81, HKY, GTR, JC+G, K80+G, SYM+G, F81+G, HKY+G, GTR+G, JC+I, K80+I, SYM+I, F81+I, HKY+I, GTR+I, JC+I+G, K80+I+G, SYM+I+G, F81+I+G, HKY+I+G, GTR+I+G
model_selection : aicc
search : all

Best partitioning scheme

Scheme Name : 203
Scheme lnL : -25497.593627929688
Scheme AICc : 51273.7423809
Number of params : 133
Number of sites : 2973
Number of subsets : 6

Subset	Best Model	# sites	subset id	Partition names
1	GTR+I+G	1009	dbb1f009713256a64f462726a798bb1a	18S
2	GTR+G	819	4d391b446f6180648ddfacd1f9af325c	28S
3	GTR+I+G	210	8249a96feca9aeae948e49b3e375cc7b	COIcodon1
4	GTR+G	210	55a4029b1a7e672603190dc88575dc0b	COIcodon2
5	SYM+I+G	209	6005fc13df64db8a442b1ecb4b22f43b	COIcodon3
6	GTR+I+G	516	5dd563034423d305cc8e6e1d4e17cc34	ITS2

Scheme Description in PartitionFinder format

Scheme_203 = (18S) (28S) (COIcodon1) (COIcodon2) (COIcodon3) (ITS2);

MrBayes block for partition definitions

Warning: MrBayes only allows a relatively small collection of models. If any model in your analysis is not one that is included in MrBayes (e.g. by setting nst = 1, 2, or 6 for DNA sequences; or is not in the available list of protein models for MrBayes) then this MrBayes block will just set that model to nst = 6 for DNA, or 'wag' for Protein. Similarly, the only additional parameters that this MrBayes block will include are +I and +G. Other parameters, such as +F and +X, are ignored. If you want to use this MrBayes block for your analysis, please make sure to check it carefully before you use it we've done our best to make it accurate, but there may be errors that remain!

begin mrbayes;

charset Subset1 = 1-1009;
charset Subset2 = 1010-1828;

Supplementary Data S1. Evolutionary models and partitioning scheme retrieved by PartitionFinder2

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```
charset Subset3 = 1829-2457\3;
charset Subset4 = 1830-2457\3;
charset Subset5 = 1831-2457\3;
charset Subset6 = 2458-2973;

partition PartitionFinder = 6:Subset1, Subset2, Subset3, Subset4, Subset5, Subset6;
set partition=PartitionFinder;

lset applyto=(1) nst=6 rates=invgamma;
lset applyto=(2) nst=6 rates=gamma;
lset applyto=(3) nst=6 rates=invgamma;
lset applyto=(4) nst=6 rates=gamma;
lset applyto=(5) nst=6 rates=invgamma;
prset applyto=(5) statefreqpr=fixed(equal);
lset applyto=(6) nst=6 rates=invgamma;

prset applyto=(all) ratepr=variable;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all) tratio=(all);

end;
```

Model selection for RaxML - GAMMA

Settings used

alignment : ./infile.phy
branchlengths : linked
models : JC+G, K80+G, TRNEF+G, K81+G, TVMEF+G, TIMEF+G, SYM+G, F81+G, HKY+G, TRN+G, K81UF+G, TVM+G, TIM+G, GTR+G
model_selection : aicc
search : all

Best partitioning scheme

Scheme Name : 203
Scheme lnL : -25542.124877929688

Scheme AICc : 51349.6775239

Number of params : 127
Number of sites : 2973
Number of subsets : 6

Subset	Best Model	# sites	subset id	Partition names
1	GTR+G	1009	dbb1f009713256a64f462726a798bb1a	18S
2	GTR+G	819	4d391b446f6180648ddfacd1f9af325c	28S

Supplementary Data S1. Evolutionary models and partitioning scheme retrieved by PartitionFinder2

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3	TVM+G	210	8249a96feca9aeae948e49b3e375cc7b COIcodon1
4	TVM+G	210	55a4029b1a7e672603190dc88575dc0b COIcodon2
5	SYM+G	209	6005fc13df64db8a442b1ecb4b22f43b COIcodon3
6	GTR+G	516	5dd563034423d305cc8e6e1d4e17cc34 ITS2

Scheme Description in PartitionFinder format

Scheme_203 = (18S) (28S) (COIcodon1) (COIcodon2) (COIcodon3) (ITS2);

RaxML-style partition definitions

Warning: RAXML allows for only a single model of rate heterogeneity in partitioned analyses. I.e. all partitions must be assigned one of three types of model: No heterogeneity (e.g. GTR); +G (e.g. GTR+G); or +I+G (e.g. GTR+I+G). If the best models for your dataset contain different types of model for different subsets you will need to decide on the best rate heterogeneity model before you run RAXML. If you prefer to do things more rigorously, you can run separate PartitionFinder analyses for each type of rate heterogeneity. Then choose the scheme with the lowest AIC/AICc/BIC score. Note that these re-runs will be quick!

DNA, Subset1 = 1-1009

DNA, Subset2 = 1010-1828

DNA, Subset3 = 1829-2457\3

DNA, Subset4 = 1830-2457\3

DNA, Subset5 = 1831-2457\3

DNA, Subset6 = 2458-2973

Model selection for RaxML – GAMMA + I

Settings used

alignment : ./infile.phy

branchlengths : linked

models : JC+I+G, K80+I+G, TRNEF+I+G, K81+I+G, TVMEF+I+G, TIMEF+I+G, SYM+I+G, F81+I+G, HKY+I+G, TRN+I+G, K81UF+I+G, TVM+I+G, TIM+I+G, GTR+I+G

model_selection : aicc

search : all

Best partitioning scheme

Scheme Name : 203

Scheme lnL : -25496.86407470703

Scheme AICc : 51272.2832745

Supplementary Data S1. Evolutionary models and partitioning scheme retrieved by PartitionFinder2

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Number of params : 133

Number of sites : 2973

Number of subsets : 6

Subset	Best Model	# sites	subset id	Partition names
1	GTR+I+G	1009	dbb1f009713256a64f462726a798bb1a	18S
2	GTR+I+G	819	4d391b446f6180648ddfacd1f9af325c	28S
3	TVM+I+G	210	8249a96feca9aeae948e49b3e375cc7b	COIcodon1
4	TVM+I+G	210	55a4029b1a7e672603190dc88575dc0b	COIcodon2
5	SYM+I+G	209	6005fc13df64db8a442b1ecb4b22f43b	COIcodon3
6	GTR+I+G	516	5dd563034423d305cc8e6e1d4e17cc34	ITS2

Scheme Description in PartitionFinder format

Scheme_203 = (18S) (28S) (COIcodon1) (COIcodon2) (COIcodon3) (ITS2);

RaxML-style partition definitions

Warning: RAXML allows for only a single model of rate heterogeneity in partitioned analyses. I.e. all partitions must be assigned one of three types of model: No heterogeneity (e.g. GTR); +G (e.g. GTR+G); or +I+G (e.g. GTR+I+G). If the best models for your dataset contain different types of model for different subsets you will need to decide on the best rate heterogeneity model before you run RAXML. If you prefer to do things more rigorously, you can run separate PartitionFinder analyses for each type of rate heterogeneity. Then choose the scheme with the lowest AIC/AICc/BIC score. Note that these re-runs will be quick!

DNA, Subset1 = 1-1009

DNA, Subset2 = 1010-1828

DNA, Subset3 = 1829-2457\3

DNA, Subset4 = 1830-2457\3

DNA, Subset5 = 1831-2457\3

DNA, Subset6 = 2458-2973

RaxML model selection:

Gamma

Scheme AICc : 51349.6775239

Gamma + I

Scheme AICc : 51272.2832745

The Gamma+I model had a lower AICc so it was chosen for the RaxML analysis