*Journal of Biogeography*

**SUPPORTING INFORMATION**

**Mountain uplift, miniaturisation and diversification in New Guinea Frogs (Choerophryne, Microhylidae)**

Paul M. Oliver, Amy Iannella, Stephen J. Richards and Michael S.Y. Lee

**Appendix S.** BEAST xml file for state evolution analyses (convert to xml format to run)

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 <!-- The list of taxa to be analysed (can also include dates/ages). -->

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 <!-- The unique patterns from 1 to end -->

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 <alignment idref="alignment1"/>

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 <!-- The unique patterns from 1 to end -->

 <!-- npatterns=1 -->

 <patterns id="alt\_1.patterns" from="1" strip="false">

 <alignment idref="alignment3\_alt\_1"/>

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 <!-- npatterns=1 -->

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 <alignment idref="alignment4\_ecology"/>

 </patterns>

 <!-- A prior on the distribution node heights defined given -->

 <!-- Using birth-death model on tree: Gernhard T (2008) J Theor Biol, Volume 253, Issue 4, Pages 769-778 In press-->

 <birthDeathModel id="birthDeath" units="substitutions">

 <birthMinusDeathRate>

 <parameter id="birthDeath.meanGrowthRate" value="270.0" lower="0.0"/>

 </birthMinusDeathRate>

 <relativeDeathRate>

 <parameter id="birthDeath.relativeDeathRate" value="0.5" lower="0.0"/>

 </relativeDeathRate>

 </birthDeathModel>

 <!-- This is a simple constant population size coalescent model -->

 <!-- that is used to generate an initial tree for the chain. -->

 <constantSize id="initialDemo" units="substitutions">

 <populationSize>

 <parameter id="initialDemo.popSize" value="100.0"/>

 </populationSize>

 </constantSize>

 <!-- Generate a random starting tree under the coalescent process -->

 <coalescentSimulator id="startingTree">

 <coalescentSimulator>

 <taxa idref="Ingroup"/>

 <constantSize idref="initialDemo"/>

 </coalescentSimulator>

 <taxa idref="taxa"/>

 <constantSize idref="initialDemo"/>

 </coalescentSimulator>

 <!-- Generate a tree model -->

 <treeModel id="treeModel">

 <coalescentTree idref="startingTree"/>

 <rootHeight>

 <parameter id="treeModel.rootHeight"/>

 </rootHeight>

 <nodeHeights internalNodes="true">

 <parameter id="treeModel.internalNodeHeights"/>

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 <parameter id="treeModel.allInternalNodeHeights"/>

 </nodeHeights>

 </treeModel>

 <!-- Taxon Sets -->

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 <taxa idref="Albericus"/>

 </mrca>

 <treeModel idref="treeModel"/>

 </tmrcaStatistic>

 <tmrcaStatistic id="tmrca(Choerophryne)" includeStem="false">

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 <taxa idref="Ingroup"/>

 </mrca>

 <treeModel idref="treeModel"/>

 </tmrcaStatistic>

 <monophylyStatistic id="monophyly(Ingroup)">

 <mrca>

 <taxa idref="Ingroup"/>

 </mrca>

 <treeModel idref="treeModel"/>

 </monophylyStatistic>

 <!-- Generate a speciation likelihood for Yule or Birth Death -->

 <speciationLikelihood id="speciation">

 <model>

 <birthDeathModel idref="birthDeath"/>

 </model>

 <speciesTree>

 <treeModel idref="treeModel"/>

 </speciesTree>

 </speciationLikelihood>

 <!-- The uncorrelated relaxed clock (Drummond, Ho, Phillips & Rambaut (2006) PLoS Biology 4, e88 ) for molecular data-->

 <discretizedBranchRates id="molec.branchRates">

 <treeModel idref="treeModel"/>

 <distribution>

 <logNormalDistributionModel meanInRealSpace="true">

 <!-- set the mean to some sensible value, e.g. 1% per lineage per million years-->

 <mean>

 <parameter id="ucld.mean" value="0.01"/>

 </mean>

 <stdev>

 <parameter id="ucld.stdev" value="0.3333333333333333" lower="0.0"/>

 </stdev>

 </logNormalDistributionModel>

 </distribution>

 <rateCategories>

 <parameter id="branchRates.categories"/>

 </rateCategories>

 </discretizedBranchRates>

 <rateStatistic id="meanRate" name="meanRate" mode="mean" internal="true" external="true">

 <treeModel idref="treeModel"/>

 <discretizedBranchRates idref="molec.branchRates"/>

 </rateStatistic>

 <rateStatistic id="coefficientOfVariation" name="coefficientOfVariation" mode="coefficientOfVariation" internal="true" external="true">

 <treeModel idref="treeModel"/>

 <discretizedBranchRates idref="molec.branchRates"/>

 </rateStatistic>

 <rateCovarianceStatistic id="covariance" name="covariance">

 <treeModel idref="treeModel"/>

 <discretizedBranchRates idref="molec.branchRates"/>

 </rateCovarianceStatistic>

 <!-- the strict clock for alt\_1 (Uniform rates across branches) -->

 <strictClockBranchRates id="alt\_1.branchRates">

 <rate>

 <parameter id="alt\_1.clock.rate" value="0.01" lower="0.0" upper="1.0"/>

 </rate>

 </strictClockBranchRates>

 <!-- the strict clock for ecology (Uniform rates across branches) -->

 <strictClockBranchRates id="ecology.branchRates">

 <rate>

 <parameter id="ecology.clock.rate" value="0.01" lower="0.0" upper="1.0"/>

 </rate>

 </strictClockBranchRates>

 <!-- The general time reversible (GTR) substitution model and 1 partition - selected by Partitionfinder BIC -->

 <gtrModel id="gtr">

 <frequencies>

 <frequencyModel dataType="nucleotide">

 <frequencies>

 <parameter id="frequencies" value="0.25 0.25 0.25 0.25"/>

 </frequencies>

 </frequencyModel>

 </frequencies>

 <rateAC>

 <parameter id="ac" value="1.0" lower="0.0"/>

 </rateAC>

 <rateAG>

 <parameter id="ag" value="1.0" lower="0.0"/>

 </rateAG>

 <rateAT>

 <parameter id="at" value="1.0" lower="0.0"/>

 </rateAT>

 <rateCG>

 <parameter id="cg" value="1.0" lower="0.0"/>

 </rateCG>

 <rateGT>

 <parameter id="gt" value="1.0" lower="0.0"/>

 </rateGT>

 </gtrModel>

 <!-- site model -->

 <siteModel id="molec.siteModel">

 <substitutionModel>

 <gtrModel idref="gtr"/>

 </substitutionModel>

 <gammaShape gammaCategories="4">

 <parameter id="alpha" value="0.5" lower="0.0"/>

 </gammaShape>

 <proportionInvariant>

 <parameter id="pInv" value="0.5" lower="0.0" upper="1.0"/>

 </proportionInvariant>

 </siteModel>

 <frequencyModel id="alt\_1.frequencyModel">

 <kStateType idref="alt\_1"/>

 <frequencies>

 <parameter id="alt\_1.frequencies" dimension="4" value="0.250 0.250 0.250 0.250"/>

 </frequencies>

 </frequencyModel>

 <generalSubstitutionModel id="alt\_1.ord" >

 <kStateType idref="alt\_1"/>

 <frequencies>

 <frequencyModel idref="alt\_1.frequencyModel"/>

 </frequencies>

 <rates>

 <parameter id="ForeAndHind.RateMatrix" value="1.0 0.0 0.0 1.0 0.0 1.0" dimension="6" lower="0" upper="Infinity" />

<!--

As there is no operator on the starting values in this rate matrix, this enforces an ordered character.

The 3 elements above correspond to the 3 entries in the matrix, in left-right order per row.

 U M L H

 U - 1 0 0

 M - 1 0

 L - 1

 H -

-->

 </rates>

 </generalSubstitutionModel>

 <siteModel id="alt\_1.siteModel">

 <substitutionModel>

 <generalSubstitutionModel idref="alt\_1.ord"/>

 </substitutionModel>

 </siteModel>

 <!-- ecology: The general Substitution Model for binary data -->

 <!-- Note: Lewis model assumes equal rates thus same equilibrium frequencies, hence no operator-->

 <frequencyModel id="ecology.frequencyModel">

 <dataType idref="ecology"/>

 <frequencies>

 <parameter id="ecology.freqs" value="0.5 0.5"/>

 </frequencies>

 </frequencyModel>

 <lewisMk totalOrder="false" id="ecology.unord">

 <frequencies>

 <frequencyModel idref="ecology.frequencyModel"/>

 </frequencies>

 </lewisMk>

 <siteModel id="ecology.siteModel">

 <substitutionModel>

 <generalSubstitutionModel idref="ecology.unord"/>

 </substitutionModel>

 </siteModel>

 <!-- START Multivariate diffusion model -->

 <multivariateDiffusionModel id="size.diffusionModel">

 <precisionMatrix>

 <matrixParameter id="size.precision">

 <parameter id="col1" value="0.05"/>

 </matrixParameter>

 </precisionMatrix>

 </multivariateDiffusionModel>

 <multivariateWishartPrior id="size.precisionPrior" df="1">

 <scaleMatrix>

 <matrixParameter>

 <parameter value="1.0"/>

 </matrixParameter>

 </scaleMatrix>

 <data>

 <parameter idref="size.precision"/>

 </data>

 </multivariateWishartPrior>

 <!-- END Multivariate diffusion model -->

 <!-- Likelihood for tree given sequence data -->

 <treeLikelihood id="molec.treeLikelihood" useAmbiguities="false">

 <patterns idref="molec.patterns"/>

 <treeModel idref="treeModel"/>

 <siteModel idref="molec.siteModel"/>

 <discretizedBranchRates idref="molec.branchRates"/>

 </treeLikelihood>

 <ancestraltreeLikelihood id="alt\_1.treeLikelihood" useAmbiguities="false" stateTagName="alt\_1">

 <patterns idref="alt\_1.patterns"/>

 <treeModel idref="treeModel"/>

 <siteModel idref="alt\_1.siteModel"/>

 <strictClockBranchRates idref="alt\_1.branchRates"/>

 <lewisMk idref="alt\_1.ord"/>

 </ancestraltreeLikelihood>

 <ancestraltreeLikelihood id="ecology.treeLikelihood" useAmbiguities="false" stateTagName="ecology">

 <patterns idref="ecology.patterns"/>

 <treeModel idref="treeModel"/>

 <siteModel idref="ecology.siteModel"/>

 <strictClockBranchRates idref="ecology.branchRates"/>

 <lewisMk idref="ecology.unord"/>

 </ancestraltreeLikelihood>

 <!-- START Multivariate diffusion model -->

 <multivariateTraitLikelihood id="size.traitLikelihood" traitName="size" useTreeLength="true" scaleByTime="true" reportAsMultivariate="true" reciprocalRates="true" integrateInternalTraits="true">

 <multivariateDiffusionModel idref="size.diffusionModel"/>

 <treeModel idref="treeModel"/>

 <traitParameter>

 <parameter id="leaf.size"/>

 </traitParameter>

 <conjugateRootPrior>

 <meanParameter>

 <parameter value="0.0"/>

 </meanParameter>

 <priorSampleSize>

 <parameter value="0.001"/>

 </priorSampleSize>

 </conjugateRootPrior>

<!-- Jitter points with identical values -->

 <jitter window="0.001 0.001" duplicatesOnly="true">

 <parameter idref="leaf.size"/>

 </jitter>

 </multivariateTraitLikelihood>

 <!-- END Multivariate diffusion model -->

 <!-- Define operators -->

 <operators id="operators" optimizationSchedule="default">

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="ac"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="ag"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="at"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="cg"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="gt"/>

 </scaleOperator>

 <deltaExchange delta="0.01" weight="0.1">

 <parameter idref="frequencies"/>

 </deltaExchange>

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="alpha"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="0.1">

 <parameter idref="pInv"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="3">

 <parameter idref="ucld.stdev"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="10">

 <parameter idref="alt\_1.clock.rate"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="10">

 <parameter idref="ecology.clock.rate"/>

 </scaleOperator>

 <subtreeSlide size="0.1" gaussian="true" weight="15">

 <treeModel idref="treeModel"/>

 </subtreeSlide>

 <narrowExchange weight="15">

 <treeModel idref="treeModel"/>

 </narrowExchange>

 <wideExchange weight="5">

 <treeModel idref="treeModel"/>

 </wideExchange>

 <wilsonBalding weight="5">

 <treeModel idref="treeModel"/>

 </wilsonBalding>

 <FixedNodeheightSubtreePruneRegraft weight="5">

 <treeModel idref="treeModel"/>

 </FixedNodeheightSubtreePruneRegraft>

 <NearestNeighborInterchange weight="5">

 <treeModel idref="treeModel"/>

 </NearestNeighborInterchange>

 <scaleOperator scaleFactor="0.75" weight="3">

 <parameter idref="treeModel.rootHeight"/>

 </scaleOperator>

 <uniformOperator weight="30">

 <parameter idref="treeModel.internalNodeHeights"/>

 </uniformOperator>

 <scaleOperator scaleFactor="0.75" weight="3">

 <parameter idref="birthDeath.meanGrowthRate"/>

 </scaleOperator>

 <scaleOperator scaleFactor="0.75" weight="3">

 <parameter idref="birthDeath.relativeDeathRate"/>

 </scaleOperator>

 <upDownOperator scaleFactor="0.75" weight="3">

 <up>

<!--rate fixed <parameter idref="ucld.mean"/> -->

 </up>

 <down>

 <parameter idref="treeModel.allInternalNodeHeights"/>

 </down>

 </upDownOperator>

 <swapOperator size="1" weight="10" autoOptimize="false">

 <parameter idref="branchRates.categories"/>

 </swapOperator>

 <uniformIntegerOperator weight="10">

 <parameter idref="branchRates.categories"/>

 </uniformIntegerOperator>

 <upDownOperator scaleFactor="0.75" weight="3">

 <up>

 <parameter idref="alt\_1.clock.rate"/>

 </up>

 <down>

 <parameter idref="treeModel.allInternalNodeHeights"/>

 </down>

 </upDownOperator>

 <upDownOperator scaleFactor="0.75" weight="3">

 <up>

 <parameter idref="ecology.clock.rate"/>

 </up>

 <down>

 <parameter idref="treeModel.allInternalNodeHeights"/>

 </down>

 </upDownOperator>

 <!-- START Multivariate diffusion model -->

 <precisionGibbsOperator weight="1">

 <multivariateTraitLikelihood idref="size.traitLikelihood"/>

 <multivariateWishartPrior idref="size.precisionPrior"/>

 </precisionGibbsOperator>

 <!-- END Multivariate diffusion model -->

 </operators>

 <!-- Define MCMC -->

 <mcmc id="mcmc" chainLength="100000000" autoOptimize="true" operatorAnalysis="Exemplar\_ConcMuscGB\_new.ops">

 <posterior id="posterior">

 <prior id="prior">

 <booleanLikelihood>

 <monophylyStatistic idref="monophyly(Ingroup)"/>

 </booleanLikelihood>

 <gammaPrior shape="0.05" scale="10.0" offset="0.0">

 <parameter idref="ac"/>

 </gammaPrior>

 <gammaPrior shape="0.05" scale="20.0" offset="0.0">

 <parameter idref="ag"/>

 </gammaPrior>

 <gammaPrior shape="0.05" scale="10.0" offset="0.0">

 <parameter idref="at"/>

 </gammaPrior>

 <gammaPrior shape="0.05" scale="10.0" offset="0.0">

 <parameter idref="cg"/>

 </gammaPrior>

 <gammaPrior shape="0.05" scale="10.0" offset="0.0">

 <parameter idref="gt"/>

 </gammaPrior>

 <uniformPrior lower="0.0" upper="1.0">

 <parameter idref="frequencies"/>

 </uniformPrior>

 <exponentialPrior mean="0.5" offset="0.0">

 <parameter idref="alpha"/>

 </exponentialPrior>

 <uniformPrior lower="0.0" upper="1.0">

 <parameter idref="pInv"/>

 </uniformPrior>

 <exponentialPrior mean="0.3333333333333333" offset="0.0">

 <parameter idref="ucld.stdev"/>

 </exponentialPrior>

 <uniformPrior lower="0.0" upper="100000.0">

 <parameter idref="birthDeath.meanGrowthRate"/>

 </uniformPrior>

 <uniformPrior lower="0.0" upper="1.0">

 <parameter idref="birthDeath.relativeDeathRate"/>

 </uniformPrior>

 <speciationLikelihood idref="speciation"/>

 <!-- START Multivariate diffusion model -->

 <multivariateWishartPrior idref="size.precisionPrior"/>

 <!-- END Multivariate diffusion model -->

 </prior>

 <likelihood id="likelihood">

 <treeLikelihood idref="molec.treeLikelihood"/>

 <treeLikelihood idref="alt\_1.treeLikelihood"/>

 <treeLikelihood idref="ecology.treeLikelihood"/>

 <!-- START Multivariate diffusion model -->

 <multivariateTraitLikelihood idref="size.traitLikelihood"/>

 <!-- END Multivariate diffusion model -->

 </likelihood>

 </posterior>

 <operators idref="operators"/>

 <!-- write log to screen -->

 <log id="screenLog" logEvery="100000">

 <column label="Posterior" dp="4" width="12">

 <posterior idref="posterior"/>

 </column>

 <column label="Prior" dp="4" width="12">

 <prior idref="prior"/>

 </column>

 <column label="Likelihood" dp="4" width="12">

 <likelihood idref="likelihood"/>

 </column>

 <column label="rootHeight" sf="6" width="12">

 <parameter idref="treeModel.rootHeight"/>

 </column>

 <column label="alt\_1.rate" sf="6" width="18">

 <parameter idref="alt\_1.clock.rate"/>

 </column>

 <column label="ecology.rate" sf="6" width="18">

 <parameter idref="ecology.clock.rate"/>

 </column>

 </log>

 write log to file -->

 <log id="fileLog" logEvery="100000" fileName="Choero\_run\_2\_new.log" overwrite="false">

 <posterior idref="posterior"/>

 <prior idref="prior"/>

 <likelihood idref="likelihood"/> <!-- total likelihood of molec and phenotypic data -->

 <parameter idref="treeModel.rootHeight"/>

 <tmrcaStatistic idref="tmrca(Albericus)"/>

 <tmrcaStatistic idref="tmrca(Choerophryne)"/>

 <tmrcaStatistic idref="tmrca(Ingroup)"/>

 <parameter idref="birthDeath.meanGrowthRate"/>

 <parameter idref="birthDeath.relativeDeathRate"/>

 <parameter idref="ac"/>

 <parameter idref="ag"/>

 <parameter idref="at"/>

 <parameter idref="cg"/>

 <parameter idref="gt"/>

 <parameter idref="frequencies"/>

 <parameter idref="alpha"/>

 <parameter idref="pInv"/>

 <parameter idref="ucld.mean"/> <!-- fixed -->

 <parameter idref="ucld.stdev"/>

 <rateStatistic idref="meanRate"/>

 <rateStatistic idref="coefficientOfVariation"/>

 <rateCovarianceStatistic idref="covariance"/>

 <parameter idref="alt\_1.clock.rate"/>

 <parameter idref="ecology.clock.rate"/>

 <!-- START Multivariate diffusion model -->

 <matrixParameter idref="size.precision"/>

 <!-- END Multivariate diffusion model -->

 <!-- START Multivariate diffusion model -->

 <multivariateTraitLikelihood idref="size.traitLikelihood"/>

 <!-- END Multivariate diffusion model -->

 <treeLikelihood idref="molec.treeLikelihood"/>

 <treeLikelihood idref="alt\_1.treeLikelihood"/>

 <treeLikelihood idref="ecology.treeLikelihood"/>

 <speciationLikelihood idref="speciation"/>

 </log>

 <!-- write tree log to file -->

 <logTree id="treeFileLog" logEvery="100000" nexusFormat="true" fileName="Choero\_run\_2\_time.trees" sortTranslationTable="true">

 <treeModel idref="treeModel"/>

 <ancestralTreeLikelihood idref="alt\_1.treeLikelihood"/>

 <ancestralTreeLikelihood idref="ecology.treeLikelihood"/>

 <multivariateTraitLikelihood idref="size.traitLikelihood"/>

 <trait name="rate" tag="rate">

 <discretizedBranchRates idref="molec.branchRates"/>

 </trait>

 <posterior idref="posterior"/>

 </logTree>

 <logTree id="substTreeFileLog" logEvery="100000" nexusFormat="true" fileName="Choero\_run\_2\_sub.trees" branchLengths="substitutions">

 <treeModel idref="treeModel"/>

 <discretizedBranchRates idref="molec.branchRates"/>

 <trait name="rate" tag="rate">

 <discretizedBranchRates idref="molec.branchRates"/>

 </trait>

 </logTree>

 </mcmc>

 <!-- START Marginal Likelihood Estimator -->

 <!-- Define marginal likelihood estimator settings -->

 <marginalLikelihoodEstimator chainLength="1000" pathSteps="100" pathScheme="betaquantile" alpha="0.3">

 <samplers>

 <mcmc idref="mcmc"/>

 </samplers>

 <pathLikelihood id="pathLikelihood">

 <source>

 <posterior idref="posterior"/>

 </source>

 <destination>

 <prior idref="prior"/>

 </destination>

 </pathLikelihood>

 <log id="MLELog" logEvery="1000" fileName="Choero\_run\_2.log">

 <pathLikelihood idref="pathLikelihood"/>

 </log>

 </marginalLikelihoodEstimator>

 <!-- Path sampling estimator from collected samples -->

 <pathSamplingAnalysis fileName="Exemplar\_ConcMuscGB\_new.mle.log">

 <likelihoodColumn name="pathLikelihood.delta"/>

 <thetaColumn name="pathLikelihood.theta"/>

 </pathSamplingAnalysis>

 <!-- Stepping-stone sampling estimator from collected samples -->

 <steppingStoneSamplingAnalysis fileName="Exemplar\_ConcMuscGB\_new.mle.log">

 <likelihoodColumn name="pathLikelihood.delta"/>

 <thetaColumn name="pathLikelihood.theta"/>

 </steppingStoneSamplingAnalysis>

 <!-- END Marginal Likelihood Estimator -->

 <report>

 <property name="timer">

 <mcmc idref="mcmc"/>

 </property>

 </report>

</beast>