*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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</alignment>

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

<!-- 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">

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<taxa idref="Ingroup"/>

<constantSize idref="initialDemo"/>

</coalescentSimulator>

<taxa idref="taxa"/>

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</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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</treeModel>

<!-- Taxon Sets -->

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</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>