**S2 Text: Example XML code to specify the skew-normal distributed molecular clock**

Specifying the molecular clock:

<arbitraryBranchRates id="branchRates" exp="true" centerAtOne="false">

 <treeModel idref="treeModel"/>

 <rates>

 <parameter id="branchRates.rates" dimension="245" value="-9"/>

 </rates>

</arbitraryBranchRates>

<distributionLikelihood id="branchRates.prior">

<distribution>

 <skewNormalDistributionModel>

 <location>

 <parameter id="rate.prior.location" value="0" lower="-Infinity"/>

 </location>

 <scale>

 <parameter id="rate.prior.scale" value="1" lower="0.0"/>

 </scale>

 <shape>

 <parameter id="rate.prior.shape" value="0"/>

 </shape>

 </skewNormalDistributionModel>

 </distribution>

 <data>

 <parameter idref="branchRates.rates"/>

 </data>

</distributionLikelihood>

Operators:

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

 <parameter idref="rate.prior.scale"/>

</scaleOperator>

<randomWalkOperator windowSize="0.1" weight="3">

 <parameter idref="rate.prior.location"/>

</randomWalkOperator>

<randomWalkOperator windowSize="0.1" weight="3">

 <parameter idref="rate.prior.shape"/>

</randomWalkOperator>

Priors:

<exponentialPrior mean="1">

<parameter idref="rate.prior.scale"/>

</exponentialPrior>

<normalPrior mean="0.0" stdev="100">

<parameter idref="rate.prior.location"/>

</normalPrior>

<normalPrior mean="0.0" stdev="3">

 <parameter idref="rate.prior.shape"/>

</normalPrior>