

# Using DISSECT in BEAST2

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DISSECT is an add-on package for BEAST2 [1] aimed at species delimitation. This manual only deals with the mechanics of using DISSECT. You should read the paper [3] and its supplementary information in order to understand what you are doing.

The model is also implemented in the development version v1.8.0pre of BEAST1 [2]). At the moment (2014-03-04) this has been better tested than the the BEAST2 implementation, and there are currently some issues with BEAST2

(<https://groups.google.com/forum/?fromgroups&hl=en#!topic/beast-users/6eILzAon5HY>) which cause inconvenience. However, future development is likely to be in BEAST2.

A tool called SpeciesDelimitationAnalyser for analysing the sampled trees is also available.

Web site: [www.indriid.com](http://www.indriid.com).

## Running a Dissect analysis

The model has two extra user-chosen parameters compared to a standard \*BEAST analysis: one ( $\epsilon$  in paper, `collapseHeight` in BEAST2 XML) controls the degree of approximation, and the second ( $w$  in paper, `collapseWeight` in BEAST2 XML) controls the prior distribution on the numbers of species.

BEAUTi can be used to set up most of the analysis. The taxa in the analysis contain **minimal clusters** of individuals which are assumed a priori to belong to a single species.

Two changes need to be made to the XML. The `birthDeathModel` must be replaced with a `birthDeathCollapseModel`, and an operator must be added for the origin height. Note that the initial value of `originHeight` is ignored.

The value of  $w$  can be set using the element `collapseWeight`. It can either be fixed or estimated.

The value of  $\epsilon$  is fixed for the analysis and is set in the `birthDeathModel` using the attribute `collapseHeight`.

The Yule model for speciation can be used with Dissect, by setting the initial values of `birthDeathCollapse.relativeDeathRate` to 0, and removing the operator which changes it.

### XML for the birth-death-collapse model

This goes in the prior distribution (<distribution id="prior"...> element, and replaces the usual birth-death or Yule prior. This change is necessary.

```
<distribution id="SpeciesTreeDivergenceTimesPrior"
    spec="dissect.BirthDeathCollapseModel"
    tree="@speciesTree"
    collapseHeight='0.00003'>
  <birthDiffRate spec='parameter.RealParameter' id="birthDiffRate"
    value='100.0' lower='0' upper='10000' />
  <relativeDeathRate spec='parameter.RealParameter' id="relativeDeathRate"
    value='0.5' lower='0' upper='1.0' />
  <originHeight spec='parameter.RealParameter' id="originHeight"
    value='100.0' lower='0' upper='10000000' />
  <collapseWeight spec='parameter.RealParameter' id="collapseWeight"
    value='0.5' lower='0' upper='1.0' />
</distribution>
```

### XML for the operator for origin height

This change is necessary.

```
<operator id="originHeightScaler" spec="ScaleOperator" weight="3"
  parameter="originHeight" scaleFactor="0.75" degreesOfFreedom="1"/>
```

### XML for a number-of-clusters statistic

This can go in any <logger> element. It is optional.

```
<log spec="dissect.BirthDeathCollapseNClustersStatistic" spptree="@speciesTree"
    bdc="@SpeciesTreeDivergenceTimesPrior"/>
```

### XML for a prior and an operator for w.

Use these two bits of XML if you want to estimate  $w$ .

This goes in the prior distribution (<distribution id="prior"...> element:

```
<distribution id='collapseWeightPrior' spec='distributions.Prior' x='@collapseWeight'>
  <distr id='collapseWeightBeta' spec='beast.math.distributions.Beta' alpha="4" beta="2" />
</distribution>
```

This goes in the operators element:

```
<operator degreesOfFreedom="1" id="collapseWeightScaler" scaleFactor="0.75"
  spec="ScaleOperator" parameter="@collapseWeight" weight="1.0"/>
```

## References

- [1] Remco Bouckaert, Joseph Heled, Denise Kuehnert, Tim Vaughan, Chieh-Hsi Wu, Dong Xie, Marc Suchard, Andrew Rambaut, Alexei J Drummond (accepted 2014). BEAST 2: A software platform for Bayesian evolutionary analysis. *PLOS Computational Biology*
- [2] Drummond, Alexei J., Suchard, Marc A., Xie, Dong, and Rambaut, Andrew (2012) Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Molecular Biology and Evolution*, **29**, 1969–1973.
- [3] Graham Jones and Bengt Oxelman (2014). DISSECT: an assignment-free Bayesian discovery method for species delimitation under the multispecies coalescent. *BIORARXIV*, doi: 10.1101/003178, <http://biorxiv.org/content/early/2014/03/03/003178>