

Beast II 101: Part 2



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2. Operator **calls** `input.get()` **instead of** `input.get(this)`.

When an `Operator` does a proposal, it should change a `StateNode`. This `StateNode` needs to be one of its inputs. So, to get the `StateNode` normally a call to `input.get()` would give the value. However, for the `State` to know that a `StateNode` changes, the method `input.get(this)`; should be called.

Note that this only applies to the `proposal()` method, not to `initAndValidate()` (though it does not hurt in the latter) since only in `proposal()` a `StateNode` should be changed.

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2. Operator **calls** `input.get()` **instead of** `input.get(this)`.

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Note that this only applies to the `proposal()` method, not to `initAndValidate()` (though it does not hurt in the latter) since only in `proposal()` a `StateNode` should be changed.

You can happily get all you like and set what you like on `StateNodes` that are in the State

3. **Shadow a StateNode in a CalculationNode.**

It is tempting to use a pattern like this:

```
public Input<RealParameter> m_p = new Input<>...;
    private RealParameter m_pShadow;

    public void initAndValidate() {
        m_pShadow = m_p.get();
    }

    double calculateSomethingOld() {
        // uses non-current value
        return m_pShadow.getValue() * 2.0;
    }

    double calculateSomethingNew() {
        // uses current value
        return m_p.get().getValue() * 2.0;
    }
```

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3. **Shadow a StateNode in a CalculationNode.**

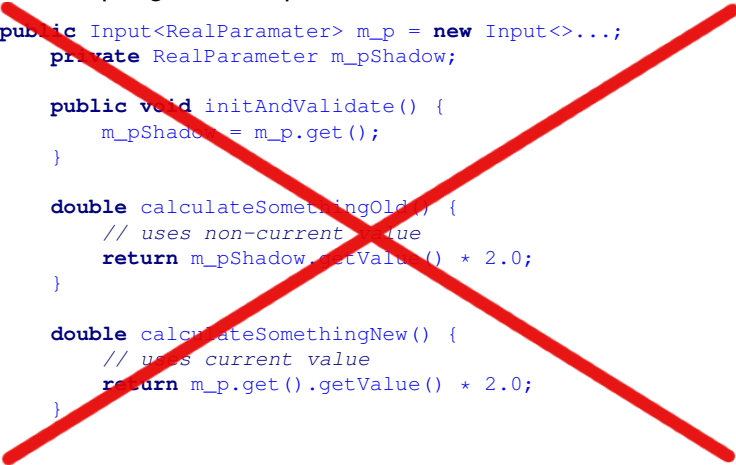
It is tempting to use a pattern like this:

```
public Input<RealParameter> m_p = new Input<>...;
private RealParameter m_pShadow;

public void initAndValidate() {
    m_pShadow = m_p.get();
}

double calculateSomethingOld() {
    // uses non-current value
    return m_pShadow.getValue() * 2.0;
}

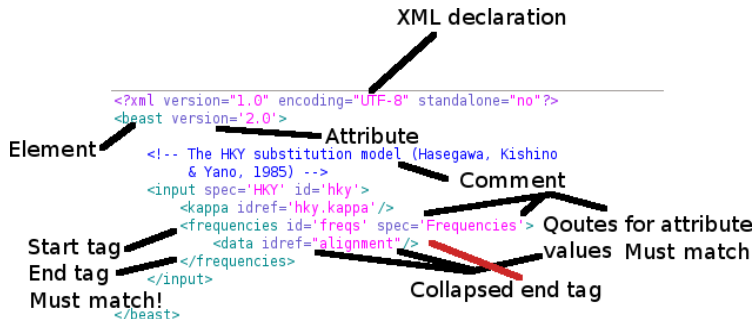
double calculateSomethingNew() {
    // uses current value
    return m_p.get().getValue() * 2.0;
}
```



You can happily shadow anything you like

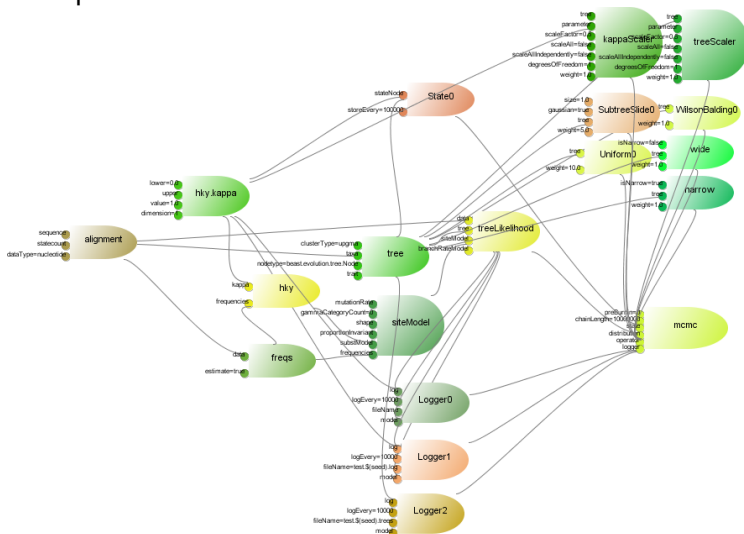
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What is XML?



Reserved characters in attribute values: " (") ' (') < (<) > (>) & (&) e.g. x="""

Let's put this model into XML



First the hky-scale operator

name, spec, id, idref

- XML element `input` can be used for every plugin.
- Specify `name` to match with input name.
- Specify `spec` to identity Plugin.
- XML id/idref mechanism to reuse Plugins.
- XML attributes for primitives (Integer, Double, Boolean, String).

```
<input name='operator' id='kappaScaler'  
  spec='beast.evolution.operators.ScaleOperator'  
  scaleFactor='0.5' weight='1'>  
  <input name='parameter' idref='hky.kappa' />  
</input>
```


Top level `beast` element can be used to define namespaces in the usual Java fashion.

```
<beast namespace="beast.core:beast.evolution.operators">
```

This allows shortening of spec-values:

```
<input name='operator' id='kappaScaler'  
  spec='beast.evolution.operators.ScaleOperator'  
  scaleFactor='0.5' weight='1'>  
  <input name='parameter' idref='hky.kappa' />  
</input>
```

becomes

```
<input name='operator' id='kappaScaler' spec='ScaleOperator'  
  scaleFactor='0.5' weight='1'>  
  <input name='parameter' idref='hky.kappa' />  
</input>
```

Input elements with name attributes equal the name's value as element name

```
<input name='xyz'></input> == <xyz></xyz>
```

so

```
<input name='operator' id='kappaScaler' spec='ScaleOperator'  
  scaleFactor='0.5' weight='1'>  
  <input name='parameter' idref='hky.kappa' />  
</input>
```

equals

```
<operator id='kappaScaler' spec='ScaleOperator'  
  scaleFactor='0.5' weight='1'>  
  <parameter idref='hky.kappa' />  
</operator>
```

If idref is only attribute in element, an attribute with element name and before the idref.

```
<name idref="some-id"/> == name='@some-id'
```

So

```
<operator id='kappaScaler' spec='ScaleOperator'  
  scaleFactor='0.5' weight='1'>  
  <parameter idref='hky.kappa' />  
</operator>
```

equals

```
<operator id='kappaScaler' spec='ScaleOperator'  
  scaleFactor="0.5" weight="1" parameter="@hky.kappa"/>
```

```
<beast version='2.0' namespace='x.y.z:a.b.c' >
```

```
<map name='xyz' >x.y.z.Class </map>
```

element <xyz> is expanded to

```
<input name='xyz' spec='x.y.z.Class'>
```

<input >

<run > spec must be `beast.core.Runnable`

<distribution > spec must be `beast.core.Distribution`

<operator > spec must be `beast.core.Operator`

<logger > spec=`beast.core.Logger`

<data > spec=`beast.evolution.alignment.Alignment`

<sequence > spec=`beast.evolution.alignment.Sequence`

<state > spec=`beast.core.State`

<parameter > spec=`beast.core.parameter.RealParameter`

<tree > spec=`beast.evolution.tree.Tree`

<plate > mainly for `Beauti` templates

```
<input name='substModel' id="hky" spec="HKY">
  <input name='kappa' idref="hky.kappa" >
    <input name='frequencies' id="freqs" spec="Frequencies">
      <input name='data' idref="alignment"/>
    </input>
  </input>
</input>
```

```
<input spec="TreeLikelihood">
  <input name='data' idref='alignment' />
  <input name='tree' idref='tree' />
  <input name='siteModel' spec="SiteModel">
    <input name='substModel' idref='hky' />
  </input>
</input>
```

Assuming namespace='beast.evolution.sitemodel:
beast.evolution.substitutionmodel:
beast.evolution.likelihood'

Input elements with name attributes equal the name's value as element name

```
<input name='xyz'></input> == <xyz></xyz>
```

Applying to the example

```
<substModel id="hky" spec="HKY">  
  <kappa idref="hky.kappa" >  
    <frequencies id="freqs" spec="Frequencies">  
      <data idref="alignment"/>  
    </frequencies>  
  </substModel>
```

```
<distribution spec="TreeLikelihood">  
  <data idref='alignment' />  
  <tree idref='tree' />  
  <siteModel spec="SiteModel">  
    <substModel idref='hky' />  
  </siteModel>  
</distribution>
```

if idref is only attribute in element, an attribute with element name and before the idref.

```
<name idref="some-id"/> == name='@some-id'
```

Applying to the example

```
<substModel id="hky" spec="HKY" kappa="@hky.kappa" >  
  <frequencies id="freqs" spec="Frequencies"  
    data="@alignment"/>  
</substModel>
```

```
<distribution data="@alignment" spec="TreeLikelihood"  
  tree="@tree">  
  <siteModel spec="SiteModel" substModel='@hky' />  
</distribution>
```

Note: you still can use any of the previous versions!
These are just short-cuts.

- specified in name attribute

```
<input name="xyz" >
```

- if not, use element name

```
<xyz value="3" >
```

- if input, use 'value' when there is text content, but no element content

```
<input>3</input>
```


- if idref is specified, use the referred object

```
<xyz idref="other" > or xyz='@other'
```

- specified in value attribute

```
<xyz value="3" >
```

- if not, use value of (non-reserved) attribute

```
<input xyz="3" >
```

- if not, use text content when there is text content, but no element content

```
<input>3</input>
```

```

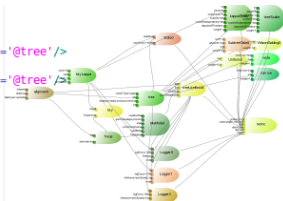
<run chainLength="1000000" id="mcmc" preBurnin="0" spec="MCMC">
  <state>
    <parameter id="hky.kappa" name="stateNode" value="1.0"/>
    <tree id="tree" name="stateNode" spec="beast.util.ClusterTree">
      <taxa idref="alignment"/>
    </tree>
  </state>

  <distribution id="likelihood" spec="TreeLikelihood" tree="@tree" data="@alignment">
    <siteModel spec="SiteModel">
      <substModel id="hky" kappa="@hky.kappa" spec="HKY">
        <frequencies spec="Frequencies" data="@alignment" estimate="true"/>
      </substModel>
    </siteModel>
  </distribution>

  <operator id='kappaScaler' spec='ScaleOperator' scaleFactor="0.5" weight="1" parameter="@hky.kappa"/>
  <operator id='treeScaler' spec='ScaleOperator' scaleFactor="0.5" weight="1" tree="@tree"/>
  <operator spec='Uniform' weight="10" tree="@tree"/>
  <operator spec='SubtreeSlide' weight="5" gaussian="true" size="1.0" tree="@tree"/>
  <operator id='narrow' spec='Exchange' isNarrow='true' weight="1" tree="@tree"/>
  <operator id='wide' spec='Exchange' isNarrow='false' weight="1" tree="@tree"/>
  <operator spec='WilsonBalding' weight="1" tree="@tree"/>

  <logger logEvery="10000" fileName="test.%(seed).log">
    <model idref='likelihood'/>
    <log idref='likelihood'/>
    <log idref='hky.kappa'/>
    <log spec='beast.evolution.tree.TreeHeightLogger' tree="@tree"/>
  </logger>
  <logger logEvery="10000" fileName="test.%(seed).trees" log="@tree"/>
  <logger logEvery="10000">
    <model idref='likelihood'/>
    <log idref='likelihood'/>
    <ESS spec='ESS' name='log' arg="@likelihood"/>
    <log idref='hky.kappa'/>
    <ESS spec='ESS' name='log' arg="@hky.kappa"/>
  </logger>
</run>

```



XMLParser produces semi sensible parser error messages:

Error 124 parsing the xml input file

This plugin (treeLikelihood) has no input with name xxx. Choose one of these inputs: data,tree,siteModel,branchRateModel,useAmbiguities

Error detected about here:

```
<beast>
  <run id='mcmc' spec='MCMC'>
    <distribution id='posterior' spec='CompoundDistribution'>
      <distribution id='treeLikelihood' spec='TreeLikelihood'>
```

and

Error 122 parsing the xml input file

Cannot create class: CompoundDistribution. Class could not be found.
Did you mean beast.core.util.CompoundDistribution?

Error detected about here:

```
<beast>
  <run id='mcmc' spec='MCMC'>
    <distribution id='posterior' spec='CompoundDistribution'>
```

A Beast 2 add-on is a library based on Beast 2

Why add-ons:

- Making work easier citable
- Making the core easier to learn – it's a lot smaller / cleaner
- Separating out stable / experimental code / dead code
- ...

- SnAP - multi-species coalescent for SNP and AFLP data <http://code.google.com/p/snap-mcmc/>
- beastii - utilities, Peter Will's AARS substitution model <http://code.google.com/p/beastii/>
- Subst-BMA - Bayes model averaging over subst. models
<http://code.google.com/p/subst-bma/>
- EBSP/*BEAST - Joseph's thesis work
- Experimental phylogeography
- David Welch's Prevalence/SI-likelihood
- Sibon's MCMC monitoring thing
- ...

- A jar file that contains the code
- A jar file with the source
- Example XML files
- Documentation
- A Beauti 2 template

Recommended directory structure:

<code>myAddOn/ ../beast2</code>	Beast 2 files
<code>myAddOn/src</code>	source files
<code>myAddOn/examples</code>	XML examples
<code>myAddOn/build</code>	class files
<code>myAddOn/build/dist</code>	jar files
<code>myAddOn/lib</code>	libraries used (if any)
<code>myAddOn/doc</code>	documentation
<code>myAddOn/templates</code>	Beauti templates (optional)

Setting up an Add-on

Checkout Beast 2 code, available at

<http://code.google.com/p/beast2>

Setting up an add-on in IntelliJ, basic steps

- Make a project containing Beast 2
- Create new module, e.g. called MyAddOn
- Create module dependency of MyAddOn on Beast 2

see SDK documentation for more details.

Setting up an add-on in Eclipse, basic steps

- Make a project containing Beast 2
- Create new project, e.g. called MyAddOn
- Add beast 2 to the Java build path of MyAddOn

see SDK documentation for more details.

Setting up an add-on in Hudson (for automatic regression testing): ask Walter

- Create Add-on files containing add-on classes only
- Put on a web-site
- Download to \$BEAST_HOME/beastlib
- It will be picked up from there when running BeastMCMC or Beauti

Future work: automate this process, provide catalogue, GUI, etc.

Beauti 2: replacement of Beauti 1

Beast II 101

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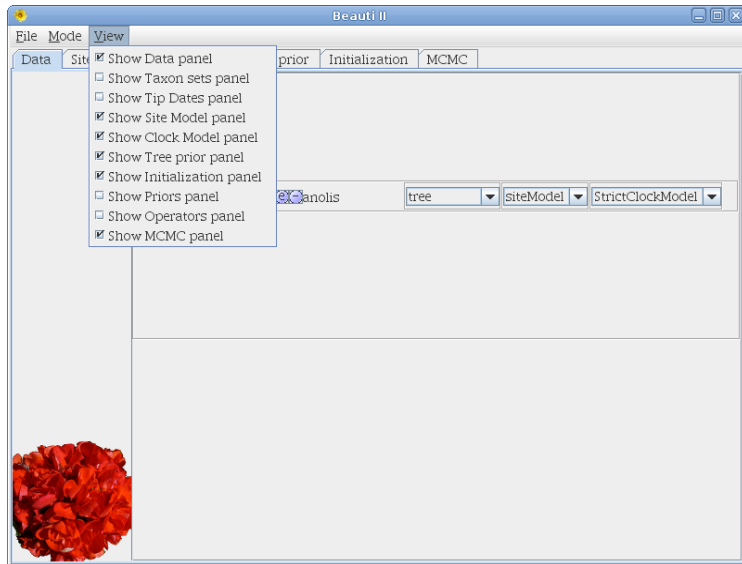


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More about Beauti in Part III

Model builder: GUI for graphical manipulation of Plugins

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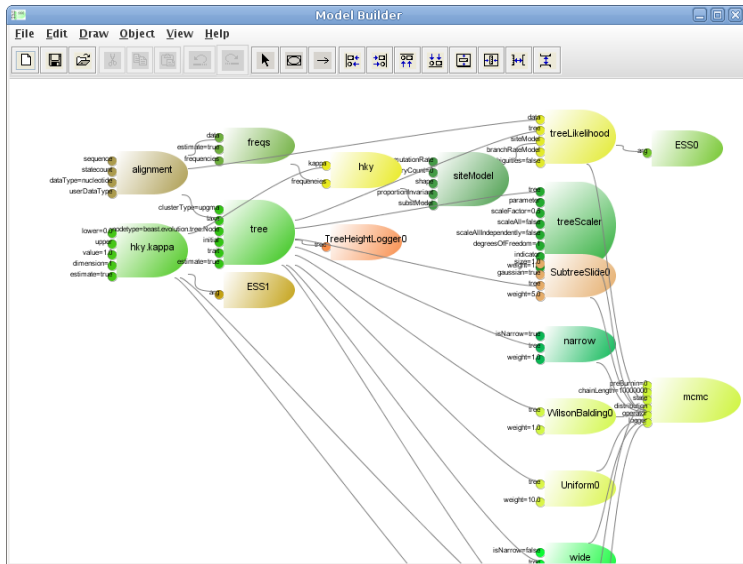


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In development...

Spreadsheet: calculates partial results on the fly

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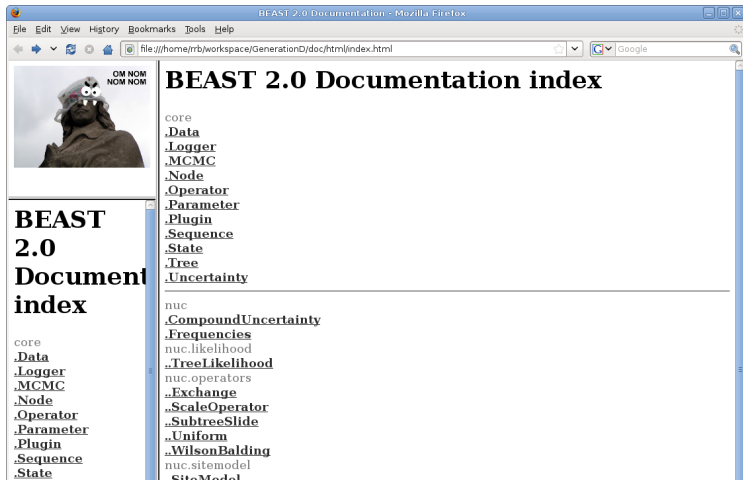
Beast II Calculator		
File Edit Window Help		
A	B	C
1	State	State([\$B2,\$B3],100000)
2	hky.kappa	RealParameter(0,0,null,2,0,1,true) 4.0
3	tree	ClusterTree(upgma,\$B5,beast.evolution.tree.Node,null,null,true) 0.107031...
4		
5	alignment	Alignment([\$B6,\$B7,\$B8,\$B9,\$B10,\$B11],null,nucleotide)
6	Sequence	Sequence(4,human, AGAAATATGTCTGATAAAAGAGTTACT...
7	Sequence	Sequence(4,chimp, AGAAATATGTCTGATAAAAGAGTTACTT...
8	Sequence	Sequence(4,bonobo, AGAAATATGTCTGATAAAAGAGTTACTT...
9	Sequence	Sequence(4,gorilla, AGAAATATGTCTGATAAAAGAGTTACTT...
10	Sequence	Sequence(4,orangutan, AGAAATATGTCTGACAAAAGAGTTA...
11	Sequence	Sequence(4,siamang, AGAAATACGTCTGACAAAAGAGTTAC...
12		
13	treeLikelihood	TreeLikelihood(\$B5,\$B3,\$B14,null,false) -1986.84...
14	siteModel	SiteModel(null,0,null,null,\$B15)
15	hky	HKY(\$B2,\$B16)
16	frequencies	Frequencies(\$B5,true,null)
17		
18	kappaScaler	ScaleOperator(null,\$B2,0.5,false,false,1,1.0)
19	treeScaler	ScaleOperator(\$B3,null,0.5,false,false,1,1.0)
20	Uniform	Uniform(\$B3,10.0)
21	SubtreeSlide	SubtreeSlide(1.0,true,\$B3,5.0)
22	narrow	Exchange(true,\$B3,1.0) 33
23	wide	Exchange(false,\$B3,1.0) 66.0
24	WilsonBalding	WilsonBalding(\$B3,1.0)
25		
26	Logger	Logger([\$B13,\$B27,\$B2,\$B28],10000,null,\$B13,autodetect)
27	ESS	ESS(\$B13)
28	ESS	ESS(\$B2)
29		
30	Logger	Logger([\$B13,\$B2,\$B31],10000,test.\$(seed).log,\$B13,autodetect)
31	TreeHeightLog...	TreeHeightLogger(\$B3)
32		
33	Logger	Logger([\$B3],10000,test.\$(seed).trees,null,autodetect)
34	mcmc	MCMC(0,10000000,\$B1,\$B13,[\$B18,\$B19,\$B20,\$B21,\$B22,\$B2...
35		
36		

In development...

Documentation

XML documentation provided through

- @Description annotation on plug in
- Tooltip text on inputs
- getCitation method
- Input validation rules



The screenshot shows a Mozilla Firefox browser window titled "BEAST 2.0 Documentation - Mozilla Firefox". The address bar displays the file path: "file:///home/rfb/workspace/GenerationD/doc/html/index.html". The page content is the "BEAST 2.0 Documentation index". On the left, there is a sidebar with a small image of a statue and the text "OM NOM NOM NOM". Below the image, the text "BEAST 2.0 Document index" is displayed. The main content area lists various components and methods, including "core", ".Data", ".Logger", ".MCMC", ".Node", ".Operator", ".Parameter", ".Plugin", ".Sequence", ".State", ".Tree", ".Uncertainty", "nuc", ".CompoundUncertainty", ".Frequencies", "nuc.likelihood", ".TreeLikelihood", "nuc.operators", ".Exchange", ".ScaleOperator", ".SubtreeSlide", ".Uniform", ".WilsonBalding", "nuc.sitemodel", and ".SiteModel".

- o Sequence generator, for simulation studies
- o Sequence with XML merging through Beauti, handy for scripting
- o XMLParser to beautify XML

```
~> java beast.app.BeastMCMC
```

Usage: BeastMCMC [options] <Beast.xml>

where <Beast.xml> the name of a file specifying a Beast run
and the following options are allowed:

- resume : read state that was stored at the end of the last run from file and append log file
- overwrite : overwrite existing log files (**if** any). By **default**, existing
- seed [<**int**>|random] : sets random number seed (**default** 127), or picks a
- threads <**int**> : sets number of threads (**default** 1)
- beastlib <path> : Colon separated list of directories. All jar files in