

PoMoCoV manual

Graham Jones, www.indriid.com

2020-05-16, May 16, 2020

1 Introduction

The program PoMoCoV and this manual are at a very preliminary stage.

`_PoMoCoV2.jar` is a BEAST2 program which can be run from the command line. It consists of BEAST 2.5.1 plus a modified version of the BADTRIP package.

Simple example:

```
java -jar PoMoCoV2.jar your.XML
```

This requires both `PoMoCoV2.jar` and `your.XML` to be in the current directory.

```
java -ea -Dbadtrip.debug="true" -jar PoMoCoV2.jar -working path\to\your.XML
```

The `-ea -Dbadtrip.debug="true"` part turns on some debugging code, which is a sensible thing to do given how new the code is. `-working` tells BEAST2 to put the output files (log and tree files) in the same directory as the XML, `path\to\` in this case.

```
java -ea -Dbadtrip.debug="true" -jar PoMoCoV2.jar -working -overwrite path\to\your.XML
```

will overwrite any old output files.

```
java -ea -Dbadtrip.debug="true" -jar PoMoCoV2.jar -working -resume path\to\your.XML
```

will resume an existing MCMC chain.

2 Notes on BEAST XML for PoMoCoV

This section explains the differences from XML for BADTRIP and the new model implemented in PoMoCoV.

There is no change to the alignment or data (`alignmentPoMo` element).

```
<TraitSetPoMo spec='beast.evolution.tree.TraitSetPoMo' id='traitSet' direction="forward"
  units="day" unobservedCases="true"
  samplesHostsValue="t1001=H1, t4001=H4, t5001=H5, t2001=H2, t7001=H7"
  samplesDatesValue="t1001=9.9, t4001=12.2, t5001=9.4, t2001=11.2, t7001=7.4"
  HostDatesStartValue="H1=-0.1, H4=2.2, H5=-0.6, H2=1.2, H7=-2.6"
  HostDatesEndValue="H1=10.4, H4=12.7, H5=9.9, H2=11.7, H7=7.9">
  <taxa spec='beast.evolution.alignment.TaxonSet' alignment='@alignment' />
</TraitSetPoMo>
```

Same as BADTRIP, except that `unobservedCases="true"` can optionally be added.

```
<treePoMo spec='beast.evolution.tree.TreePoMo' id='tree' estimate='true'>
  <traits spec='beast.evolution.tree.TraitSetPoMo' idref='traitSet' />
</treePoMo>
<siteModel spec="SiteModelPoMo" id="siteModel">
  [...]
</siteModel>
```

Same as BADTRIP.

```
<input spec='CompoundDistribution' id='parameterPriors'>
<distribution spec='beast.math.distributions.Prior' x="@PoMo.mutRates">
  <distr spec='LogNormalDistributionModel' M="-7.0" S="2.0"/>
</distribution>
<distribution spec='beast.math.distributions.Prior' x="@mutationRate">
  <distr spec='LogNormalDistributionModel' M="-7.0" S="2.0"/>
</distribution>
  <distribution spec='beast.math.distributions.Prior' x="@PoMo.bottleneck">
    <distr spec='LogNormalDistributionModel' M="6.0" S="3.0"/>
  </distribution>
</input>
```

Same as BADTRIP, except that I have changed the hyperparameters M and S.

```
<input spec='TreePoMoCoVPrior' id="treePrior" tree="@tree">
</input>
```

New, and optional. Provides a prior for the transmission tree based on observed distributions for transmission times. [*Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing*, Ferretti et al. <https://science.sciencemag.org/content/early/2020/04/09/science.abb6936>] This is a built-in prior with no hyperparameters (at the moment). It uses Burr distributions with various hyperparameters to approximate “waiting times” [*The intensity of COVID-19 outbreaks is modulated by SARS-CoV-2 free-living survival and environmental transmission*, Ogbunugafor et al, <https://www.medrxiv.org/content/10.1101/2020.05.04.20090092v2>] between host, transmission times after infection in one hosts, and durations of chains of unobserved hosts.

```

<input spec='PoMoCoVTreeLikelihood' id="treeLikelihood" treePoMo="@tree">
  <seqError spec='RealParameter' id="PoMo.seqError" value="0.0001" upper="0.01"/>
  <bottleneck spec='RealParameter' id="PoMo.bottleneck" value="1.0" upper="10000"/>
  <data idref="alignment"/>
  <siteModel idref='siteModel'/>
</input>

```

Same as BADTRIP, except that PoMoCoVTreeLikelihood replaces TreeLikelihoodPoMoTransmission or TreeLikelihoodPoMoTransmissionSlow.

```

<run spec="MCMC" id="mcmc" chainLength="1000000" storeEvery="50000">
  <state>
    [...]
  </state>
  <distribution spec='CompoundDistribution' id='posterior'>
    <distribution idref="treeLikelihood"/>
    <distribution idref="treePrior"/>
    <distribution idref="parameterPriors"/>
  </distribution>

```

Same as BADTRIP, except that <distribution idref="treePrior"/> added.

```

<operator spec='ScaleOperator' id='mutScalerAll' parameter="@PoMo.mutRates"
  scaleFactor="0.95" weight="5" scaleAll="true"/>
<operator spec='ScaleOperator' id='mutScalerOne' parameter="@PoMo.mutRates"
  scaleFactor="0.98" weight="5" scaleAll="false"/>
<operator spec='ScaleOperator' id='errScaler' parameter="@PoMo.seqError"
  scaleFactor="0.95" weight="5"/>
<operator spec='ScaleOperator' id='muRateScaler' parameter="@mutationRate"
  scaleFactor="0.95" weight="5"/>
<operator spec='ScaleOperator' id='bottleneckScaler' parameter="@PoMo.bottleneck"
  scaleFactor="0.9" weight="5"/>
<operator spec='UpDownOperator' id='RelativeScalerMuHKY'
  scaleFactor="0.95" weight="5" down="@mutationRate" up="@PoMo.mutRates"/>
<operator spec='UniformTransmission' weight="50" tree="@tree"/>
<operator spec='WilsonBaldingTransmission' weight="50" tree="@tree"/>
<operator spec='ParentChildExchange' weight="50" tree="@tree"/>
<operator spec='PoMoCoVCountsWalker' weight="50" tree="@tree"/>

```

I added the scaleAll="true" version of ScaleOperator for PoMo.mutRates (maybe helps mixing a bit). The SubtreeSlideTransmission operator is omitted (not yet implemented for PoMoCoV). The PoMoCoVCountsWalker operator is added for changing the number of unobserved hosts linking a host to the originating observed host.

The tree operators PoMoCoVCountsWalker, UniformTransmission, WilsonBaldingTransmission, and ParentChildExchange take note of the unobservedCases flag in TraitSetPoMo. PoMoCoVCountsWalker does nothing and the other three revert to the BADTRIP versions if unobservedCases is false. They have new implementations when unobservedCases is true.

```

<logger logEvery="1000" fileName="transmission-uo.log">
  <model idref='posterior'/>
  [...]
</logger>

```

```
<logger logEvery="1000" fileName="transmission-uo.trees" mode="tree">  
  <log idref="tree"/>  
</logger>
```

```
<logger logEvery="1000">  
  [...]  
</logger>
```

I have just changed file names and screen output. The new parameters (counts of unobserved hosts and originating times) are in the trees file as metadata, like this:

```
[&host=H1,height=7.549999999999999,originHeight=11.454827615148464,unobservedCount=1]
```
