

Section 4: BEAST2 Howto



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Tools needed

BEAST2

Software implementing MCMC for model parameter and tree inference

BEAUti

Part of BEAST2 package for setting up the input file

Tracer

Analysis of BEAST2 output files (.log)

Tree Annotator

Analysis of BEAST2 output files (.trees)

FigTree/IcyTree/DensiTree

Visualisation of trees (.trees)

Workflow

 **ACACACCC**
 **TCACACCT**
 **ACAGACTT**



BEAUi



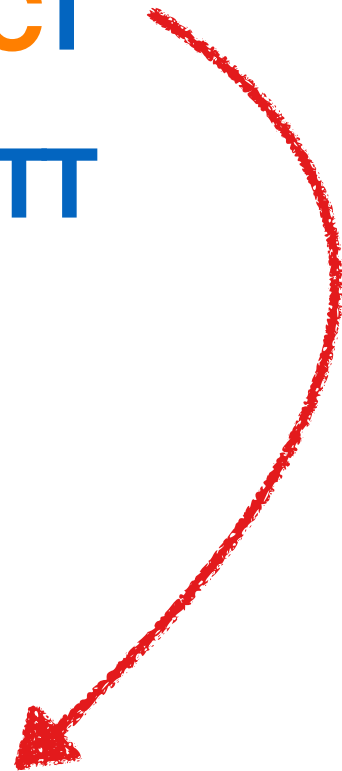
Tracer



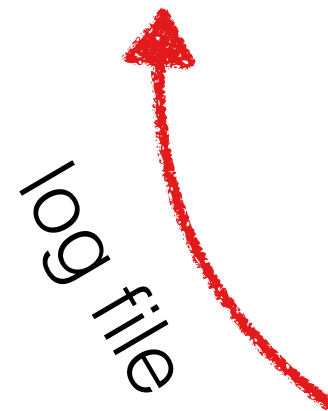
TreeAnnotator



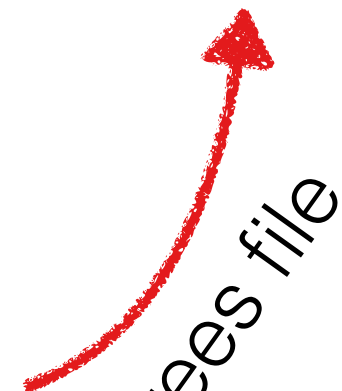
BEAST2



xml file

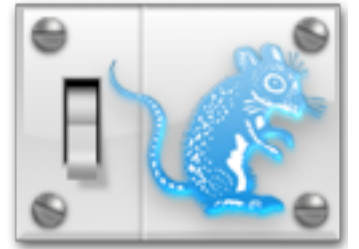


log file



trees file

BEAUti



GUI for setting up BEAST2 input file in xml format

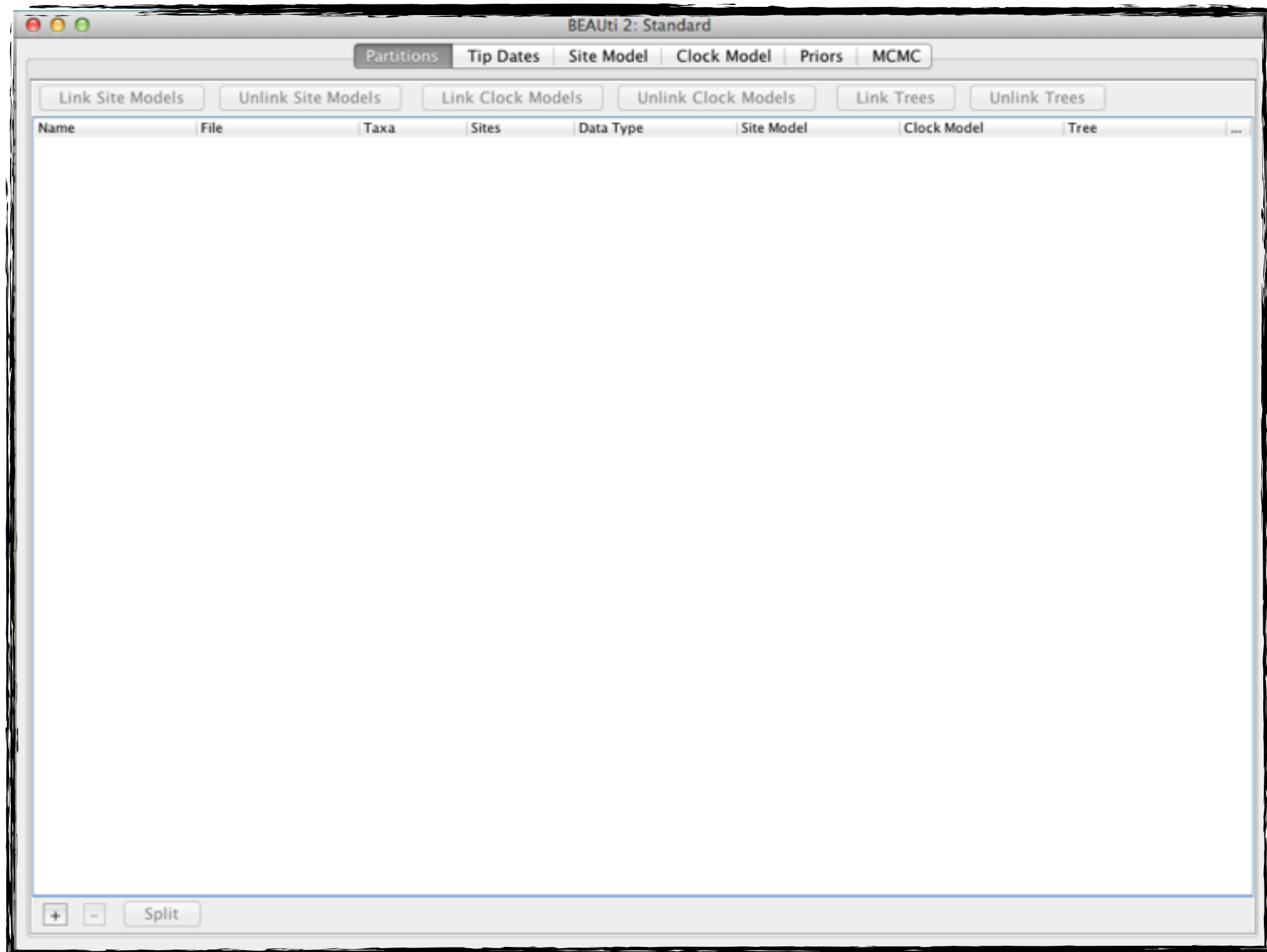
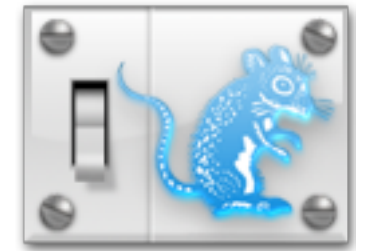
Input:

- Sequence alignment

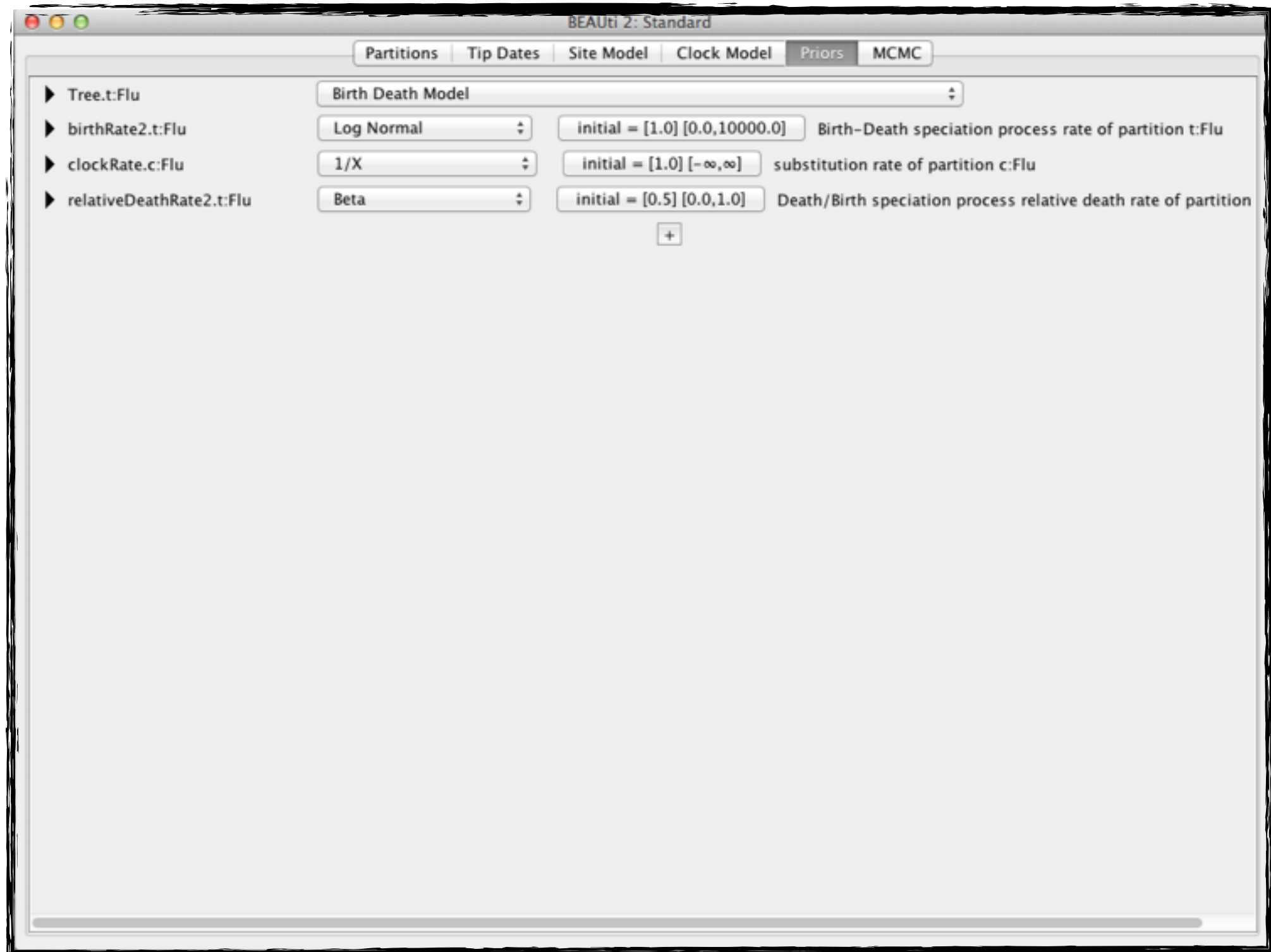
Output:

- xml file

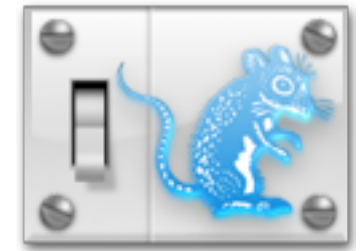
BEAUti



BEAUti



BEAUti



```
testHKY.xml
<beast version='2.0' namespace='beast.evolution.alignment:beast.core:beast.evolution.tree.coalescent:beast.core.ut...
1 <!-- The sequence alignment -->
2 <!-- ntax=6 nchar=768 -->
3 <!-- npatterns=69 -->
4 <data id="alignment" dataType="nucleotide">
5   <sequence taxon="human">
6     AGAAATATGTCTGATAAAAGAGTTACTTTGATAGAGTAAATAATAGGAGCTTAAACCCCTTATTTCTACTAGGACTATGAGAATCGAACCCAT
7     CCCTGAGAATCCAAAATTCTCCGTGCCACCTATCACACCCCATCCTAAGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTT
8     GGTTATACCCCTTCCCGTACTAAGAAATTTAGGTTAAATACAGACCAAGAGCCTTCAAAGCCCTCAGTAAGTTG-
9     CAATACTTAATTTCTGTAAGGACTGCAAAACCCCACTCTGCATCAACTGAACGCAAAATCAGCCACTTTAATTAAGCTAAGCCCTTCTAGACCAA
10    TGGGACTTAAACCCACAAACACTTAGTTAACAGCTAAGCACCTAATCAAC-TGGCTTCAATCTAAAGCCCCGGCAGG-
11    TTTGAAGCTGCTTCTTGAATTTGCAATTCAATATGAAAA-
12    TCACCTCGGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
13    CTCAGCCATTTTACCACAAAAAAGGAAGGAATCGAACCCCAAGCTGGTTTCAAGCCAACCCCATGGCCTCCATGACTTTTTTCAAAGGTAT
14    TAGAAAAACCATTTTATAAATTTGTCAAAGTTAAATTATAGGCT-AAATCCTATATATCTTA-
15    CACTGTAAAGCTAACTTAGCATTAACTTTTAAAGTTAAAGATTAAGAGAACCAACACCTCTTTACAGTGA
16  </sequence>
17  <sequence taxon="chimp">
18    AGAAATATGTCTGATAAAAGAATTACTTTGATAGAGTAAATAATAGGAGTTCAAATCCCCTTATTTCTACTAGGACTATAAGAATCGAACTCAT
19    CCCTGAGAATCCAAAATTCTCCGTGCCACCTATCACACCCCATCCTAAGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTT
20    GGTTACACCCCTTCCCGTACTAAGAAATTTAGGTTAAGCACAGACCAAGAGCCTTCAAAGCCCTCAGCAAGTTA-
21    CAATACTTAATTTCTGTAAGGACTGCAAAACCCCACTCTGCATCAACTGAACGCAAAATCAGCCACTTTAATTAAGCTAAGCCCTTCTAGATTAA
22    TGGGACTTAAACCCACAAACATTTAGTTAACAGCTAAACACCTAATCAAC-TGGCTTCAATCTAAAGCCCCGGCAGG-
23    TTTGAAGCTGCTTCTTGAATTTGCAATTCAATATGAAAA-
24    TCACCTCAGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
25    CTCAGCCATTTTACCACAAAAAAGGAAGGAATCGAACCCCTAAAGCTGGTTTCAAGCCAACCCCATGACCTCCATGACTTTTTTCAAAGATAT
26    TAGAAAACTATTTTATAAATTTGTCAAAGTTAAATTACAGGTT-AACCCCGTATATCTTA-
27    CACTGTAAAGCTAACCTAGCATTAACTTTTAAAGTTAAAGATTAAGAGGACCGACACCTCTTTACAGTGA
28  </sequence>
29  <sequence taxon="bonobo">
30    AGAAATATGTCTGATAAAAGAATTACTTTGATAGAGTAAATAATAGGAGTTTAAATCCCCTTATTTCTACTAGGACTATGAGAGTCGAACCCAT
31    CCCTGAGAATCCAAAATTCTCCGTGCCACCTATCACACCCCATCCTAAGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTT
32    GGTTATACCCCTTCCCGTACTAAGAAATTTAGGTTAAACACAGACCAAGAGCCTTCAAAGCTCTCAGTAAGTTA-
33    CAATACTTAATTTCTGTAAGGACTGCAAAACCCCACTCTGCATCAACTGAACGCAAAATCAGCCACTTTAATTAAGCTAAGCCCTTCTAGATTAA
34    TGGGACTTAAACCCACAAACATTTAGTTAACAGCTAAACACCTAATCAGC-TGGCTTCAATCTAAAGCCCCGGCAGG-
35    TTTGAAGCTGCTTCTTGAATTTGCAATTCAATATGAAAA-
36    TCACCTCAGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
```

BEAST2 (<http://beast2.org>)



- **B**ayesian **e**volutionary **a**nalysis by **s**ampling **t**rees
- Performs MCMC analyses of sequences under selected sequence evolution and tree (epidemiological/speciation) model
- Initially planned to be an extension to BEAST1
→ now two separate software packages
- BEAST2 has most of the functionality of BEAST1
- BEAST2 has a modular design that makes it easy to extend

Input:

- xml file

Outputs:

- log file
- trees file
- state file

BEAST2 (<http://beast2.org>)



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- Pe
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m

- In



- BE

- BE

COALESCENT TREE PRIORS

Constant size	drum-mond2002	drum-mond2002	king-man1982		
Exponential growth	drum-mond2002	drum-mond2002	kuhner1998		
Bayesian skyline	drum-mond2005	drum-mond2005	drum-mond2005		
Extended Bayesian skyline	heled2008	heled2008	heled2008		
Bayesian skygrid	x	gill2013	gill2013		
Deterministic closed SIR	in preparation	dearlove2013	volz2012		

BIRTH-DEATH TREE PRIORS

Yule			yule1924		
Yule with one calibration	heled2012		heled2012		
Birth-death			gern-hard2008		
Calibrated birth-death	heled2013	x	heled2013		
Birth-death with incomplete sampling		x	stadler2009		

BEAST2 (<http://beast2.org>)



- **Bayesian evolution**

- Performs MCMC sequence evolution model

- Initially planned for one processor → now two

- BEAST2 has

- BEAST2 has

Input:

- xml file



selected
(specification)

to extend

Tracer



- Analyse log files from BEAST2 runs
- Check mixing, ESS, ACT, parameter correlations
- Overview of posterior parameter estimates
- Comparisons of several analyses

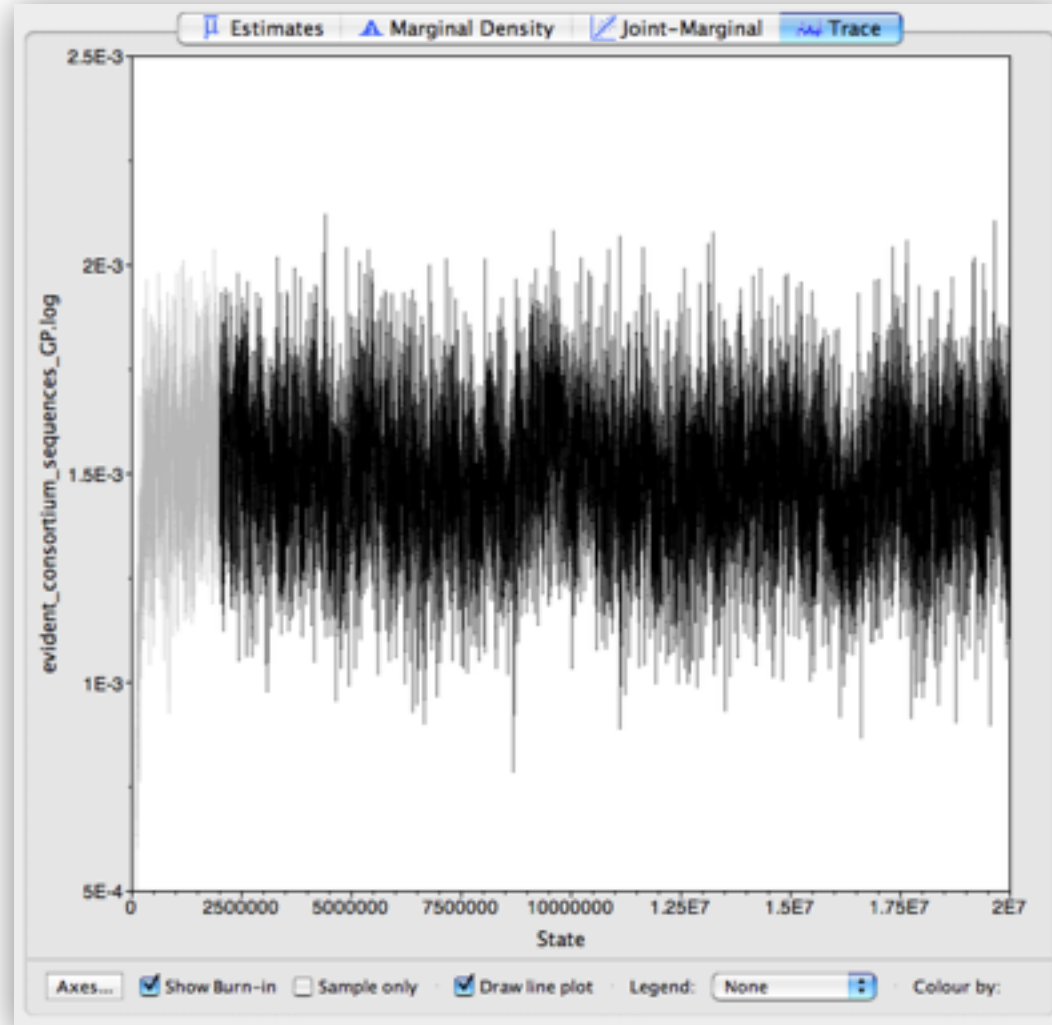
Input:

- log file

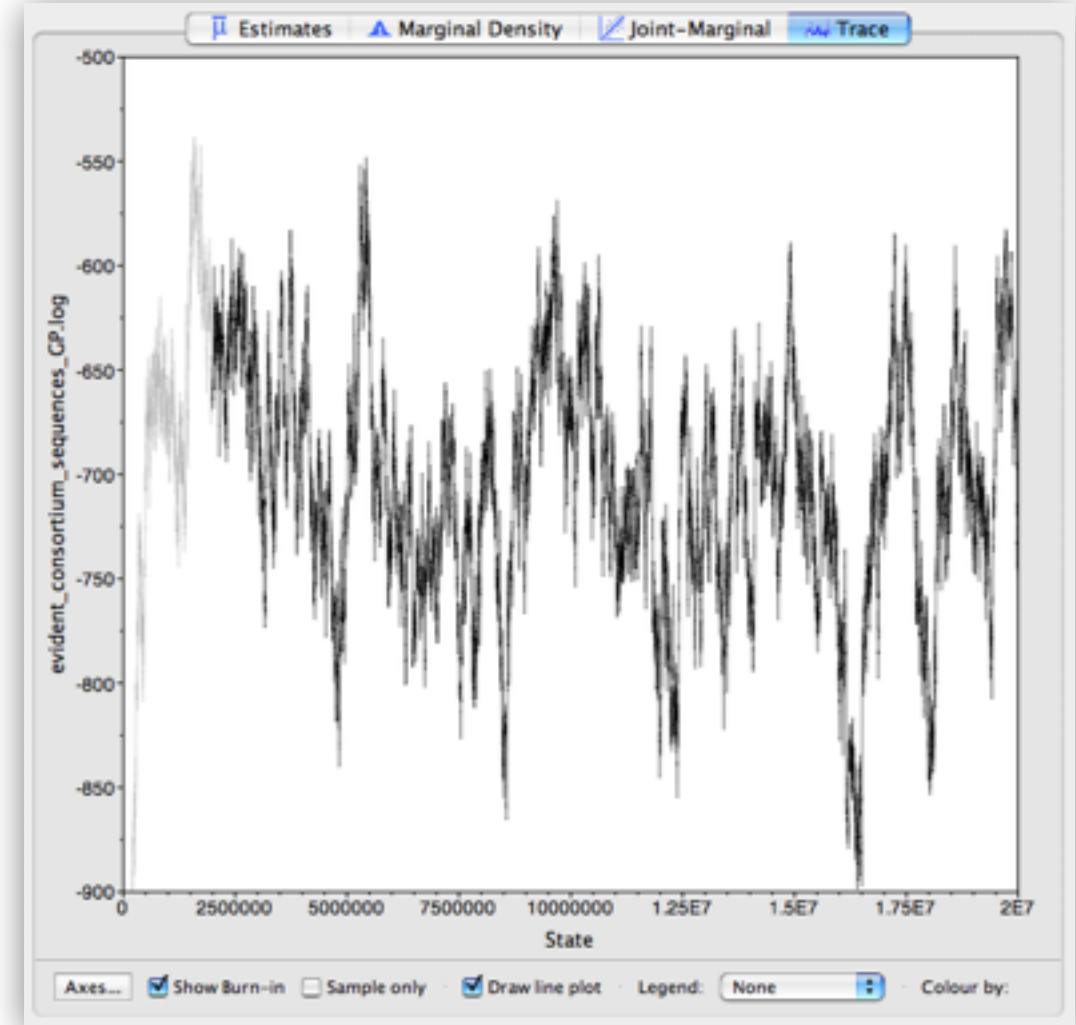
Output:

- Gain insight

Tracer



Mixing well! 😊



Not mixing! 😭

TreeAnnotator



- Analyze trees file from BEAST2 runs
- Produces MCC tree with node annotations (posterior probability)
- Note that the MCC tree may never actually appear in the trees file

Input:

- trees file

Output:

- MCC tree

TreeAnnotator



- A
- P
- N

TreeAnnotator v2.3.0

Burnin percentage:

Posterior probability limit:

Target tree type:

Node heights:

Target Tree File:

Input Tree File:

Output File:

n



```

;
tree
End;

```

FigTree/IcyTree/DensiTree

- Analyze trees file from BEAST2 runs
- Visual analysis only

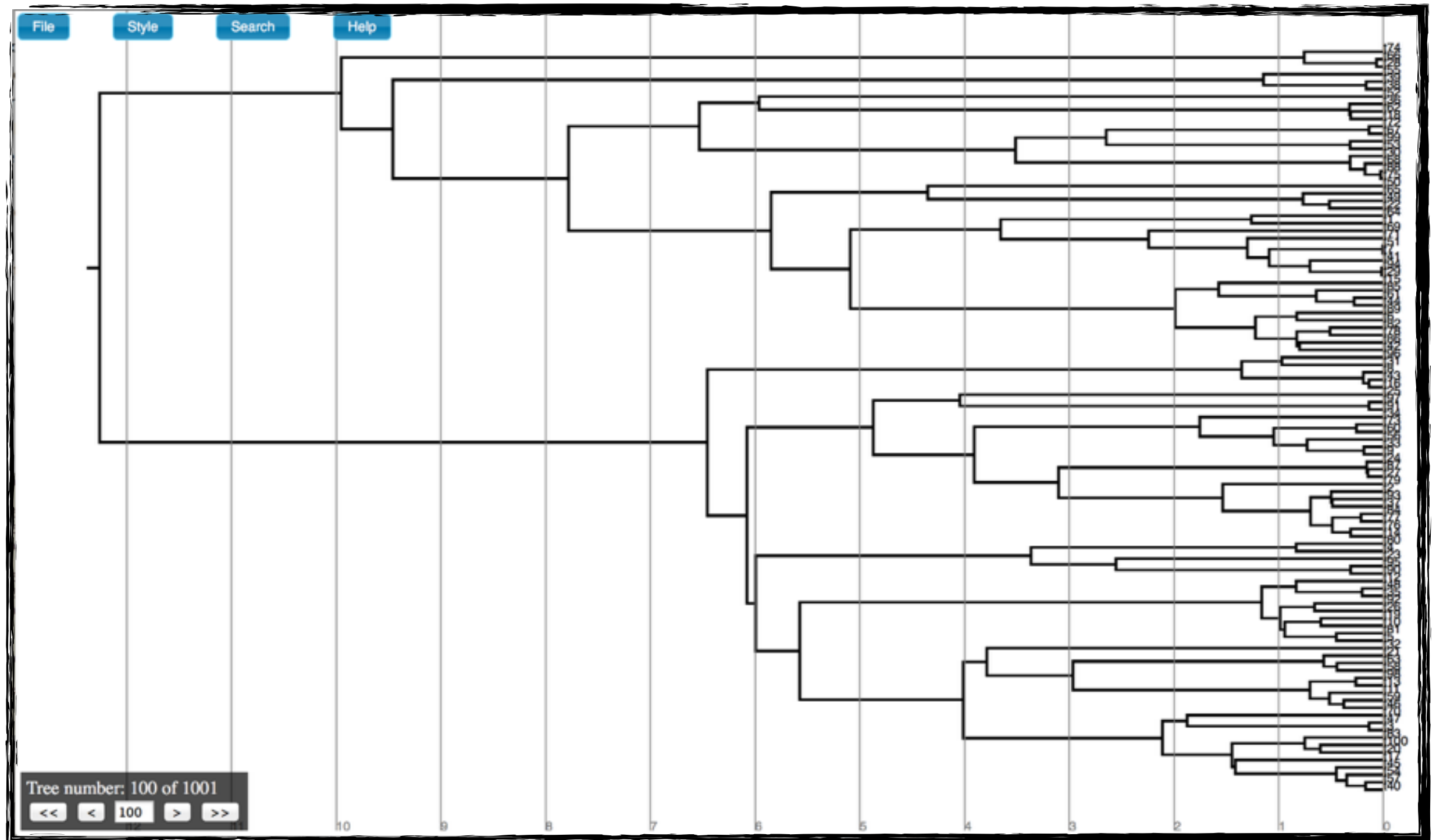
Input:

- trees file

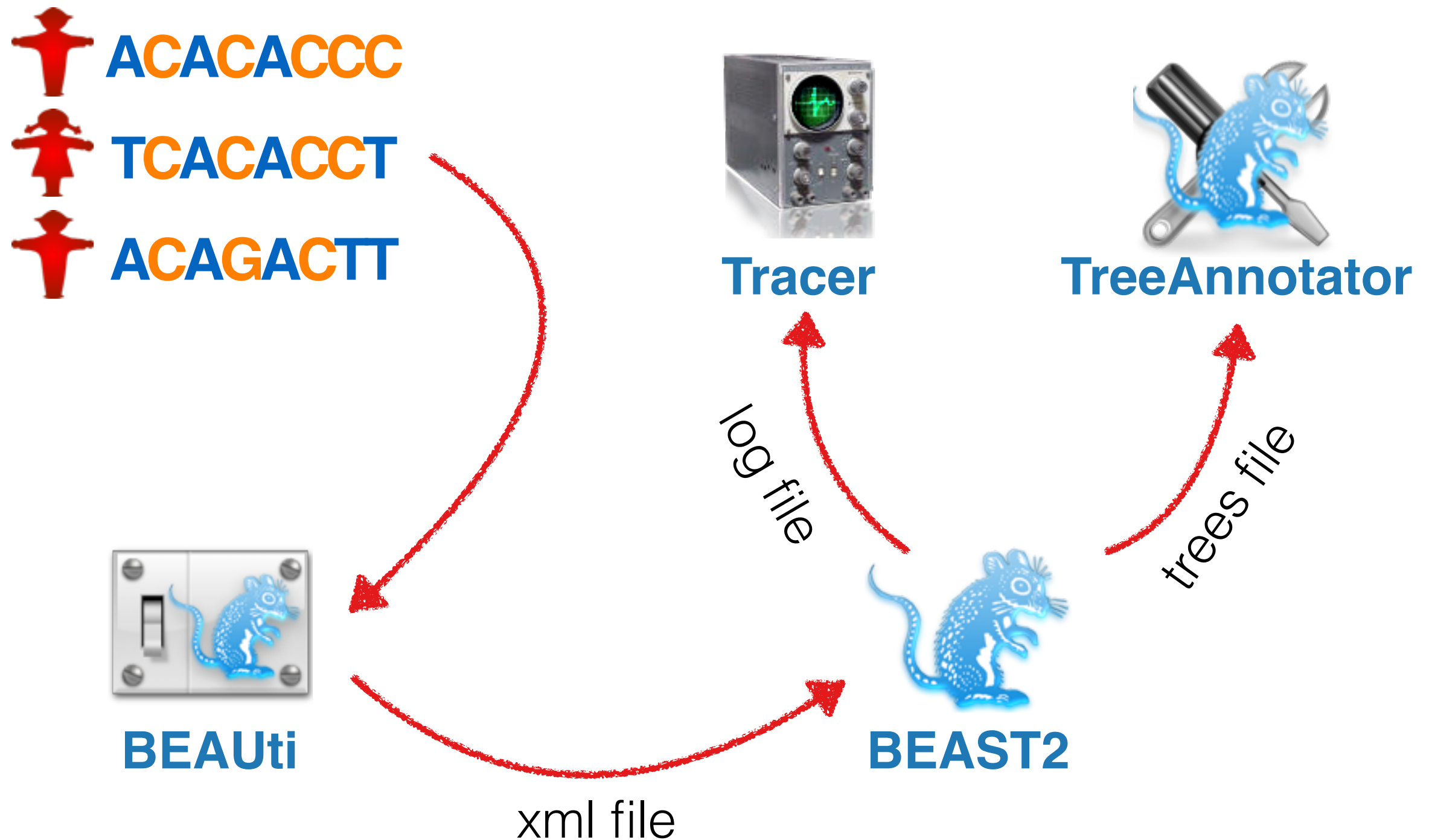
Output:

- Gain insight

FigTree/IcyTree/DensiTree



Workflow revisited



Tweaking xml files

- If runs are not mixing properly
 - adjust sampling frequency
 - adjust run length
 - ...
- If we want to fix an input tree and only sample parameters of tree and evolutionary model
- If ... it is easier to do by hand than in Beauti ...

Installing a new add-on for BEAST2

Very straightforward in BEAST2 GUI

USING Beauti: File > Manage Packages

