

Section 4: BEAST2 Howto









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)

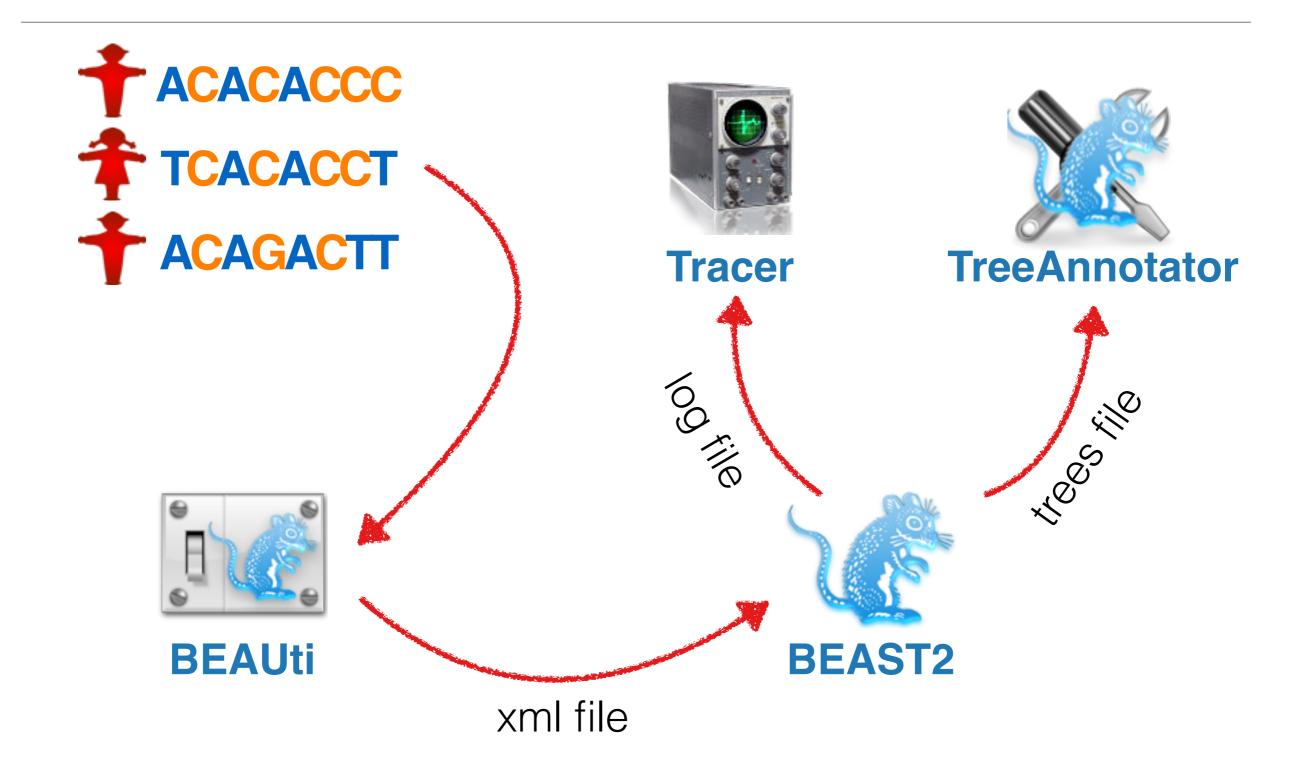
Tree Annotator

Analysis of BEAST2 output files (.trees)

FigTree/lcyTree/DensiTree

Visualisation of trees (.trees)

Workflow





GUI for setting up BEAST2 input file in xml format

Input:

 Sequence alignment

Output:

• xml file











```
testHKY.xml
  Seast version='2.0' namespace='beast.evolution.alignment:beast.core:beast.evolution.tree.coalescent:beast.core.ut...
   <beast version='2.0'</pre>
        namespace='beast.evolution.alignment:beast.core:beast.evolution.tree.coalescent:beast.core.util:
           beast.evolution.nuc:beast.evolution.operators:beast.evolution.sitemodel:
           beast.evolution.substitutionmodel:beast.evolution.likelihood'>
      <!-- The sequence alignment
      <!-- ntax=6 nchar=768
      <!-- npatterns=69
      <data id="alignment" dataType="nucleotide">
         <sequence taxon="human">
               AGAAATATGTCTGATAAAAGAGTTACTTTGATAGAGTAAATAATAGGAGCTTAAACCCCCTTATTTCTACTAGGACTATGAGAATCGAACCCAT
               GGTTATACCCTTCCCGTACTAAGAAATTTAGGTTAAATACAGACCAAGAGCCTTCAAAGCCCTCAGTAAGTTG-
               TGGGACTTAAACCCACAAACACTTAGTTAACAGCTAAGCACCCTAATCAAC-TGGCTTCAATCTAAAGCCCCGGCAGG-
               TTTGAAGCTGCTTCTTCGAATTTGCAATTCAATATGAAAA-
               TCACCTCGGAGCTTGGTAAAAAGAGGCCTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
               CTCAGCCATTTTACCACAAAAAAGGAAGGAATCGAACCCCCCAAAGCTGGTTTCAAGCCAACCCCATGGCCTCCATGACTTTTTCAAAAGGTAT
               TAGAAAAACCATTTCATAACTTTGTCAAAGTTAAATTATAGGCT-AAATCCTATATATCTTA-
               CACTGTAAAGCTAACTTAGCATTAACCTTTTAAGTTAAAGATTAAGAGAACCAACACCTCTTTACAGTGA
         </sequence>
12
         <sequence taxon="chimp">
               AGAAATATGTCTGATAAAAGAATTACTTTGATAGAGTAAATAATAGGAGTTCAAATCCCCTTATTTCTACTAGGACTATAAGAATCGAACTCAT
               GGTTACACCCTTCCCGTACTAAGAAATTTAGGTTAAGCACAGACCAAGAGCCTTCAAAGCCCTCAGCAAGTTA-
               TGGGACTTAAACCCACAAACATTTAGTTAACAGCTAAACACCCTAATCAAC-TGGCTTCAATCTAAAGCCCCGGCAGG-
               TTTGAAGCTGCTTCTTCGAATTTGCAATTCAATATGAAAA-
               TCACCTCAGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
               CTCAGCCATTTTACCACAAAAAAGGAAGGAATCGAACCCCCTAAAGCTGGTTTCAAGCCAACCCCATGACCTCCATGACTTTTTCAAAAGATAT
               TAGAAAAACTATTTCATAACTTTGTCAAAGTTAAATTACAGGTT-AACCCCCGTATATCTTA-
               CACTGTAAAGCTAACCTAGCATTAACCTTTTAAGTTAAAGATTAAGAGGACCGACACCTCTTTACAGTGA
         </sequence>
15
         <sequence taxon="bonobo">
               AGAAATATGTCTGATAAAAGAATTACTTTGATAGAGTAAATAATAGGAGTTTAAATCCCCTTATTTCTACTAGGACTATGAGAGTCGAACCCAT
               GGTTATACCCTTCCCGTACTAAGAAATTTAGGTTAAACACAGACCAAGAGCCTTCAAAGCTCTCAGTAAGTTA-
               TGGGACTTAAACCCACAAACATTTAGTTAACAGCTAAACACCCTAATCAGC-TGGCTTCAATCTAAAGCCCCGGCAGG-
               TTTGAAGCTGCTTCTTTGAATTTGCAATTCAATATGAAAA-
               TCACCTCAGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
```

BEAST2 (http://beast2.org)



- Bayesian evolutionary analysis by sampling trees
- 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)



	COALESCENT TREE PRIORS						
3 8	Constant size	drum- mond2002	drum- mond2002	king- man1982			
Pe	Exponential growth	drum- mond2002	drum- mond2002	kuhner1998			
se m	Bayesian skyline	drum- mond2005	drum- mond2005	drum- mond2005			
	Extended Bayesian skyline	heled2008	heled2008	heled2008			
n	Bayesian skygrid	x	gill2013	gill2013			
	Deterministic closed SIR	in prepara- tion	dearlove2013	volz2012			
3	BIRTH-DEATH TREE PRIORS						
	Yule			yule1924			
3	Yule with one calibration	heled2012		heled2012			
	Birth-death			gern- hard2008			
	Calibrated birth-death	heled2013	x	heled2013			
	Birth-death with incomplete sampling		x	stadler2009			

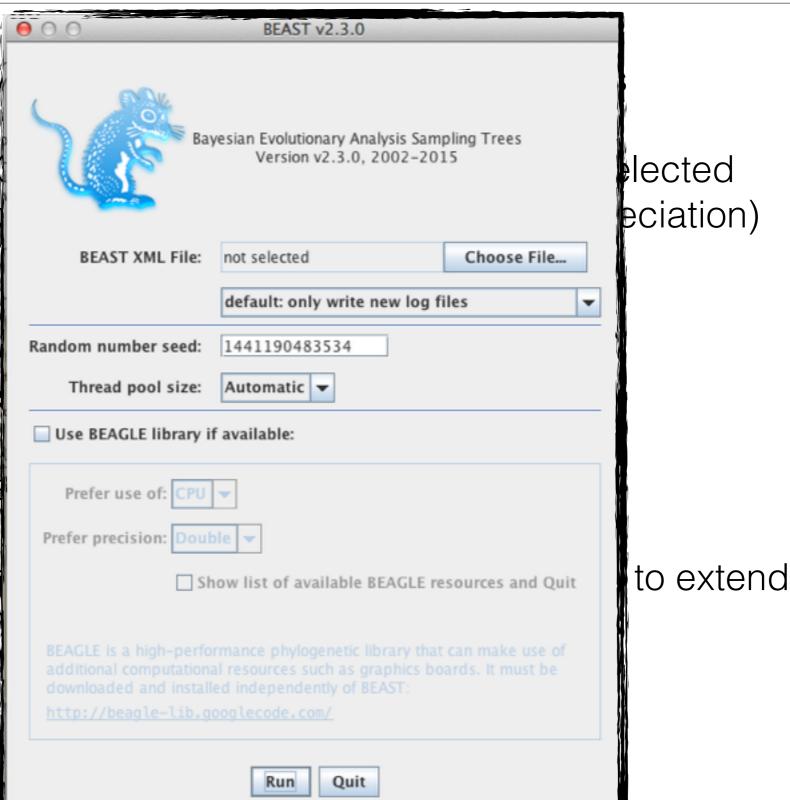
BEAST2 (http://beast2.org)



- Bayesian ev
- Performs Model
 model
- Initially plan
 → now two
- BEAST2 has
- BEAST2 has

Input:

xml



Tracer



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

Input:

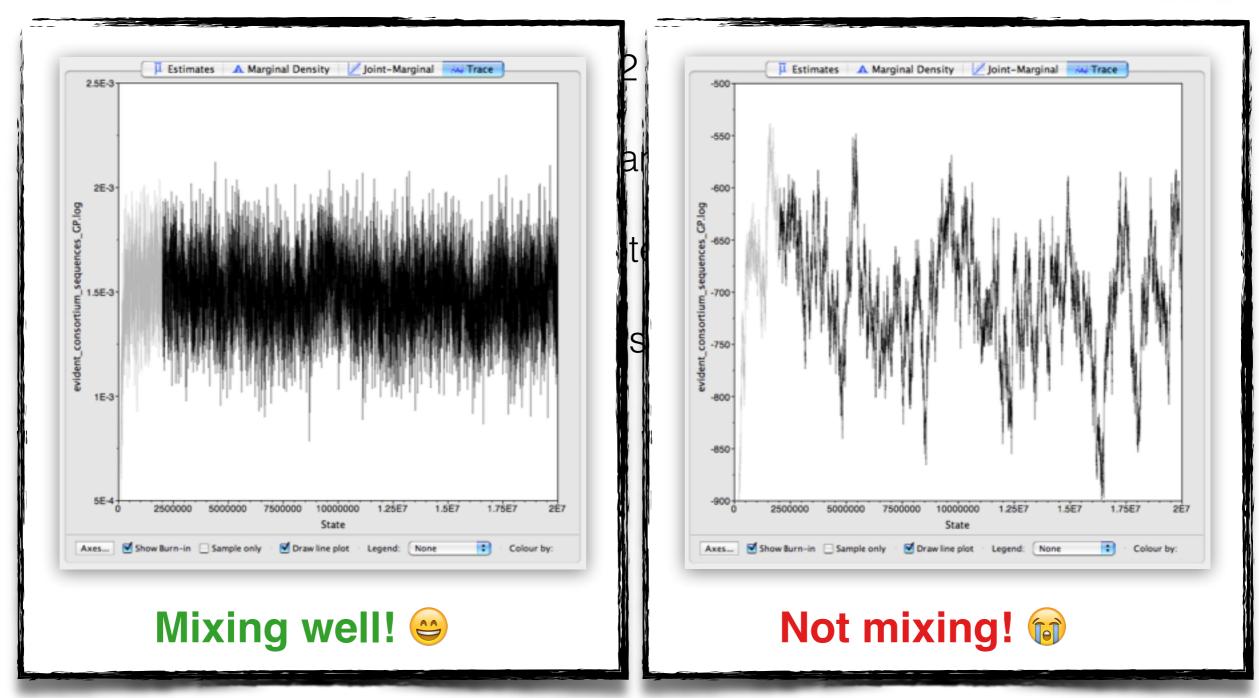
log file

Output:

Gain insight

Tracer





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





000	TreeAnnotator v2.3.0		
Burnin percentage:	Ō		
Posterior probability limit:	0.0		
Target tree type:	Maximum clade credibility tree \$		
Node heights:	Common Ancestor heights ‡		
Target Tree File:	not selected Choose File		
Input Tree File:	not selected Choose File		
Output File:	not selected Choose File		





```
284
          95 t95.
205
          97 t97,
286
207
          98 t98,
208
          99 t99,
289
          100 t100
210
211
    tree STATE_0 = (1:16.8300000000000000, (2:16.66, (3:16.4900000000000, (4:16.32, (5:16.15000)
    tree STATE_500 = (1:3.424288759134244,((2:2.8289726122912633,(((((3:1.8173871407955537,6:
212
213
    tree STATE_1000 = (((((1:3.450318951872839,11:3.450318951872839):0.14647283015070478,(8:
    214
    tree STATE_2000 = (((((((((1:0.06491254311659068,90:0.06491254311659068):0.8662921134487
215
    tree STATE_2500 = (((((((1:0.4880067781633301,(4:0.11338463693035995,(24:0.1019304106560
    tree STATE_3000 = ((((((((((((((1:0.1274035868530727,89:0.1274035868530727):0.5550781084639)
217
    tree STATE_3500 = (((((((((((1:0.3948510435842721,92:0.3948510435842721):0.07701664630721)
218
    tree STATE_4000 = (((((((((((((1:0.366816666467208,48:0.366816666467208):1.0150599347002545
219
    tree STATE_4500 = (((((((((((((1:2.1639601022519055,(((10:0.14341236948453426,(37:0.080278
    tree STATE 5000 = ((((((((1:0.39115026047794904,90:0.39115026047794904):1.32341934377836)
    tree STATE_5500 = (((((((((1:0.15980578031835888,47:0.15980578031835888):1.35168384003905
222
    tree STATE_6000 = (((((((((1:0.8738261503426664,100:0.8738261503426664):0.13411236740774)
223
224
    tree STATE_6500 = (((((1:0.1561475243628339,100:0.1561475243628339):3.491302266843568,((
    tree STATE_8000 = (((((((((1:0.5966593524257285,89:0.5966593524257285):0.134001372013521
228
    231
    Tree STATE 17500 = [[[[[[[[[[1]]]]]]]]1.0.08371053170104415 [45:0.060343615503408166.05:0.06034
                                                                    99 t99,
                                                                   100 t100
```

FigTree/IcyTree/DensiTree

- Analyze trees file from BEAST2 runs
- Visual analysis only

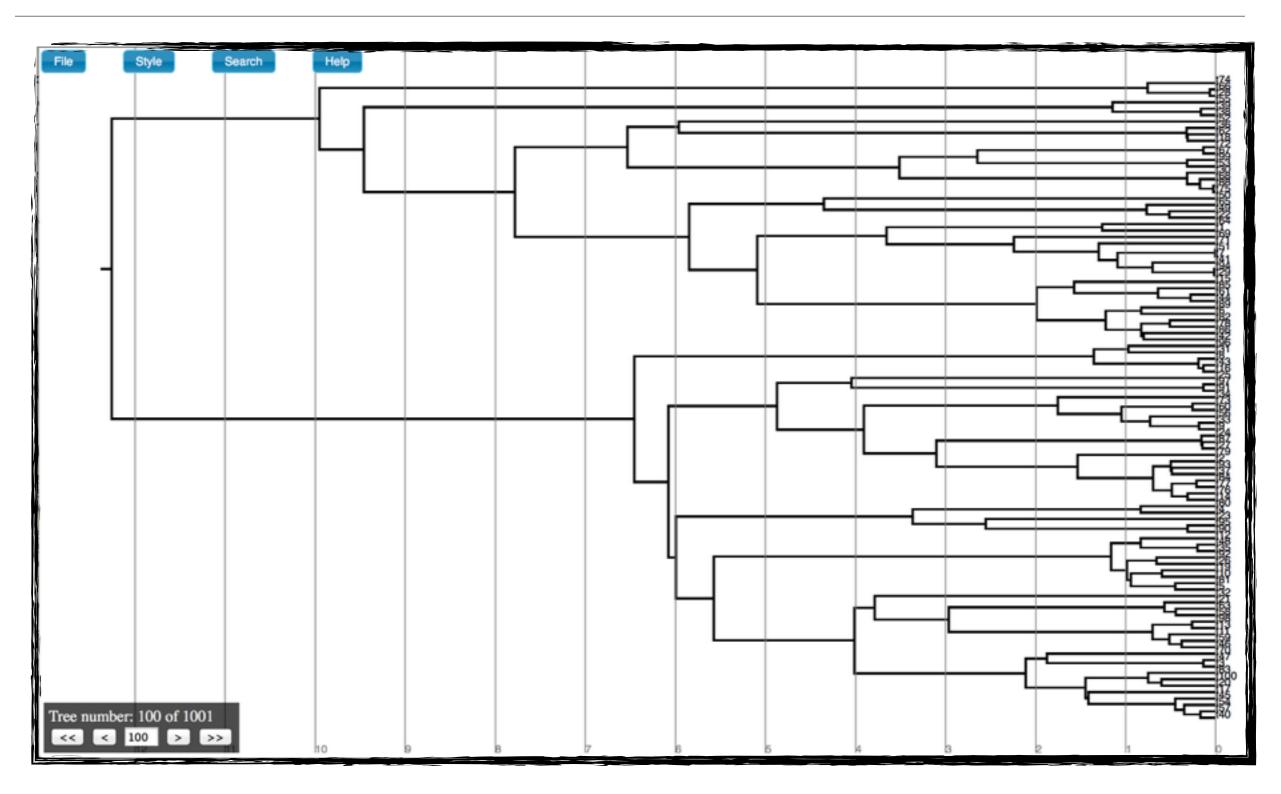
Input:

• trees file

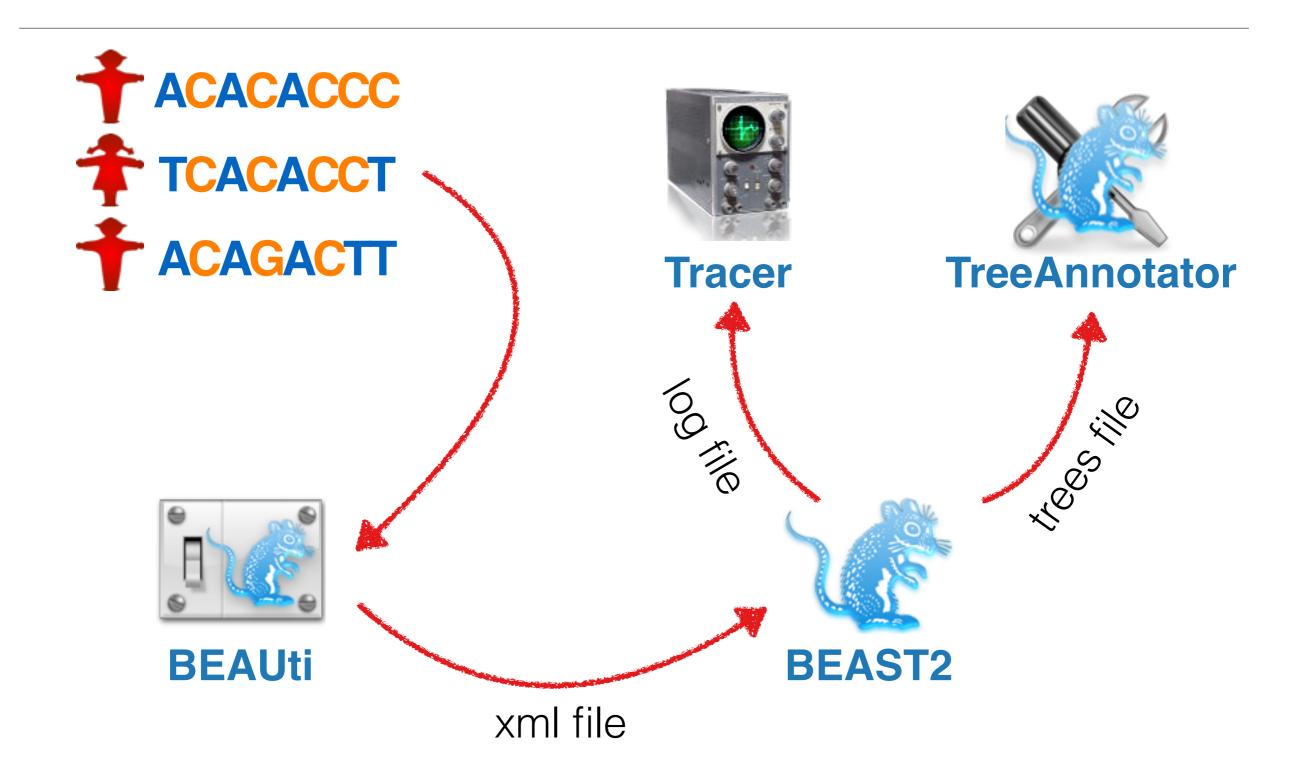
Output:

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

0.00		25467225								
0 0		BEAST 2 Packa	ge Manager							
List of available packages for BEAST v2.3.*										
Name	Status/Version	Latest	Dependencies	Detail						
bacter	un-installed	1.0.0-pre		ClonalOrigin ARG inference.						
BASTA	un-installed	2.0.1		Bayesian structured coalescent approx						
BDSKY	un-installed	1.2.2		birth death skyline - handles serially s						
BEAST_CLASSIC	un-installed	1.2.1	BEASTLabs	BEAST classes ported from BEAST 1 in						
BEASTLabs	un-installed	1.3.1		BEAST utilities, such as multi threaded						
BEASTShell	un-installed	1.1.1		BEAST Shell - BeanShell scripting for B						
bModelTest	un-installed	0.1.1		Bayesian model test for nucleotide sub						
CA	un-installed	1.1.0		CladeAge aPackage for fossil calibratio.						
DISSECT	un-installed	1.2.0		Species delimitation with *BEAST						
GEO_SPHERE	un-installed	0.0.9		Whole world phylogeography						
MASTER	un-installed	4.1.1		Stochastic population dynamics simulat.						
MGSM	un-installed	0.1.3		Multi-gamma and relaxed gamma site						
MODEL_SELECTION	un-installed	1.1.1		Select models through path sampling/						
morph-models	un-installed	1.0.3		Enables models of morphological chat						
MultiTypeTree	un-installed	5.3.0		Structured coalescent inference.						
phylodynamics	un-installed	1.1.2	BDSKY	birth death skyline model						
RBS	un-installed	1.2.4		Reversible-jump Based substitution m						
SA	un-installed	1.1.3		Sampled ancestor trees						
SNAPP	un-installed	1.2.2		SNP and AFLP Phylogenies						
STACEY	un-installed	1.0.4		Species delimitation and species tree						
SubstBMA	un-installed	1.2.0		Substitution Bayesian Model Averaging						
☑ install/uninstall a	II dependencies Ins	tall/Upgrade U	Ininstall Packa	ge repositories Close ?						