SNAPP

- Empirical mutation rates use "Calc mutation rates" button
- Pay attention to values in "prior" panel defaults are almost certainly wrong
- Start with small number of lineages, say 50, and see how SNAPP behaves scaling things up
 NB: In diploid data, each sequence counts as 2 lineages!
- Threads can help or hinder experiment to see how many for your data

How to do species delimitation?

Bayesian Factor Delimitation

- consider different species assignments in a multi species coalescent analysis
- use path sampling to calculate marginal likelihoods (MLs)
- determine Bayes factors from MLs
- BFD for *BEAST. BFD* for SNAPP

Fujita et al, Trends Eco & Evo, 2012, Leach et al, Sys Bio, 2014, model-selection, SNAPP



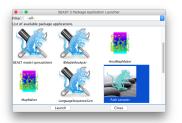
How to do species delimitation?

STACEY: Species Tree And Classification Estimation, Yarely

- joint estimate of species tree and species assignment
- ullet considers a species everything joined with branch lengths $<\epsilon$
- faster than *BEAST: integrates out population sizes + better MCMC operators (but keep an eye on StartBeast2)

Jones, Journal of Mathematical Biology, 2016, STACEY

Set up through XML or GUI





Creates subdirectory structure, one for each step containing all log files.

Set up through command line

- to list BEAST apps in Windows: \path\to\appstore -list
 OSX, Linux: /path/to/appstore -list
- To show PathSampler options: /path/to/appstore -PathSampler -help
- To set up PathSampler analysis: /path/to/appstore PathSampler -nrOfSteps 64 -rootdir dir/withs/steps -burnInPercentage 50 -model beast.xml

To set up on a HPC cluster

- Set up locally, using 'doNotRun' flag = true
- Move steps to cluster, and run steps in paralel there
- Estimate ML using PathSampleAnalyser available via BEAST appstore/BEAUti File/AppLauncher menu

/path/to/appstore PathSampleAnalyser -nrOfSteps 64 -rootdir dir/withs/steps -burnInPercentage 50

Hacking the XML:

```
<run spec="beast.inference.PathSampler"
    chainLength="1000" alpha="0.3"
    rootdir="/home/desktop/BFD*-tutorial/runA/"
    doNotRun="true" deleteOldLogs="true" nrOfSteps="24">

cd $(dir)
    java -cp $(java.class.path) beast.app.beastapp.BeastMain \
    $(resume/overwrite) -java -seed $(seed) beast.xml
<mcmc ...</pre>
```

Edit script for clusters, e.g. add load module java Run beast on XML with say 8 threads to create 8 run files for starting jobs