

## Automated Simultaneous Analysis Phylogenetics (ASAP)

### Quick-start tutorial for OS X users

This brief tutorial provides details for how to download, install, and use the ASAP software. The tutorial is done within the context of a customized set of FASTA formatted files, the most common data format used for ASAP analyses.

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***STEP 0: Install PAUP\* and MUSCLE, and make sure that they are accessible from your \$PATH.***

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ASAP requires that the command-line version of PAUP\* and MUSCLE are installed on your computer and are accessible from your path. You can verify this by typing ‘which PAUP’ or ‘which muscle’, the directory where PAUP and MUSCLE are installed should be returned. If this is not the case for either, contact your systems administrator for assistance.

```
Turing:ASAP sarkar$ which PAUP
/usr/local/bin/PAUP
```

```
Turing:ASAP sarkar$ which muscle
/usr/local/bin/muscle
```

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## *STEP 1: Download the ASAP installer for OS X*

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From the ASAP website (<http://www.ubio.org/ASAP>), download the latest ASAP installation package:

**Downloading and Installing ASAP**

Once you have met the system requirements listed above, installation is a two step process:

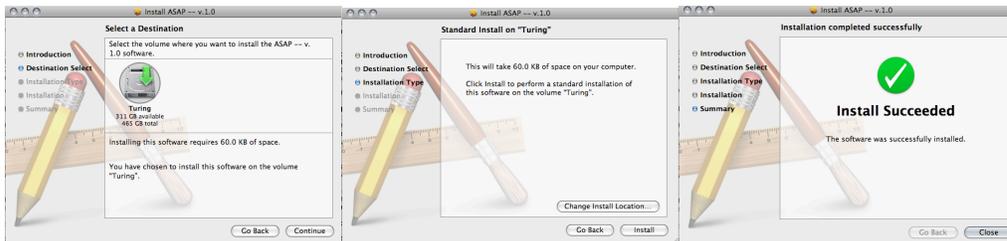
For OS X:

1. Download and uncompress the latest ASAP installation package ([ASAP OSX.pkg.zip](#))
2. Double-click the downloaded file.

For \*NIX:

1. Download and uncompress the latest ASAP .zip file ([ASAP.zip](#))
2. Move or copy the contents of the .zip file into /usr/bin.

This will download the package, which you then double-click (on OS X 10.4 and above, it should automatically start the install program):



After you click on the Install button above, ASAP will be installed on your machine.

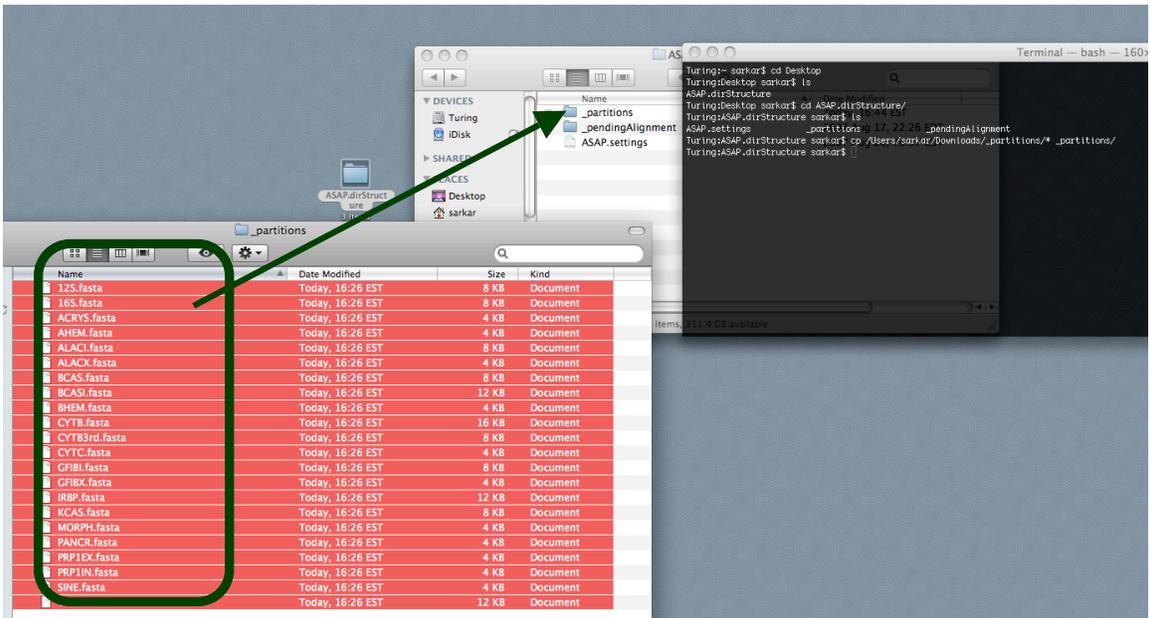
***ASAP is a COMMAND-LINE SCRIPT; YOU WILL NOT SEE AN 'APPLICATION' in your Applications Folder.***

You can verify installation by typing 'which ASAP' in the Terminal Application:

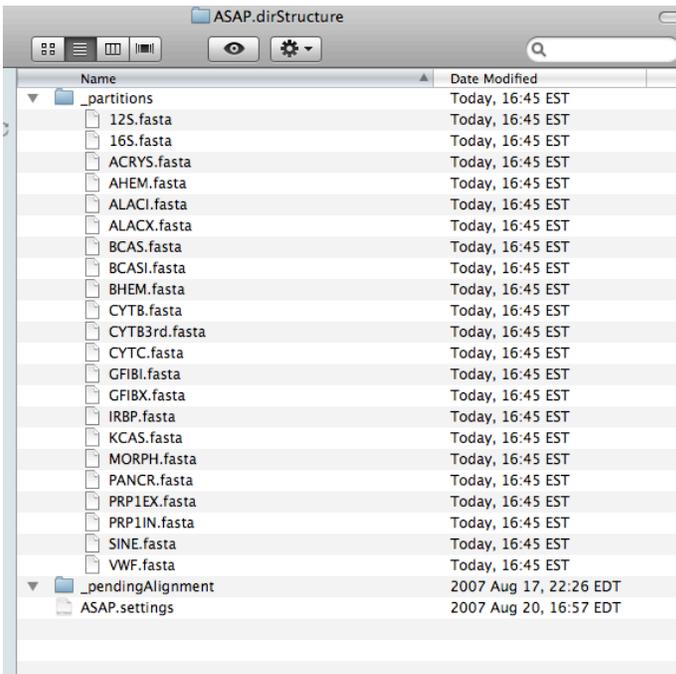
```
Terminal — bash — 80x24
Turing:~ sarkar$ which ASAP
/usr/bin/ASAP
Turing:~ sarkar$
```

The terminal application should return 'usr/bin/ASAP'





The `_partitions` folder in your `ASAP.dirStructure` should now contain all the files copied:



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### *STEP 3: Run ASAP*

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From a new Terminal window, go to your Desktop directory (using the `cd` command), then invoke the ASAP script giving it the directory to process:

```
Turing:~ sarkar$ cd
Turing:~ sarkar$ cd Desktop/
Turing:Desktop sarkar$ ASAP ASAP.dirStructure/
```

ASAP will then run. A number of new directories and files are generated as the script processes the data and runs the phylogenetic analyses through PAUP\*:

- **\_branchSupports.txt** - this file contains the tab-delimited results of the branch supports at each node.
- **\_NEXUS.nex** - this file is the multi-partitioned dataset assembled from the `_partition` directory.
- **currList** - this is an internal file name for ASAP to keep track of files that are in the `_pendingAlignment` or `_partition` directories. This prevents ASAP from repeating an already completed analysis. This can be overridden by entering "forceASAP" at the command line (e.g., `ASAP asapDirName forceASAP`).
- **getTrees.cmd** - this file is a PAUP command file that is used to generate all the individual partition trees as well as the simultaneous analysis tree.
- **supportTests** - this directory contains all the individual results from each of the performed tests
- **trees** - this directory contains the results of the individual partition and simultaneous analysis trees (three files exist for each tree search performed: AllTrees, Bootstrap, and Consensus).