With the Fasta and Newick files in hand…
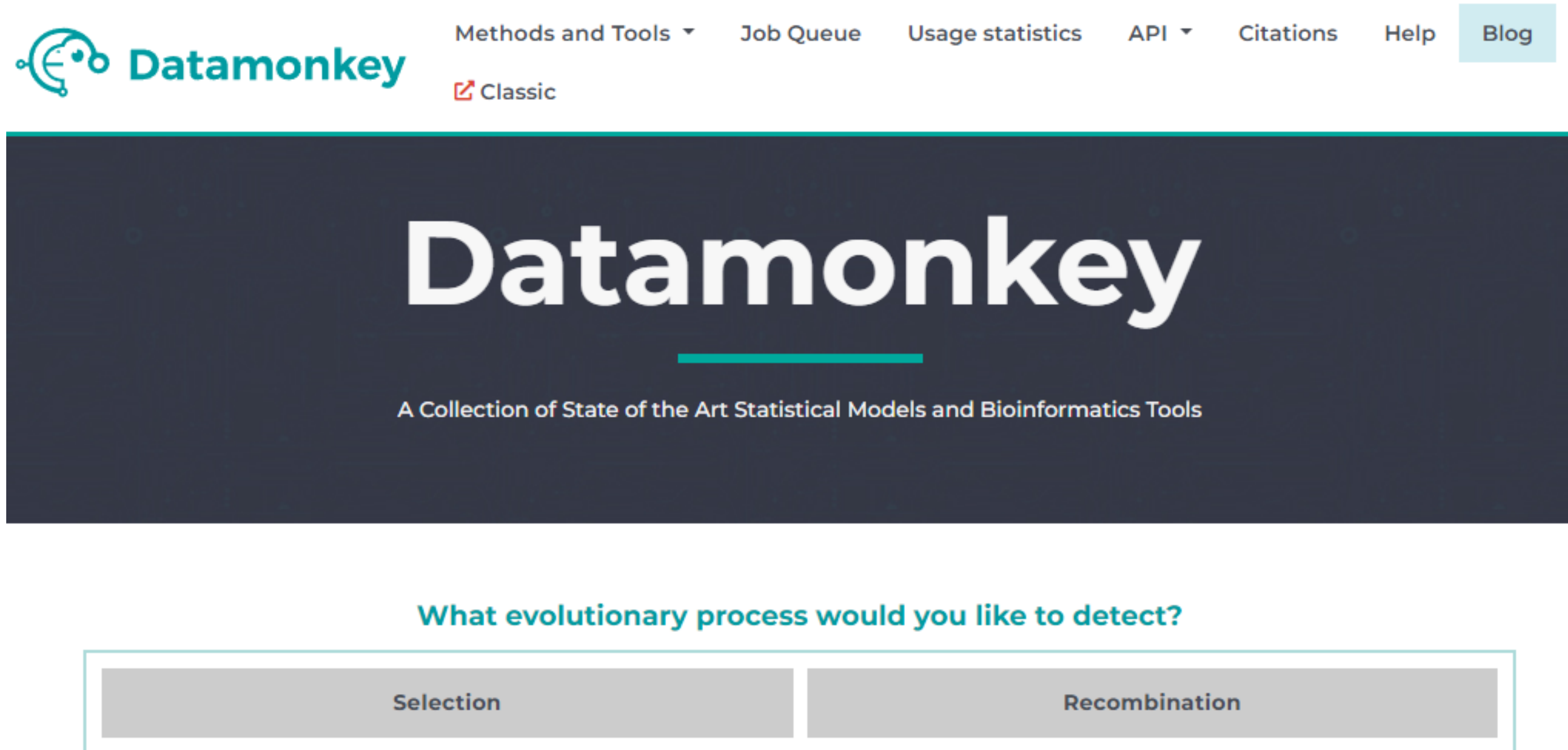
You now have two files:

A codon-based multiple sequence alignment

And a phylogenetic tree.

These can be used for all downstream selection analyses in HyPhy

Happy Hunting!

<u>datamonkey.org</u> will create a NJ-tree for your small dataset