

# With the Fasta and Newick files in hand...

**You now have two files:**

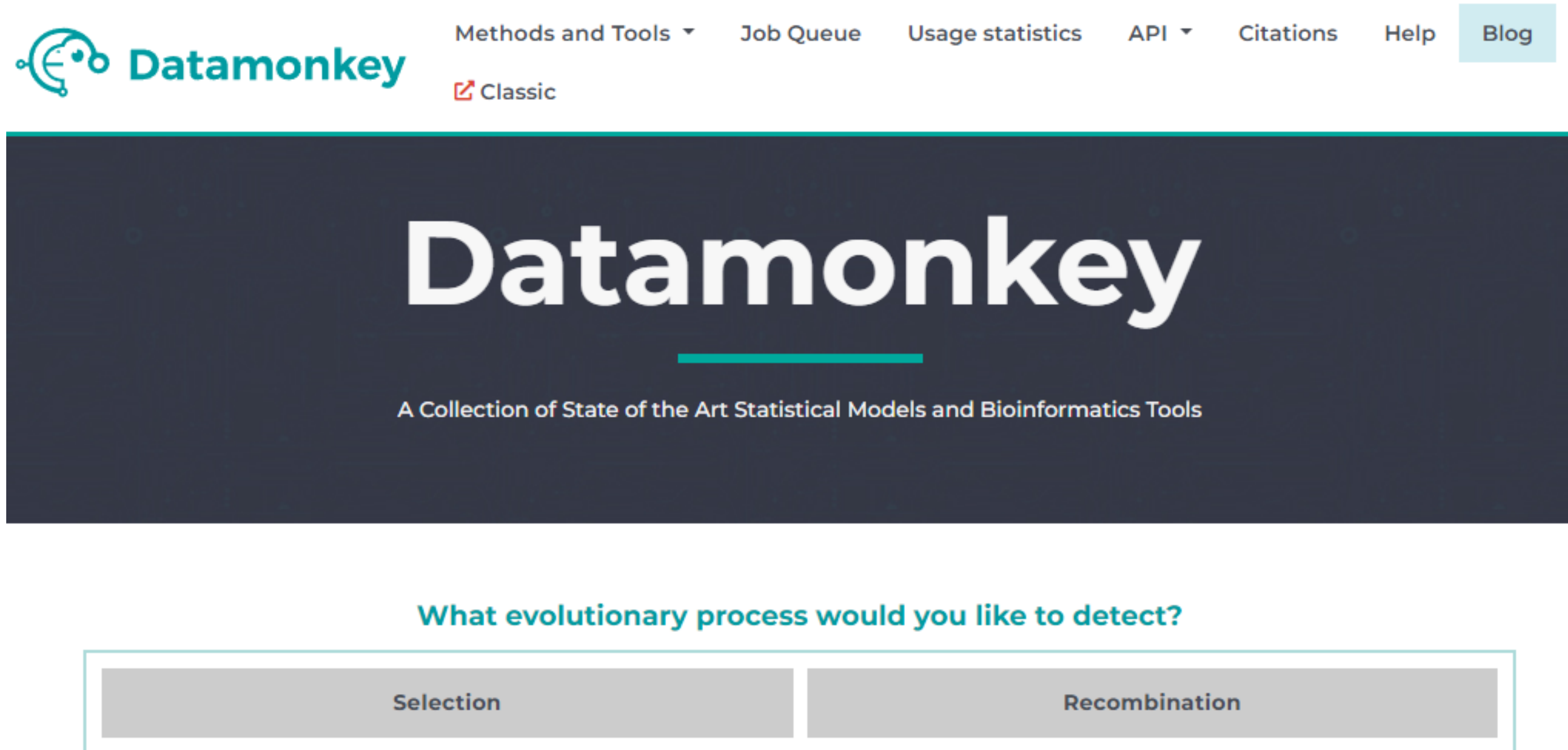
A codon-based multiple sequence alignment

And a phylogenetic tree.

These can be used for all downstream selection analyses in HyPhy

Happy Hunting!

datamonkey.org will create a NJ-tree for your small dataset



The screenshot shows the Datamonkey website. At the top, there is a navigation bar with the Datamonkey logo on the left and several links on the right: "Methods and Tools", "Job Queue", "Usage statistics", "API", "Citations", "Help", and "Blog". Below the navigation bar, there is a large dark blue banner with the word "Datamonkey" in large white letters. Underneath the banner, it says "A Collection of State of the Art Statistical Models and Bioinformatics Tools". Below this, there is a question "What evolutionary process would you like to detect?" followed by two buttons: "Selection" and "Recombination".

Datamonkey

Methods and Tools Job Queue Usage statistics API Citations Help Blog

Classic

**Datamonkey**

A Collection of State of the Art Statistical Models and Bioinformatics Tools

What evolutionary process would you like to detect?

Selection Recombination