Create an FNA file

HyPhy uses a custom data format (Fasta + Newick or FNA) to make things easier

Simply open your Fasta file and paste the Newick string right below

```
TTGAGCAGAATAAATCATTTTGAGAAGATTCTGATCATCCCCAAGAGTTCCTGGCCAAAT
CATGAAACATCACTAGGGGTGAGCGCAGCTTGTCCATACCAGGGAGCGCCCTCCTTTTTC
AGAAATGTGGTGTGGCTTATCAAAAAGAACGATGCATACCCAACAATAAAGATAAGCTAC
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TACGTGAAGTCAAACAAGTTGGTCCTTGCGACTGGGCTCAGAAATAGTCCTCTAAGAGAA
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GCGGACAAAGAATCCACCCAAAAGGCAATAGATGGAGTTACCAATAAGGTCAACTCAATC
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TTACAGTGCAGAATTTGCATTTAG
(OQ963804.1_|Calidris_alba|USA|NY|2022-02-21:0.048365, ((((OQ958820.1_||USA|NY|2022-04-
04:0.000000, OQ958812.1_||USA|NY|2022-04-
04:0.000000):0.000000, OQ958804.1_||USA|NY|2022-04-04:0.000000):0.010594, OQ961564.1_|Bubo_virginianus|USA|NY|2022-
04:0.010594):0.032642, (OQ961068.1_|Corvus_ossifragus|USA|NY|2022-04-04:0.029003, (OQ959564.1_|Haliaeetus_leucocephalus|USA|NY|2022-04-
21:0.030490, ((((OQ963300.1_|Phasianus_colchicus|USA|NY|2022-04-26:0.000000, OQ961548.1_|Bubo_virginianus|USA|NY|2022-04-
07:0.000000):0.000000, OQ961556.1_|Bubo_virginianus|USA|NY|2022-04-07:0.000000):0.015892, OQ962772.1_|Phasianinae|USA|NY|2022-03-
22:0.015892):0.012392, ((OQ958780.1_||USA|NY|2022-03-28:0.005297, OQ958772.1_||USA|NY|2022-03-28:0.005297):0.018590, (OQ965100.1_|
Bubo_scandiacus|USA|NY|2022-03-22:0.023278, ((OQ958764.1_||USA|NY|2022-02-22:0.000000, OQ958756.1_||USA|NY|2022-02-
22:0.000000):0.022835, (OQ963812.1_|Calidris_alba|USA|NY|2022-04-11:0.019082, ((OQ961228.1_|Ardea_herodias|USA|NY|2022-03-02:0.005814,
(OQ964204.1_|Anser_caerulescens|USA|NY|2022-03:0.005562, (((((((((OQ965188.1_|Cathartes_aura|USA|NY|2022-04-12:0.000000, OQ963252.1_|
Aythya_americana|USA|NY|2022-03:0.000000):0.000000, OQ960660.1_|Branta_canadensis|USA|NY|2022-03-21:0.000000):0.000000, OQ958788.1_||
USA|NY|2022-04-04:0.000000):0.000000, OQ958796.1_||USA|NY|2022-04-04:0.000000):0.000000, OQ959068.1_|Sibirionetta_formosa|USA|NY|2022-
03-23:0.000000):0.000000, OQ962516.1_||USA|NY|2022-03-21:0.000000):0.000000, OQ960876.1_|Accipiter_cooperii|USA|NY|2022-03-
31:0.000000):0.005297, OQ967076.1_|Aix_sponsa|USA|NY|2022-04-11:0.005297):0.000265):0.000252):0.007909, ((OQ965172.1_|
Cygnus_columbianus|USA|NY|2022-04-01:0.010594, OQ964212.1_|Anser_caerulescens|USA|NY|2022-03:0.010594):0.001980, (OQ962524.1_||USA|NY|
2022-04-05:0.012597, (OQ959548.1_|Haliaeetus_leucocephalus|USA|NY|2022-04-06:0.011306, (OQ963044.1_|Buteo_jamaicensis|USA|NY|2022-04-
06:0.005814, (OQ963036.1_|Buteo_jamaicensis|USA|NY|2022-03-29:0.005562, (OQ959556.1_|Haliaeetus_leucocephalus|USA|NY|2022-04-
12:0.005297, OQ959540.1_|Haliaeetus_leucocephalus|USA|NY|2022-03-30:0.005297):0.000265):0.000252):0.005492):0.001292):-
0.000023):0.001148):0.005359):0.003753):0.000443):0.000609):0.004396):0.002206):-0.001486):0.014233):0.005129);
```

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!