Species Catalog Arabidopsis thaliana Drosophila melanogaster Homo sapiens Genome -chr1 chrX Genetic maps HapMap II (1000 Genomes Project 2007) DECODE (Kong *et al.* 2010) Models Out of Africa [YRI, CEU, CHB] (Gutenkunst et al. 2009) ----- American admixture (Browning et al. 2011)

```
B) Python API
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```
example.py

1 import stdpopsim

2

3 species = stdpopsim.get_species("HomSap")

4 contig = species.get_contig(

5    "chr22", genetic_map="HapMapII_GRCh37")

6 model = species.get_model("OutOfAfrica_3G09")

7 samples = model.get_samples(10)

8 engine = stdpopsim.get_default_engine()

9 ts = engine.simulate(model, contig, samples)

10 print("simulated:", ts.num_trees, ts.num_sites)
```

(C) Command Line Interface

```
$ stdpopsim HomSap
--seed 12345
--chromosome chr22
--genetic-map HapmapII_GRCh37
--model OutOfAfrica_3G09
--output simulation.trees 10 10 10
```