A 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

```python
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_demographic_model(
7      "OutOfAfrica_3G09")
8  samples = model.get_samples(10)
9  engine = stdpopsim.get_engine("msprime")
10 ts = engine.simulate(model, contig, samples)
11 print("simulated:", ts.num_trees, ts.num_sites)
```

C Command Line Interface

```
$ stdpopsim
  --engine msprime
  HomSap
  --seed 12345
  --chromosome chr22
  --genetic-map HapMapII_GRCh37
  --demographic-model OutOfAfrica_3G09
  --output simulation.trees 10 10 10
```