A. Catalog

```
Heliconius melpomene
Homo sapiens

    Genome

        chr 1
   - Genetic Map

Hapmap II

         (1000 Genomes Project 2007)
      ..... DeCODE
         (Kong et al. 2010)
    -Demographic Model
        Out-of-Africa [YRI, CEU, CHB]
          (Gutenkunst et al. 2009)
         Ancient Eurasian 9 population model
         (Kamm et al. 2019)

    Annotations

         ensembl Havana exons
          (Hunt et al. 2018)
        ensembl Havana CDS
          (Hunt et al. 2018)

    Distribution of Fitness effects DFEs

         Deleterious Gamma DFE
         (Kim et al. 2017)
      Deleterious Log Normal DFE
         (Huber et al. 2017)
      Deleterious Gamma DFE plus lethals
          (Kyriazis et al. 2013)
```

B. Python API

```
example_with_selection.py
1 import stdpopsim
3 species = stdpopsim.get_species("HomSap")
4 contig = species.get_contig(
     "chr22".
     genetic map="HapMap GRCh37"
8 model = species.get_demographic_model(
     "OutOfAfrica 3G09"
10)
11 samples = {"YRI": 5, "CEU": 5, "CHB": 5}
12 # Adding DFE to exons
13 dfe = species.get dfe("Gamma K17")
14 exons = species.get_annotations("ensembl_havana_104_exons")
15 exon_intervals = exons.get_chromosome_annotations("chr22")
16 contig.add_dfe(intervals=exon_intervals, DFE=dfe)
17 engine = stdpopsim.get_engine("slim")
18 # Performing the simulation
19 ts = engine.simulate(
20
     model.
21
     contig,
22
     samples,
23
     seed=236.
     slim_scaling_factor=20,
24
     slim_burn_in=10,
25
26)
```

C. Command Line Interface

```
$ stdpopsim -e slim --slim-scaling-factor 20 HomSap \
-c chr22 \
--dfe Gamma_K17 \
--dfe-annotation ensembl_havana_104_CDS \
-o example.ts -d OutOfAfrica_3G09 YRI:5 CEU:5 CHB:5
```