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")
7 model = species.get_demographic_model(
     "OutOfAfrica 3G09")
9 samples = {"YRI": 5, "CEU": 5, "CHB": 5}
10 # adding selection to exons
11 dfe = species.get dfe("Gamma K17")
12 exons =
species.get_annotations("ensembl_havana_104_exons")
13 exon intervals =
exons.get chromosome annotations("chr22")
14 contig.add_dfe(intervals=exon_intervals, DFE=dfe)
15 engine = stdpopsim.get_engine("slim")
16 ts = engine.simulate(
     model,
18
    contig,
19
     samples.
20
     seed=236,
     slim scaling factor=20,
     slim burn in=10,
22
23)
```

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_2T12 AFR:1 EUR:2
```