## 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
   import stdpopsim
   species = stdpopsim.get_species("HomSap")
  contig = species.get_contig(
        "chr22".
        genetic_map="HapMap_GRCh37"
   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(
       model,
20
21
       contiq,
       samples,
22
23
       seed=236.
       slim scaling factor=1,
24
       slim_burn_in=10,
25
26
```

## C. Command Line Interface

```
$ stdpopsim -e slim --slim-scaling-factor 1 HomSap \
   -c chr22 \
   --dfe Gamma_K17 \
   --dfe-annotation ensembl_havana_104_exons \
   -o example.ts -d OutOfAfrica_3G09 YRI:5 CEU:5 CHB:5
```