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)
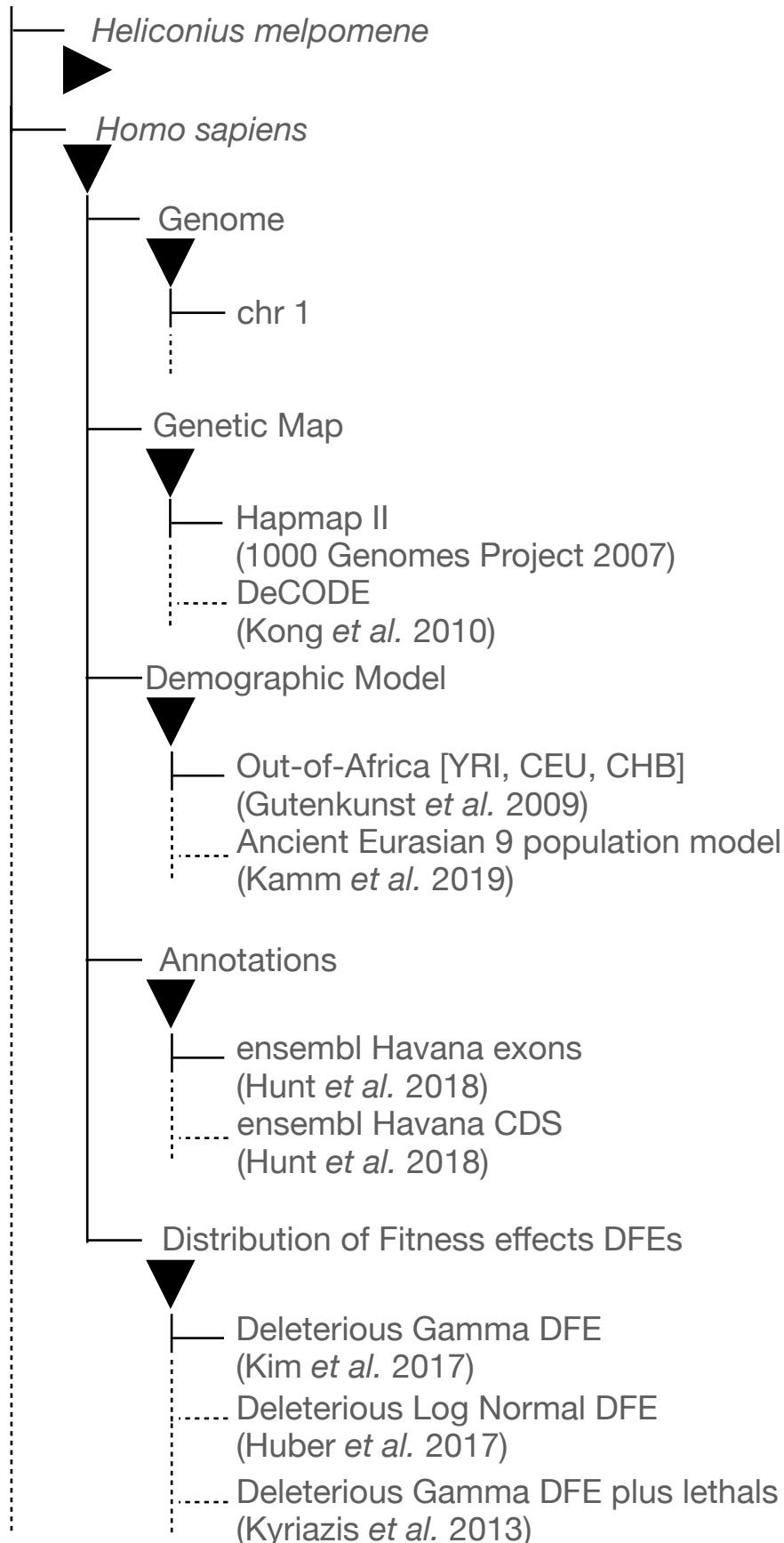   - Deleterious Gamma DFE plus lethals
      (Kyriazis *et al.* 2013)

B. Python API

```python
example_with_selection.py
1  import stdpopsim
2
3  species = stdpopsim.get_species("HomSap")
4  contig = species.get_contig(
5      "chr22",
6      genetic_map="HapMap_GRCh37")
7  model = species.get_demographic_model(
8      "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(
17     model,
18     contig,
19     samples,
20     seed=236,
21     slim_scaling_factor=20,
22     slim_burn_in=10,
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
```