A. Species 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)
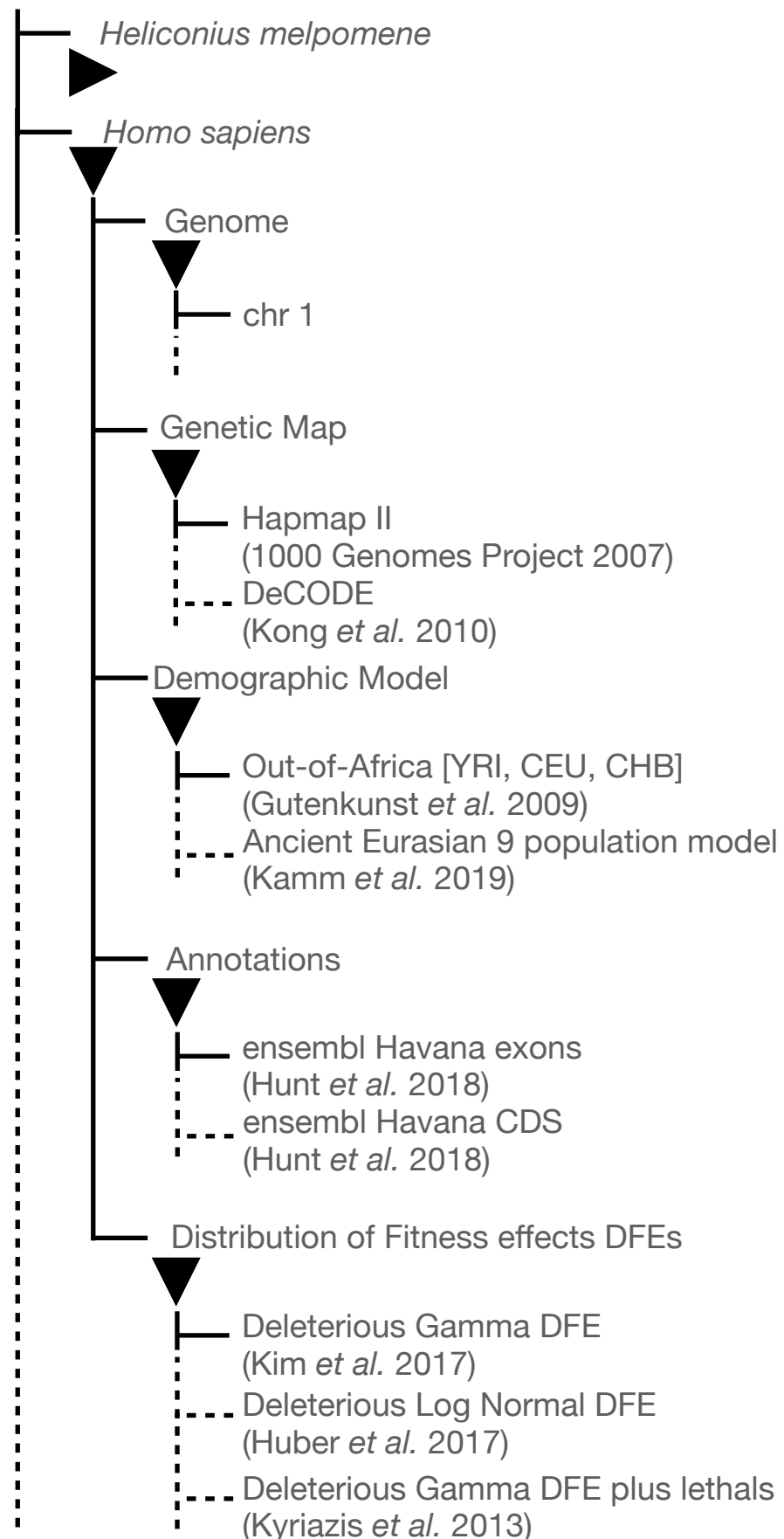
B. Python API

```python
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 # selection additions
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 foo.ts -d OutOfAfrica_2T12 AFR:1 EUR:2
```