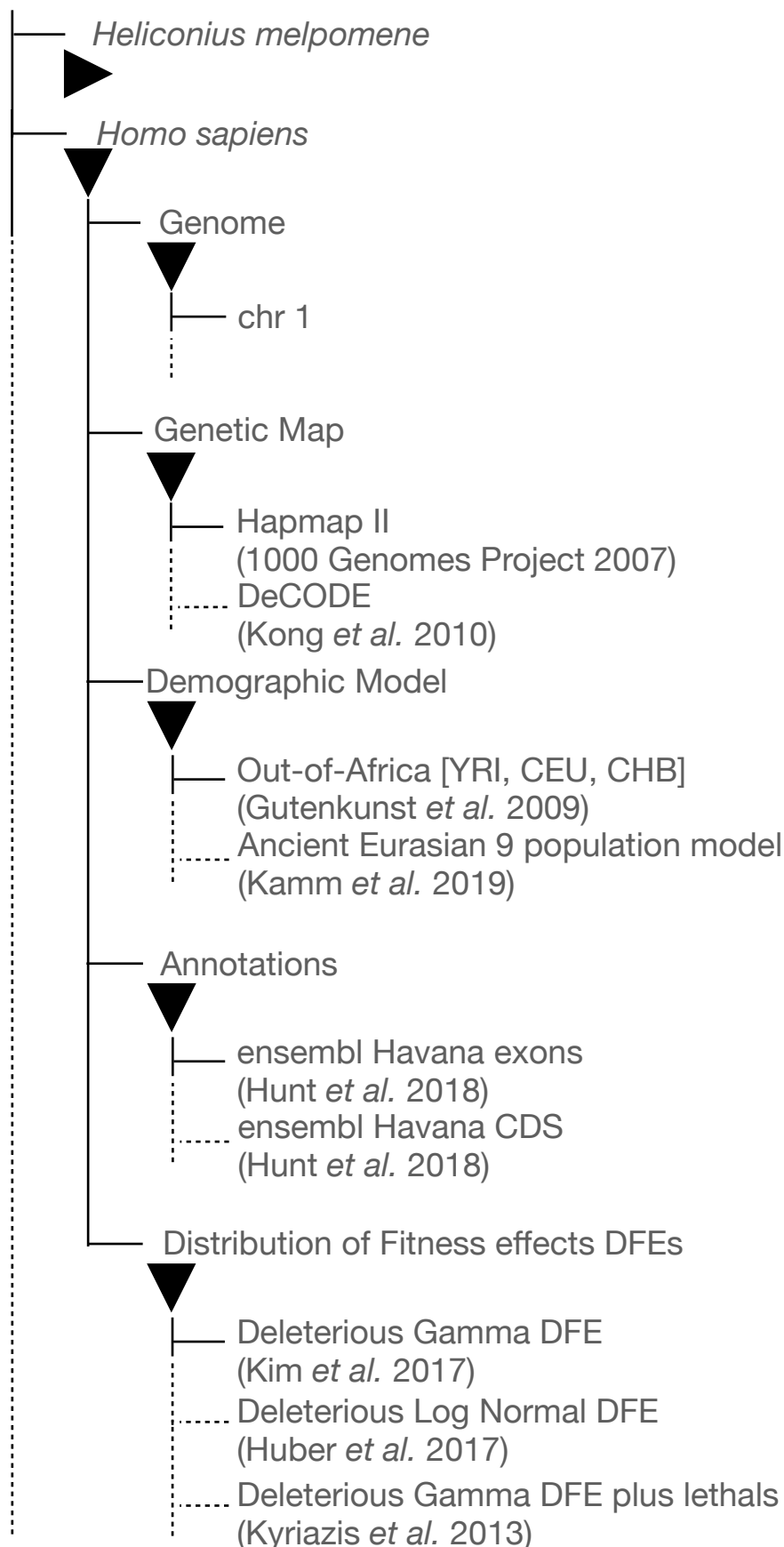


# A. Catalog



# B. Python API

```
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
```