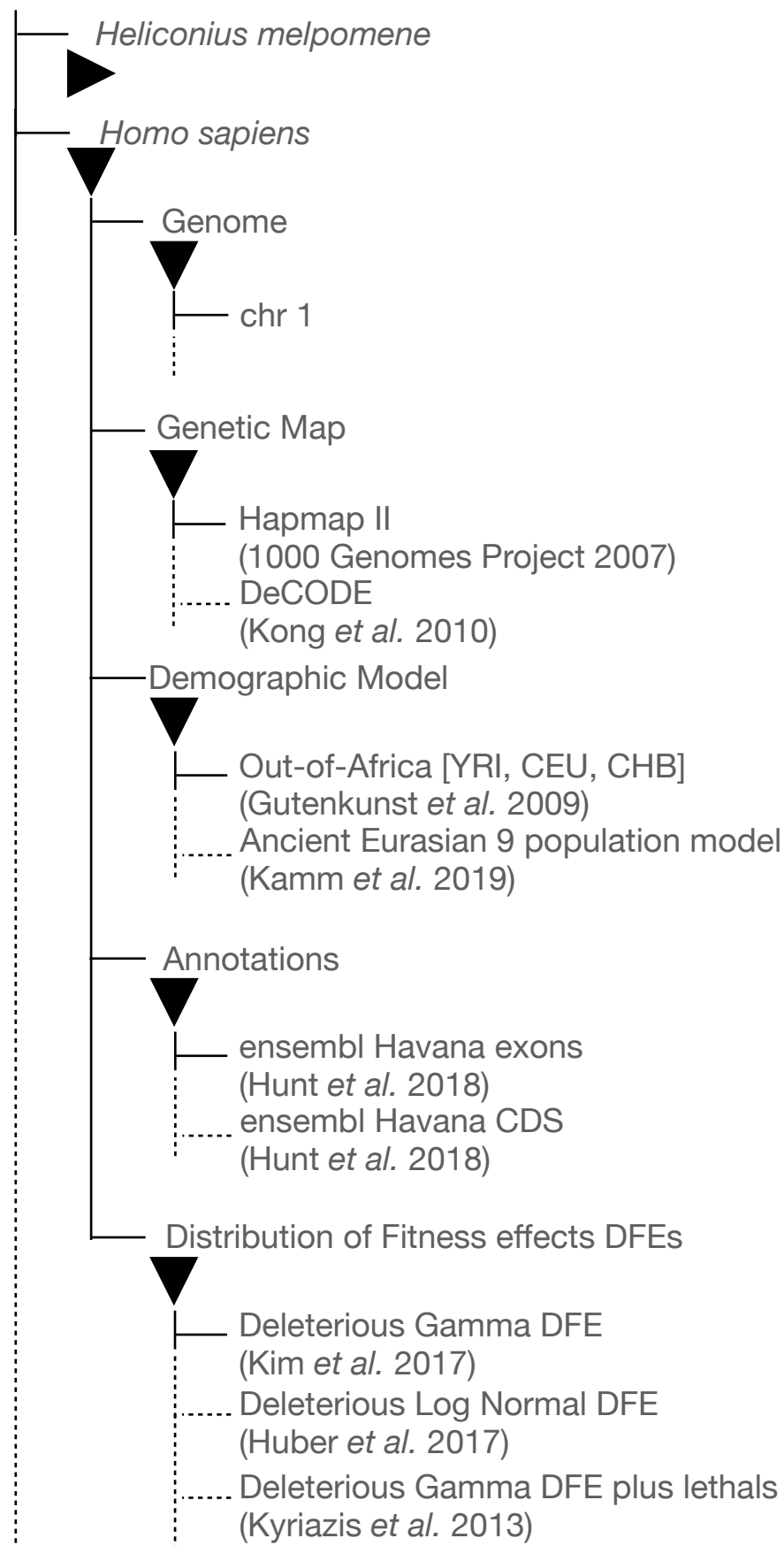


A. Catalog



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 )
8 model = species.get_demographic_model(
9     "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(
20     model,
21     contig,
22     samples,
23     seed=236,
24     slim_scaling_factor=1,
25     slim_burn_in=10,
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
```