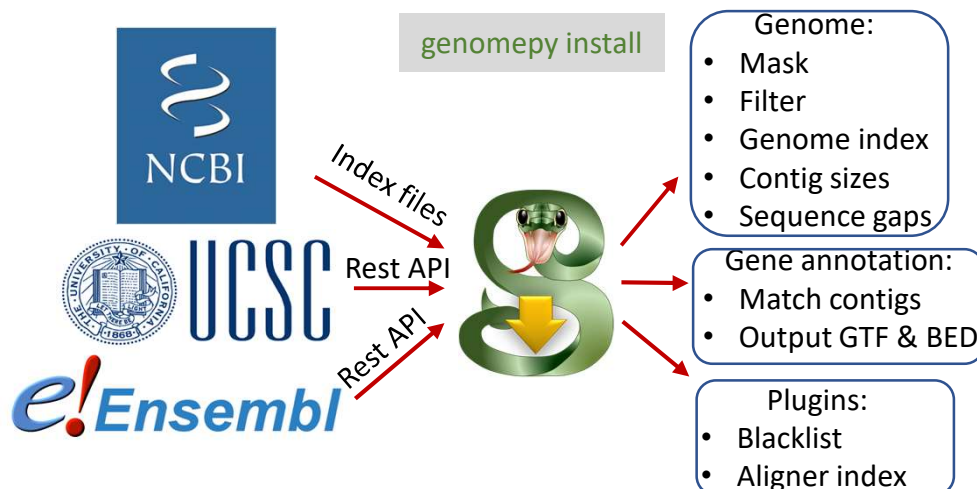


A



B

```
$ genomepy search "drosophila mel" --provider ucsc
name provider accession species tax_id ot
dm1 UCSC na Drosophila melanogaster 7227
dm2 UCSC na Drosophila melanogaster 7227
dm3 UCSC GCA_000001215.2 Drosophila melanogaster
dm6 UCSC GCA_000001215.4 Drosophila melanogaster
^
```

Use name for genomepy install

```
$ genomepy install dm3 --annotation
```

```
$ ls -l ~/.local/share/genomes/dm3
dm3.annotation.bed.gz
dm3.annotation.gtf.gz
dm3.blacklist.bed
dm3.fa dm3.fa.fai
dm3.fa.sizes
dm3.gaps.bed
index
README.txt
```

C

```
>>> import os
>>> import genomepy

>>> for row in genomepy.search("melanogaster", "ucsc"):
>>>     print("\t".join([x.decode('utf-8') for x in row]))

dm1 UCSC na Drosophila melanogaster 7227 Ja
dm2 UCSC na Drosophila melanogaster 7227 Ap
dm3 UCSC GCA_000001215.2 Drosophila melanog
dm6 UCSC GCA_000001215.4 Drosophila melanog

>>> p = genomepy.ProviderBase.create("ucsc")
>>> p.download_genome("dm3", annotation=True)

>>> path = os.path.expanduser("~/local/share/genomes/dm3")
>>> os.listdir(path)
['dm3.annotation.gtf.gz', 'dm3.blacklist.bed',
'dm3.gaps.bed', 'dm3.fa', 'index', 'dm3.annotation.bed.gz',
'README.txt', 'dm3.fa.sizes', 'dm3.fa.fai']
```

D

```
>>> genome = genomepy.Genome("dm3")
>>> plugins = genomepy.plugin.init_plugins()
>>> plugins["star"].after_genome_download(genome)
Creating star index...

>>> plugins["blacklist"].after_genome_download(genome)
Downloading blacklist http://mitra.stanford.edu/kundaje/akundaje/release/blacklists/dm3-D.melanogaster/dm3-blacklist.bed.gz

>>> p.download_annotation("dm3")
Downloading annotation from UCSC.
Target URL: http://hgdownload.soe.ucsc.edu/goldenPath/dm3/bigZips/genes/dm3.ensGene.gtf.gz...
Annotation download successful

>>> genomepy.utils.sanitize_annotation(genome)
```