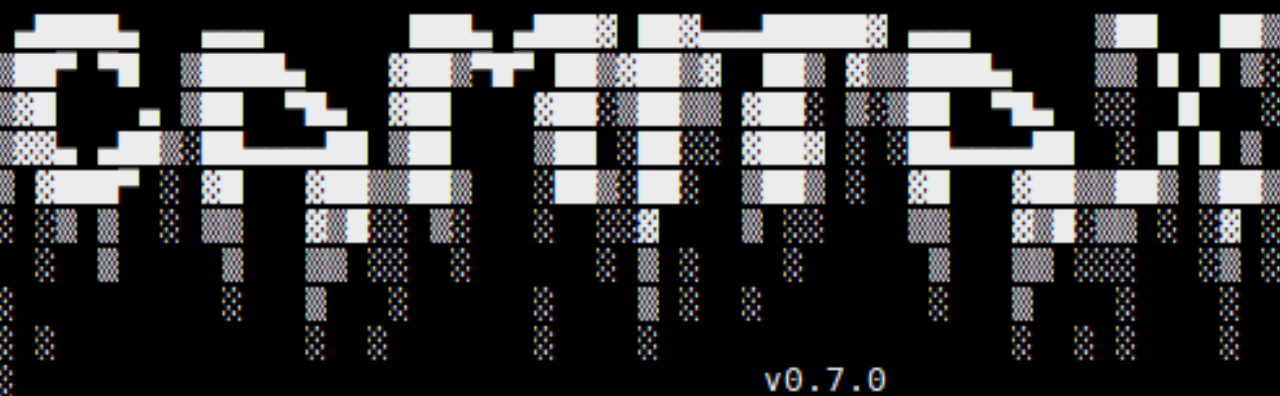


```
(docker) wirth@zebra:~$ nextflow run CAMI-challenge/CAMITAX -profile docker --db ~/cami_dat/ --i PLS/1_11.fasta --x fasta
NEXTFLOW ~ version 20.04.1
Launching `CAMI-challenge/CAMITAX` [marvelous_fourier] - revision: 6ac30c998f [master]
```



```
Input genomes:
[-          ] process > mash          -
[-          ] process > checkm        -
[-          ] process > dada2         -
[-          ] process > prodigal      -
[-          ] process > centrifuge    -
[-          ] process > kaiju         -
[-          ] process > taxonomy      -
[-          ] process > summary       -
```

```
(docker) wirth@zebra:~$ █
```