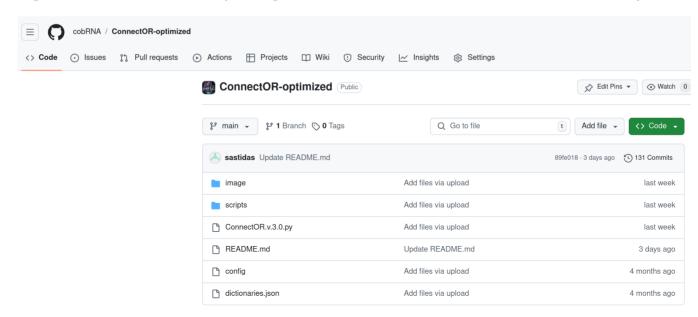
# ConnectOR-optimized

#### **Optimized & modified**

by

barbara uszczyńska-ratajczak & sasti Gopal Das

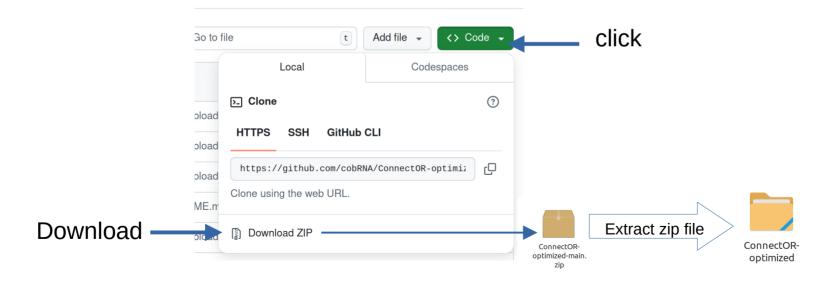
Download github link https://github.com/cobRNA/ConnectOR-optimized

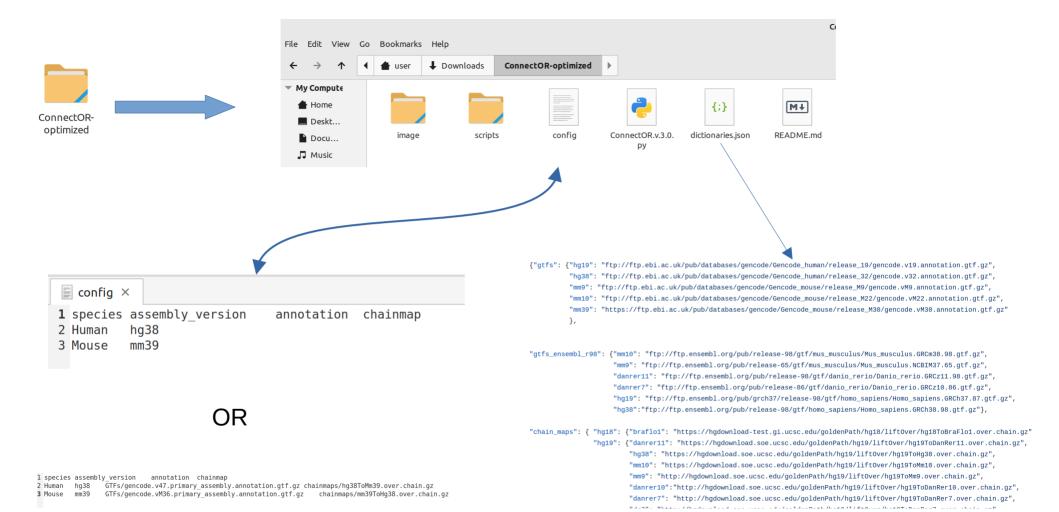


## **Download**

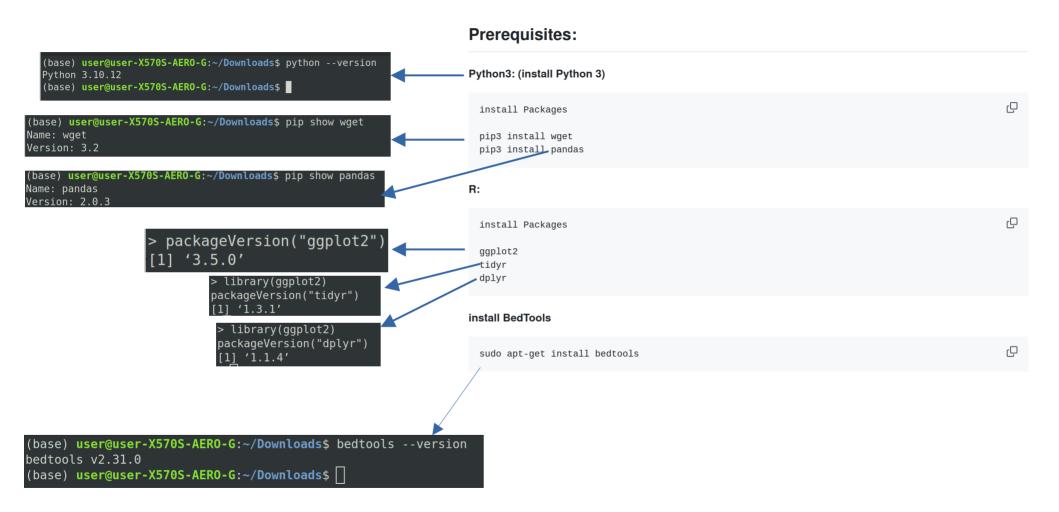
```
(base) user@user-X570S-AERO-G:~/Downloads$ git clone https://github.com/cobRNA/ConnectOR-optimized Cloning into 'ConnectOR-optimized'...
remote: Enumerating objects: 385, done.
remote: Counting objects: 100% (84/84), done.
remote: Compressing objects: 100% (59/59), done.
remote: Total 385 (delta 64), reused 25 (delta 25), pack-reused 301 (from 1)
Receiving objects: 100% (385/385), 18.87 MiB | 29.06 MiB/s, done.
Resolving deltas: 100% (175/175), done.
```

#### OR





### **Prerequisites:**

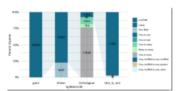


## Run ConnectOR

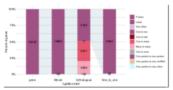
## python3 ConnectOR.v.3.0.py

```
(base) user@user-X570S-AERO-G:~/Downloads$ cd ConnectOR-optimized/
(base) user@user-X570S-AERO-G:~/Downloads/ConnectOR-optimized$ python3 ConnectOR.v.3.0.py
Checkina Confia file...
gencode.v43.annotation.gtf.gz downloaded succesfully...
                                                                                   hg38ToMm39.over.chain.gz downloaded succesfullv...
<u>100% [......] 73017320 / 73017320 </u>
                                                                                   gencode.vM32.annotation.gtf.gz downloaded succesfully..
<u>100% [......] 29299972 / 29299972 </u>
mm39ToHq38.over.chain.qz downloaded succesfully...
Config file is correct..
Generating geneID - geneName - geneBiotype - transcripts maps...
      Maps for hg38... generating
      Maps for mm39... generating
      Maps for mm39... generated
      Maps for hg38... generated
Generating BED files for exons and genes...
      Exons BEDs for hg38... generating
      Exons BEDs for mm39... generating
      Genes BEDs for hg38... generating
      Genes BEDs for mm39... generating
      BEDs for mm39... generated
      BEDs for hg38... generated
LiftOver features between species...
      hg38 exons to mm39... mapping
      mm39 exons to hq38... mapping
Reading liftover chains
Reading liftover chains
Mapping coordinates
Mapping coordinates
      mm39 exons to hq38... done
      hq38 exons to mm39... done
Intersecting LiftOver...
      Human exons to Mouse... done
      Mouse exons to Human... done
Predicting orthologues...
      Human exonStrand to Mouse... done
      Mouse exonStrand to Human... done
completed
```

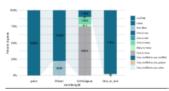
# **ConnectOR** result



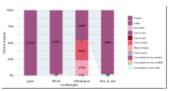
hg38tomm39\_lncRNA\_Orthologous.pdf 5,5 kB Fri 13 Sep 2024 02:49:00 PM CEST



hg38tomm39\_protein\_Orthologous.pdf 5,5 kB Fri 13 Sep 2024 02:49:01 PM CEST



mm39tohg38\_lncRNA\_Orthologous.pdf 5,5 kB Fri 13 Sep 2024 02:49:01 PM CEST



mm39tohg38\_protein\_Orthologous.pdf 5,6 kB Fri 13 Sep 2024 02:49:02 PM CEST