**Mitochondrial genomes:**

Mitochondrial genomes generated in the Reich Lab are also available in this release.

These are compressed, and may be extracted using: mtdna\_uncompress\_v3.py (in this version).  
  
Then, the full mitogenome dataset may be extracted into a single multisample fasta file, using: Mitogenomes maybe accessed in the following way:  
(i) For the full dataset: zcat aadr\_v54.1.p1\_MT\_v1.gz | python mtdna\_uncompress\_v3.py   
  
(ii) Or: a subset of samples may be pulled using a comma separated list, eg:  
zcat aadr\_v54.1.p1\_MT\_v1.gz | python mtdna\_uncompress\_v3.py --id=I0026,I0018   
  
(iii) Or: a subset of samples may be pulled using a file of ids, eg:  
zcat aadr\_v54.1.p1\_MT\_v1.gz | python mtdna\_uncompress\_v3.py --file=my.id.file   
  
You may check to see if ids exist using the --check option, eg:  
zcat aadr\_v54.1.p1\_MT\_v1.gz | python mtdna\_uncompress\_v3.py --file=my.id.file --check   
  
Notes:   
(a) python 2.7 is used.  
(b) 'zcat' is used, expecting:  
(i) that the dataset is not automatically uncompressed by your browser, and,  
(ii) that 'zcat' operates directly on gzipped files (which is the norm for linux systems, but not on some macs).   
If (i) is not true, then your browser may decompress the file to aadr\_v54.1.p1\_MT\_v1. In this case use 'cat' instead of 'zcat'.  
If (ii) does not work, one solution might be to directly uncompress aadr\_v54.1.p1\_MT\_v1.gz on your local system using: 'gunzip aadr\_v54.1.p1\_MT\_v1.gz' and then using 'cat' instead of 'zcat'.   
  
Please let us know if there are any changes that may be useful.   
  
  
  
*Update history:*   
[2022\_11.16]: repo built