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Mitogenome Assembly with GetOrganelle

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Protocol status: Working

We use this protocol and it's working

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Abstract

Basic instructions for assembling mitogenomes with the GetOrganelle Program



Installation

1

Note

This protocol includes instructions for a conda install of GetOrganelle, which requires that you have Anaconda or Miniconda already installed on your system.

Detailed installation information and additional installation options for various systems can be found here: <https://github.com/Kinggerm/GetOrganelle> and here: <https://github.com/Kinggerm/GetOrganelle/wikihttps://github.com/Kinggerm/GetOrganelle/wiki>

Before installation, activate your python environment (example code below for python3 environment):

Command

new command name

```
conda activate python3
```

2 Install GetOrganelle with the following code:

Command

new command name

```
conda install -c bioconda getorganelle
```



You may need to install updates, be sure to say yes (type **y** and hit enter) when prompted to update any conda-related programs.

```
Downloading and Extracting Packages
libgfortran-5.0.0      | 19 KB      | ##### | 100%
libblas-3.9.0         | 11 KB      | ##### | 100%
urllib3-1.26.6        | 99 KB      | ##### | 100%
mpc-1.1.0             | 100 KB     | ##### | 100%
gmpy2-2.1.0b5        | 190 KB     | ##### | 100%
sympy-1.8             | 11.2 MB    | ##### | 100%
pigz-2.6              | 88 KB      | ##### | 100%
libgfortran5-9.3.0    | 1.7 MB     | ##### | 100%
mpfr-4.0.2            | 573 KB     | ##### | 100%
openssl-1.1.1k        | 1.9 MB     | ##### | 100%
llvm-openmp-11.1.0    | 268 KB     | ##### | 100%
bowtie2-2.4.4         | 1.3 MB     | ##### | 100%
ca-certificates-2021  | 136 KB     | ##### | 100%
perl-5.32.1           | 13.4 MB    | ##### | 100%
libcxx-11.1.0         | 1.0 MB     | ##### | 100%
lz4-c-1.9.3           | 155 KB     | ##### | 100%
tbb-2020.2            | 132 KB     | ##### | 100%
zstd-1.4.9            | 460 KB     | ##### | 100%
mpmath-1.2.1          | 437 KB     | ##### | 100%
liblapack-3.9.0       | 11 KB      | ##### | 100%
getorganelle-1.7.5.0  | 164 KB     | ##### | 100%
idna-2.10             | 52 KB      | ##### | 100%
cryptography-3.4.7    | 763 KB     | ##### | 100%
libopenblas-0.3.15    | 8.7 MB     | ##### | 100%
scipy-1.7.0           | 19.8 MB    | ##### | 100%
blast-2.6.0           | 113.0 MB   | ##### | 100%
spades-3.12.0         | 12.3 MB    | ##### | 100%
libblas-3.9.0         | 11 KB      | ##### | 100%
certifi-2021.5.30     | 141 KB     | ##### | 100%
chardet-4.0.0         | 204 KB     | ##### | 100%
numpy-1.21.0          | 5.8 MB     | ##### | 100%
gmp-6.2.1             | 774 KB     | ##### | 100%
requests-2.25.1       | 51 KB      | ##### | 100%
brotlipy-0.7.0        | 357 KB     | ##### | 100%
pyopenssl-20.0.1     | 48 KB      | ##### | 100%
pysocks-1.7.1        | 27 KB      | ##### | 100%
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
```

Printout of successful installation of GetOrganelle (for reference).

Initialization

- 3 Next we need to download and initialize the database of your preferred organelle genome type.

Options include: embplant_pt, embplant_mt, embplant_nr, fungus_mt, fungus_nr, animal_mt, and/or other_pt

For animal mitochondrial genomes, use **animal_mt**:



Command

new command name

```
get_organelle_config.py --add animal_mt
```

If you would like to download and initialize multiple organelle genome types, you can list them after the **--add** command above, separated by spaces.

```
[(python3) marina@Lamellibrachia ~ % get_organelle_config.py --add animal_mt  
Python 3.8.5 | packaged by conda-forge | (default, Aug 29 2020, 01:18:42) [Clang 10.0.1 ]  
DEPENDENCIES: Bowtie2 2.4.4; Blast 2.6.0  
WORKING DIR: /Users/marina  
/Users/marina/miniconda3/envs/python3/bin/get_organelle_config.py --add animal_mt  
  
Existing databases(s):  
  
Downloading animal_mt.fasta  
Downloading animal_mt.fasta [=====] 100%  
Downloaded animal_mt.fasta (30285897 bytes), cost 1.82 s  
bowtie2-build animal_mt.fasta ... Making - bowtie2 index ...  
Making - bowtie2 index finished.  
finished  
Downloading animal_mt.fasta  
Downloading animal_mt.fasta [=====] 100%  
Downloaded animal_mt.fasta (6674918 bytes), cost 0.72 s  
makeblastdb animal_mt.fasta ... finished
```

Printout of successful initialization (for reference). Note that working directories will be different on your system.

- 4 If you have trouble with the above command (connection to GitHub fails) try a few times more, as the problem generally resolves itself. If you're still having trouble, you can download the repository manually, as in Option 2 available here:

<https://github.com/Kinggerm/GetOrganelle/wiki/Initialization#default-directory>