

Starling-May18
Projects/Katarina Stuart/KStuart.Starling-Aug18/Sv3_Genome/Annotation/2020-04-06.Mites

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Katarina Stuart (z5188231@ad.unsw.edu.au)

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MITES-minature inverted-repeat transposable elements

Step 1 of 'Repeat Library Construction-Advanced'

http://weatherby.genetics.utah.edu/MAKER/wiki/index.php/Repeat_Library_Construction-Advanced

Previously tried in [2018-09-26.Species specific repeat library](#)

- **mitehunter2011**: didn't work
- **detectmite**: worked

MITE-Tracker

<https://github.com/INTABiotechMJ/MITE-Tracker>

Usage:

```
python3 -m MITETracker -g /path/to/your/genome.fasta -w 3 -j jobname
```

or to run in background

```
nohup python3 -m MITETracker -g /path/to/your/genome.fasta -w 3 -j jobname &
```

```
cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/programs
git clone https://github.com/INTABiotechMJ/MITE-Tracker.git
cd MITE-Tracker
module load blast+/2.6.0
module load python/3.6.5
```

VSearch:

```
wget https://github.com/torognes/vsearch/archive/v2.7.1.tar.gz
tar xzf v2.7.1.tar.gz
cd vsearch-2.7.1
sh autogen.sh
./configure
make
```

Running MITE-tracker from within program directory

```
GENOMEDIR=/srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/genome_assembly
GENBASE=Sturnus_vulgaris_2.2
GENOME=${GENOMEDIR}/${GENBASE}.fasta
```

```
python3 -m MITTracker -g $GENOME -w 3 -j trial
```

This worked, now submitting as a script below:

```
#!/bin/bash

#PBS -N 2020-05-05.MITE-tracker.pbs
#PBS -l nodes=1:ppn=16
#PBS -l mem=124gb
#PBS -l walltime=100:00:00
#PBS -j oe
#PBS -M katarina.stuart@student.unsw.edu.au
#PBS -m ae

module load blast+/2.6.0
module load python/3.6.5

cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/programs/MITE-Tracker

GENOMEDIR=/srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/genome_assembly
GENBASE=Sturnus_vulgaris_2.3.simp
GENOME=${GENOMEDIR}/${GENBASE}.fasta

python3 -m MITTracker -g $GENOME -w 16 -j Sturnus_vulgaris_2.3.simp
```

MITE-hunter

Reattempting to set up after being unable to last time

```
module add perl/5.28.0
module add blast/2.2.26
module add mdust/2006

perl MITE_Hunter_Installer.pl \
-d /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/adv_repeats/programs/ \
-f /apps/blast/2.2.26/bin/formatdb \
-b /apps/blast/2.2.26/bin/blastall \
-m /apps/mdust/2006/bin/mdust \
-M /apps/muscle/3.8.31/bin/muscle

cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/genome_assembly
perl -/simplifyFastaHeaders.pl ${GENOME} ${PREFIX} ${GENOME%.fasta}.simp.fasta ${GENOME%.fasta}.map
INPUT=${GENOME%.fasta}.simp.fasta
```

```
cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/adv_repeats/MITE
perl ../programs/MITE_Hunter/MITE_Hunter_manager.pl -i ${INPUT} -g ${PREFIX} -n ${CPU} -S 12345678
```

```
perl MITE_Hunter_manager.pl -i ${INPUT} -g ${PREFIX} -n ${CPU} -S 12345678
```

still not working

Error:

```
Can't open perl script "/srv/scratch/z5188231/KStuart.Starling-
Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/adv_repeats/programs/blast_formatdb_index.pl": No such file or directory
Can't open perl script "/srv/scratch/z5188231/KStuart.Starling-
Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/adv_repeats/programs/fasta_windows_maker.pl": No such file or directory
Can't open perl script "/srv/scratch/z5188231/KStuart.Starling-
Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/adv_repeats/programs/fasta_splitter.pl": No such file or directory
cat: *.TSD.*: No such file or directory
Can't open perl script "/srv/scratch/z5188231/KStuart.Starling-
Aug18/Sv3_Genome/Sv3.4_GenomeAnnotation/data_2020/adv_repeats/programs/low_complexity_filter.pl": No such file or directory
No such file or directory
```