

## Supplementary Note - Manual

This note provides a guide to help users use DeepTE in annotation of transposons in a genome.

### Prerequisites

#### 1. Python

Available at <https://www.python.org/downloads/>. Developed and tested with version 3.7.1.

#### 2. Python packages

- 1) biopython: pip install biopython
- 2) numpy: pip install numpy==1.16.0 (Developed and tested with version 1.16.0)
- 3) tensorflow: pip install tensorflow==1.14.0 (Developed and tested with version 1.14.0)
- 4) keras: pip install keras==2.2.4 (Developed and tested with version 2.2.4)

### Optional tools

#### 1. HMMER

Available at <http://hmmer.org/download.html>. Developed and tested with version 3.1b1.

### DeepTE Installation

#### 1. Download DeepTE

git clone <https://github.com/LiLabAtVT/DeepTE.git>

### Example Run

In this example we use maize 'B73' genome (maize.fas) which can be download from [https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org\\_Zmays](https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Zmays). We provide a simple example to help users annotate TEs in this maize genome with help of DeepTE.

#### 1. Create a transposon library from genomes.

Users can choose one or more following tools to develop transposon library in the maize genome:

RepeatModeler (<http://www.repeatmasker.org/RepeatModeler/>);

LTR\_retriever ([https://github.com/oushujun/LTR\\_retriever](https://github.com/oushujun/LTR_retriever));

LTR\_finder (<https://code.google.com/archive/p/ltr-finder/downloads>);

LTRharvest (<http://genometools.org/>);

miteFinder (<https://github.com/screamer/miteFinder>)

Users can also develop the library based on other tools that are not listed as above.

##### 1) RepeatModeler

###### Command:

```
RepeatModeler_Path/BuildDatabase -name maize maize.fas
```

```
mv consensi.fa.classified repeatmodeler.lib
```

**Note:** RepeatModeler will generate **consensi.fa.classified** file that is **maize transposon library**. The '**consensi.fa.classified**' is changed to '**repeatmodeler.lib**' to make the output more clear.

##### 2) LTR-retriever

###### Command:

```
ltr_finder -D 15000 -d 1000 -L 7000 -l 100 -p 20 -C -M 0.9 maize.fas > ltrfinder.scn;
```

```
gt suffixerator -db maize.fas -indexname index_maize -tis -suf -lcp -des -ssp -sds -dna;
```

```
gt ltrharvest -index index_maize -similar 90 -vic 10 -seed 20 -seqids yes -minlenltr 100 -maxlenltr 7000 -mintsd 4 -maxtsd 6 -motif TGCA -motifmis 1 > ltrharvest.scn;
```

```
LTR_retriever -genome maize.fas -inharvest ltrharvest.scn -infinder ltrfinder.scn
```

**Note:** LTR\_retriever will generate multiple outputs, and **\*.LTRlib.fa** is **maize transposon library**.

3) **miteFinder**

**Command:**

```
miteFinder -input maize.fas -output maize_miteFinder.lib -pattern_scoring mite_finder2_profile/
pattern_scoring.txt -threshold 0.5
```

**Note:** pattern\_scoring.txt is from profile directory of miteFinder downloaded from <https://github.com/screamer/miteFinder/tree/master/profile>. The output file (maize\_miteFinder.lib) is **maize transposon library**.

2. **Use DeepTE to classify transposons in the libraries into families.**

1) Create working and output directories

**Command:**

```
mkdir working_dir
mkdir output_dir
```

2) Download plant model directory

([https://drive.google.com/file/d/1dQf1zUdqKGb9EorpPPoLtr\\_67hpiOUo/view](https://drive.google.com/file/d/1dQf1zUdqKGb9EorpPPoLtr_67hpiOUo/view))

**Command:**

```
tar -xvzf Plants_model.tar.gz
```

3) Run DeepTE

a. Run DeepTE without modification.

**Command:**

```
python DeepTE.py -d working_dir -o output_dir -i repeatmodeler.lib -m Plants_model -sp P -fam All
```

**Note:** Users can use transposon libraries generated from the previous step. The libraries can be derived from single tool or multiple tools listed above. The combined library can be generated using 'cat'. For example: cat repeatmodeler.lib ltr\_retriever.lib miteFinder.lib > combine.lib. This example will use library from RepeatModeler. The output\_dir will contains opt\_DeTE.fasta file that is the input transposon library in RepeatMasker tool.

b. Run DeepTE with modification.

Users need to download and install hmmscan tool (<http://hmmer.org/>).

**Command:**

```
mkdir working_dir_md
```

```
mkdir output_dir_md
```

```
python DeepTE_domain.py -d working_dir_md -o output_dir_md -i repeatmodeler.lib -s
DeepTE/supfile_dir --hmmscan hmmscan
```

```
python DeepTE.py -d working_dir -o output_dir -i repeatmodeler.lib -m Plants_model -sp P -fam All -
modify opt_te_domain_pattern.txt
```

**Note:** If users detect domains of TEs to improve performance of DeepTE, they need to use DeepTE\_domain.py with help of hmmscan tool. The opt\_te\_domain\_pattern.txt can be found in the output\_dir\_md. The output\_dir will contains opt\_DeTE.fasta file that is the input transposon library in RepeatMasker tool.

3. **Use RepeatMasker to mask individual transposons in the maize genome**

Users need to download and install RepeatMasker (<http://www.repeatmasker.org/RMDownload.html>).

**Command:**

```
mkdir repeatmasker_opt_dir
```

```
RepeatMasker maize.fas -lib opt_DeepTE.fasta -gff -dir repeatmasker_opt_dir
```

**Note:** The output file \*.out.gff is the annotation information of transposons.

### An overview of all parameters

**Table 1. All parameters for DeepTE.py**

Required parameters	
-d [working directory]	Working directory stores intermediate files of each step.
-o [output directory]	Output directory stores the output files.
-i [input fasta file]	Input sequences that are unknown transposons or DNA sequences. If -UNS is not initiated, the input sequences are unknown transposons, otherwise, are DNA sequences.
-m [model directory]	Model directory that can be downloaded from links in <a href="https://github.com/LiLabAtVT/DeepTE">https://github.com/LiLabAtVT/DeepTE</a> . If users set -UNS yes, please provide UNS_model.h5 that can be downloaded in the above link. Note: this model is used for plants rather than metazoans and fungi.
-sp [species type]	Specify which species the input sequences belong to. P or M or F or O. P: Plants, M: Metazoans, F: Fungi, and O: Others.
-fam [transposon family name]	Provide TE family name for the input transposon sequence. Default: All. All: the input sequence is unknown TEs. ClassI: the input sequence is ClassI TEs. ClassII: the input sequence is ClassII TEs. LTR: the input sequence is LTR TEs. nLTR: the input sequence is nLTR TEs. LINE: the input sequence is LINE TEs. SINE: the input sequence is SINE TEs. Domain: the input sequence is Class II TEs with specified super families.
Optional parameters	
-modify [domain information file]	Domain file is generated from script: DeepTE_domain.py in <a href="https://github.com/LiLabAtVT/DeepTE">https://github.com/LiLabAtVT/DeepTE</a> . This modification argument helps to increase performance of DeepTE tool.
-UNS [Yes]	If set this argument, users need change the input fasta file to the DNA sequences instead of unknown transposons; This argument will classify the sequences into transposons (TEs), coding sequences (CDS), or Intergenic sequences (INS). Also, -sp and -fam do not need to provide.

**Table 2. All parameters for DeepTE\_domain.py**

Required parameters	
-d [working directory]	Working directory stores intermediate files of each step.
-o [output directory]	Output directory stores the output files.
-i [input fasta file]	Input sequences that are unknown transposons.
-s [supplementary directory]	Specify supplementary directory that contains required files to generate domain information of the transposons. It is from supfile_dir from <a href="https://github.com/LiLabAtVT/DeepTE">https://github.com/LiLabAtVT/DeepTE</a> .
--hmmscan [hmmscan tool]	Specify file path to hmmscan executable. For example, /usr/bin/hmmscan.