

MATLAB code of plotting a phylogenetic tree of 3 miRNAs

```
fastawrite('m129','miR-129','GGAUCUUUUUGCGGUCUGGGCUUGCUGUCCU  
CUCAACAGUAGUCAGGAAGCCCUUACCCCAAAAAGUAUCU');
```

```
R129=fastaread('m129');
```

```
fastawrite('m555','miR-555','GGAGUGAACUCAGAUGUGGAGCACUACCUUUG  
UGAGCAGUGUGACCCAAGGCCUGUGGACAGGGUAAGCUGAACCUUGA  
UAAAACUCUGAUCUAU');
```

```
R555=fastaread('m555');
```

```
fastawrite('m19a','miR-19a','GCAGUCCUCUGUUAGUUUUGCAUAGUUGCACU  
ACAAGAAGAAUGUAGUUGUGCAAUCUAUGCAAACUGAUGGUGGCCU  
GC');
```

```
R19a=fastaread('m19a');
```

```
seqs = [R129, R555, R19a];
```

```
distances = seqpdist(seqs,'method','jukes-cantor','Alphabet', 'NT');
```

```
%distances = seqpdist(seqs,'method','alignment-score','Alphabet', 'NT');
```

```
%distances = seqpdist(seqs,'method','p-distance','Alphabet', 'NT');
```

```
phyлотree = seqlinkage(distances,'average',seqs);
```

```
%phyлотree = seqlinkage(distances,'single',seqs);
```

```
%phyлотree = seqlinkage(distances,'median',seqs);
```

```
view(phyлотree)
```

