```
┌─────────────────────────────────┐   ┌─────────────────────────────────┐   ┌─────────────────────────────────┐
│ Jellyfish on individual         │   │ Align k-mers to retrotransposons│   │ LTRHarvest, default parameters  │
│ chromosomes                     │   │ (inner sequence and LTRs) to    │   └─────────────────────────────────┘
└─────────────────────────────────┘   │ determine if families are       │                    │
                 │                     │ overrepresented with a specific │                    ▼
                 ▼                     │ type                            │   ┌─────────────────────────────────┐
┌─────────────────────────────────┐   └─────────────────────────────────┘   │ Extract individual LTR sequences│
│ Find overrepresented k-mers on  │                    │                     │ (LTRHarvest provides total fasta│
│ chromosome pairs                │                    │                     │ location table +                │
└─────────────────────────────────┘                    │                     │ get_fastas_from_LTRout.pl)      │
                 │                                      ▼                     └─────────────────────────────────┘
                 ▼                     ┌─────────────────────────────────┐                    │
┌─────────────────────────────────┐   │ 5' vs 3' distances of same      │                    ▼
│ Take union of k-mers that are   │   │ retroelement are assumed to     │   ┌─────────────────────────────────┐
│ differential across all pairs   │   │ represent insertion time, while │   │ All-vs-All BLASTN with 1e-2     │
└─────────────────────────────────┘   │ peaks in cross-species activity │   │ and 90% length cutoff           │
                 │                     │ is assumed to represent the     │   └─────────────────────────────────┘
                 ▼                     │ speciation event, allowing for  │                    │
┌─────────────────────────────────┐   │ calibration to a known time with│                    ▼
│ Map differential k-mers to      │   │ LTR distance space              │   ┌─────────────────────────────────┐
│ genome, determine MB-bin        │   └─────────────────────────────────┘   │ Use MAFFT to perform a          │
│ density for each population     │                                         │ multiple sequence alignment     │
└─────────────────────────────────┘                                         │ within each family              │
                 │                                                           └─────────────────────────────────┘
                 ▼                                                                            │
┌─────────────────────────────────┐                                                          ▼
│ Train HMM on visually "pure"    │                                         ┌─────────────────────────────────┐
│ chromosome pair (Chr01/Chr02    │                                         │ Compute Jukes-Cantor            │
│ here;R "HMM" package)           │                                         │ distances in R (R "ape"         │
└─────────────────────────────────┘                                         │ package, visualized using       │
                                                                            │ "dendextend")                   │
                                                                            └─────────────────────────────────┘
```