Using Hidden Markov Models (HMMs) to call PRO-seq transition points in transcriptional elongation speed assays.

## Quickstart

1. Use tar2 to call global transcription units (TUs)

```
tar2 –p (plus strand bedgraph pre-treatment) –m (minus strand bedgraph
pretreatment) –mp (mappability bedgraph)  > global_TU.bed
```

2. Use hmm-select script to select only the genes with un-ambiguous TSS and 3´ ends, and are long enough for elongation speed assays.

```
hmm-select –a global_TU.bed –b (genelist
bed file) –p (plus strand bedgraph
pretreatment) –m (minus strand pre-
treatment) –mp (mappability bedgraph)  >
selected_genes.txt
```
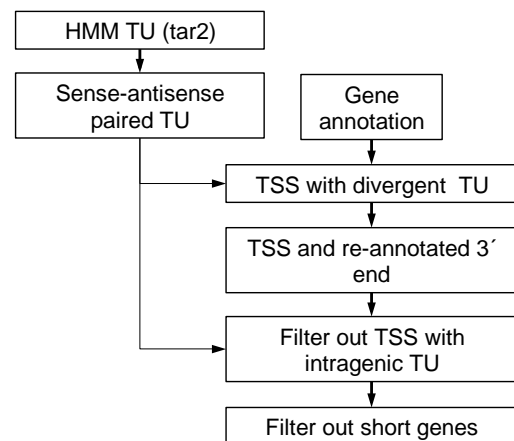

3. Use hmm2 to call transition points

```
hmm2 –p (plus strand bedgraph post-treatment) -m (minus strand bedgraph
posttreatment) -p0 (plus strand bedgraph pre-treatment) -m0 (minus strand
bedgraph pretreatment) -g (genelist bed file) -b 5000  >
transition_points.txt
```

4. Filter the transition point data by the selected genes.