

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

## Quickstart

### 1. Use hmm2 to call transition points

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

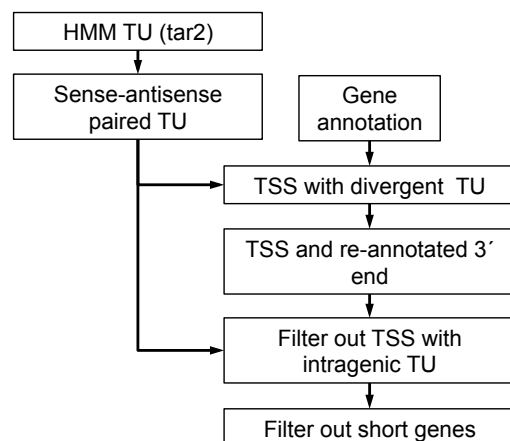
### 2. Use tar2 to call global transcription units (TUs)

```
tar2 -p (plus strand bedgraph pre-treatment) -m (minus strand bedgraph pre-treatment) -mp (mappability bedgraph) -b 5000 > global_TU.bed
```

### 3. 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 pre-treatment) -m (minus strand pre-treatment) -mp (mappability bedgraph) > selected_genes.txt
```

### 4. Intersect the transition point list with genes that are filtered by the hmm-select script.



Schematics of hmm-select procedure