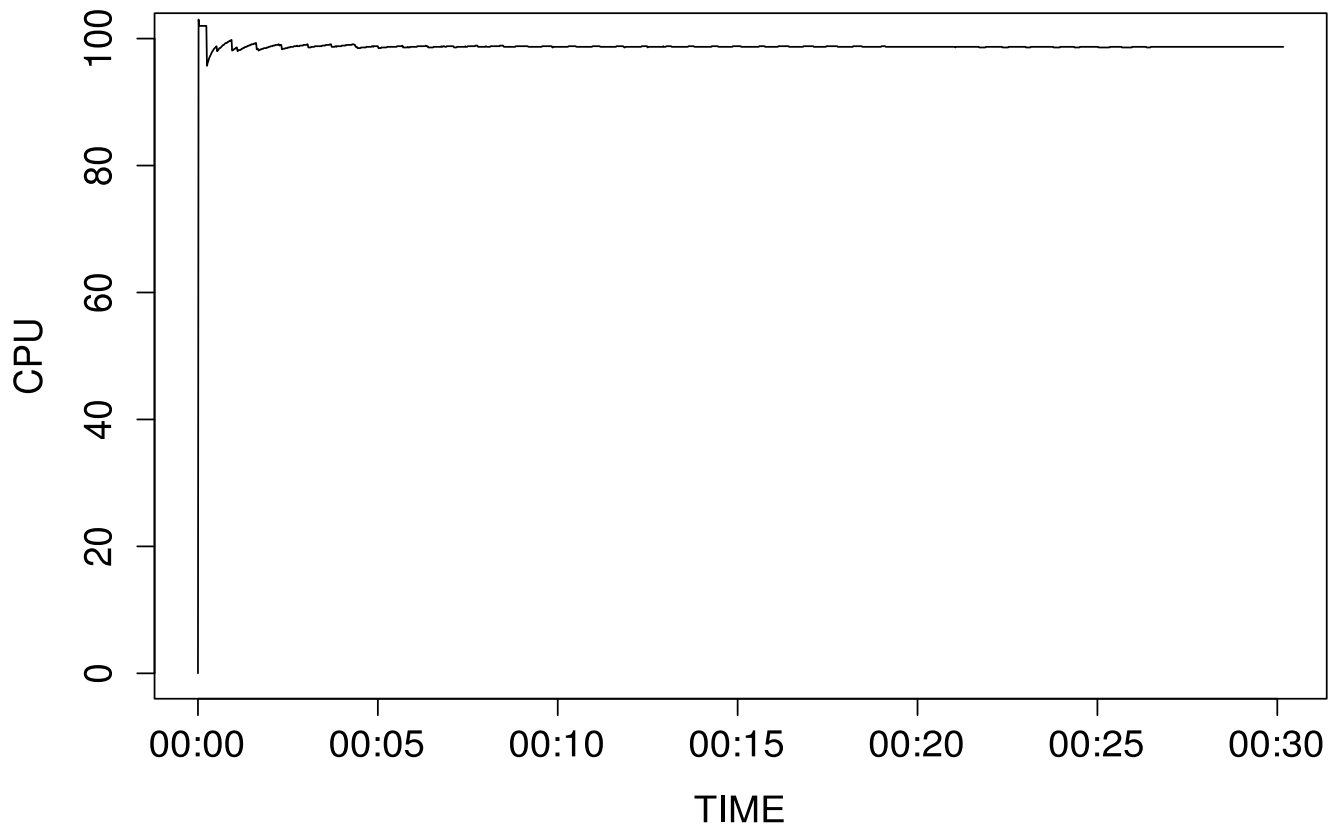
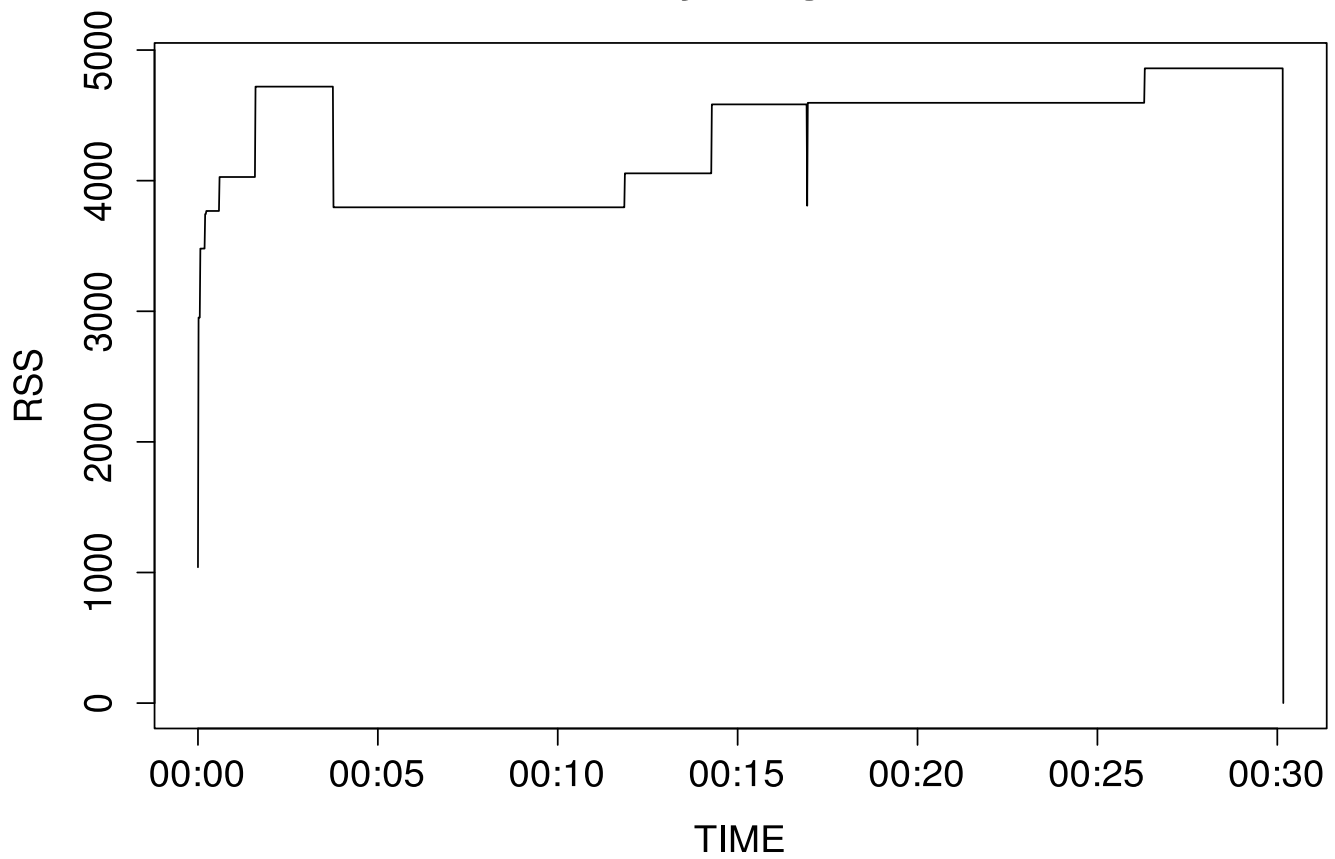


## Example 1: Compute genetic distances

**Processor usage (%)**

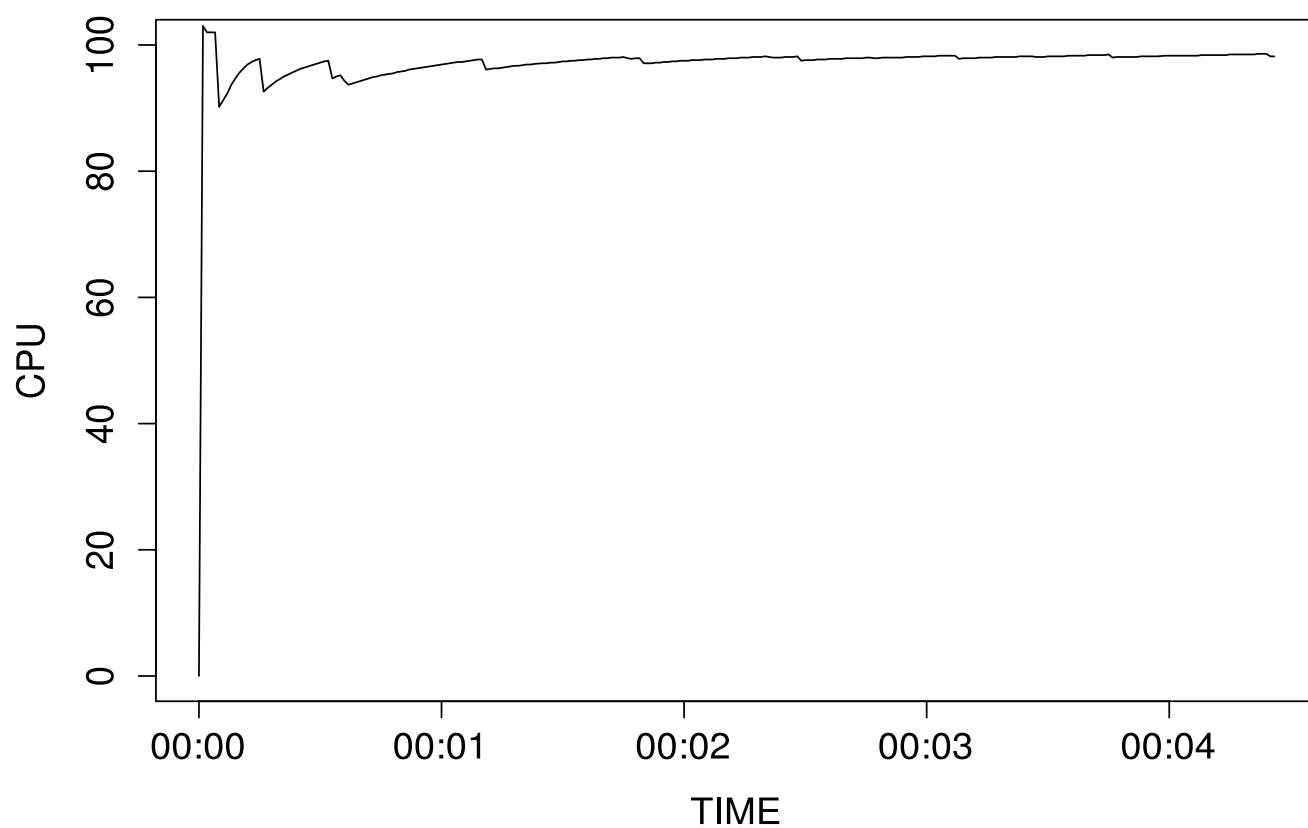


**Memory usage (kB)**

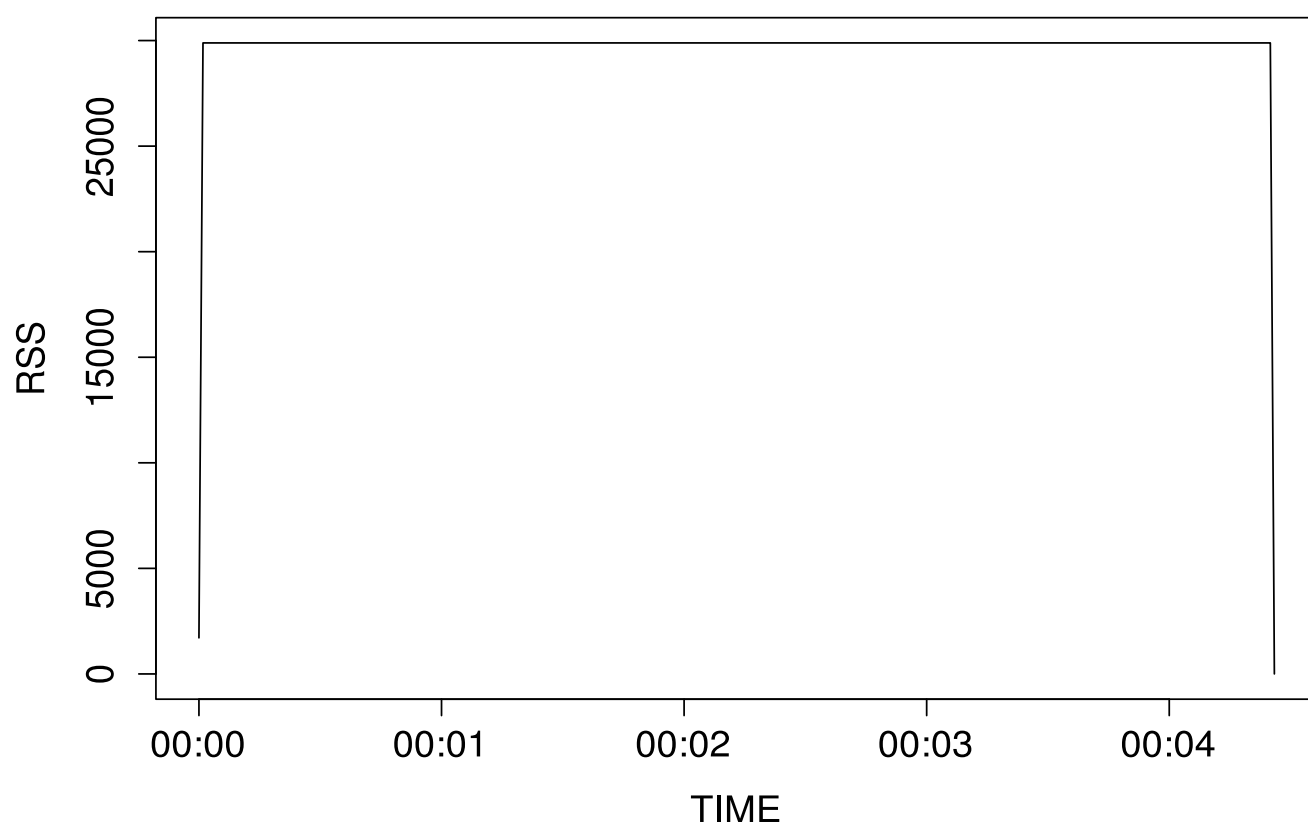


## Example 2: Extract non-coding regions and compute GC content

**Processor usage (%)**

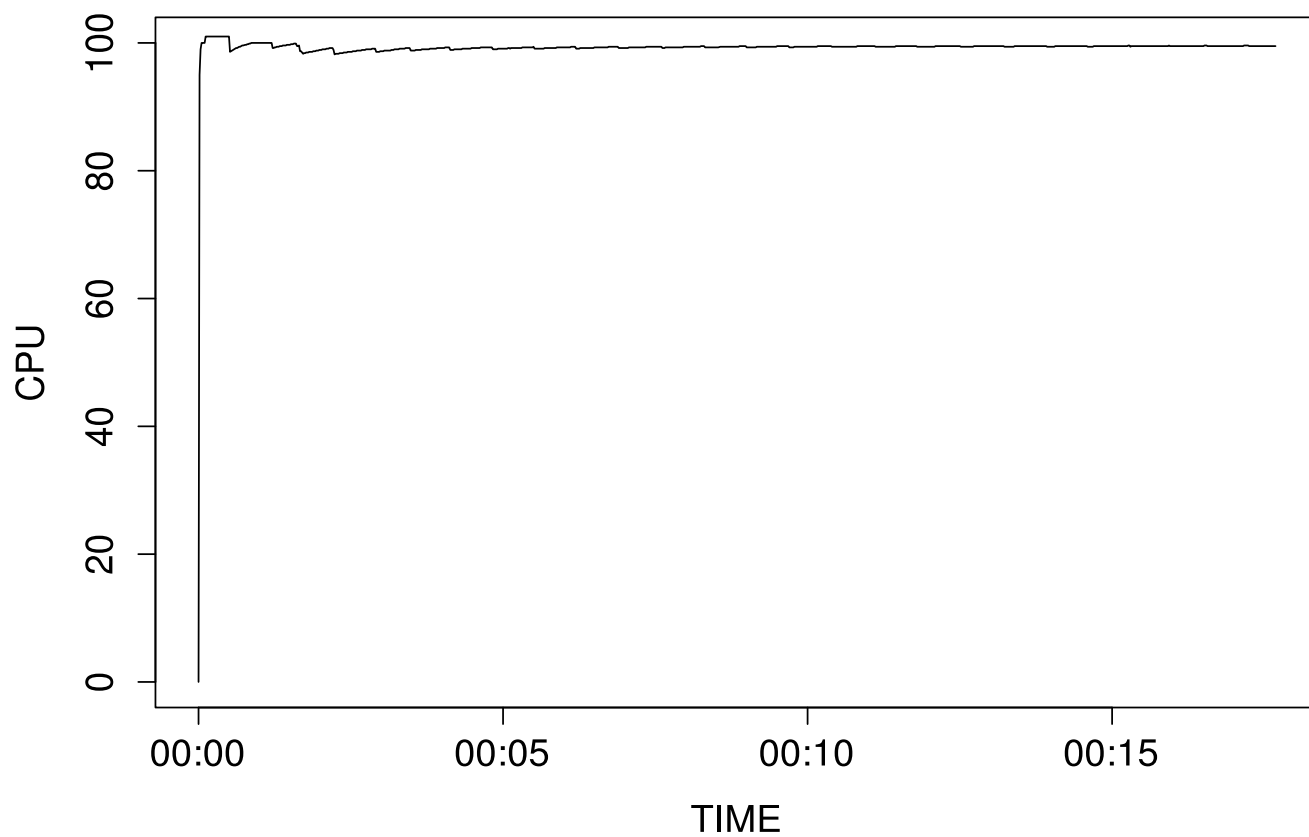


**Memory usage (kB)**



### Example 3: Extract homologous gene sets

**Processor usage (%)**



**Memory usage (kB)**

