

## Additional Figures

**Manuscript:** SigWin-detector: a Grid-enabled workflow for discovering enriched windows of genomic features related to DNA sequences

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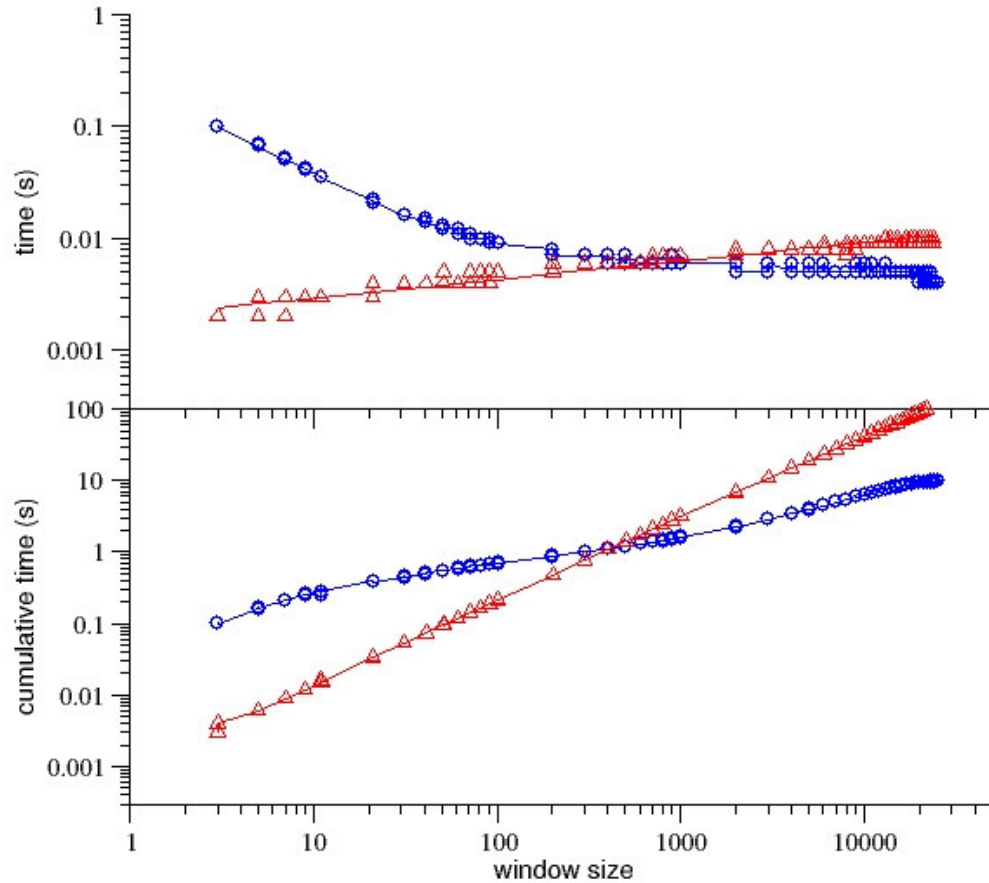


**Figure A1 - Moving medians comparison**

Upper: Time in seconds (s) to compute a moving median profile as a function of the window size for a sequence of size 25.000. Lower: Corresponding cumulative time to compute moving median profiles for a range of windows sizes  $S=3, 5, \dots, S_{max}$  as a function of maximum window size  $S_{max}$ . Triangles: Hardle and Steiger's algorithm [26]. Circles: our algorithm.

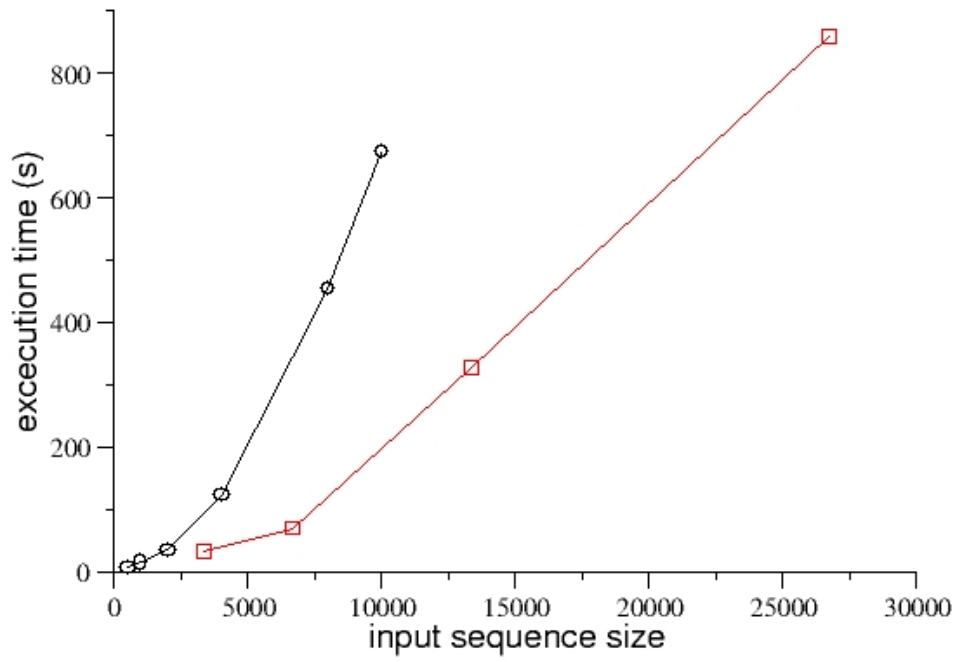


**Figure A2 - SigWin-detector performance**

Timing results of the SigWin-detector basic workflow as a function of the input sequence size  $N$  for different window ranges  $S=3, 5, \dots, S_{max}$ . Squares:  $S_{max} \sim N$ . Circles line:  $S_{max} \sim N/10$ .

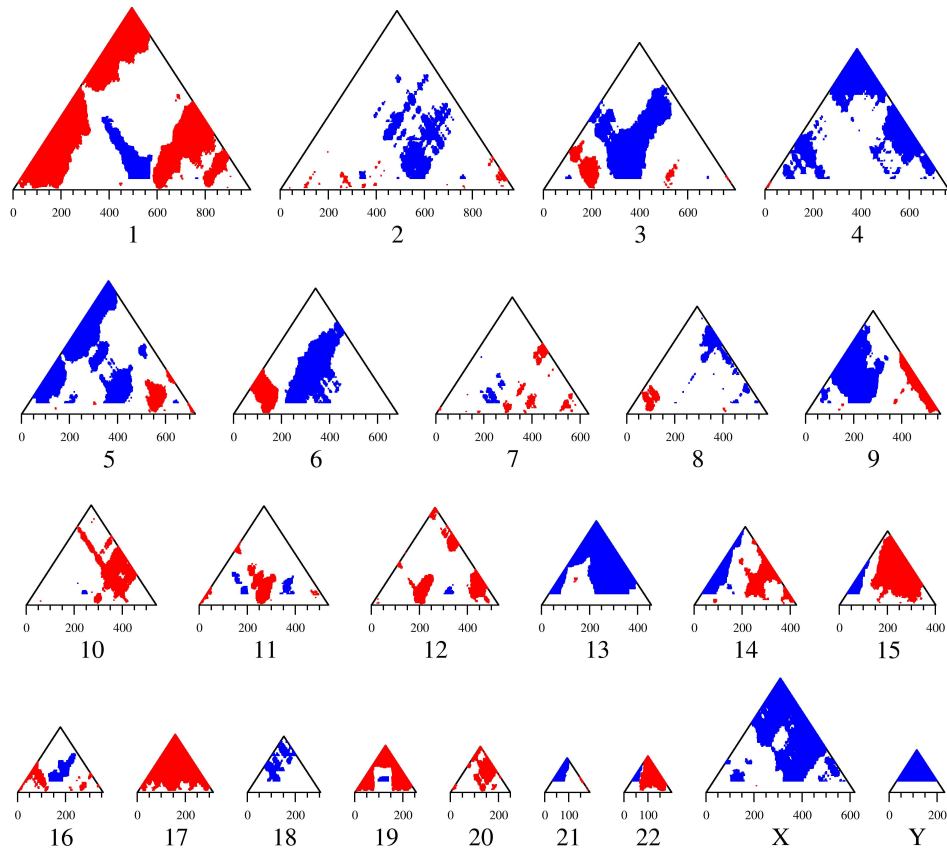


**Figure A3 - Positional RIDGES in a human transcriptome map (HTM)**

Positional genome-wide RIDGEOGRAMS per chromosome for the HTM based on the UCSC release hg18 [4] at 5% mmFDR level, made using SigWin-detector Config-Sub2 (additional information). The expression levels are mapped to chromosome position. RIDGES are in red, anti-RIDGES are in blue.