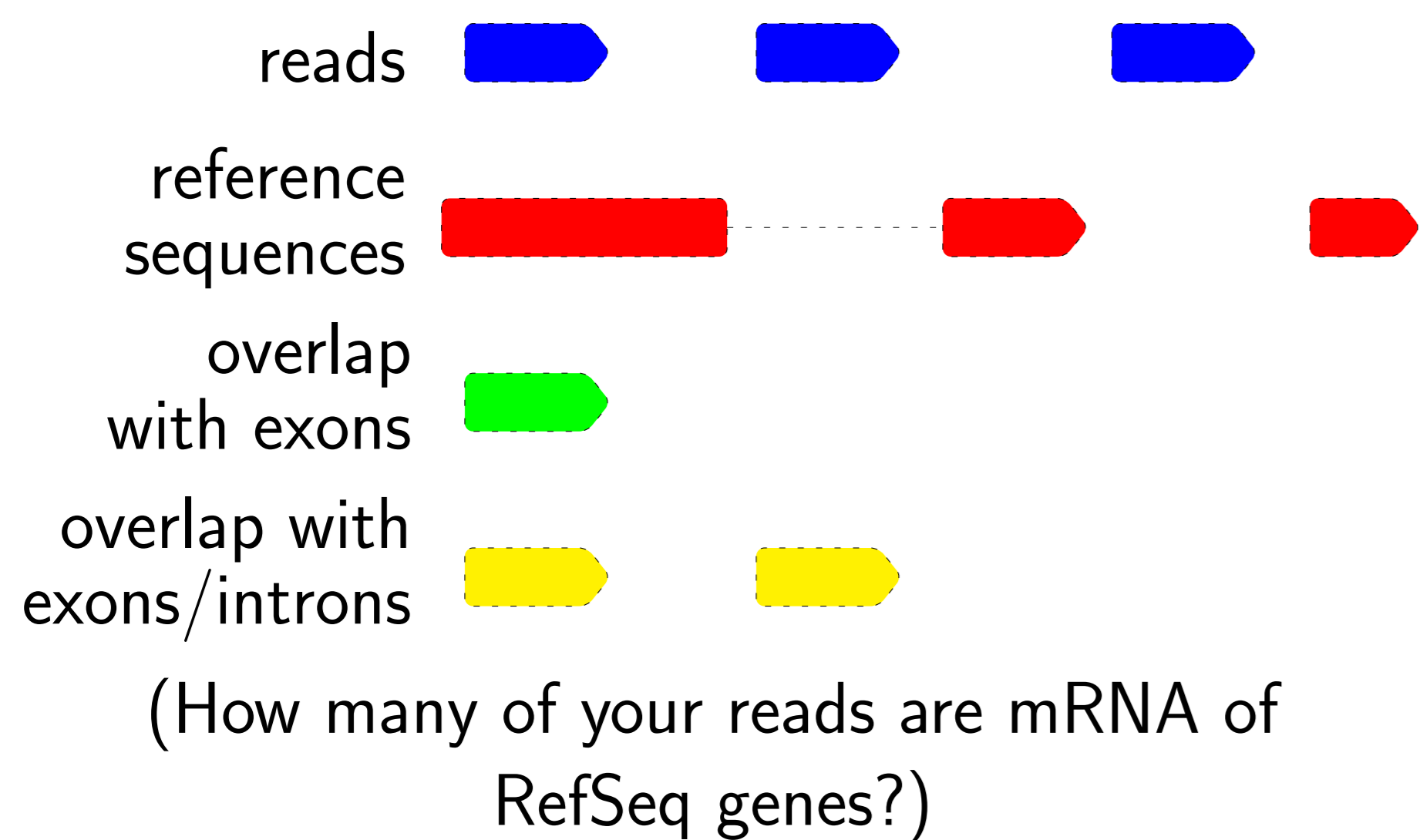


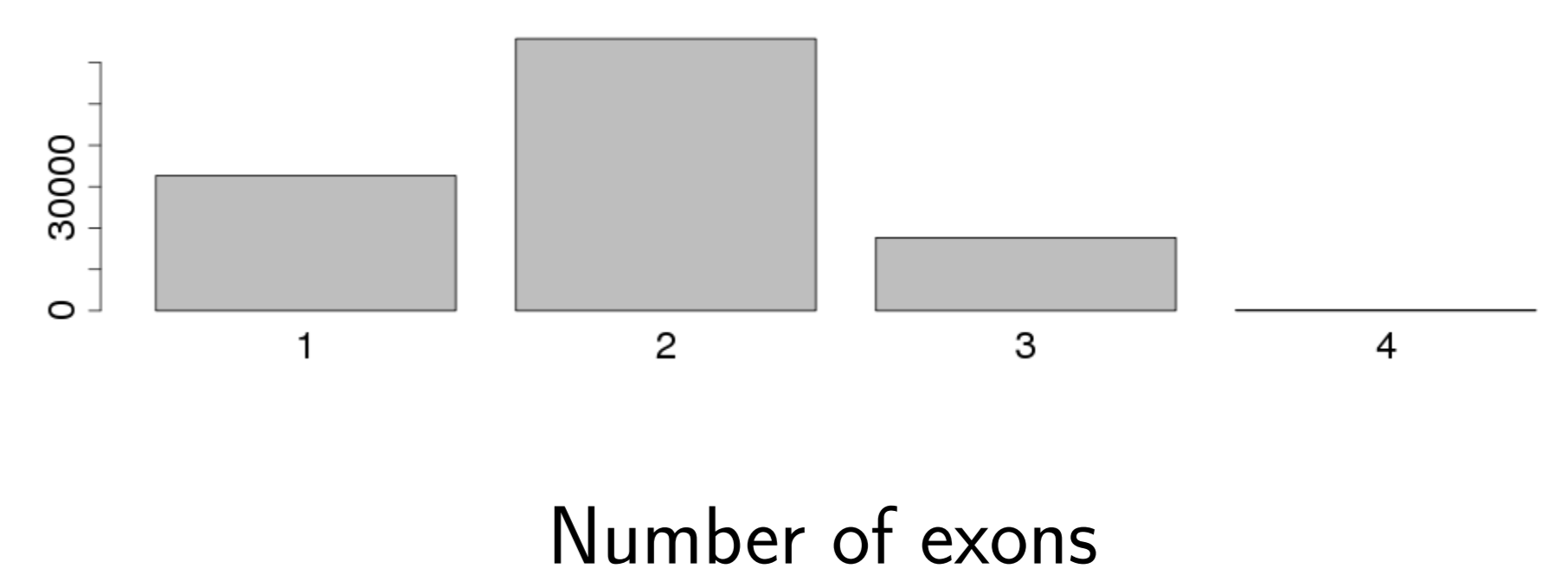
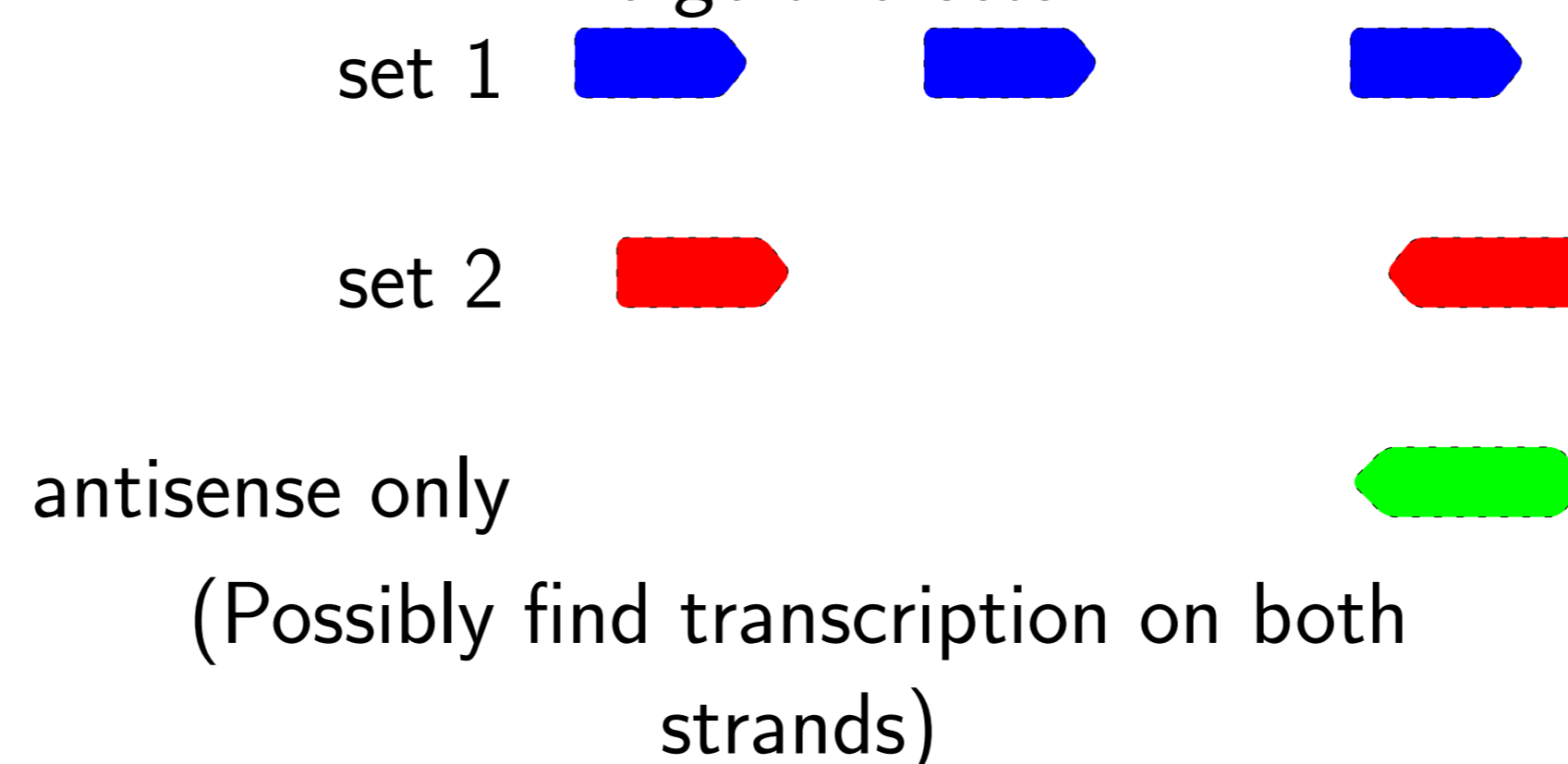
You have your high-throughput RNA/ChIP-Seq data. You know that many mapping tools exist (Maq, ZOOM, Mosaik, etc.), but what can you do with a set of genomic coordinates? Will you code another set of Perl scripts to analyze them? Better use S-MART!

Features

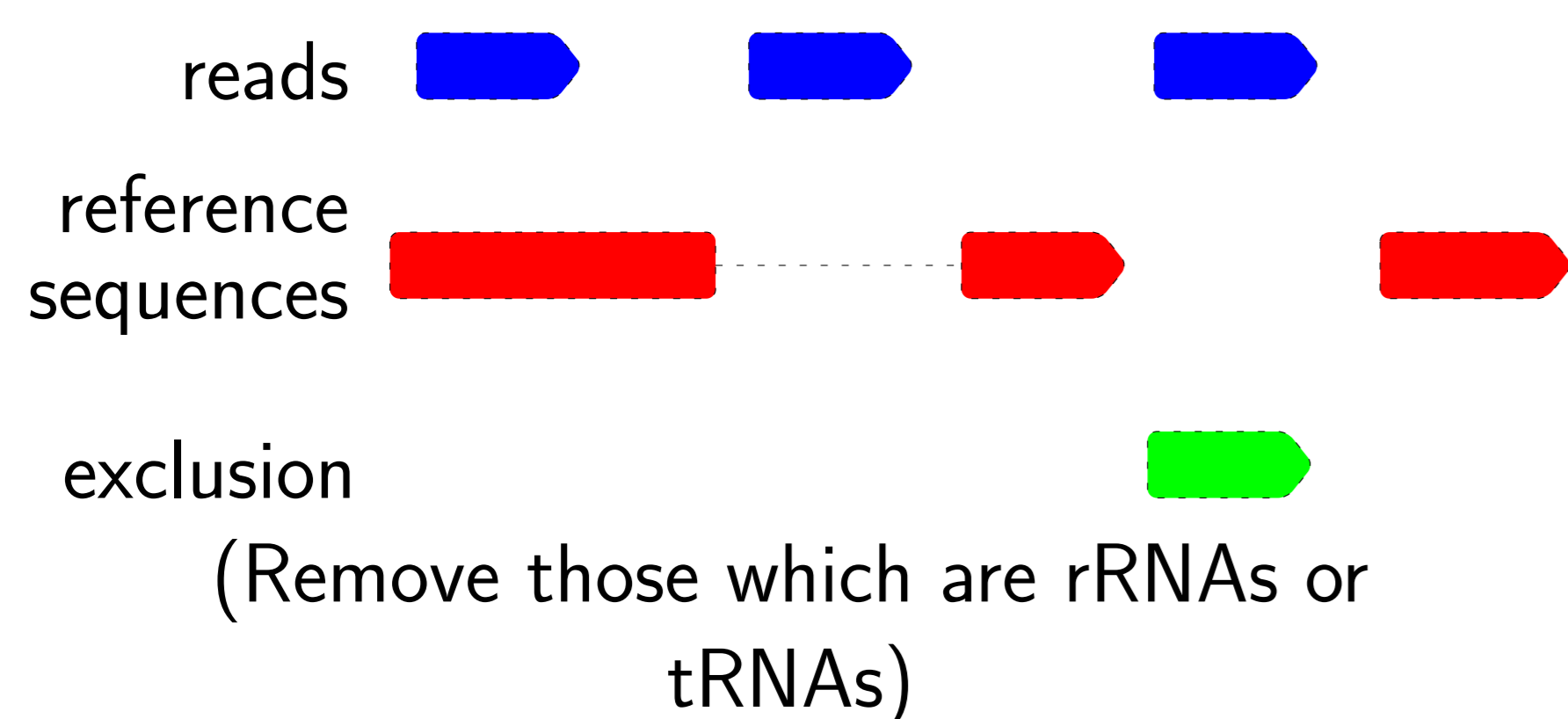
Check overlap with a reference set



Merge two sets

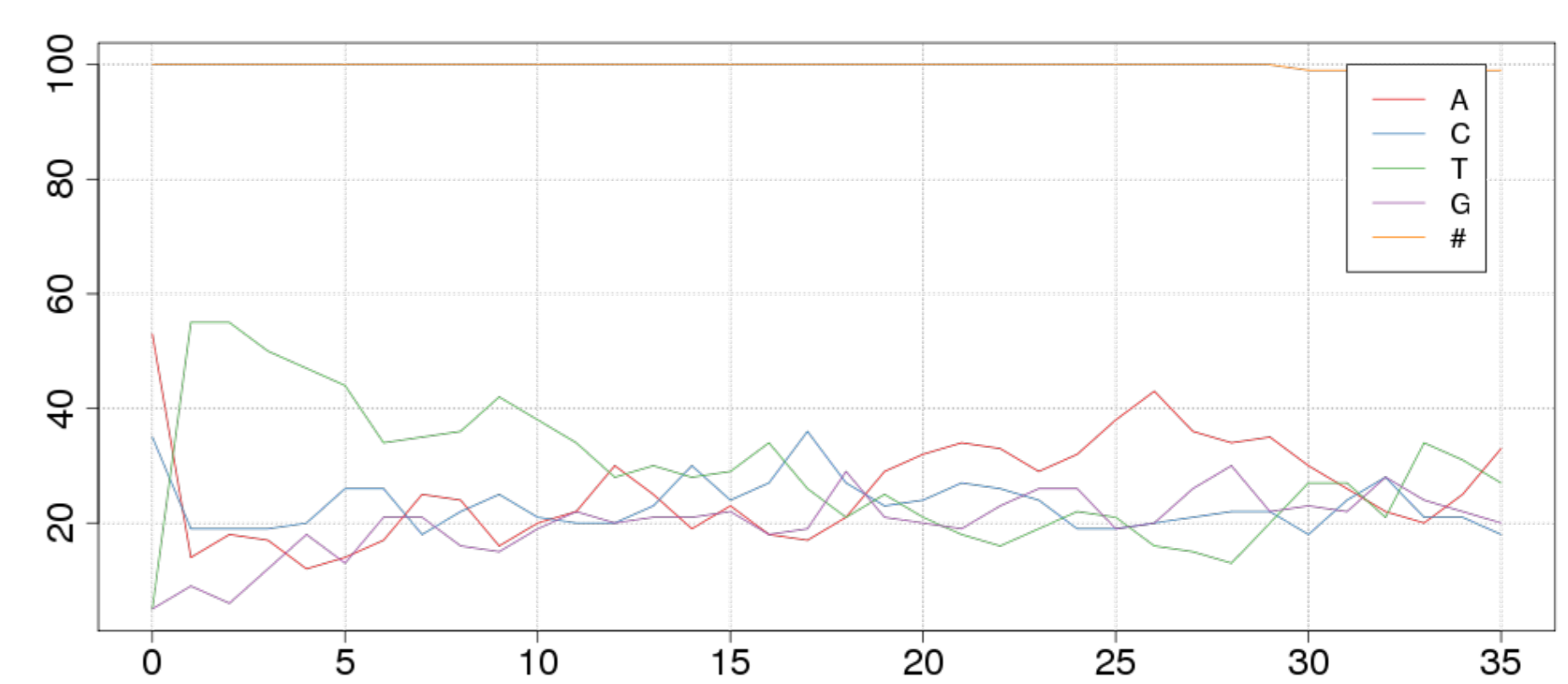
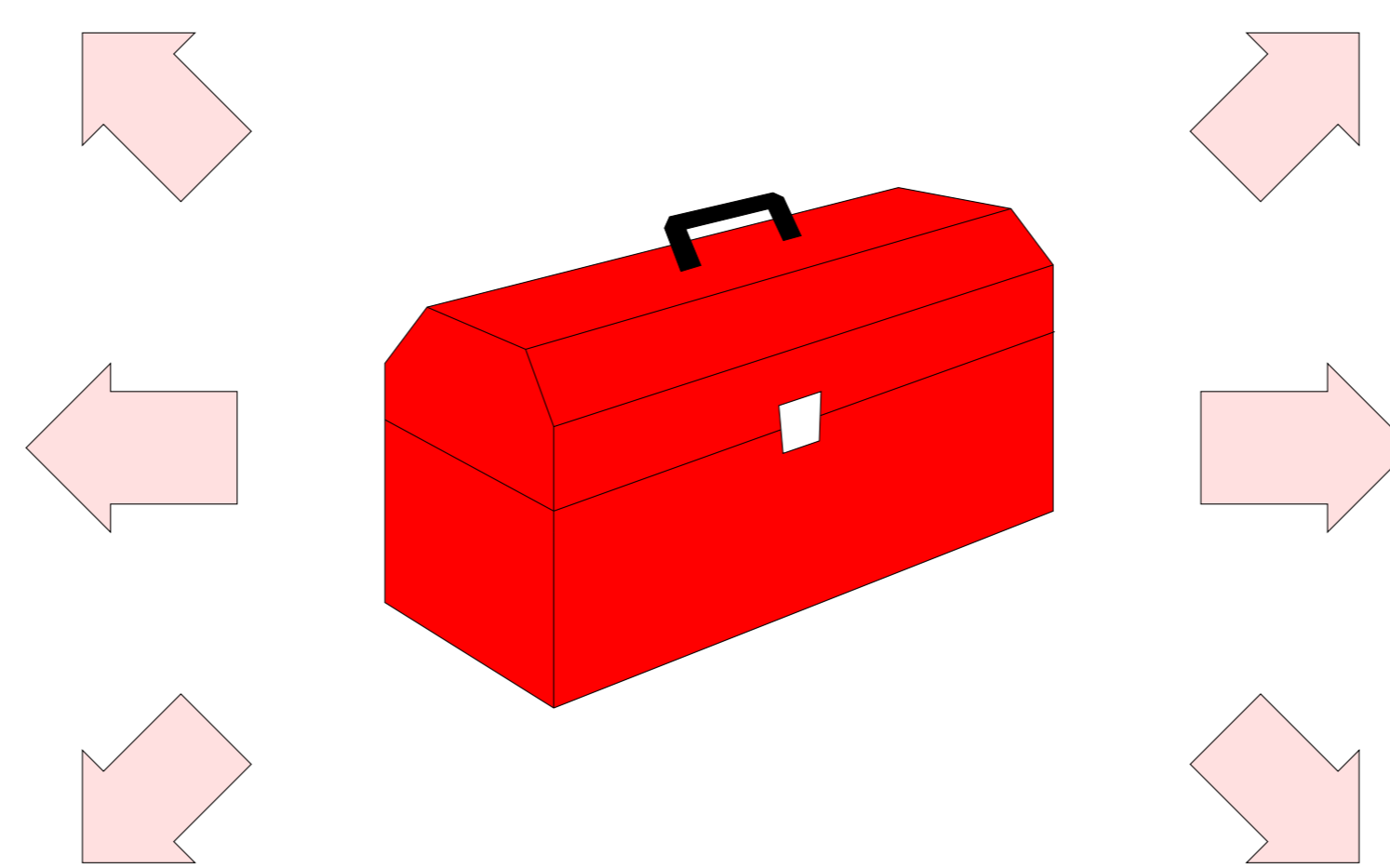


Exclude the reads which overlap with another set

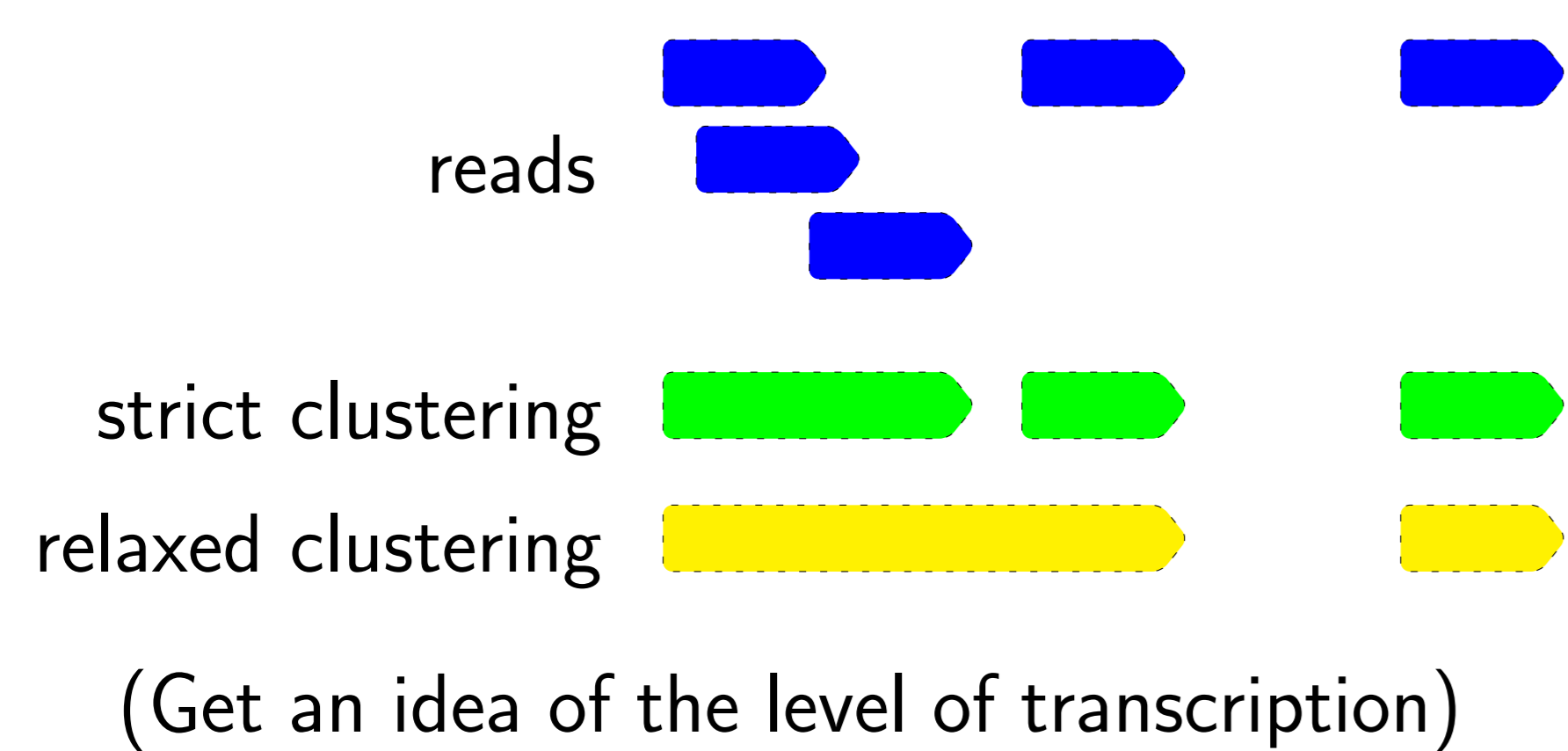


Transformation tools

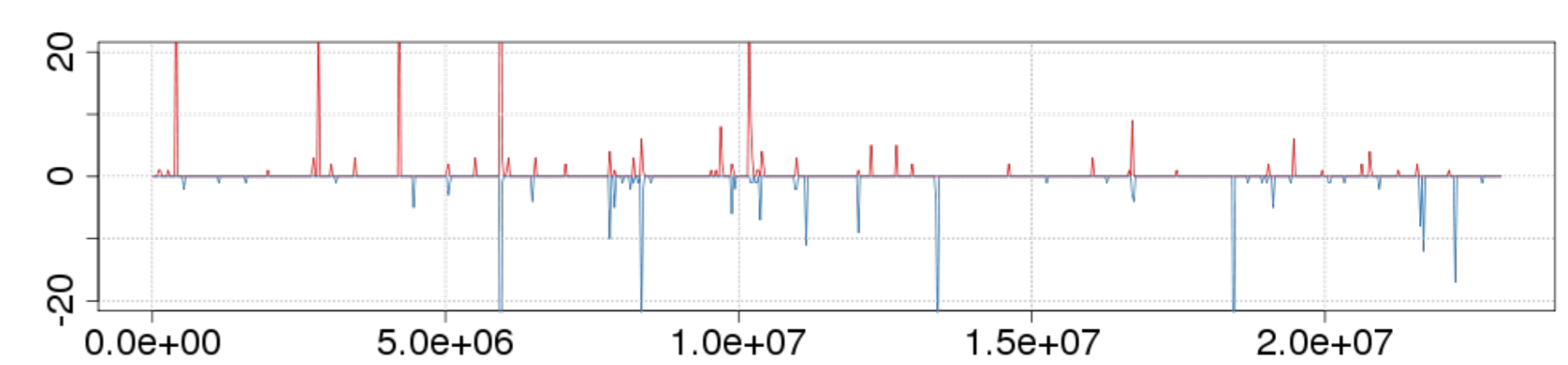
S-MART can select, remove, gather all or part of you data, depending on the task you want to perform



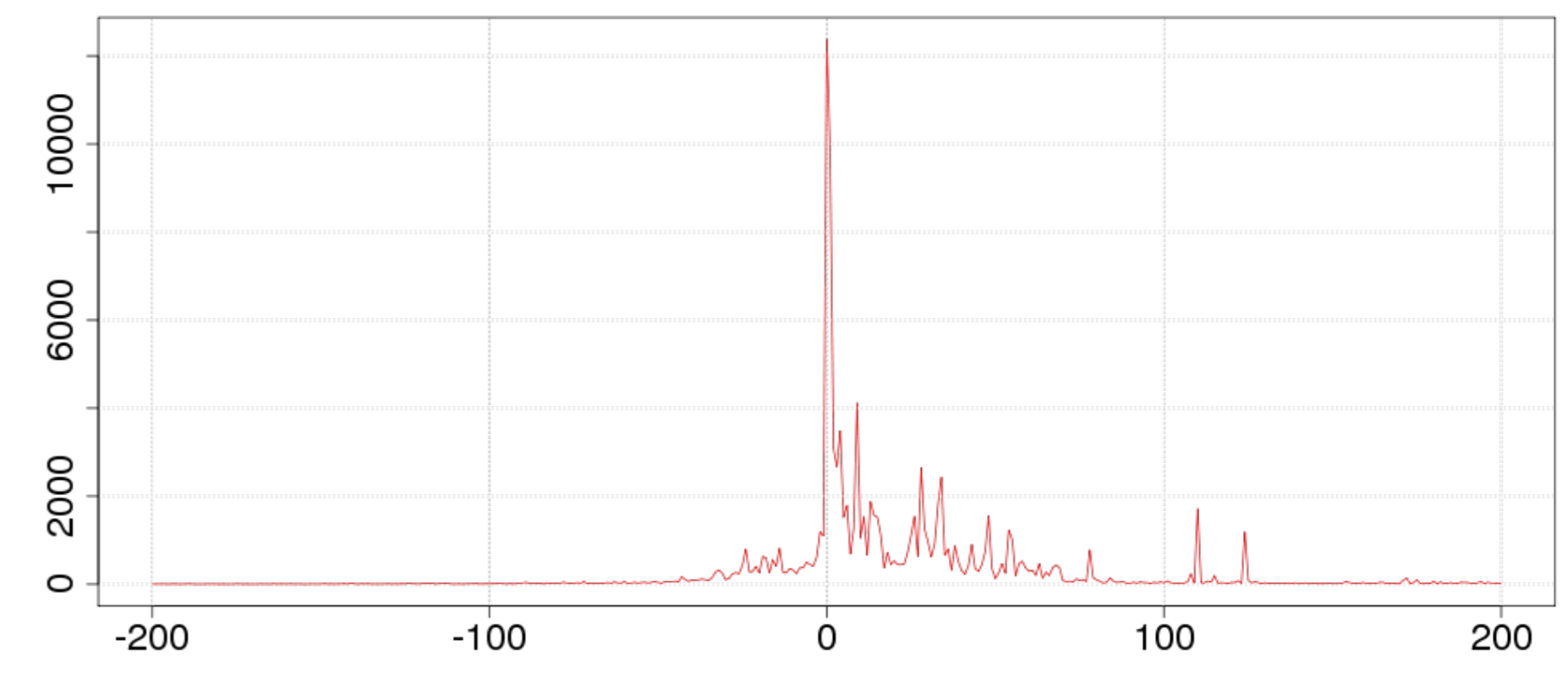
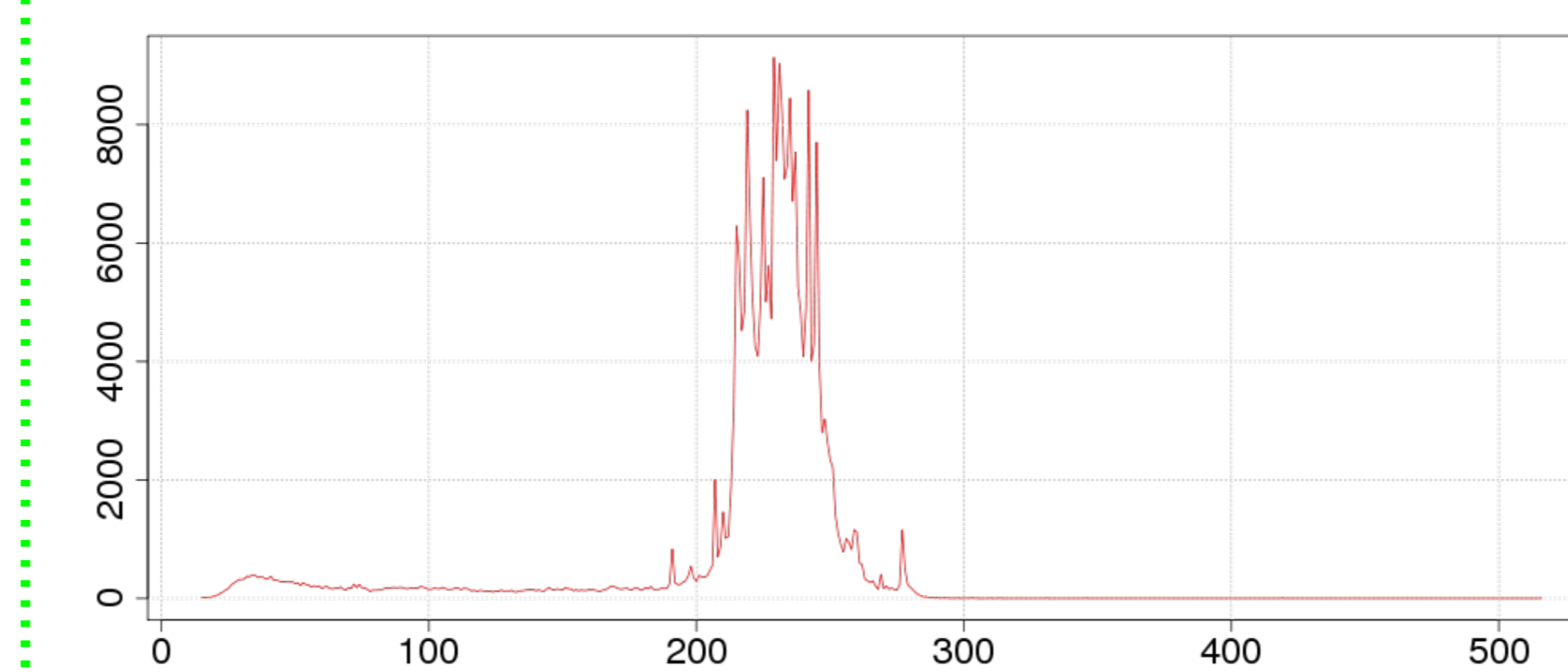
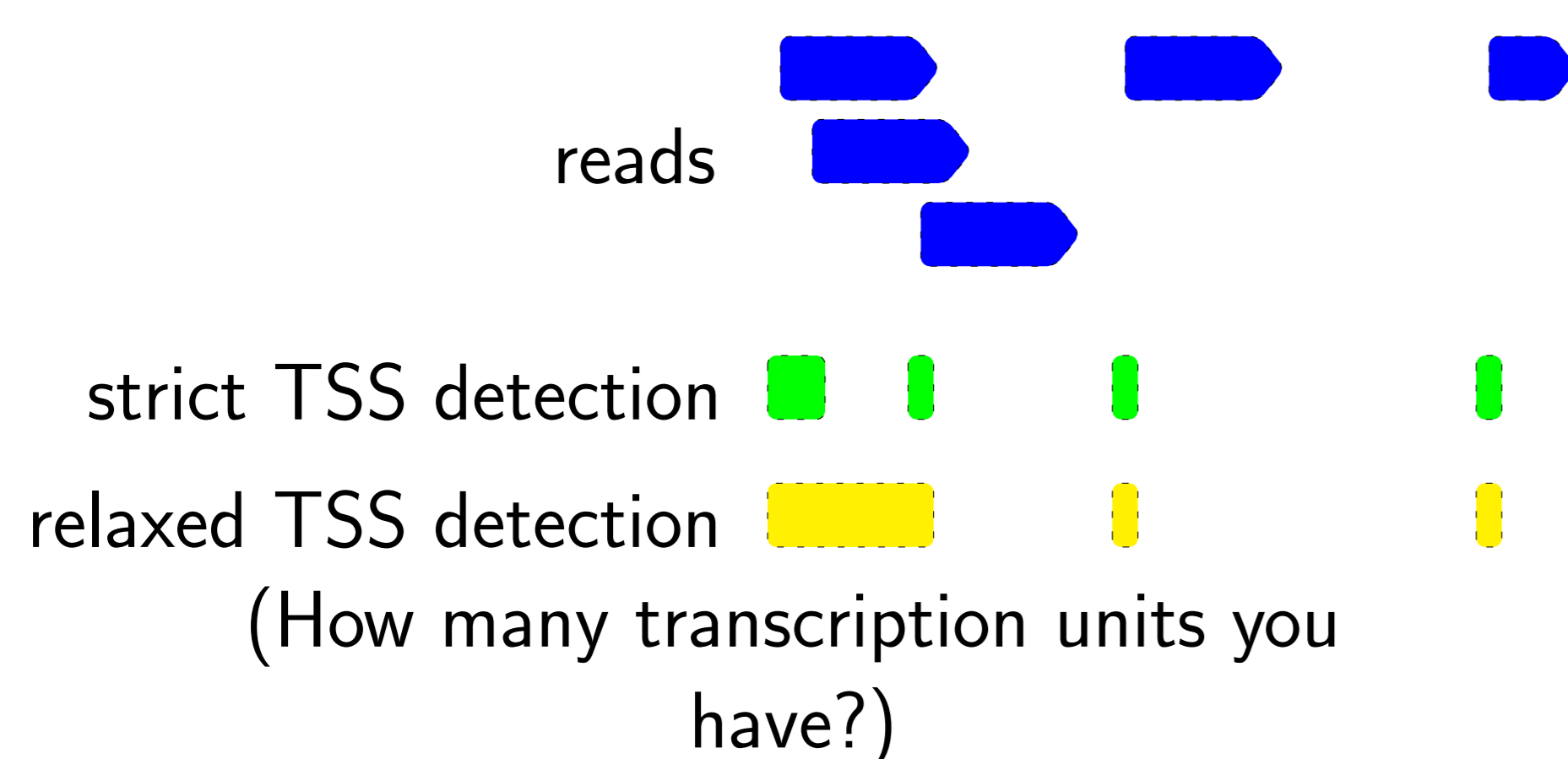
Cluster your data



S-MART provides you with different graphs in order to control your data or publish them
Visualization tools ↓ →



Find the TSS of the transcripts (when sets are capped)



Results

S-MART has been successfully to analyze our set of Solexa (> 5,000,000 reads, 36 nt. long) and 454 (> 250,000 reads, ~ 250 nt. long) data on *Drosophila melanogaster*.

We studied the impact of heterochromatin and transposable elements on the transcriptome. First results show that heterochromatin is actively transcribed and that transposable elements have an active role in this process.

We also studied the role of transposable elements in the formation of heterochromatin. We identified genomic regions possibly producing double-stranded transcripts linked with promoters of nearby transposable elements and producing small RNAs.

Implementation & Requirements

S-MART is a set of Python scripts which use MySQL to efficiently store genomic intervals. Nested bins are used to retrieve them quickly.

S-MART is made for use on a standard personal computer, under Linux. MySQL and R (freely available) are required. The tool is available from the authors.