## 4.1-Segment Graph


(ii) they describe the exon-intron structures of all transcripts spanning s (completeness)

## Unknown macro: 'mathinline'

(iii) they either differ in mode or in supporting transcripts (discrimination) <br> Unknown macro: 'mathinline'}

To ensure the properties of

## Unknown macro: 'mathinline'

 connected to an artificial source node, and all cleavage sites are connected to an artificial sink node [Sammeth 2008]. Once the segment graph
## Unknown macro: 'mathinline'

has been constructed for a locus, the edge set $E$ describes the backbone of exonic segments and introns from the $3^{\prime}$-most transcription start to the $5^{\prime}$-most cleavage site, with additional introns, source and sink links that allow to navigate alternative transcripts (Fig.1, panel A and B).

A


B


C


Figure 1: segment graph inferred on an alternatively spliced locus. (A) The exon-intron structure of a locus with two alternative transcripts. (B) Segment graph elements with links by exonic edges shown as solid arrows, links by intronic edges as dashed arrows, and source/sink links as dotted arroes. (C) Expansion of the segment graph by super-edges coalesced from adjacent exon segments or from splice junctions. (D) Super-edges formed by paired-end mappings within the bounds of the three windows marked, to keep (super-) edge combinations within graphical resolution bounds.

