4.2 - Read Mapping

To avoid redundancy caused by overlapping exons of alternative transcripts, we employ read mappings to the genome. However, our data structure also permits mappings to *de novo* transcriptome assemblies given that one provides coordinates relative to the projected contig of the assembled locus. The annotation mapping algorithm then assigns genomic read mappings to edges of the segment graph, following Definition 2.



Figure 2: mapping reads to the segment graph spanned by the annotation. (A) Exon segments and their respective super-edges in the case of overlapping exons. (B) Super-edges inferred by alternative splice-junctions. (C) Paired-end mappings to super-edges coalesced by (super-) edges constructed in (A) and (B).