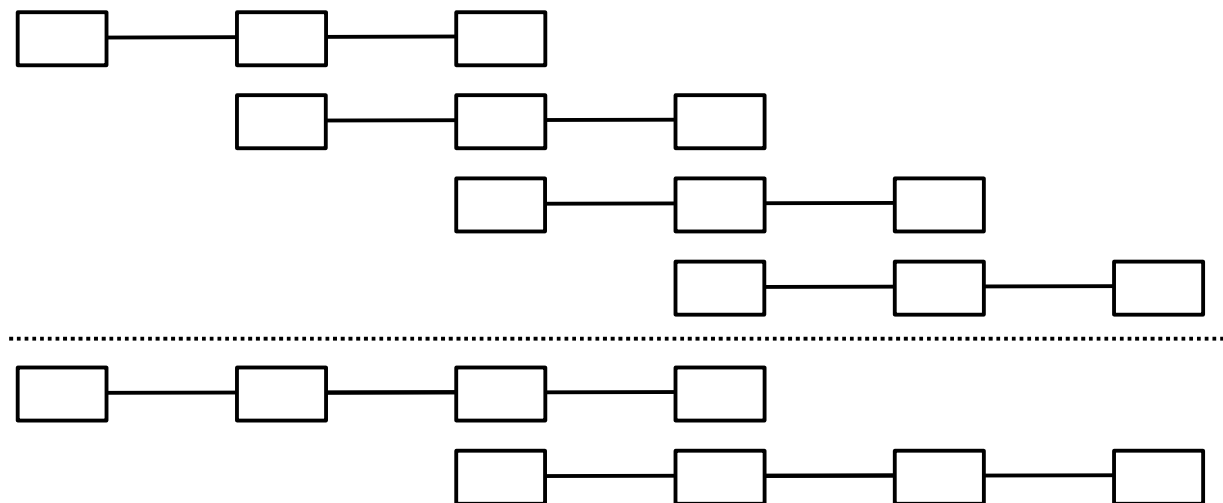
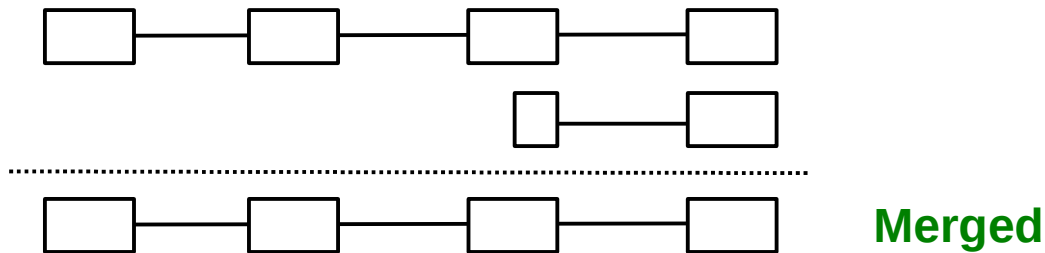
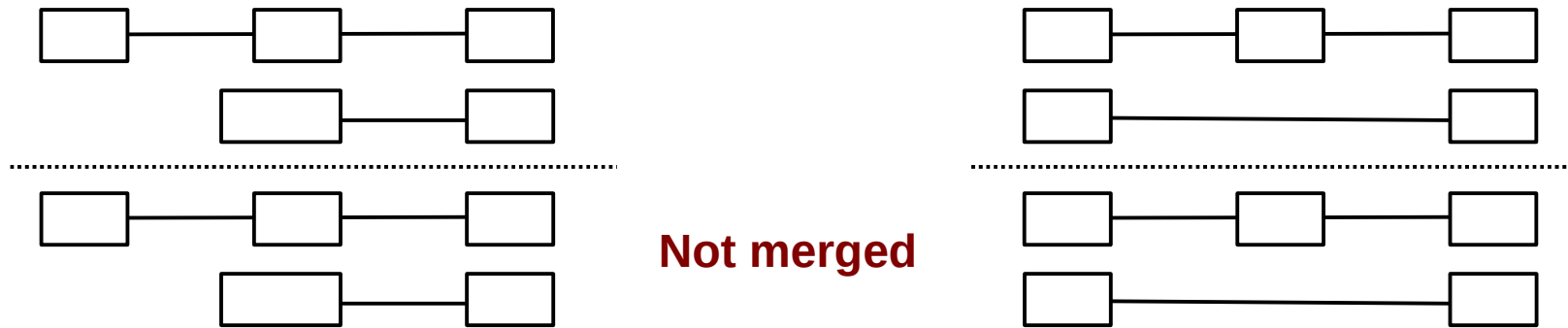


When and how does compmerge merge spliced transcripts?



Merged two by two
(3rd one does not have any
intronic bp in common with 1st)

compmerge rules

- Considers mono-exonic and spliced transcripts separately
- Merges mono-exonic transcripts based on stranded overlap (1bp)
- Merges spliced transcripts only if they fullfill the following pairwise rules:
 - their extents overlap by at least 1 intronic bp
 - all their overlapping introns are the same
 - no bp in their union is exonic in one and intronic in the other
- Spliced transcript merging:
 - is done from 5' to 3' (note: might give a different result than if done from 3' to 5'), merges transcripts as they come and records the individual transcripts present in a merged transcript
 - makes a partition of the input transcripts = 1 transcript can only be included in 1 merged transcript
 - each new transcript is compared to all the individual transcripts already present in each merged transcript
- The output file provides the ids of each individual transcript a merged transcript is composed of