When and how does `compmerge` merge spliced transcripts?

Not merged

Merged

2 first merged and 2 last merged
(3rd one does not have any intronic bp in common with 1st)
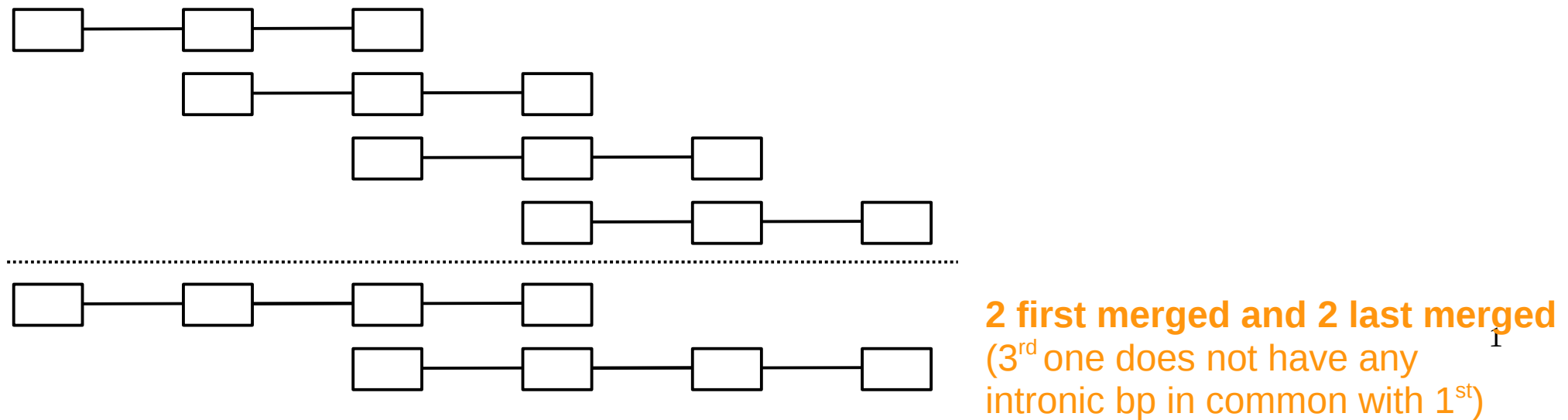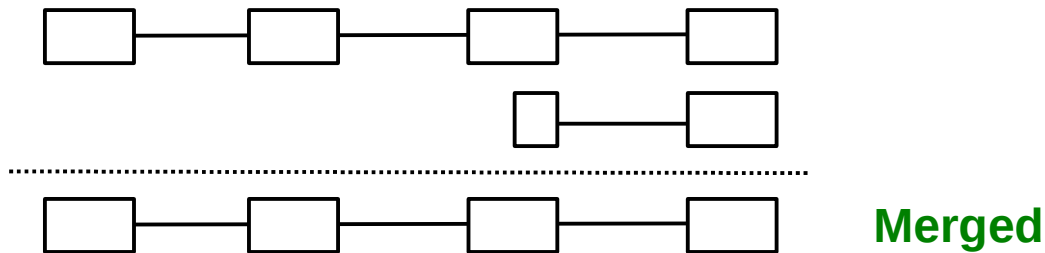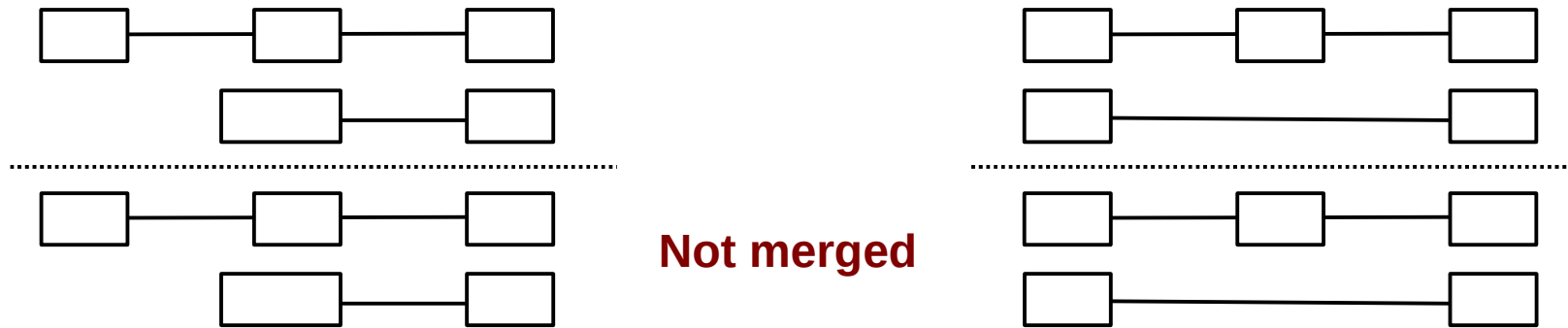
compmerge rules

- Considers mono-exonic and spliced transcripts separately

- Merges mono-exonic transcripts based on stranded overlap (1bp)

- Merges spliced transcripts if they fullfill the following pairwise rules with all the transcripts already in the merged transcript cluster:

    - 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