Guided RNA-Seq assembly

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Objective

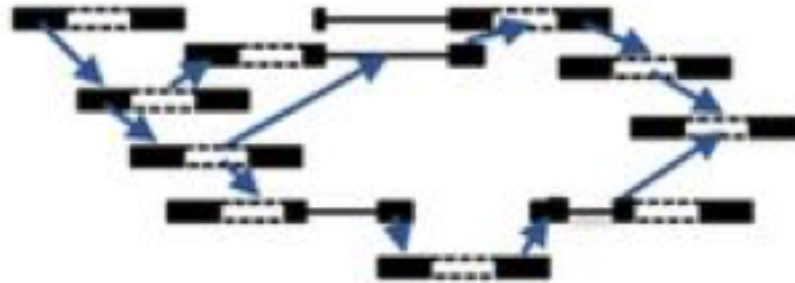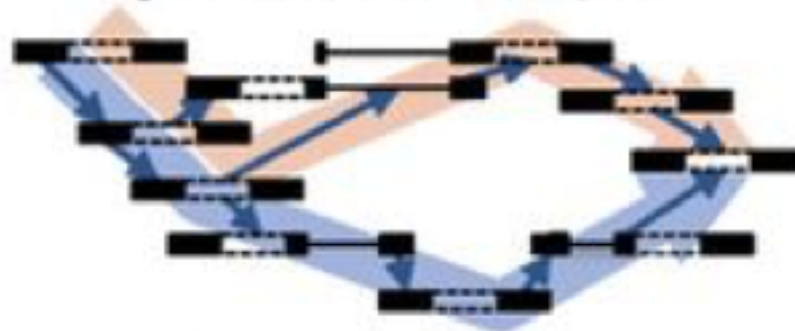RNA-seq reads
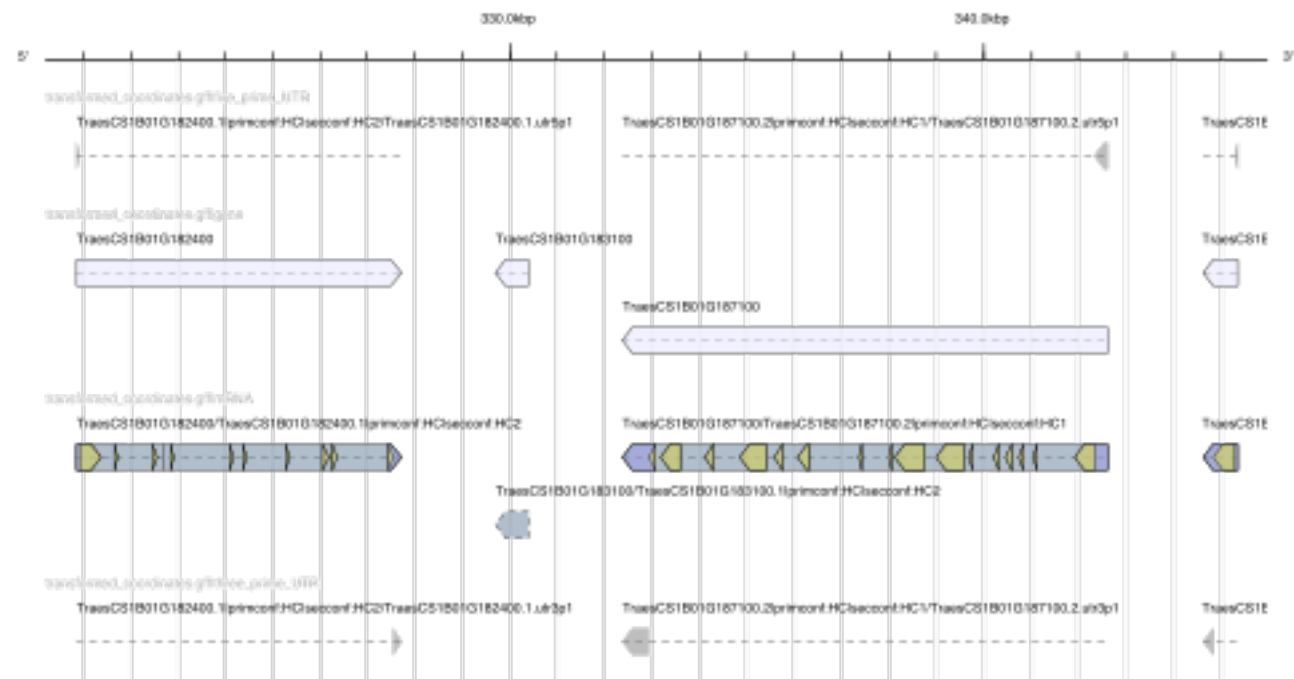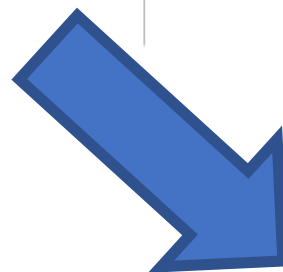
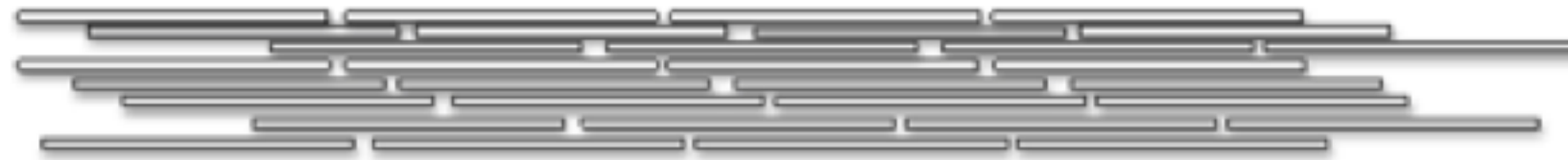# We have a reference genome!

Cufflinks

Build overlap graph

Compute minimum path cover to generate transcripts
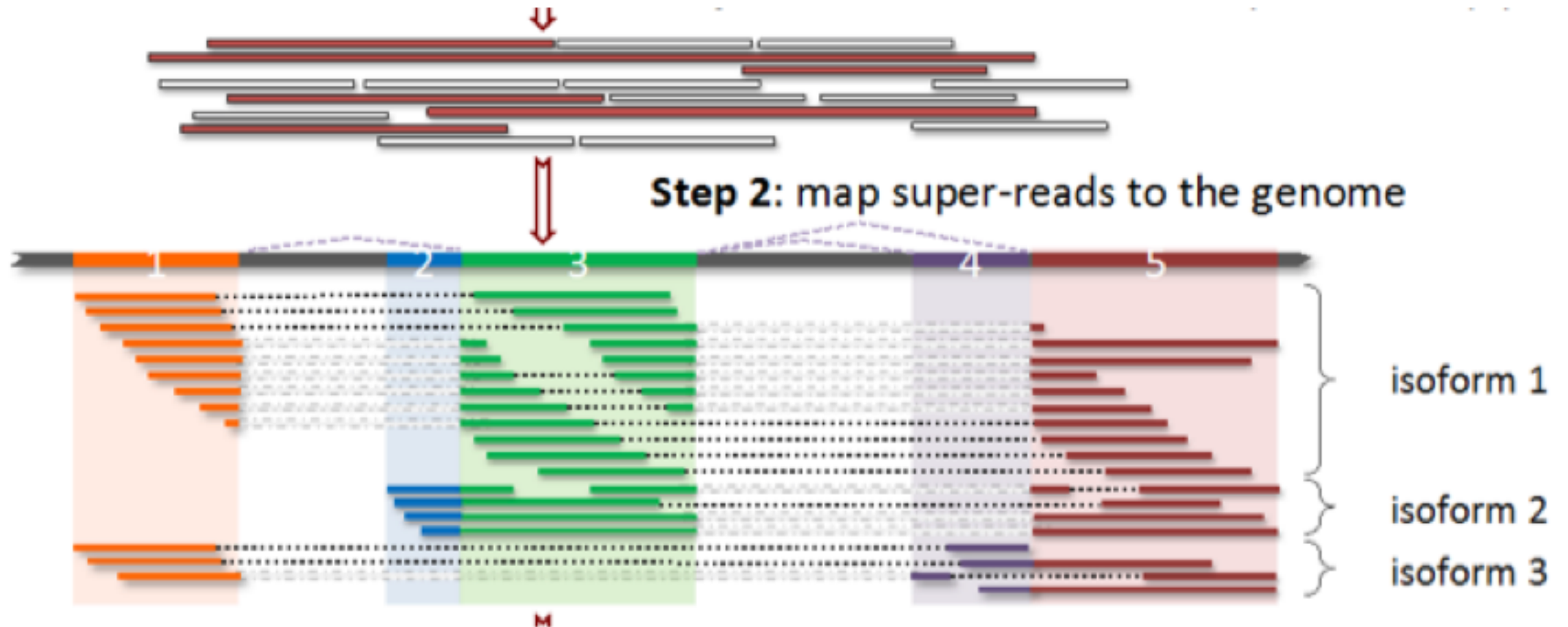
Maximum likelihood abundance estimation

StringTie

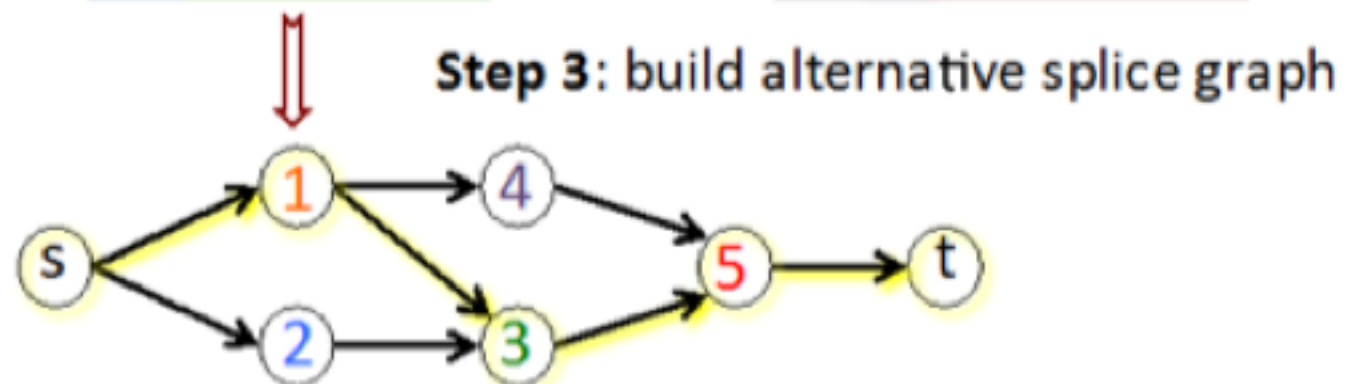**Step 1**: assemble reads into "super-reads"

StringTie

Step 2: map super-reads to the genome

isoform 1

isoform 2

isoform 3

StringTie

Step 3: build alternative splice graph

StringTie

Step 3: build alternative splice graph

Step 4: construct flow network for path in splice graph with heaviest coverage

Step 5: assemble transcripts and update coverage