

Week 5 Report

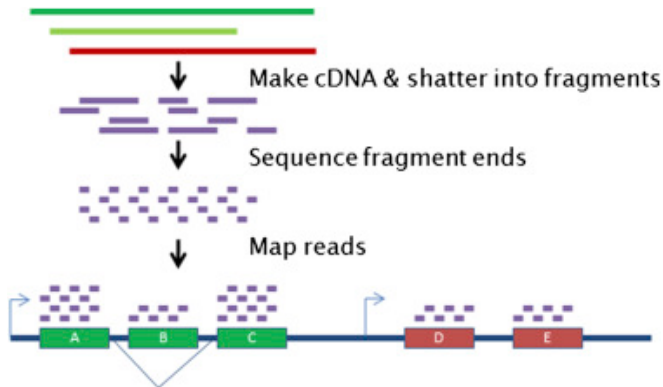
Chen, Pin-Jui

Oct 17, 2025

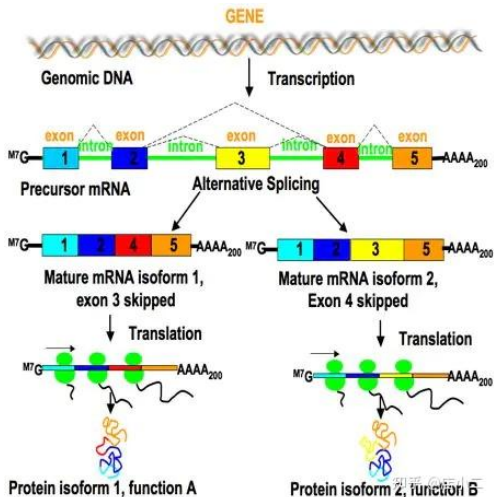
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- 1 RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome

Read

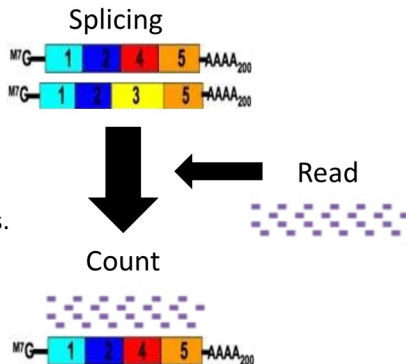


Alternative Splicing

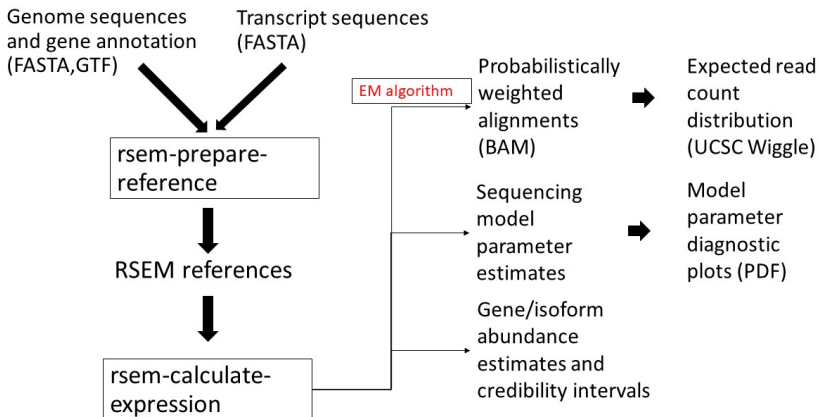


count

- Throws away data and produces biased estimates if “mappability” is not taken into account.
- Produces incorrect estimates for alternatively-spliced genes.
- Does not extend well to the task of estimating isoform abundances.



RSEM



參考文獻 I