Analysis of poly(A) tails by sequencing

Maria Nizik
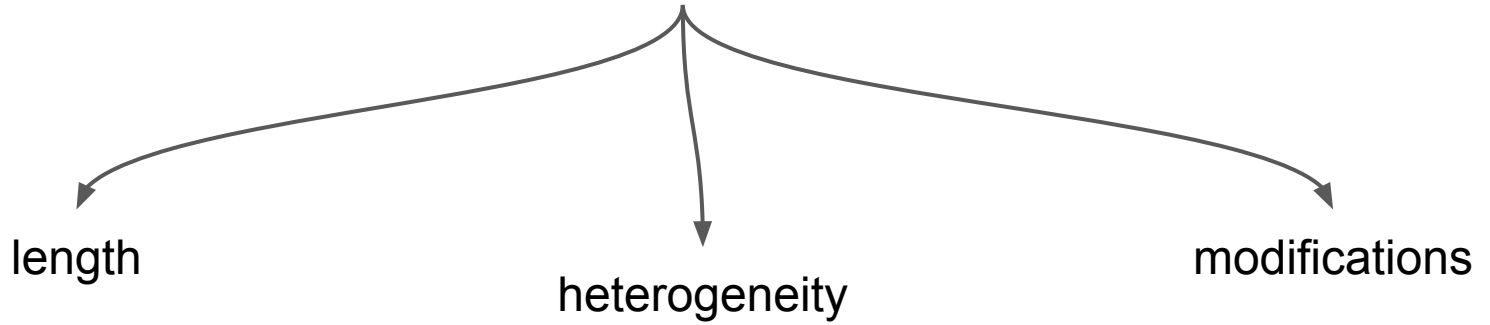
mRNA processing
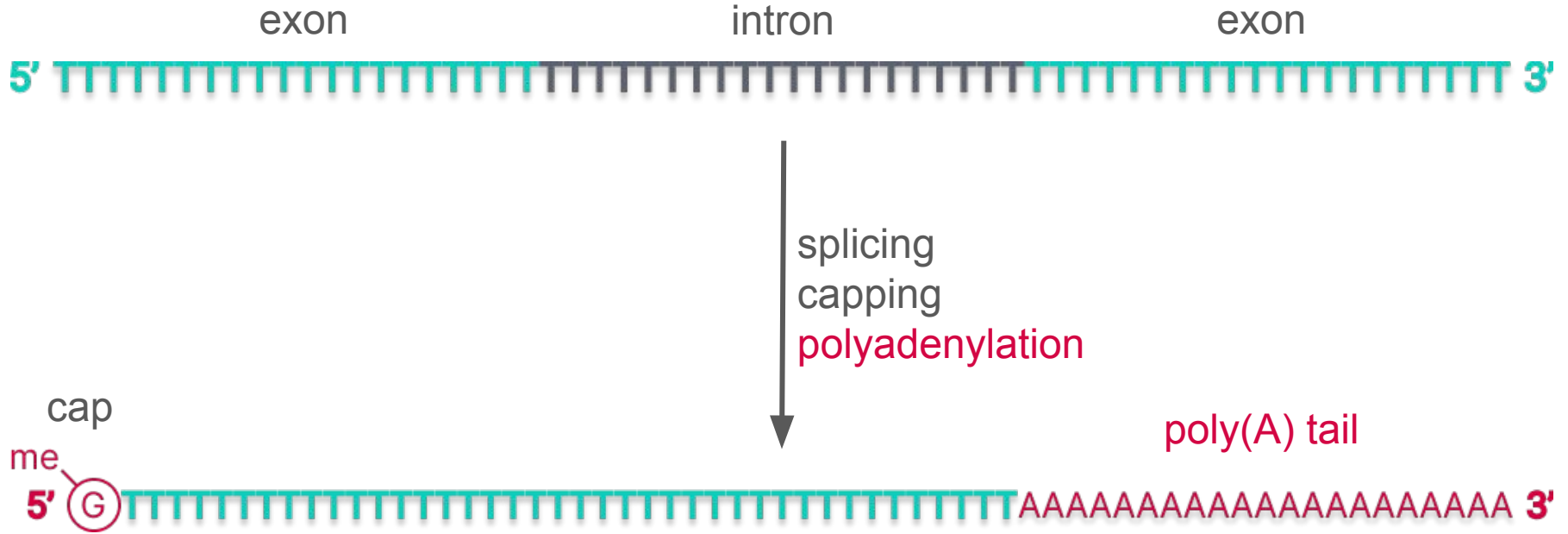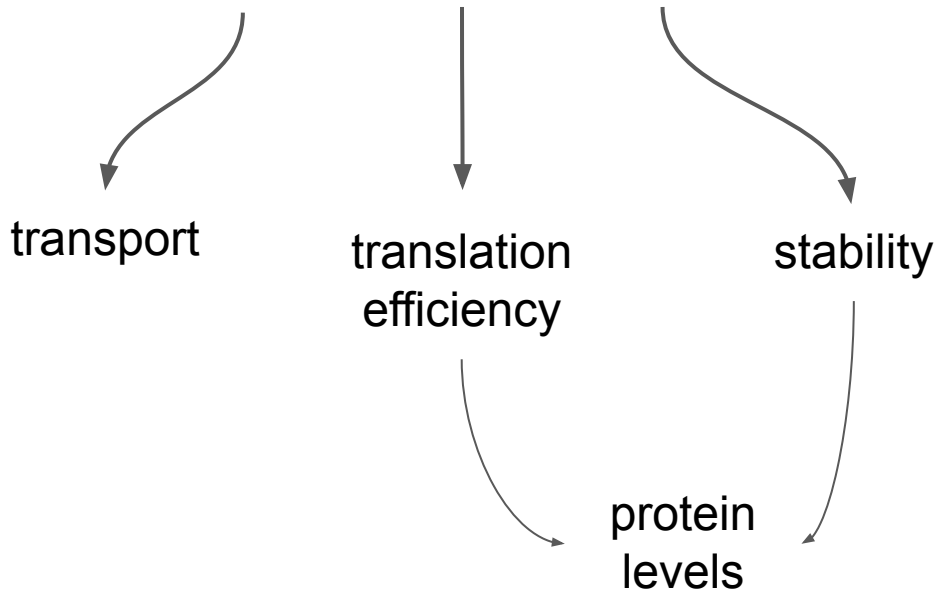
exon   intron   exon

5'   3'

splicing
capping
polyadenylation

cap

poly(A) tail

me

5' G   AAAAAAAAAAAAAAAAAAAAAAAA 3'

poly(A) tails diversity
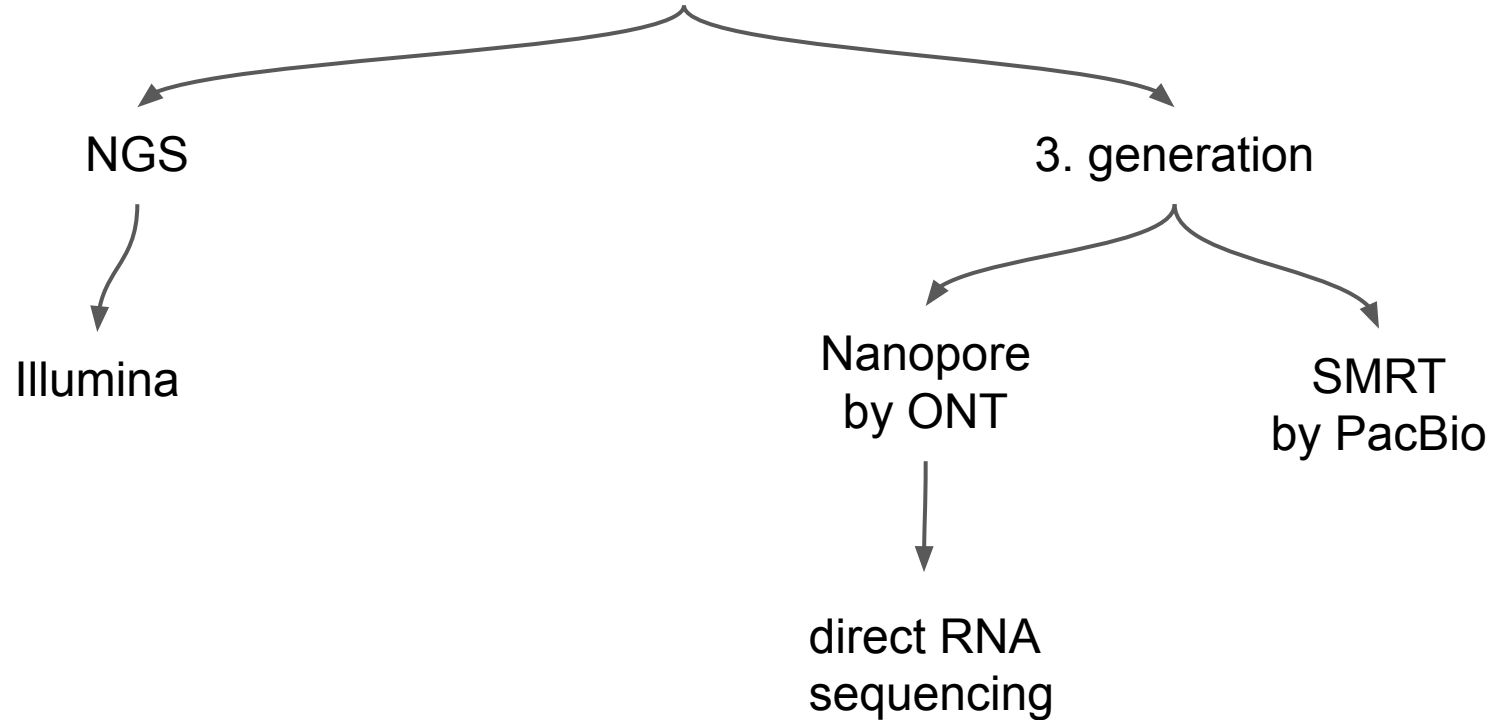
length

heterogeneity

modifications

AAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

AAAAAUAAACAAAGCAAAA

m6A

Tails are dynamic!

High-throughput
transcriptome sequencing

NGS

3. generation

Illumina

Nanopore
by ONT

SMRT
by PacBio

direct RNA
sequencing

Ilumina

PAL-Seq: poly(A) tail length estimated from the fluorescence signal intensity normalized to cluster density

TAIL-Seq and **m-TAIL-Seq**: identification of the transcript from read 1 (51 nt) and examination of the poly(A) tail with read 2 (231 nt)

SMRT by PacBio

FLAM-Seq (full-length mRNA sequencing)

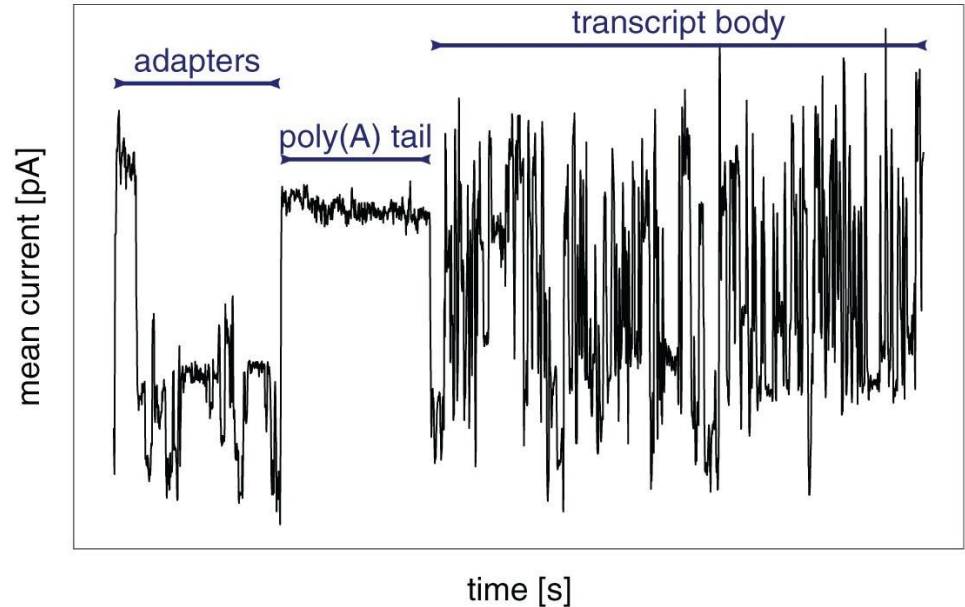**PAIso-Seq** (poly(A) inclusive RNA isoform sequencing)
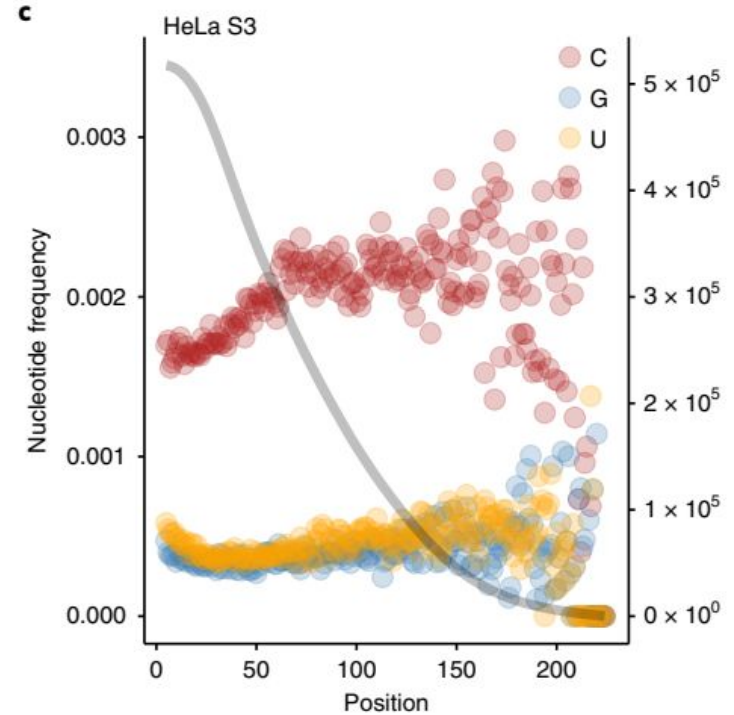
Leginini, et al., 2019

Nanopore - direct RNA sequencing

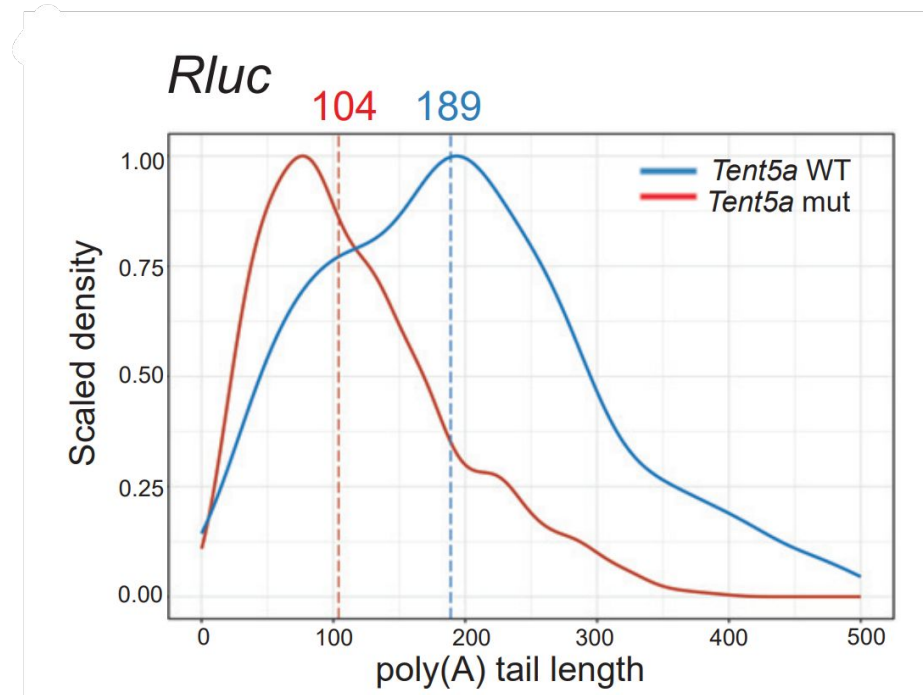Captures modifications and
enables precise length
measurements.

Nanopolish polya, TailfindR -
poly(A) tail length measurement

Brouze et al., 2023

DRS-based pol(A) analysis in action

Role of cytoplasmic polyadenylation in bone formation.

Gewartowska et al., 2021

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https://github.com/jts/nanopolish

https://github.com/adnaniazi/tailfindr

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