Sequencing RNA in New Ways: Engineering the Future of Nanopore Direct RNA Sequencing at the RNA Bioscience Initiative Laura K. White, PhD

- "master copy" of genetic information
- transcribed into "working instructions" for making proteins (mRNA)
- very stable, limited number of chemical modifications
- high turnover molecules that may contain DNA-derived instructions or perform other functional roles in cells
- 3 letter code for matching mRNA instructions with the correct amino acid
- many different chemical modifications

are tRNAs?



- Essential adapter molecules for making proteins
- At the bottom, the tRNA anticodon enables specific pairing with a corresponding codon sequence in mRNA
- At the top, tRNAs are charged with **amino acids** (the building blocks of proteins) that match their anticodon
- Chemical modifications impart stability & function

What is nanopore sequencing?

uncharged

Mean Current (pA)

- Compact, commercially available emerging technology for sequencing **RNA or DNA** with chemical modifications intact
- The only way to directly sequence RNA molecules
- RNA is pulled through **biological nanopores** embedded in ionically charged membranes
- Different RNA nucleotides (A,C,G,U) produce distinct changes in the flow of **ionic current** through the nanopores
- Additional distortions in ion flow due to **chemical modifications** can be identified using **machine learning** algorithms



peptide bond formation

In the image above, the yellow shapes are individual tRNAs whose anticodons are paired up with matching codons in mRNA to make sure the right amino acids are added to the growing protein



We developed a new approach to nanopore

sequence tRNAs with their amino acids intact.

1. Proprietary chemical ligation to amino acids

- 2. Attach additional sequencing adapters
- 3. **Sequence** on nanopore RNA flow cells
- 4. Classify tRNAs as aminoacylated or "uncharged" using custom trained **machine learning** models

We want to use this to:

study how tRNA aminoacylation is disrupted in childhood and neurological diseases

 understand relationships between tRNA modifications and amino acids

 develop machine learning models to identify amino acids from nanopore signal (new ways to sequence proteins using nanopores?)

Want to know more? Read all about it here! \rightarrow

White, Radakovic et al. <u>Nanopore</u> sequencing of intact aminoacylated tRNAs. BioRxiv preprint. Nov. 2024





Position

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