**Abstract:**

Given the similarity of ring molecules and their corresponding linear mRNAs, reconstructing circular RNA sequences (loops) from short RNA sequence reads has proven challenging. High-throughput full-length ring circuits cannot be detected using previous sequencing methods. Compared with previous methods, circular reverse transcription and size selection achieve 20-fold higher enrichment of RNA than total RNA. To reconstruct the sequence of looped molecules, we generated an algorithm called the siRNA identifier using long-read (CIRI-long) sequence data. A new form of intronic self-linked RNA. Our method uses long readouts from the nanopore to reconstruct full-length CircRNA sequences.

**Introduction:**

CircRNA has been associated with disease progression and prediction.Circular RNAs (circRNAs) are a broad class of RNAs with a covalent circular structure that regulate a variety of biological processes. The majority of circRNAs studied so far have been proposed to

1. act as microRNA (miRNA) sponges
2. act as RNA-binding protein (RBP) sponges
3. enhance protein function & encode peptides
4. form RNA duplex structures

The majority of current methods depend on the alignment of Illumina short RNA sequence reads (RNA-seq), and their detection ability is severely restricted due to the Illumina sequence reads' short duration. so we found long-read sequencing techniques such as Oxford and nanopore. PacBio sequencing was recently used to assess the full-length loop sequences of reverse transcription products for polymerase chain reaction in a recent report (RT-PCR). Specific PCR primers, on the other hand, were designed to target a subset of candidate ring loops and were only able to detect full-length sequences of selected ring molecules one at a time. Using nanoscale sequencing technology, we present an experimental and computational method (CIRI-long) for mass profiling of full-length looped rings. In contrast to currently available approaches, to discover and recreate ring molecules, and to provide new insights into the diversity of ring molecules and their biosynthesis.