**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

* act as microRNA (miRNA) sponges
* act as RNA-binding protein (RBP) sponges
* enhance protein function & encode peptides
* 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.

**Related Work:**

Using nanopore sequencing, we present an experimental and computational protocol for detecting full-length circRNA isoforms. To provide clear evidence of the circular structure of the transcripts, several rounds of circular amplification of the same circRNA molecule are reverse transcribed. CIRI-long has been thoroughly tested using simulated datasets and Illumina RNA-seq data. The reliability of our method in decoding the complex array of circular transcripts and splicing events that have not been studied previously has been demonstrated using virtual datasets, Illumina RNA-seq data, and experimental validation. It was discovered that the selection of section length is the main factor affecting RNA detection efficiency, When opposed to Illumina-based traditional sequencing, choosing the right length ( 1 kb) and optimising other processing conditions resulted in a 20-fold rise in circular readings. Many species of vertebrates have been shown to have an excessive amount of ring particles, according to recent research. CircAtlas, for example, gathered a total of 252,811 electrical circuits found in mice, while the GENCODE project only explained 138,835 versions. Check the diversity of the fields specified in the specified fields; unlike other existing methods that extend through BSJs, this approach checks the diversity of the fields specified in the specified fields. This method demonstrated that, each cloned cDNA molecule contained multiple copies of the corresponding full-length CircRNA sequence, and each long reading provided direct evidence of the existence and sequence of CircRNA. CIRI-long can accurately quantify additional alternate generalization and alternative splicing events and provide a more than five-fold increase in alternate generalization events compared to results obtained with Illumina RNA-seq. In addition, nanopore sequence libraries have detected multiple cirexons and AS events Compared to those detected with Illumina data