Alternative polyadenylation (APA) is a gene regulation mechanism by which a single gene encodes multiple RNA isoforms with different polyadenylation (polyA) sites. Most APA sites lead to identical protein products but variable 3’ untranslated region lengths, indicating a regulatory mechanism by which a single gene is expressed differently in a cell. Alternative polyadenylation (APA) is a gene regulation mechanism. The regulation of APA can be studied using RNA-seq data. The process of extracting APA sites from RNA-seq data can be done using various tools, including aptardi. The aptardi pipeline and machine learning model are robust.

**REFERENCES**


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**RESULTS**

- Alternative polyadenylation (APA) is a gene regulation mechanism by which a single gene encodes multiple RNA isoforms with different polyadenylation (polyA) sites. Most APA sites lead to identical protein products but variable 3’ untranslated region lengths, indicating a regulatory mechanism by which a single gene is expressed differently in a cell. Alternative polyadenylation (APA) is a gene regulation mechanism. The regulation of APA can be studied using RNA-seq data. The process of extracting APA sites from RNA-seq data can be done using various tools, including aptardi. The aptardi pipeline and machine learning model are robust.

**CONCLUSIONS**

- We devised a machine learning algorithm that takes a "use-all-data" approach for identifying polyadenylation sites expressed in a sample. Namely, aptardi incorporates both RNA sequencing and DNA sequence when making predictions. We first established that aptardi is applicable across datasets. We next established that aptardi improves upon current transcriptome reconstruction methods that do not consider DNA sequence. Finally, we showed that incorporating aptardi into transcriptome assembly may lead to novel insights when performing downstream analyses such as differential expression. Aptardi is freely available (https://github.com/lusk/aptardi).