

## **Modelling and detection of transcription termination sites of genes induced during low oxygen response in Arabidopsis**

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### **ABSTRACT**

Plants vary in their responses to low/without oxygen environment. The mechanism that controls such stress condition is still unknown. A number of researchers have been trying to find out the control of expression of genes under low/without oxygen mainly at transcription initiation sites as these regions have been populated with most of the regulatory signals. However, it is also equally important to look at the transcription termination sites of those genes as improper termination may lead to further complications such as non-functioning proteins that could lead to many other undesirable issues.

In this work, we have developed a model to investigate the region surrounding the poly(A) sites i.e. the site for transcription termination. This algorithm has been developed with the help of Support Vector Machines and Receiver Operation Characteristics. The program can distinguish between the up-stream and down-stream sequences of a poly(A) site. It can also distinguish between true and false poly(A) sites. Using our program, we are analysing the poly(A) site for about 100 genes (having 10, 000 nt downstream relative to transcription start sites) those were induced during low oxygen response in Arabidopsis.