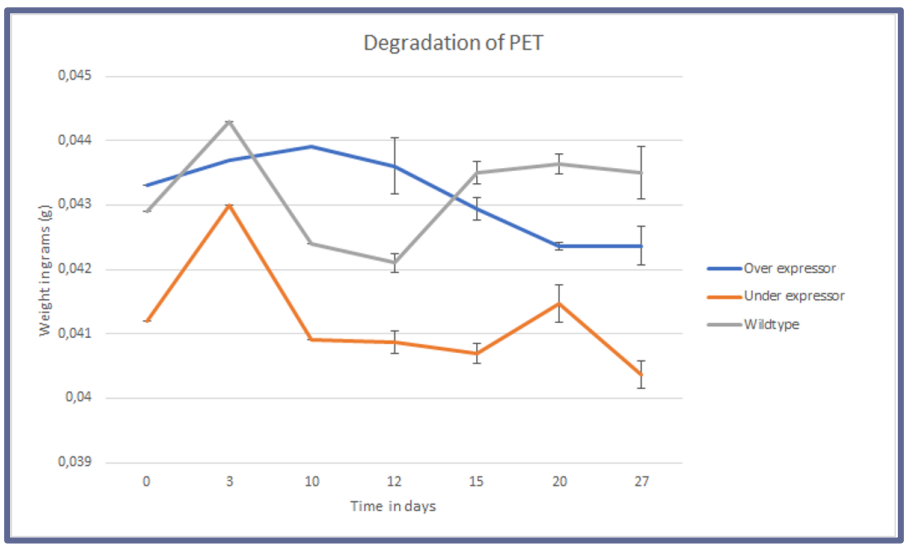
Analysis of Fungal enzyme mediated polymer degradation

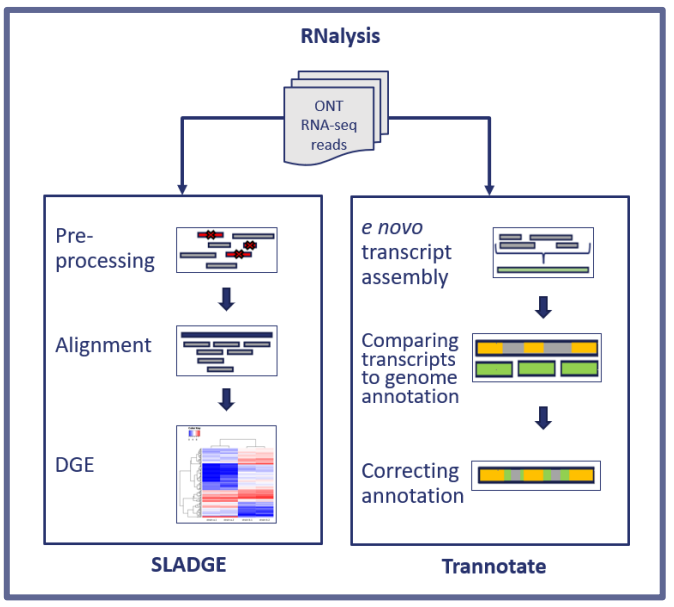
Case

In recent years scientist have been looking for microorganisms capable of biodegrading plastics. A certain fungal species with enzymes that show the potential to degrade polymers was discovered. To determine if this is really the case three strains of this fungal species were grown in a liquid minimal medium with a polymer as the sole carbon source. The three strains consists of a **wildtype**, an **over expressor** and an **under expressor**. To analyze differences in expression between these strains **ONT MinION** RNA-seq analysis is the most suitable choice. However no standardized analysis tools are available for this type of RNA-seq. Thus, one had to be created.

Polymer degradation

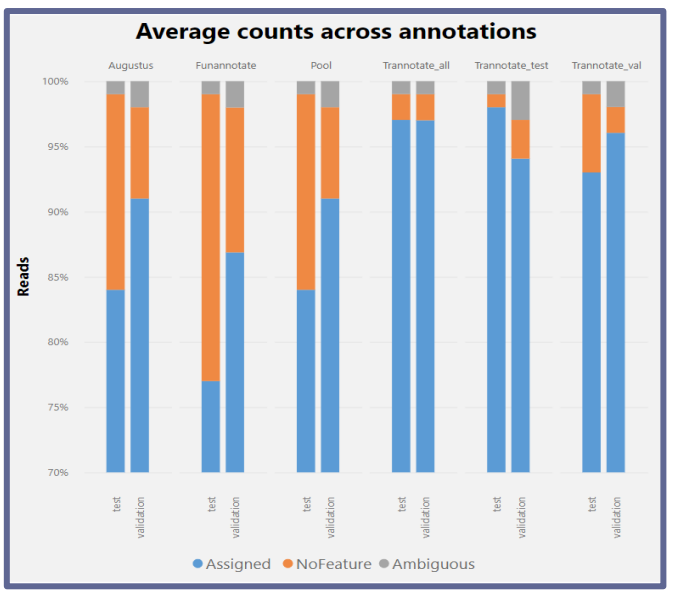
The three strains of the fungal species were cultivated in a liquid minimal medium with either **PU**, **PET** or **LDPE**. The degradation of the polymers was tracked by taking the weight of the pieces at certain intervals (see Graph). After 27 days of fungal growth and weight measurements a statistical analysis was done. The analysis showed that there was no biodegradation caused by the three strains. It was also determined that there was no difference in degradation between the wildtype, the over expressor and the under expressor. This could be because the enzyme activity was not high enough so it is recommended to change the medium to a solid one without a nitrogen source.





Creating RNA-seq analysis tools

RNA form the tree cultured fungal strains was isolated and sequenced using ONT MinION RNA-seq sequencing. The resulting RNA-seq data was used to test the created **RNalysis** package (shown above). Differential gene expression was perfumed by **SLADGE**, indicating no difference in expressed genes between the tree strains. Transcript annotation was perfumed by **Trannotate**, indicating increases in assigned reads (shown below). The **RNalysis** package must still be further tested and validated. However, it already proved to be a capable analysis package.



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