

FAIRification of IsoSeq Evidence-driven annotation of the biodiversity



The project will leverage SQANTI3 – a quality control tool for long-read transcriptomic data, which filters inaccurate models to enhance genome annotations – alongside the FAIR principles, to create an open-source, standardised IsoSeq evidence-driven annotation pipeline. This initiative will refine genome annotation practices, support broader European and global genomic projects, and facilitate the characterisation of genomes for all species on Earth.



Challenge

The project tackles the urgent need to understand species' resilience to climate change, impacting ecosystems and conservation efforts. A major challenge lies in improving genome annotation, essential for organising and preserving genomic data.

Solution

A benchmarked pipeline for long-read-driven genome annotation, designed for seamless integration with existing genome annotation efforts, significantly enhancing the quality of annotations. It will utilise existing IsoSeq data and promote the generation of new data to further improve annotation accuracy.

Scientific Impact

This project is expected to significantly enhance the quality of both current and future genome annotations.

Partners

Spanish National Research Council-Institute for Integrative Systems Biology