OSCARS
Open Science Clusters' Action for Research & Society

Funded Project

FAIRification of IsoSeq Evidence-driven annotation of the biodiversity

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CSIC — Consejo Superior de Investigaciones Científicas

Genomics of Gene Expression Lab

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- Understanding species' resilience is crucial for conservation, but genome annotation remains a major hurdle

- Long-read RNA sequences present challenges in the integration into pipelines, due to noise and innacuracies

- Existing guidelines lack clear instructions on using full-length RNA sequences, limiting data integration and reuse

- Development and implementation of a FAIR workflow to perform IsoSeq-driven genome annotation

- Connecting databases and pipelines:
  - European Nucleotide Archive
  - European Reference Genome Atlas

- Encouraging the generation of IsoSeq data for non-model organisms

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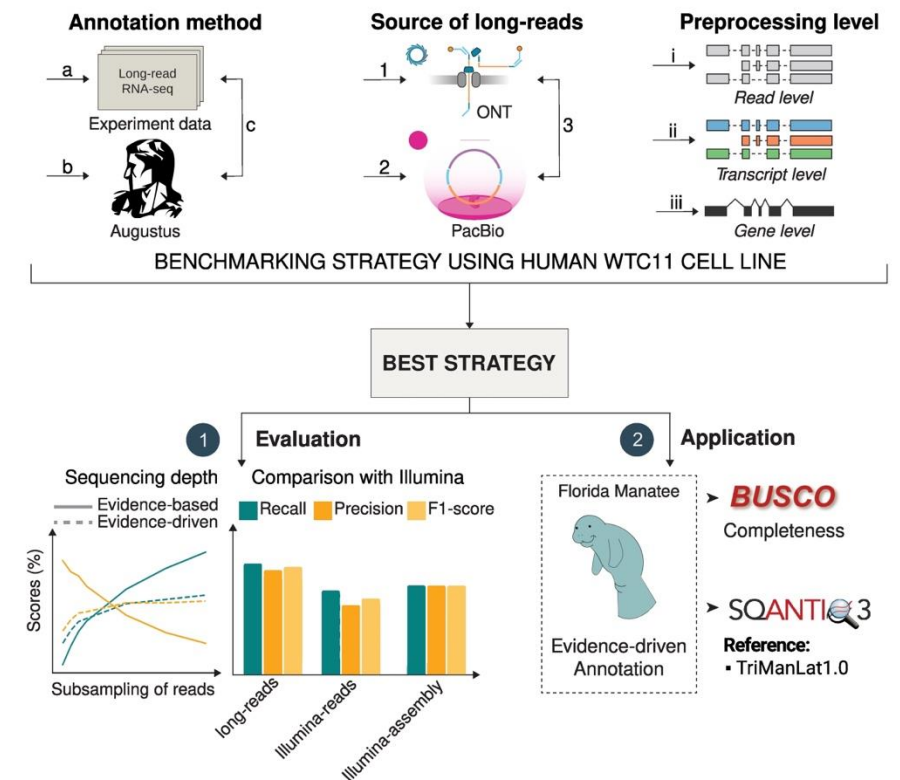
- Pipeline development and integration into the existing workflows

- Training to scientists through ERGA and web resources

- Annotation of non-model organisms with IsoSeq data available

- Lack of multi-tissue samples and IsoSeq data for a wide range of organisms

- Quality standards on RNA sequencing

- Spreading and educating the community

- Set a golden standard for genome annotation quality
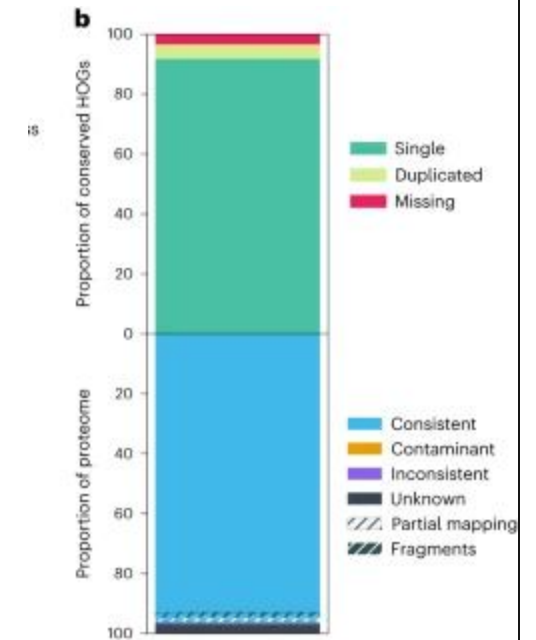
Yannis et al., 2025

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