OSCARS
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Funded Project

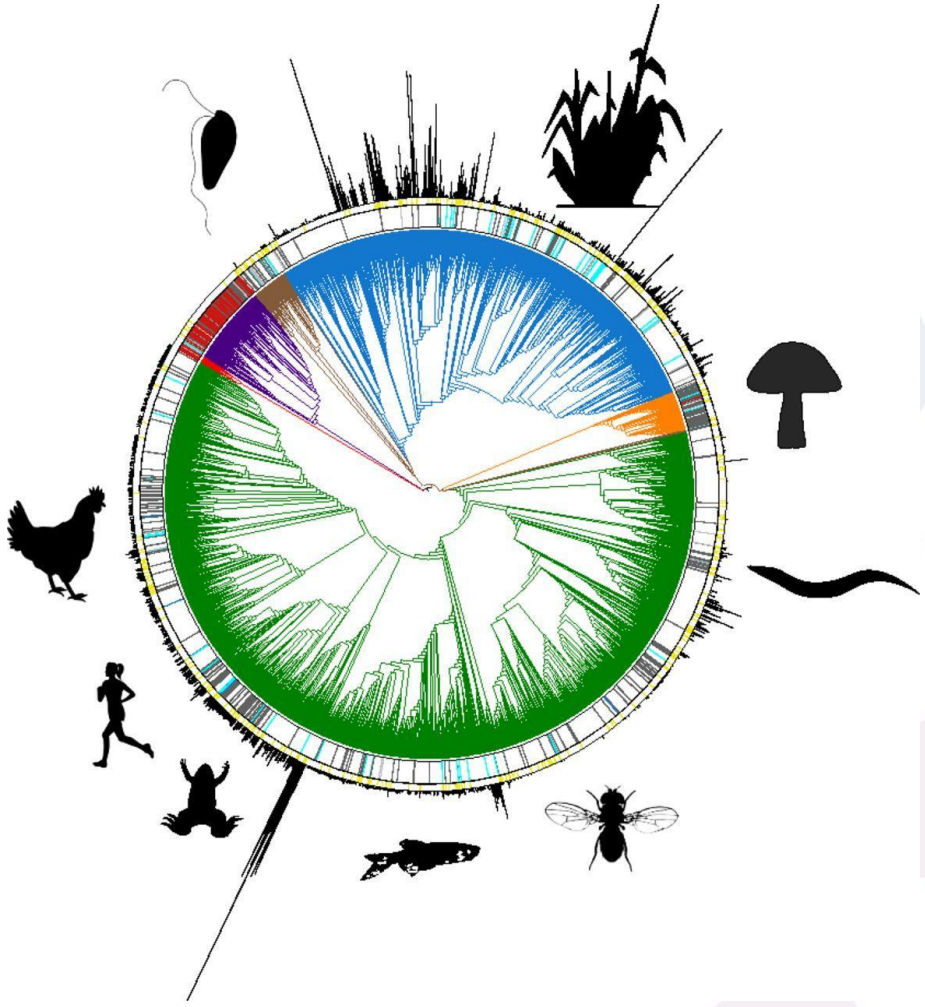
FAIRification of IsoSeq Evidence-driven annotation of the biodiversity

Presenter: Pablo Atienza, Genomics of Gene Expression Lab (CSIC), 0009-0002-1093-693X

CSIC
Consejo Superior de Investigaciones Científicas
i2sysbio Institute for Integrative Systems Biology
Genomics of Gene Expression Lab
eosc

Funded by the European Union

CHALLENGE ADDRESSED



- 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

SOLUTION

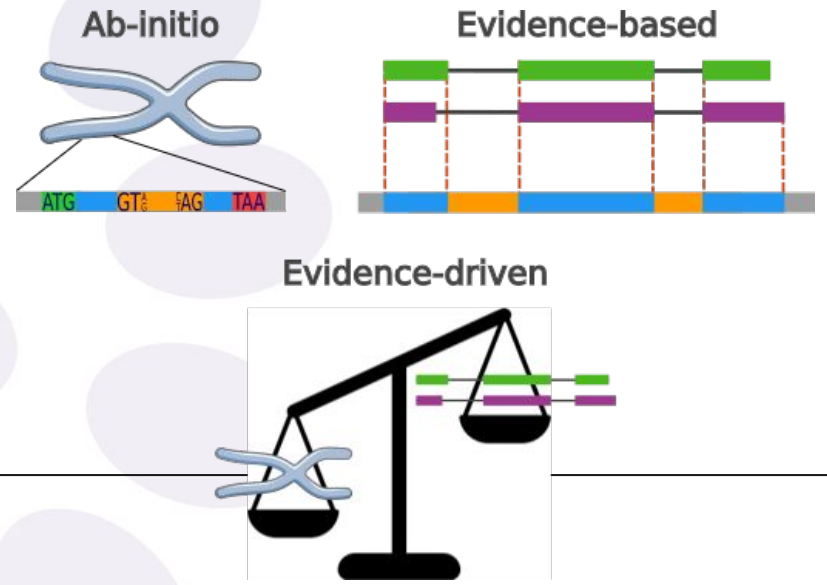
- Development and implementation of a FAIR workflow to perform IsoSeq-driven genome annotation

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

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

- Using data from public repositories

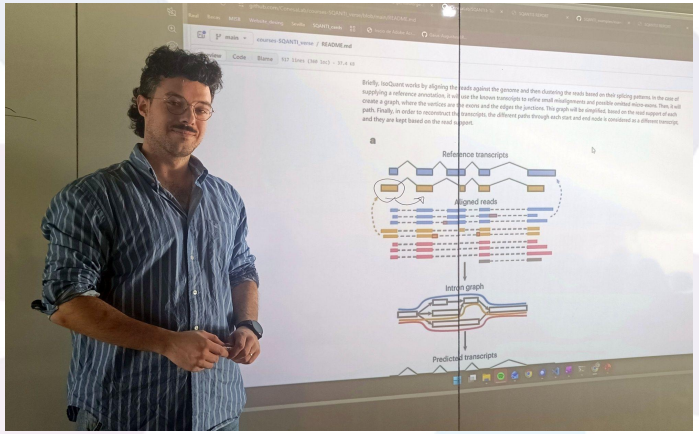
SQANTI evidence



RESULTS

- Pipeline initial version available on GitHub (SQANTI_evidence)

- Training scientists through ERGA and web resources



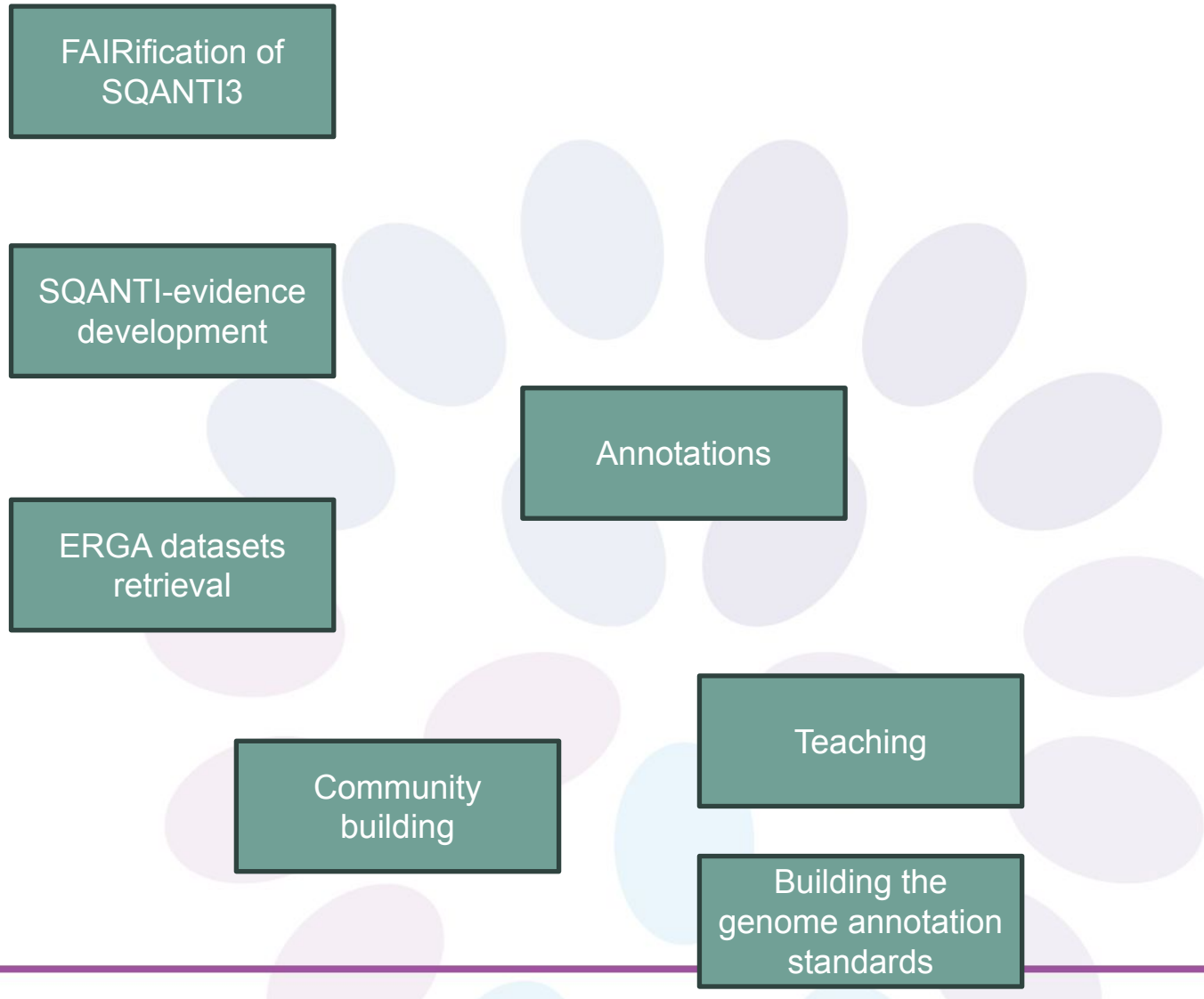
- Annotation of non-model organisms with IsoSeq data available (WIP)

TEAM

Ana Conesa
Team Leader

Alejandro Paniagua
PhD student

Pablo Atienza
Bioinformatician


FAIRification of SQANTI3
SQANTI-evidence development
Annotations
ERGA datasets retrieval
Teaching
Community building
Building the genome annotation standards