

FAIRFUN4Biodiversity – FAIR AI models for functional annotation of biodiversity genomics resources



FAIRFUN4Biodiversity aims to enhance functional annotation of genomic resources generated by the biodiversity genomics community, particularly for non-model organisms. By leveraging AI-driven methodologies, it seeks to generate publicly accessible functional data, promote Open Science practices, and improve cross-domain interoperability.



Challenge	Solution	Scientific Impact	Partners
A lack of functional genome annotation leads to incomplete models of evolutionary change and limits the identification of conserved or lineage-specific features, and there is an increasing need to leverage faster and scalable sequence-based functional prediction methods.	FANTASIA (Functional ANnotation based on embedding space SImilArity), a novel pipeline leveraging AI models from natural language processing, which overcomes the current limitations of homology-based methods and recovers functional annotation with great informativeness for virtually all genes in a proteome.	The project advances biodiversity genomics by addressing functional annotation for non-model organisms. By expanding publicly available functional annotation of the generated genomic resources, it enhances downstream biological analyses and fosters collaboration among European RIs. https://www.oscars-project.eu/projects/fairfun4biodiversity-fair-ai-models-functional-annotation-biodiversity-genomics-resources	Institute of Evolutionary Biology (CSIC-UPF), Andalusian Center of Developmental Biology (Ana Rojas, CABD-CSIC), Institute of Plant Molecular and Cell Biology (Aureliano Bombarely, IBMCP-CSIC)