

Using comparative genomics to develop 'digital twins' to support ecotoxicological predictions



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BACKGROUND

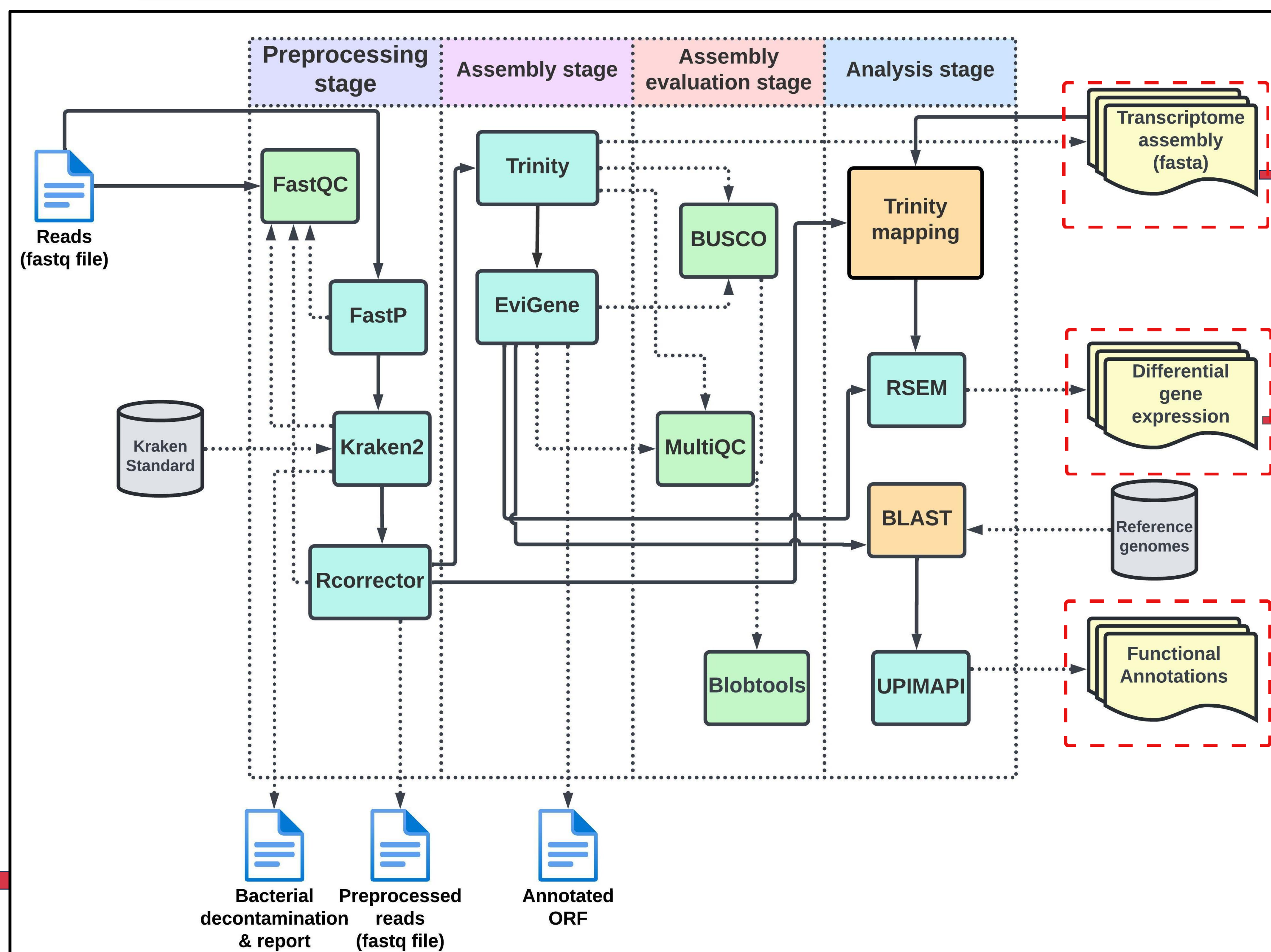
- Our rapidly changing world is placing ecosystems under unprecedented pressure, including exposure to a wide range of chemical toxicants [1].
- Traditional toxicity testing methods are inadequate for diverse non-model organisms, highlighting the need for innovative ecotoxicological approaches [2].
- By harnessing genomic data & generating *in silico* representations of organisms, this project seeks to reveal key characteristics underlying comparative ecotoxicological responses

AMBITION

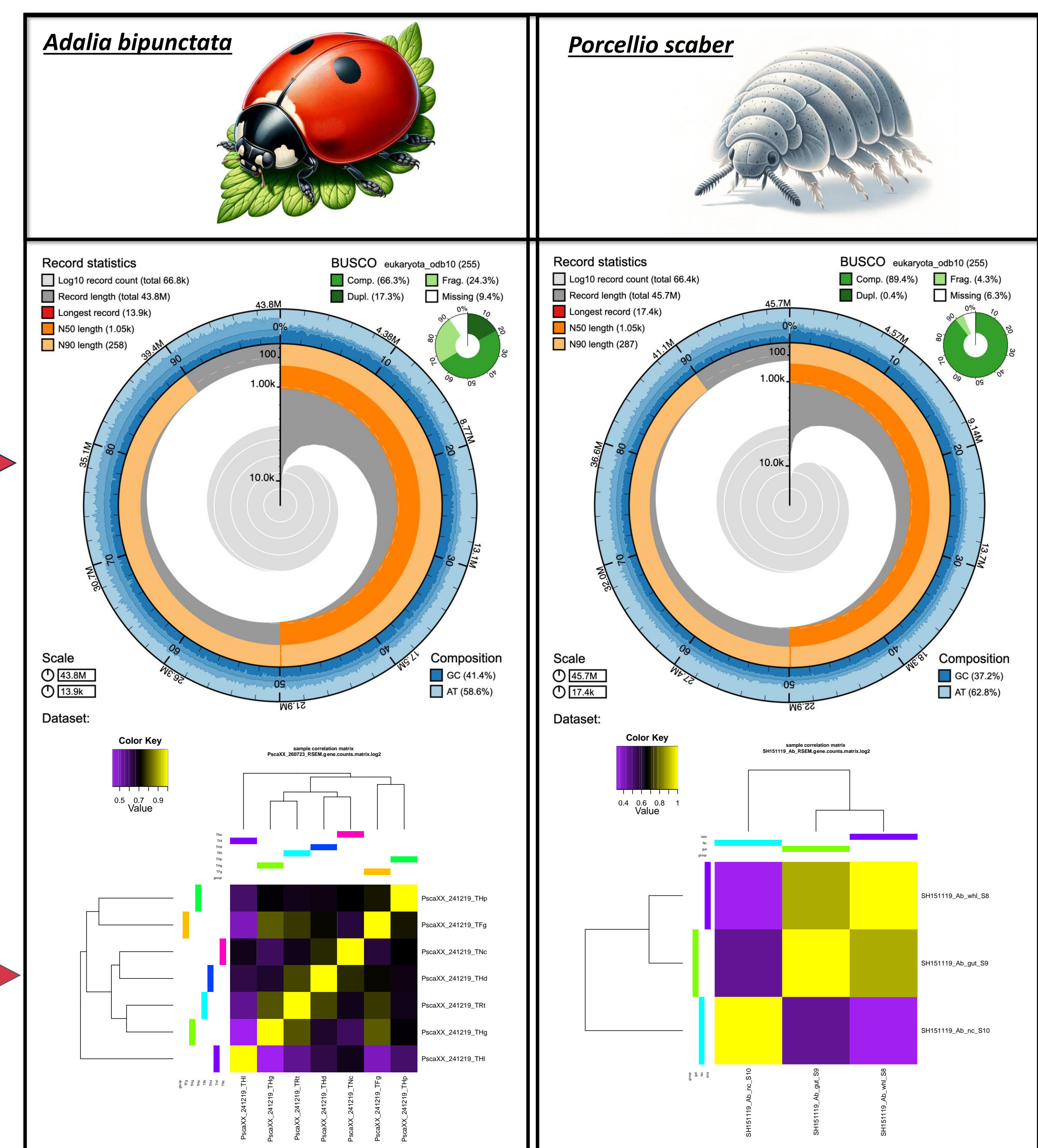
- Develop streamlined & automated pipelines to process large-scale publicly available transcriptomic data of non-model organisms.
- Develop an interactive data platform to map the processed transcriptomes onto toxicological databases, focusing on Adverse Outcome Pathways (AOPs) to provide mechanistic insight into comparative Toxicodynamics (TD).
- Predict species sensitivities to different toxicants, thereby protecting species critical for ecosystem processes or of high conservation value.

ANALYSIS PIPELINE

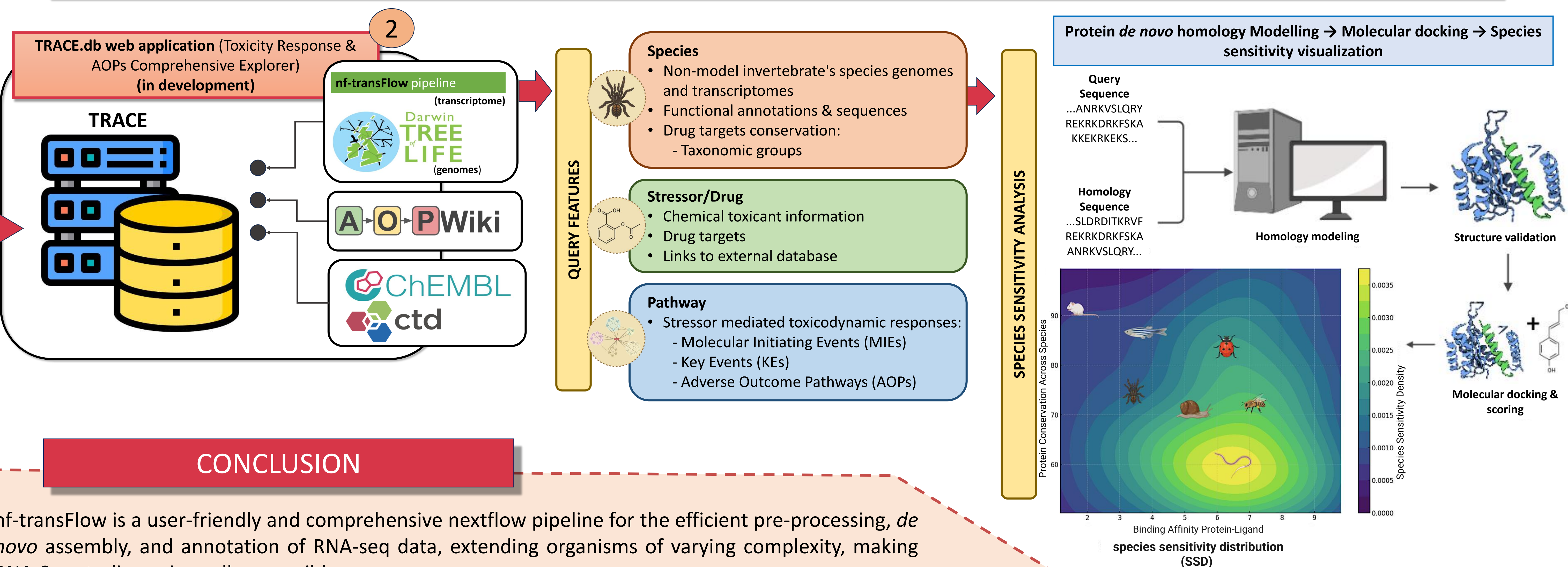
nf-transFlow Preprocessing → De novo Assembly → Annotation



nf-transFlow analysis on non-model species RNA-seq data



FUTURE RESEARCH



CONCLUSION

- nf-transFlow is a user-friendly and comprehensive nextflow pipeline for the efficient pre-processing, *de novo* assembly, and annotation of RNA-seq data, extending organisms of varying complexity, making RNA-Seq studies universally accessible.
- Incorporating nf-transFlow, we are developing TRACE, a web tool to map transcriptome/genomic data onto toxicological databases to support AOP-based species sensitivity distributions (SSD) predictions.

REFERENCES

