



These projects have received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No. 963845 (ONTOX), No. 965406 (PrecisionTox), No. 964537 (RISK-HUNT3R)

This output reflects only the author's view and the Directorate-General for Research and Innovation (DG RTD) cannot be held responsible for any use that may be made of the information contained therein.

Open **2-3 July 2026** Symposium

Maastricht
The Netherlands

aspis-cluster.eu



R-ODAF-Shiny : A Web-Based Tool for RNA-seq Analysis and Reporting

Saad Lodhi

Department of Translational Genomics (TGX) Maastricht University

saad.lodhi@maastrichtuniversity.nl

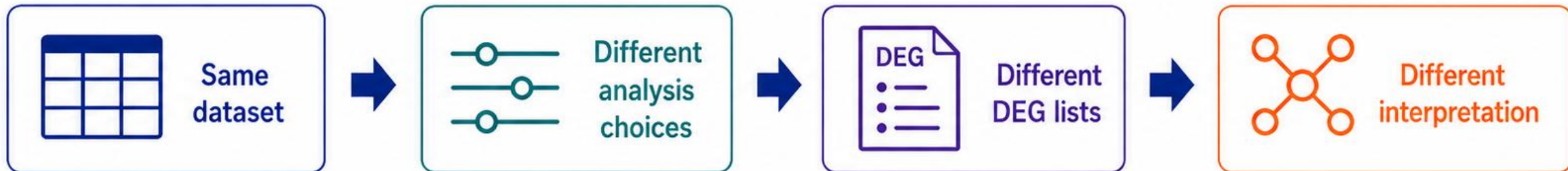


BACKGROUND

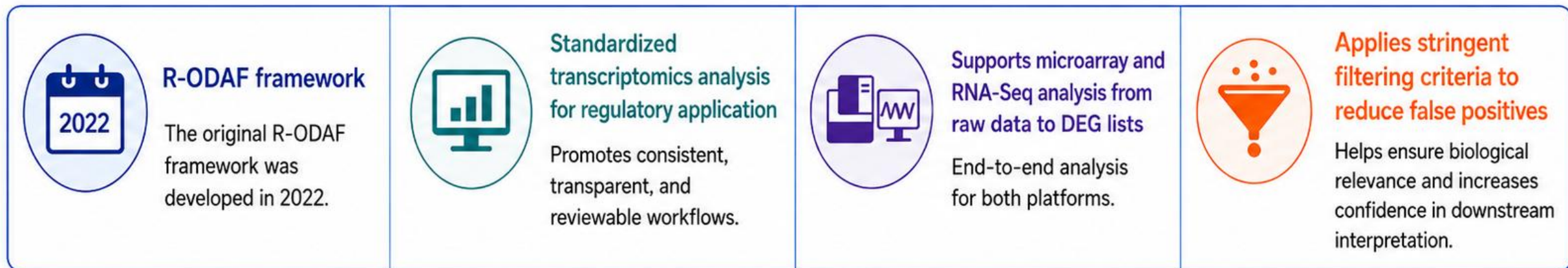


Transcriptomics is increasingly used in NAMs, mechanistic toxicology, and NGRA, so standardized analysis is needed.

THE PROBLEM



THE SOLUTION



Standardization reduces variation and improves reproducibility.



Building on the R-ODAF Framework

This study adds **R-ODAF-Shiny**: an interactive web interface for differential expression analysis.

WHAT THIS STUDY ADDS



User-friendly web interface

Intuitive interface for seamless analysis without programming.



Fixed R-ODAF logic

Consistent, validated analysis with fixed methodology and parameters.



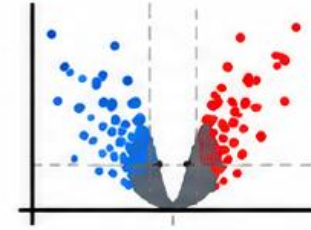
Multi-dataset handling

Analyze and compare multiple datasets within a unified workflow.



Quality control & outlier review

QC metrics, PCA plots, and sample flagging to support data quality assessment.



DEG analysis

Differential expression analysis with robust statistics and multiple testing correction.



Reporting & export

Export results, figures, and session information in reproducible formats.



Impact: Empowers researchers to perform standardized, reproducible differential expression analysis through an accessible, web-based platform.

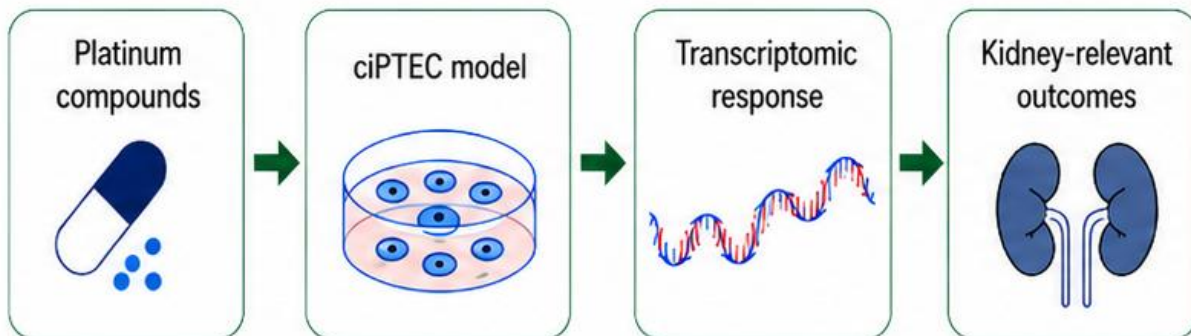
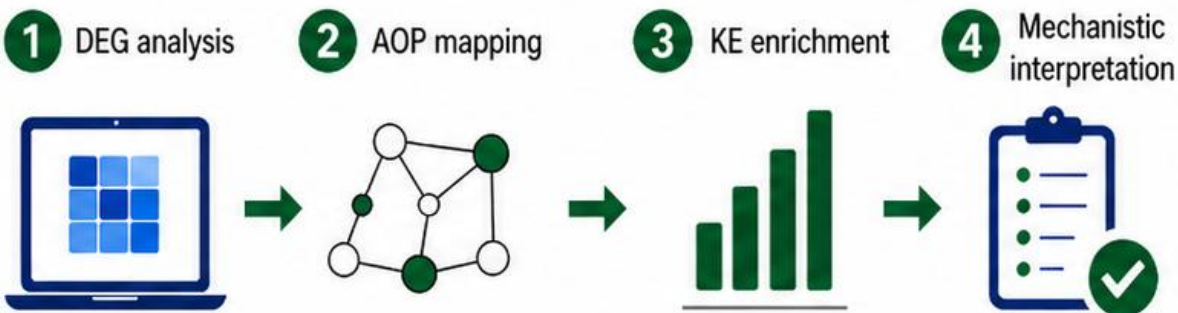


CURRENT DEVELOPMENTS AND FUTURE APPLICATIONS

Extending toward broader NAM and NGRA workflows

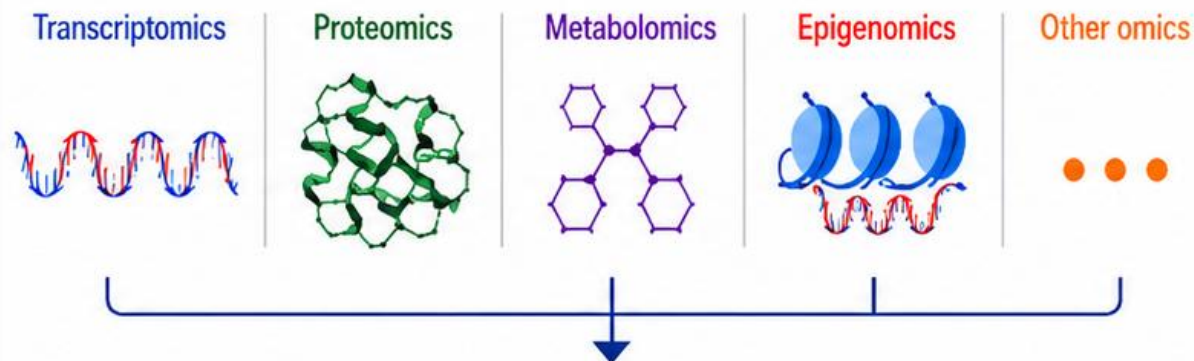
1. TRANSCRIPTOMICS TO AOPs

Kidney case study example



Links early gene expression changes to key events and adverse outcomes.

2. MULTIOMICS INTEGRATION



Integrated interpretation



Cross-omics comparison



Biomarker discovery



Mechanistic insight



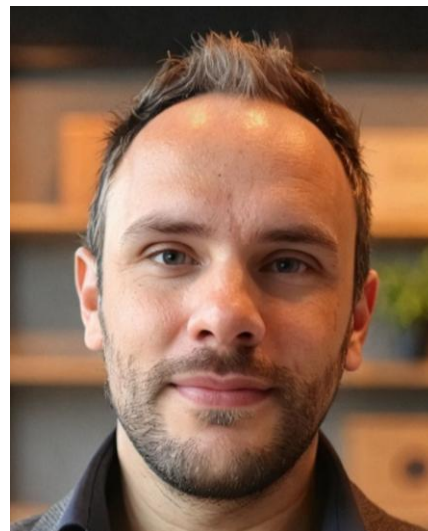
Supports a more complete understanding of biological responses.



Theo de Kok



Danyel Jennen



Florian Caiment



Marcha Verheijen



<https://platform.vhp4safety.nl/>
<https://r-odaf.nl>

Supported by



Maastricht University



TRANSLATIONAL
GENOMICS

