

# DARTpaths, an in silico platform to investigate molecular mechanisms of compounds

*Commonly used acronym: DARTpaths*

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## Contact person

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## Organisation

**Name of the organisation** Katholieke Universiteit Leuven (KUL)

**Department** Faculty of Bioscience Engineering

**Country** Belgium

**Geographical Area** Flemish Region

## Partners and collaborations

Open Analytics, Hogeschool Utrecht , Vivaltes

## SCOPE OF THE METHOD

<b>The Method relates to</b>	Human health
<b>The Method is situated in</b>	Basic Research, Regulatory use - Routine production
<b>Type of method</b>	In silico

## DESCRIPTION

### Method keywords

Data analysis

phenotype ontology

pathways

chemoinformatics

### **Scientific area keywords**

computational modelling

data modeling

data integration

bioinformatics

### **Method description**

DARTpaths is an integrative app to support the prioritisation of chemicals. The Open Source R shiny application allows for the prediction of compound-induced molecular mechanisms of action. The tool integrates phenotypic endpoints of different species induced by compounds and genetic variants, *in vitro* targets, adverse outcomes, molecular pathways and evolutionary conservation. The toolbox proposes follow-up tests for model organisms to validate the predictions of which molecular pathways are causative for phenotypes.

- All code for the application and a dockerized version are available on

<https://github.com/Xpaths/dartpaths-app>

- Demonstration of use-cases of the application are available on

<https://www.vivaltes.com/dartpaths/>

### **Lab equipment**

Computer.

### **Method status**

Internally validated

## **PROS, CONS & FUTURE POTENTIAL**

### **Advantages**

The application integrates different data sources and combines them to find the most likely underlying molecular pathway for an adverse outcome of a compound. Based on knowledge generated over decades in model organisms, it can also predict expected phenotypes (endpoints) when disturbing this pathway in a non-vertebrate

model organism.

## Challenges

Phenotypes induced by compounds as well as *in vitro* target data are incomplete and for specific compounds often only available inside companies that develop new compounds. For accurate pathway and phenotype prediction, complete data is ideal.

## Modifications

Users can install the application on their own site and connect (private) data to the app to improve pathway and phenotype prediction.

## Future & Other applications

- The species conservation of molecular pathways can inform researchers in life sciences research interested in specific pathways if studies in alternative, non-vertebrate model organisms are useful and informative.
- The NLP pipeline for identification of connections between compounds and phenotypes in full-text reports is widely applicable in toxicology and pharmacology.

## REFERENCES, ASSOCIATED DOCUMENTS AND OTHER INFORMATION

### References

DARTpaths, an *in silico* platform to investigate molecular mechanisms of compounds. Diksha Bhalla<sup>1\*</sup>, Marvin N. Steijaert<sup>2\*</sup>, Eefje S. Poppelaars<sup>3\*</sup>, Marc Teunis<sup>4\*</sup>, Monique van der Voet<sup>3</sup>, Marie Corradi<sup>4</sup>, Elisabeth Dévière<sup>2</sup>, Luke Noothout<sup>5</sup>, Wilco Tomassen<sup>5</sup>, Martijn Rooseboom<sup>6</sup>, Richard A. Currie<sup>7</sup>, Cyrille Krul<sup>4</sup>, Raymond Pieters<sup>4,8</sup>, Vera van Noort<sup>1,9^</sup>, and Marjolein Wildwater<sup>3^</sup>  
Bioinformatics, submitted

### Associated documents

[Supplement\\_DARTapplication\\_20220504\\_V8.docx](#)

[Manuscript\\_DARTapplication\\_20220504\\_V8.docx](#)

### Links

[GitHub repository](#)

[Demo page](#)

### **Other remarks**

A manuscript about the application has been submitted to the journal Bioinformatics.

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