OASIS software
Environmental/Fate endpoints
ADVANCED AGENDA
2023

I. CATALOGIC platform

The OASIS CATALOGIC software is a platform for models and databases related to the environmental fate of chemicals such as abiotic and biotic degradation, bioaccumulation and acute aquatic toxicity. The biodegradation is modelled by simulating degradation pathways. OASIS CATALOGIC is unique software which combines on a single modelling platform biodegradation model that explicitly simulates the microbial metabolism (biodegradation pathways) and calculates the amounts of metabolites and their properties. Thus, the modelling formalism allows estimation of the magnitude of the degradation products and prediction of their phys-chem properties and acute aquatic toxicity. The CATALOGIC models for bioaccumulation are based on the maximum bioaccumulation potential of the chemicals defined by their passive diffusion, only. A set of mitigating factors are used to reduce the maximum bioaccumulation potential accounting for fish metabolism, 3D size, water solubility and ionization which are analyzed individually and explicitly. Acute aquatic toxicity models are based on the base-line (base surface) concept. All narcotic chemicals are populating the response-surface. The reactive chemicals are above the surface, and they are organized into reactivity classes. A single model predicts the chemicals falling in the base surface where the parameter for bioavailability (logKow) is combined with quantum-chemical electronegativity parameter. The models predicting reactive chemicals are organized depending on the mechanism of their action. In these models the reactivity parameter associated with the reactive functionality is combined with bioavailability parameter. All CATALOGIC models are developed in accordance with Guidance Document on the Validation of (Quantitative) Structure-Activity Relationship [(Q)SAR] Models published by OECD.

1. Useful functionalities for demonstration and training purposes
    a. Searching capabilities:
        i. Simple search
        ii. Flexible search

    Searching for parents and/or metabolites in large chemical inventories meeting specific criteria. The search could be based on:

    - *structural fragments in the parents and/or metabolites*
    - *phys-chem properties*
    - *OFG using Toolbox profilers*

- *common transformation sequences*

b. Selection of analogues

The approach provides two types of analogues supporting adequacy of the endpoint prediction and simulated metabolism. The analogues are searched in the available training sets of the model with observed endpoint data and documented metabolism data.

c. AD**M**E similarity: Metabolic similarity

Assessing metabolic similarity between different chemicals, in terms of:

- *similarity between transformation pathways,*
- *structural similarity of metabolites (using TB profilers),*
- *common metabolites*
- *justifying conflicts between environmental data of structurally similar chemicals*

d. Documented metabolism data supporting metabolic transformations

i. Databases with documented metabolism data
ii. Metabolic transformations. Local training sets with documented metabolism data
iii. Access to the treatment groups associated to molecular transformations and generated metabolites

A new functionality of searching in the databases with documented metabolism data was developed. It provides experimental data support for each molecular transformation and allows the metabolic transformations to be associated with the treatment groups and to check their validity. This support is organized as local training set of the respective transformation.

e. Other functionalities:

i. Grouping of chemicals and clustering based on different criteria
ii. Selection of representatives from a list of chemicals (to minimize the testing)

The functionality is a powerful tool for assessment of the UVCB constituents. It allows grouping of the chemicals into small sets (clusters) where the chemicals in each cluster are similar with respect to predefined criteria. In addition, it is possible to select the representative chemical from a cluster for further testing.

f. Reporting functionalities:

CATALOGIC has several types of report:

- *Full report – provides results associated with prediction, such us phys-chem properties, calculated quantities, observed and predicted endpoint values, applicability domain results not only for parent, but also for metabolites.*
- *QPRF – QSAR Prediction Reporting Format is a standard report approved by OECD and accepted by regulatory organs, for example ECHA.*
- *Metabolic maps report – allows export of the metabolic information associated with the simulated maps, such us connectivity between metabolites (predecessor of each metabolite), transformations responsible for generating the metabolites, etc.*
- *Metabolic similarity report – provides the results obtained as a result of estimation of metabolic similarity between two or more chemicals.*

2. Principle/theoretical items for presentation and discussion

   a. Explicit evaluation of ionization mitigating factor (BCF base-line DP model)

   Justifying the BCF predictions for ionizing chemicals using distribution coefficient (log D) accounting for ionization.

   b. Consideration of Perfluoroalkyl and Polyfluoroalkyl Substances (PFAS) in the CATALOGIC models

   Recent work focused on expanding of the CATALOGIC models with PFAS including improvements in terms of endpoint predictions and simulated metabolism.

   c. Criteria for reliability of prediction:

      i. Biodegradation
      ii. Bioaccumulation

   List of criteria that can be used for justification of the prediction results obtained from QSAR models. The approach is already published.

II. Pipeline Profiler platform

OASIS Pipeline Profiler is a classification system based on a pipeline technology for predicting (eco)toxicity of chemicals. The Pipeline Profiler software allows coding and execution of Integrated Approaches to Testing and Assessment (IATA). The IATAs integrate and interpret nonstandard information generated for key events in a manner that can be practically useful for making decision for testing and assessment. The Pipeline

Profiler provides automatic implementation of (Q)SAR models along with the regulatory criteria for hazard/risk assessment. The system is also docked to the OECD QSAR Toolbox which allow the information from Toolbox (e.g., profilers, calculators, experimental data, (Q)SAR models) to be used.

1. Platform for predicting PBT profile of the chemicals
   PBT scheme can be used for screening and prioritization purposes of organic chemicals according to their persistency, bioaccumulation and aquatic toxicity. The scheme combines experimental data extracted from QSAR Toolbox and modelling results from CATALOGIC.

2. Platform for predicting (a)biotic stability of the chemicals
   The scheme allows assessment of stability of the chemicals in terms of abiotic and enzymatic stability using the CATALOGIC models.

Appendix I. Models available in OASIS CATALOGIC

I. Environmental fate models

1. Abiotic transformation

- Acidic hydrolysis model pH 2
- Acidic hydrolysis model pH 5
- Neutral hydrolysis rate constant model
- Autoxidation simulator
- Autoxidation Kinetic model

2. Biodegradation

- CATABOL 301B
- CATABOL 301C
- CATALOGIC 301C
- CATALOGIC Abiotic 301C
- CATALOGIC Kinetic 301B
- CATALOGIC Kinetic 301F
- CATALOGIC Soil

3. Bioaccumulation

- BCF base-line model DP (ionization term)
- BCF base-line model

II. Models for acute aquatic toxicity

1. Algae

- Acute Toxicity Algae

2. Daphnia

- Cerodaphnia dubia LC50 48h
- Daphnia magna EC50 24h
- Daphnia magna LC50 24h
- Daphnia magna EC50 48h
- Daphnia magna LC50 48h
- Daphnia pulex LC50 48h
- Daphnia pulex LC50 96h

3. Fish

- Carassius auratus LC50 24h
- Hydractinia echinata MRC50
- Lepomis macrochirus LC50 96h
- Leuciscus idus LC50 96h
- Lymnaea stagnalis LC50 96h
- Oryzias latipes LC50 48h
- Pimephales promelas LC50 96h
- Poecilia reticulate LC50 96h
- Rana japonica LC50 12h

4. Bacteria

- Vibrio_fischeri pT5
- Vibrio_fischeri pT15
- Vibrio_fischeri pT30
- Bacillius subtilis I50
- Escherichia coli EC50 12h

5. **Other organisms**

- Culex tarzalis LD50 24h
- Tetrahymena pyriformis IGC50 48h