

# Biodegradation of Water-Soluble Polymers – Reviewing In-Silico Methods (Interim state)

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## QSAR/Read-Across

- Derive substance properties based on regression or similarity
- Use descriptors/similarity indices to characterize substances
- Fit models (MLR, RF, SVM, kNN, ANN) to consistent datasets
- Examples: BIOWIN<sup>1</sup>, VEGA<sup>2</sup>

## Motivation:

- Water soluble polymers are exempt from REACH.
- If they become subject, assessing biodegradability is obliged
- In-silico are cost-effective methods used for risk assessment
- Hence, the current landscape of models is examined

## Pathway Prediction System

- Predict pathways based on rules mapping functional groups onto products
- Assign likelihood to rules based on expert knowledge or probability calculations
- Discriminate reactions and apply recursively to final degradation products
- Examples: CATABOL<sup>3</sup>, enviPath<sup>4</sup>, BESS<sup>5</sup>

## Data, Descriptors

- Crucial for reliable predictions but sufficiently large and consistent set of water soluble polymer degradation data is lacking
- Polymers need to be characterized and discriminatory descriptors identified also encompassing macroscopic properties

## Predicting Biodegradability of Polymers

## Pathways, Rules

- To establish pathways, rules for polymer degradation need to be identified and probabilities assigned.
- Due to their variability and macroscopic properties, rules need to include patterns beyond functional groups

## Connection, Complexity

- While the degradation process may be modelled at this level a derivation of biodegradability is not established
- Modelling specific polymers in itself is a non-trivial task. Including their stochastic nature increases the complexity considerably

## Outlook:

- Adaptations of the approaches are needed to predict biodegradability of polymers
- PPS might be most promising
- Establish degradation rules and assign interdependent likelihoods
- Determine set of descriptors suited or polymer characterization

## Molecular Modelling

- Model substances explicitly on the atomic/molecular level
- Compute energy minima, normal modes, binding-sites for enzymes, interaction strength
- Examples: GROMACS<sup>6</sup>, AUTODOCK<sup>7</sup>, CHARMM<sup>8</sup>

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