'Relevant' versus 'Similar' Structural Analogs to Support Genotoxicity (Q)SAR Predictions

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Background

- Structural analogs with experimental data are important for expert review of (Q)SAR model evaluations.
- Analogs help clarify uncertain (Q)SAR outcomes, making inconclusive or contradictory evaluations more definitive.
- Finding analogs is challenging when query compounds have multiple alerts of varied significance, a common scenario in statistical model evaluations.
- Conventional similarity metrics may yield structurally similar analogs but often lack relevance by failing to identify analogs with query compound's alerts.
- Here we introduce a novel approach for finding analogs, employing a sophisticated fingerprinting technique that considers both specific alerts and general structural features.

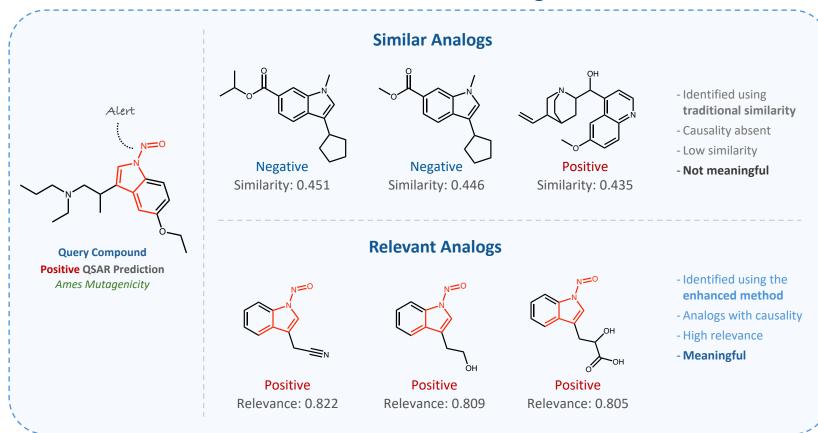
Methodology

- **Fingerprint Construction:** The fingerprint for a compound consists of two parts:
 - Alert Part Contains importance weights of toxicity alerts identified in the compound, specific to the end point. As many elements as alerts in the model.
 - Fragment Part Indicates presence of molecular fragments from the whole structure. Usually of fixed size, e.g., 256, 512 or 1024.
- Relevance Metric: Cosine similarity function was used to compute relevance.
- Software: CASE Ultra, 1.9.1.2 beta

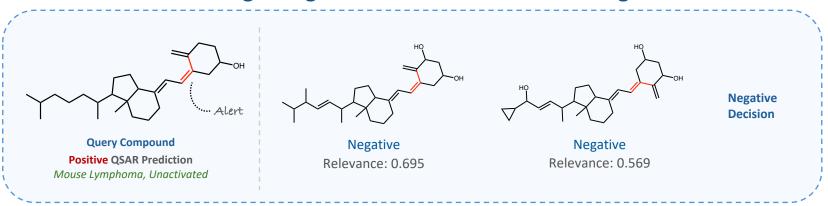
Conclusions

- This refined method improves the discovery of suitable and meaningful analogs.
- Offers a more sophisticated analysis of structural features relevant to toxicity.
- It is versatile, applicable beyond genotoxicity, compatible with both statistical and expert knowledge-based (Q)SAR models.

Relevant vs Similar Analogs



Downgrading Positive Prediction Calls to Negative



Resolving Inconclusive Prediction Calls

