Characterization of Bacterial Mutagenicity QSAR Predictions of Food Additives to Support Safety Assessments in a Regulatory Setting

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1. Abstract

Assessment of food additive safety at the U.S. FDA is often based upon guidance QSAR (GQSAR) models that are based on genetic toxicity and development toxicity models to support regulatory decision making. However, many of the GQSAR models in routine use were originally developed for drug and industrial chemical assessments. Consequently, we have conducted an assessment of how well the GQSAR models predict food additive safety.

2. Methods

Salmonella GQSAR Model Description

Salmonella mutagenicity data were generated with the U.S. FDA using the Leadscope software. The Compound Activity Database (CADD) was used to generate an initial training set of chemicals using a proprietary Salmonella mutagenicity model (GQSAR). The test set was selected using a database of 2,240 chemicals. The models were independently developed for predicting Salmonella mutagenicity. The test set was used to assess the sensitivity of the chemical space of novel compounds based on the 540 compounds in the CADD database. Sensitivity was assessed for compounds not predicted by the model. Some clusters of complexes were split to form multiple classes. Certain classes were not predicted by the model. The frequency distribution indicates that the proportion of predicted compounds at each probability interval. The predicted values indicate that the predictions are out of the model's domain. The model predicted the CFSAN test set with 84% of the clusters in common. The model has several sites that are not predicted by the model. The frequency distribution indicates that the proportion of predicted compounds at each probability interval. The predicted values indicate that the predictions are out of the model's domain. The model predicted the CFSAN test set with 84% of the clusters in common. The model has several sites that are not predicted by the model. The frequency distribution indicates that the proportion of predicted compounds at each probability interval. The predicted values indicate that the predictions are out of the model's domain. The model predicted the CFSAN test set with 84% of the clusters in common. The model has several sites that are not predicted by the model. The frequency distribution indicates that the proportion of predicted compounds at each probability interval. The predicted values indicate that the predictions are out of the model's domain. The model predicted the CFSAN test set with 84% of the clusters in common. 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