

PERPEST version 1.0, manual and technical description

a model that Predicts the Ecological Risks of PESTicides
in freshwater ecosystems

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perpest



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PERPEST version 1.0, manual and technical description

A model that Predicts the Ecological Risks of PESTicides in freshwater ecosystems

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ABSTRACT

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This report is a technical description and a user-manual of the PERPEST model, able to Predicts the Ecological Risks of PESTicides in freshwater ecosystems. This system predicts the effects of a particular concentration of a pesticide on various (community) endpoints, based on empirical data extracted from the literature. The method that it uses solves new problems (e.g., what is the effect of pesticide A?) by using past experience (e.g., published microcosm experiments). The database containing the "past experience" has been constructed by performing a review of freshwater model ecosystem studies evaluating the effects of pesticides. The PERPEST model searches for situations in the database which resemble the question case, based on relevant (toxicity) characteristics of the compound. The model is described in the scientific paper written by Van den Brink et al. (2002) and available via the enclosed CD-ROM and the website www.perpest.alterra.nl.

Keywords: Effect model, Aquatic community, Ecological risk assessment, Pesticides, Case-Based Reasoning

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Preface

We would like to thank Rene van Wijngaarden, Joost Lahr, Theo Brock and Gerben van Geest for their help in reviewing the literature on the ecological effects of pesticides in freshwater ecosystems, Marten Scheffer, Jan Roelsma and Theo Brock for their help developing the model and Mechteld ter Horst for testing the model.

Summary

This report is a technical description and a user-manual of the model PERPEST, a model that Predicts the Ecological Risks of PESTicides in freshwater ecosystems. This system predicts the effects of a particular concentration of a pesticide on various (community) endpoints, based on empirical data extracted from the literature. The method that it uses is called Case-Based Reasoning (CBR), a technique that solves new problems (e.g., what is the effect of pesticide A?) by using past experience (e.g., published microcosm experiments). The database containing the “past experience” has been constructed by performing a review of freshwater model ecosystem studies evaluating the effects of pesticides. This review assessed the effects on various endpoints (e.g. community metabolism, phytoplankton, macro-invertebrates) and classified them according to their magnitude and duration. The PERPEST model searches for situations in the database which resemble the question case, based on relevant (toxicity) characteristics of the compound. This allows the model to predict effects of pesticides for which no evaluation on a semi-field scale have been published. PERPEST results in a prediction showing the probability of classes of effects (no, slight or clear effects, plus an optional indication of recovery) on the various grouped endpoints. The model is described in the scientific paper written by Van den Brink et al. (2002). and available via the enclosed CD-ROM and the website www.perpest.alterra.nl.

1 Introduction

1.1 What is PERPEST?

The tiered ecological risk assessment of pesticides consists of a conservative first tier and more realistic higher tiers. These higher tiers can include the use of laboratory tests using more realistic exposure regimes, testing of indigenous species, the use of a variety of models (population, food-web, landscape) and conducting experiments in model ecosystems (Campbell et al. 1999). To this end many experiments performed with microcosms and mesocosms are performed during the last 20 years and published in the open literature. Brock et al. (2000a; 2000b) reviewed the open literature for microcosm and mesocosm experiments on the effects of herbicides and insecticides. This review was performed to establish ecological threshold values for pesticides in surface waters and to evaluate current standard setting methodologies.

In order to predict effects of pesticides on aquatic communities and ecosystems, large simulation models like for instance food-web models can be used (Koelmans et al. 2001; Traas et al. 1998). Ecological models, however, are either incomplete or have many uncertain parameters, so experts may predict effects of toxicants better. Anderson (1983) has shown that people use past cases as models when learning to solve new problems. Also experts solve problems by analogy, i.e. using analogous cases from memory to solve new problems. For instance if one asks an expert what the effect of 1 µg/L of the insecticide chlorpyrifos will be on the ecology of a freshwater ecosystem, he or she will look for analogous cases; i.e. experiment he or she has conducted or evaluated in the past. Obvious the type of experimental ecosystem, test design, assessed endpoints etc. are different between the experiments so the expert has to make some nuance also. In the field of artificial intelligence this process is called Case-Based Reasoning (CBR) (Kolodner 1993; Leake 1996). The basics of CBR is that it retrieves similar experience (cases) about similar situations from the memory (a database that is called the case base) and reuses this experience in the context of a new situation for a prediction.

The PERPEST model (Van den Brink et al. 2002) is based on Case-Based Reasoning. In this model the prediction of the effects of a certain concentration of a pesticide on a defined aquatic ecosystem is based on published information on effects of pesticides on the structure and function of aquatic ecosystems as observed in semi-field experiments. This CBR system consists of the database containing this information and a search routine named Weighted Analogies Prediction (WAP) (Van Nes and Scheffer 1993). The rationale behind WAP is that based on a few characteristics of the questioned case (e.g. pesticide characteristics, exposure concentration, type of exposure) analogous cases are identified in the database. These analogous cases can be weighted and summarised in a prediction. This means that although for certain pesticides no microcosm or mesocosm experiment is published, one is able to predict its effect on a semi-field scale using the results of experiments

performed with other pesticides that have a similar toxicological mode of action (TMoA) and fate characteristics.

The PERPEST model can be used in the ecological risk assessment when uncertainties are large and data availability is small, e.g. in the case of a new pesticide. Using PERPEST an idea can be obtained in which direction uncertainties are likely to be large, so in which direction data must be gathered for a refined risk assessment (e.g. endpoints and exposure concentrations of interest). Output of PERPEST can also be used to translate spatially and temporal distributed concentration data into effect concentrations, i.e. to use it as a risk indicator. In this report the methods incorporated in PERPEST are described and a manual of the graphical user interface (GUI) of the model is included.

1.2 Case-based reasoning

Case-based reasoning (CBR) is a way of solving problems that is able to utilize the specific knowledge of previously experienced, concrete analogous situations (cases) for solving new problems. CBR is an approach that enables incremental, sustained learning since new experience is retained, making it immediately available for future problems (Aamodt and Plaza 1994). The first system that might be called a case-based was the system of Kolodner (1993), a question answering system with knowledge on the various travels and meetings of the former US secretary of State Cyrus Vance. Since then the study of CBR is driven by two primary motivations: firstly to model human reasoning and learning and secondly to make Artificial Intelligence (AI) systems more effective (Leake 1996).

Early applications of CBR are, among others, in diagnosis setting (clinical audiology, heart failure, building defects, aircraft fault diagnosis and repair), legal reasoning (criminal sentencing, patent law, injuries to workers, building regulations), arbitration (dispute resolution), design (landscape, mechanical design, conceptual design) and planning (warfare planning, manufacturing planning problems, (Watson and Marir 1994)). Examples of interpretive CBR are law application and diagnosis setting. A well known application of CBR in medicine is to help medical personnel to assess patient status, assist in making a diagnosis, and facilitate the selection of a course of therapy (Frize and Walker 2000). In this example a case is defined as a set of variable values or features collected from a patient collected during a consult or visit. This case can be compared to earlier collected cases (patients) incorporated in a case base (Montani et al. 2000). From this case base the most similar cases can be extracted by applying for instance the nearest neighbor technique. From these similar cases some useful statistics like similarity in diagnosis and successful therapy between the cases can be calculated, and used for decision making. Although CBR is popular in various scientific areas, there have been described only very few applications in ecology (grasshopper pest control, Branting et al. 1997) and ecotoxicology (ecological risks of pesticides, Van den Brink et al. 2002).

Some of the advantages of the CBR technique are:

1. No prior information or assumptions about the nature of relations between variables are needed.
2. It is easy to find and browse through all available information of the most analogous cases.
3. The system can improve by adding new cases to the case-base. This learning possibility is an important feature of CBR systems.
4. It is the starting point of the LABDA approach (**L**argely **A**nalogous **B**ut **D**ifferences **A**lso) (Scheffer 1991).

The LABDA approach is a way of predicting the response of a case.

It involves two steps:

- A. Rough estimations using analogous cases (**L**argely **A**nalogous)
- B. Fine tuning of the prediction by quantitative models that predict only the differences of the question case from the analogous cases (**B**ut **D**ifferences **A**lso)

2 Methods

The main purpose of the program PERPEST is to find analogous cases based on available information in a data base (§ 2.1). In § 2.2 is explained how this is done. Based on these analogous cases it is possible to predict the response of the question case. In § 2.3 the averaging method is explained. The next question is how good this prediction is. In § 2.4 is explained how the goodness-of-fit is evaluated. The methods and parameters used by PERPEST can be optimized automatically. § 2.5 explains by which method this is done.

Table 2.1. The most important variables in the PERPEST database

Variable	Description	Type of variable
DT50	Field dissipation DT50 (days)	Float
EC50	geometric mean acute EC50 value of the most sensitive standard test species according to OECD guidelines ($\mu\text{g/L}$)	Float
FullName	Name of the substance	Memo
Henry	Partitioning coefficient air-water ($\text{Pa m}^3/\text{mol}$)	Float
Kom	Partitioning coefficient water-organic matter Kom (L/kg)	Float
Mode of action	Mode of action	String
Molecule group	Molecule group	String
Type_sub	Type of substance	String
Conc	Concentration of substance ($\mu\text{g/l}$)	Float
Expos	Exposure	String
Hydrology	Hydrology during experiment	String
Reference	Full reference	Memo
ToxUnit	Concentration as toxic unit	Calculated: Conc/EC50

2.1 The PERPEST database (case base)

The database (called the case base) consist of two different data sets, one containing the updated results of the review on effects of pesticides observed in semi-field experiments (Brock et al. 2000a; Brock et al. 2000b) and one on fate and effect characteristics of insecticides and herbicides (Table 2.1). The first data set comprises case studies in which the effect of a certain concentration of a pesticide is evaluated in a microcosm or mesocosm. Experiments were selected for evaluation when the model ecosystem simulated a realistic freshwater community, the experimental design was appropriate (ANOVA or regression design), and when the exposure concentrations were clearly described. We made a distinction between systems to which a single (single or pulse) and to which a repeated (multiple or chronic) dose was applied and between lentic (stagnant or recirculating) and lotic (flow-through) systems. Evaluated experiments normally comprised of several cases, i.e. each evaluated concentration in an experiment is a separate case in the case base.

The endpoints evaluated were classified in 8 different ecological endpoint groups, which were different for insecticides and herbicides (see Box 1). The responses

observed for various ecological endpoint groups were assigned to 0 (not evaluated) or the five effect scores (ranging from no to clear long-term effects).

Each record in the case base is composed of the name of the chemical, the concentration evaluated, the reference to the open literature, type of exposure and model ecosystem and the effect scores for the eight ecological endpoint groups.

The second data set consists of fate characteristics of the different pesticides and their toxicity for standard test species. In order to make comparisons possible between studies performed with different herbicides or insecticides, we expressed the exposure concentrations as Toxic Units (TU). For this we divided the studied exposure concentration (usually the nominal peak concentration of the pesticide in the water column) by the corresponding geometric mean acute EC50 value of the most sensitive standard test species according to OECD guidelines. In case of insecticides the most sensitive standard test species usually was *Daphnia magna*. For herbicides the most sensitive standard test alga according to OECD guidelines usually were *Scenedesmus subspicatus* or *Selenastrum capricornutum*. Values were taken from Brock et al. (2000a; 2000b).

To be able to find analogies related to fate characteristics of pesticides also the field dissipation is taken into account. This field dissipation is represented by the DT50 of the water compartment determined in a water sediment study, the Henry coefficient (partitioning coefficient air-water) and the K_{om} (partitioning coefficient water-organic matter). These variables were, when available, added to the database for each pesticide. Values were obtained from Linders et al. (1994) and the pesticide manual (Tomlin, 2000).

BOX 1. The grouped endpoints and five effect classes used in PERPEST

The grouped endpoints are:

Herbicides

Community metabolism
Phytoplankton
Periphyton
Macrophytes
Zooplankton
Macrocrustaceans & Insects
Other macro-invertebrates
Vertebrates

Insecticides

Community metabolism
Algae and macrophytes
Microcrustacea
Rotifers
Macrocrustacea
Insects
Other macro-invertebrates
Vertebrates

The five effect classes are:

- **0. blank** .Endpoint not evaluated in the study.
- **1. No effects demonstrated:** No consistent adverse effects are observed as a result of the treatment. Observed differences between treated test systems and controls do not show a clear causality.
- **2. Slight effects:** Confined responses of sensitive endpoints (e.g., partial reduction in abundance). Effects observed on individual sampling dates only and/or of a very short duration directly after treatment.
- **3. Clear short-term effects, lasting < 8 weeks:** Convincing reductions in sensitive endpoints. Recovery, however, takes place within eight weeks. Effects observed on a sequence of sampling dates.
- **4. Clear effects, recovery not studied:** Clear effects (e.g., severe reductions of sensitive taxa over a sequence of sampling dates) are demonstrated, but duration of the study is too short to demonstrate complete recovery within eight weeks after the last treatment.
- **5. Clear long-term effects, lasting > 8 weeks:** Convincing reductions in sensitive endpoints and complete recovery of these endpoints later than 8 weeks after the last treatment. Negative effects reported over a sequence of sampling dates.

2.2 How to find similar cases?

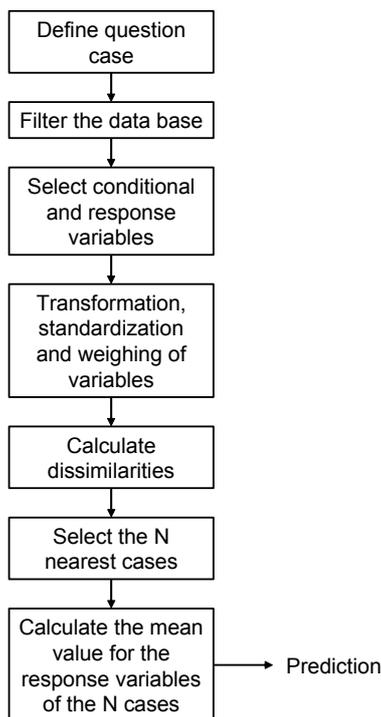


Fig. 2.1. The used method of case-based reasoning.

The steps to be taken to find analogies are summarized in Fig. 2.1. Each step is explained below.

2.2.1 Defining question case

The first step in case based reasoning is defining the question case, i.e. which circumstance do you want to predict? In PERPEST the minimum information for a question case is the pesticide name and its concentration. If the pesticide is not yet available in the fate and effects characteristics database also its CAS number, mode of action, molecule group, type of substance and lowest EC50 for standard test organisms must be entered (see also § 3.2).

2.2.2 Filter the database

The first (optional) step in the finding the similar cases, is to select a part of the database on the basis of a logical equation. Examples of such equation are: 'TU<3' or 'Exposure=multiple/constant'. These conditions can be combined in complex equations including several functions (see: calculated variables). Note that the result of the equation should be a logical value (*True* or *False*, the result of comparison and logical functions like: > < = *and or*).

There is one special kind of selection that is the relative selection. In this case the selected cases may differ from the problem case only with a certain relative value. For instance $((TU < M/2)$ and $(TU > M*2))$ in which M is the toxic unit of the problem case. The advantage of this relative selection is that this condition can be updated in the cross-validation, and therefore the relative factor (2 in the example) can be optimized (see § 2.4 and 2.5).

2.2.3 Select conditional and response variables

The next step in CBR is to select variables that are to be used in the analysis.

There are two kinds of variables:

1. *Conditional variables*

Conditional variables are called independent variables in regression analysis. They 'explain' the effect of a substance. Examples of these variables in PERPEST are the "Mode of action" and the concentration of a substance.

2. *Response variables*

Response variables are variables that express the effects of a substance. In regression these variables are called dependent variables. In PERPEST all effect classes of herbicides or insecticides are automatically selected as response variables.

Nominal variables are used as conditional variables, all cases that equal the question case get a value 1 and all other cases get value 0 assigned. When nominal variables are used as response variables, the variable is translated into binary dummy variables. Each class is one variable that can take two values: true (1) or false (0). For ordinary variables these restrictions are not made.

2.2.4 Transformation, standardization and weighing of variables

Before standardization, a non-linear transformation can be used to shrink certain parts and to stretch other parts of the scale of the variable. The most commonly used transformation is the logarithmic transformation.

The available transformations are listed in Appendix I.

The different variables need to be standardized to give equal weight to different scaled variables. There are three options implemented (see details in Appendix II):

1. *Normalization* – The variable is scaled to be a normal distribution with a mean of 1 and a standard deviation of 1.
2. *MinMax standardization* – By this method the variables are scaled between one and zero.
3. *No transformation* - Use unstandardized data. Use this option only if the data are already standardized.

The variables are weighted by multiplying their values with weights that are entered by the user. The purpose of this weighting is to give important variables more weight. The weights also can be optimized by the computer (see § 2.5).

2.2.5 Calculate dissimilarities

The distance between the 'question case' and all other cases is calculated by a dissimilarity index. Appendix III gives a list of the supported indices. At default the Euclidian distance index is used.

Optionally the dissimilarity coefficients can be scaled between the minimum and maximum dissimilarity, which is especially useful with noisy data:

$$D^* = \text{MinDist} + \frac{D - \text{MIN}(D)}{\text{MAX}(D) - \text{MIN}(D)} (\text{MaxDist} - \text{MinDist})$$

2.3 How to predict a response variable?

After calculation of the dissimilarities of all cases with the question case, the cases in the database are ranked according to the obtained values. The N nearest cases are used to make a prediction of the selected response variables (we call N the *number of nearest points*). The default number for N is 25. With the response variables of these points, the prediction is made. The following methods are implemented:

1. Inverse distance

The response variables of these cases are weighted so that the influence of the cases declines with the dissimilarity from the case being estimated.

$$P^* = \frac{\sum_{i=1}^N (y_{ki}^* D_i^p)}{\sum_{i=1}^N D_i^p}$$

in which:

- P^* = Prediction of the transformed response variable (needs to be transformed back by using the inverse of the transformation)
- N = Number of nearest points
- y_{ki} = Transformed (not standardized) response variable k of case i
- D_i = Dissimilarity of case i with the question case
- P = Distance weighting power (is always negative !)

The more negative the *distance weighting power*, the faster the decline in influence and the less the effect of points further out will have on the interpolation.

2. Moving averages

The response variables of the N nearest cases are averaged without weighing.

3. *Local multiple regression*

The response variables of the N nearest cases are estimated by multiple regression of the nearest points with the conditional variables. This method is suitable for noisy and irregular spaced data.

4. *Global multiple regression*

The response variables are estimated by multiple regression with the conditional variables.

A bootstrapping procedure calculates the confidence intervals for the different effect classes and endpoints (Manly, 1997). In this resampling technique many (default 500) random data sets are generated by selecting cases at random with replacement. To be conservative we selected a smaller amount of cases than in the original database (default 75%). With each data set a prediction is made. The generated distribution of predictions serves as an estimate of the uncertainty. The 2.5 and 97.5% percentiles from this bootstrap distribution serve as the 95% confidence interval.

2.4 How accurate is the prediction?

The performance of the prediction method is evaluated using leave-one-out cross-validation (Stone, 1974). With this technique one case is removed from the database. Subsequently, the response variables of this case is predicted, using the remaining cases. The prediction is compared with the removed case. This procedure is repeated for all cases and a goodness-of-fit measure is calculated. In case of binary results (such as the effect classes in PERPEST) only the log(likelihood) and the percentage correctly predicted are suited.

Four indices of the fit were implemented:

1. The mean adjusted R^2 of the response variables (= percentage of variance explained by the model)
2. The minimal adj. R^2 of the response variables.
3. The sum of the log(likelihood) of the response variables. This measure is only suited for binary variables (Boolean, String, Calculated string).
4. The percentage correctly predicted. This simple measure also is only suited for binary variables.

Details about these options are given in Appendix IV.

2.5 Optimization of the prediction

The CBR method implies many subjective choices of methods and weights. We used the controlled random search procedure (Price, 1979) to optimize these choices mathematically.

The following parameters used by the prediction method can be optimized automatically:

- *Weights of conditional variables*
- *Distance weighting power*
- *Number of nearest points*

The parameters are optimized iteratively, by use of the *Controlled Random Search (CRS)* algorithm (Price, 1979). This algorithm is an improvement of pure random search, an algorithm searching the best set of parameters by trying at random. After each iteration the goodness of fit (adjusted R^2) is calculated by cross validation (see § 2.4).

The CRS algorithm first selects N sets of model parameters uniformly distributed over prior parameter ranges, calculates the goodness-of-fit for each and puts them in a vase.

It then selects $m+1$ points at random from the vase and mirrors the last point over the average (centroid) of the first m . The mirrored point is the new trial point. The goodness-of-fit (R^2) is calculated. If the R^2 better than the worst set of parameters in the vase, the worst element of the vase is replaced by this new guess. This process continues until a convergence criterion is reached.

3 User manual

3.1 Installation and getting started

The program is distributed as a single file (Install PERPEST.exe). To install the program, run this file and follow the instructions on the screen. The program is installed in the *Program Files/WUR* directory, and an icon is added to the *Start | Programs* menu.

To start the program click on the PERPEST icon in the *Programs* menu. The start screen will be displayed (Fig. 3.1).

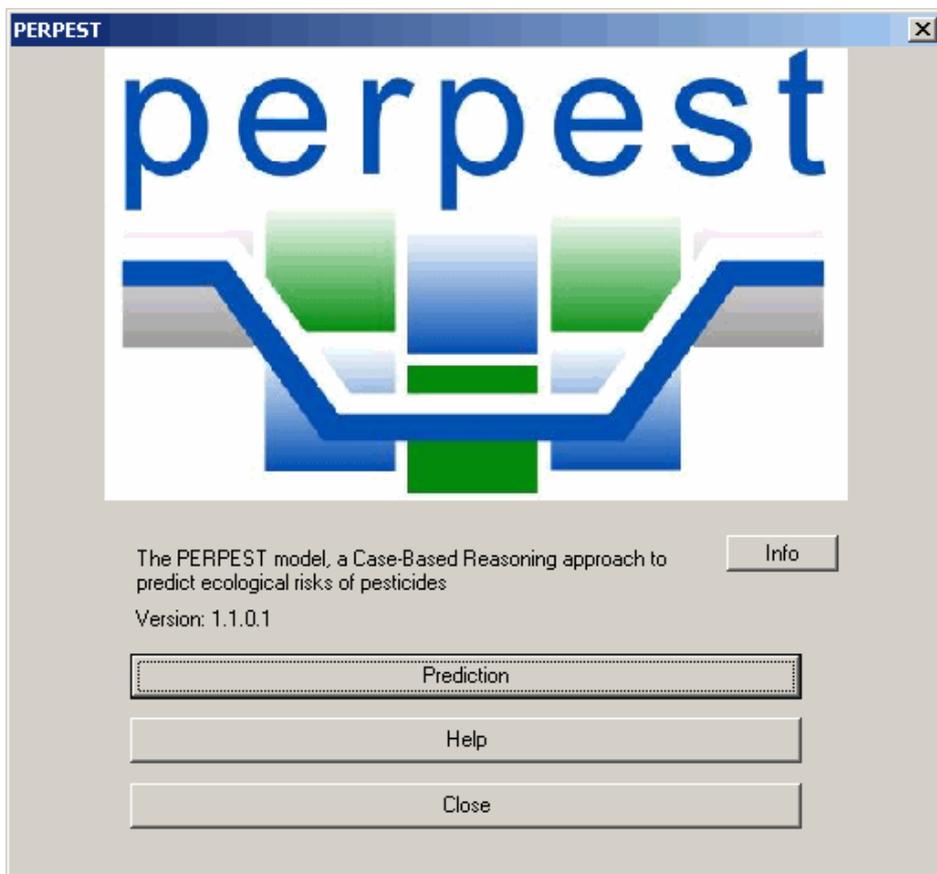


Fig. 3.1. The Start screen.

Click the *Prediction* button to make a prediction (see § 3.2).

The *Help* button opens the context sensitive Help system.

The program can be removed from the computer in the following way:

1. Open the configuration screen by selecting *Configuration* from the *Start* menu.
2. Select *Add or remove programs*
3. Select PERPEST from the list of installed software and click the *Remove* button.

3.2 Predicting an effect

After pressing the “Prediction” button in the start screen, the following dialog box appears (Fig 3.2).

Feature	Value
Code of substance	94-75-7
Name of the substance	2,4-D
Type of substance	Herbicide
Mode of action	Auxine simulator
Molecule group	Aryloxyalkanoic acid

Fig. 3.2. The substance data dialog box.

Enter in this screen the features of the experiment to be predicted. The dialog box has the following tab sheets:

- *Experiment features tab*
- *Weight/Select using tab*
- *Options tab*

If you press the **Next** button, you go to the next tab sheet, alternatively you can select tab sheets by clicking the tabs. You can also load a previous session by clicking the **Load** button. (*.lab file).

3.2.1 Experiment features tab

In this window you enter the features of the experiment that should be predicted.

- **Substance** Select here the chemical name/CAS number of the pesticide. Right of this list, the following buttons are displayed.
 - **Add New** - Add a new substance to the database (see below).
 - **Delete** - delete the current substance. This is only possible if there are no records with experiments of this substance in the database (the button is not grayed then).
 - **Edit** - edit the properties of the substance.
- **Features** - the features of the selected substance are listed in this table. Below the table, the *Number of cases* with data about this substance is displayed.

- **Concentration ($\mu\text{g}/\text{l}$)** - type here the concentration of the substance. As you type, the toxic unit of the currently selected substance is displayed.
- **Number of effect classes** - choose either 3 or 5 effect classes. In case of three effect classes, the original classes 3, 4 and 5 are fused to one “clear effects” class.
- **Reset** button. - resets the selections.

3.2.1.1 Add new substance

This form appears if you press the New button in the *Experiment features* tab of the substance data form (see above). Fill this form to enter a new substance or for editing the features of an existing substance. The following fields should be filled:

- **CAS registry number (required)**. Fill here the international CAS registry number of the substance.
- **Search on Internet button**. Use this button to find information about pesticides on a number of selected websites.
- **Chemical name (required)**. The name of the substance.
- **Type of substance (required)**. Select the type of substance (herbicide or insecticide) here.
- **Mode of action**. The mode of action (e.g. photosynthesis inhibitor) is filled here.
- **Molecule group** The active molecule group (e.g. triazin(on)e).
- **DT50 (days)**. The half-life of the chemical in water as determined in a water-sediment system,
- **EC50 ($\mu\text{g}/\text{l}$) (required)**. LC50 or EC50 of most susceptible standard test species.
- **Henry coefficient ($\text{Pa m}^3/\text{mol}$)** The partitioning coefficient air-water.
- **K_{om} (l/kg)** The partitioning coefficient between water and organic matter.

3.2.1.2 Search Internet

This dialog box may help to find information about substances on internet (CAS number, LC50, DT50 etc.).

Select a title of an internet site in the upper list. The URL and a short description is displayed. If you press OK, the default internet browser should be started with the URL in the edit box.

If nothing happens, you may not have registered the extension *.html in the Windows Explorer.

3.2.2 Weigh/Select using tab

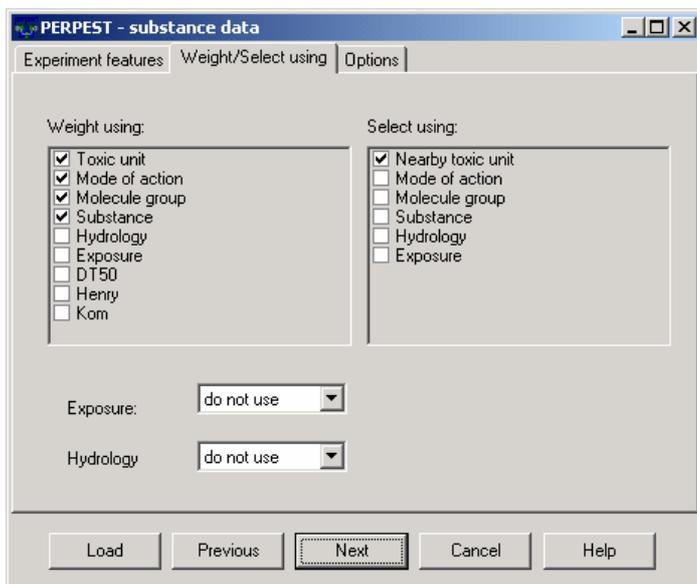


Fig. 3.3. The Weight/Select using tab sheet.

In this tabsheet (Fig 3.3) you can select or deselect conditional variables or selection variables. In the lower part of the dialog screen you can select the hydrology and exposure of the experiment to be predicted.

Left panel: Here you select the conditional variables used for weighing the similarity of cases:

- Toxic unit (*) – cases evaluating a concentration with a similar TU have a higher weight
- Mode of action (*) – cases evaluating a a compound with a similar mode of action have a higher weight
- Molecule group (*) – cases evaluating a a compound within the same molecule group have a higher weight
- Substance (*) –cases evaluating a a compound within the same substance have a higher weight
- Hydrology – cases with a similar hydrology have a higher weight
- Exposure – cases with a similar exposure have a higher weight
- DT50 – cases evaluating a substance with a similar DT50 have a higher weight
- Henry – cases evaluating a substance with a similar Henry coefficient have a higher weight
- K_{om} – cases evaluating a substance with a similar K_{om} have a higher weight

Right panel: Here you select a part of the case base based on the conditional variables:

- Nearby Toxic unit (*) - select cases within a certain range of toxic unit (factor, see options)

- Mode of action – select cases evaluating substances with the same mode of action only
 - Molecule group – select cases evaluating substances with the same active molecule group only
 - Substance – select cases evaluating the same substance only
 - Hydrology – select cases having the same hydrology only
 - Exposure– select cases evaluating the same exposure only
 -
- * *Selected as default*

3.2.3 Options tab

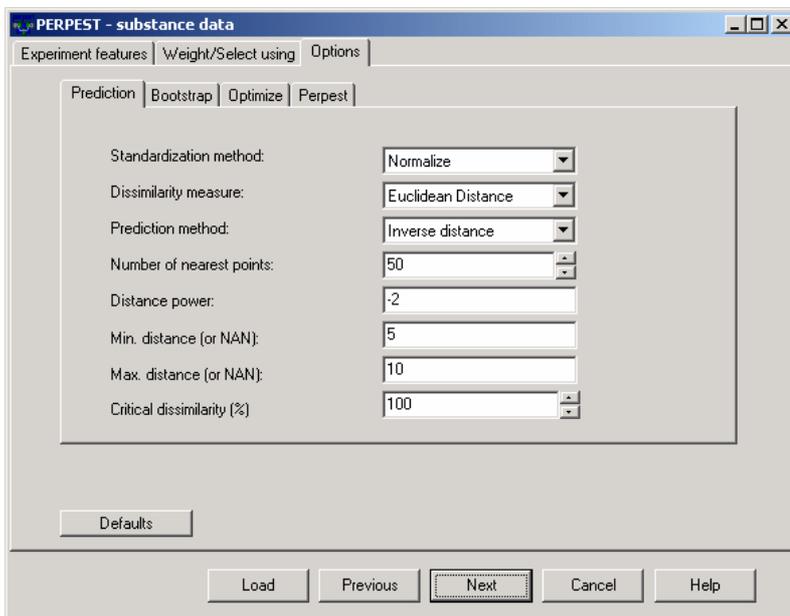


Fig. 3.4. The Options tab sheet

The option parameters of PERPEST are grouped in various tabs. Changes in the parameters are saved till the next session (Fig 3.4). Press the *Defaults* button to reset the default values of the parameters. The parameters in each tab are explained below:

- First tab sheet ('Prediction');
- Second tab sheet ('Bootstrap');
- Third tab sheet ('Optimize');
- Fourth tab sheet ('PERPEST')

The first tab sheet (Prediction):

parameter	description
Standardization method	This parameter defines the standardization method used to standardize the conditional variables before the dissimilarity with all cases can be calculated. See Appendix II.
Dissimilarity measure	This parameter defines the similarity method used to calculate the dissimilarity between the question case and all cases. See Appendix III.
Number of nearest points	For all CRS prediction methods the N most similar cases are used to calculate a prediction. The default number of nearest for N is 25. With the response variables of these points, the prediction is made using various methods.
Prediction method	Use this parameter to select the method for the prediction. See § 2.3
Distance power	With the inverse distance prediction method, the response variables of N most similar cases are weighted so that the influence of the cases declines with the dissimilarity to a power from the case being estimated.
Min. distance (or NAN)	The Min. distance defines the minimum of a scaling of the dissimilarity measures, which is especially useful with noisy data. Assign NAN (Not A Number) to this parameter if you want to keep the minimum unchanged.
Max. distance (or NAN)	The Max. distance defines the maximum of a scaling of the dissimilarity measures, which is especially useful with noisy data. Assign NAN (Not A Number) to this parameter if you want to keep the minimum unchanged.
Critical dissimilarity (%)	Optionally, the user may limit the cases that are displayed in the Cases Dialog to a certain percentage of the optimal similarity.

The second tab sheet (Bootstrap):

parameter	description
N Bootstrap	N Bootstrap defines the number of random data sets that are generated for the Bootstrap technique. The larger this number, the more accurate the bootstrapped confidence limits are.
Bootstrapped fraction	To be conservative we selected a smaller amount of cases than in the original database (Bootstrap fraction, default 75%) for each bootstrapped prediction.
Confidence limits p	This parameter sets the probability of the confidence limits of the bootstrapped predictions.

The third tab sheet (Optimize):

parameter	description
Convergence criterion	The convergence criterion is a stop criterion for the optimization. The lower this parameter, the better the optimization, but the longer the optimization takes. The convergence is defined as the relative difference in goodness-of-fit between the best and worst parameter set in the 'vase' during controlled random search.
"Vase" size	This parameter sets the size of the vase in controlled random search optimization. A higher vase size is needed if the optimization fails to find the global optimum but stays in a local optimum.
Goodness of fit	This parameter sets the used goodness of fit criterion for cross validation and optimization. See § 2.4 and Appendix IV.
Stop criterion stepwise	In a step forward analysis (optimization or prediction), the conditional variable that yields the best fit is added first. Subsequently, the next parameter is added, but only if the goodness of fit increases with a certain factor, i.e the stop criterion.
Range for optimizing:	During optimization several parameters are changed within certain

Weights of vars.	ranges. This parameter defines the minimal and maximal weights of variables.
Range for optimizing: Ranges of vars.	During optimization several parameters are changed within certain ranges. This parameter defines the minimal and maximal relative ranges of variables
Range for optimizing: Distance power	During optimization several parameters are changed within certain ranges. This parameter defines the minimal and maximal distance power.
Range for optimizing: Num. of nearest points	During optimization several parameters are changed within certain ranges. This parameter defines the minimal and maximal number of nearest points.

The fourth tab sheet (Perpest):

parameter	description
CAS	Set the default weight and (optionally) the transformation used for the CAS (substance code).
ToxUnit	Set the default weight and (optionally) the transformation used for the concentration of the substance expressed as toxic unit (Conc/EC50).
Mode of Action	Set the default weight and (optionally) the transformation used for the mode of action of the pesticide.
Molecule Group	Set the default weight and (optionally) the transformation used for the active molecule group.
Hydrology	Set the default weight and (optionally) the transformation used for the hydrology during the experiment (“Flow through” or “Stagnant/recirculating”).
Expos	Set the default weight and (optionally) the transformation used for the exposure to the substance in the experiment (“multiple/constant” or “single/pulse”).
DT50	Set the default weight and (optionally) the transformation used for the field dissipation DT50 (days).
Henry	Set the default weight and (optionally) the transformation used for the Partitioning coefficient air-water ($\text{Pa m}^3/\text{mol}$).
Kom	Set the default weight and (optionally) the transformation used for the Partitioning coefficient water-organic matter Kom (L/kg).
Max allowable difference (toxic unit), factor	At default the system selects only experiments that differ by a certain factor with the question experiment. You can set that factor here.

3.2.4 Predicted effects

After evaluating all the options and pressing the “next” button, the “predicted effects” screen appears.

In this screen, a summary of the results is given as pie charts (see Fig. 3.5). Each pie gives the predicted effect classes for that response variable. By pressing the right mouse button, a menu pops up with the following items:

- **Copy** - copy the figure as in wmf format to the clipboard. Pasting it in Microsoft Word, yields a sharp scalable picture.
- **Change Font** - change the font of the pie charts.
- **Update Figure** – updates the figure using the latest settings.

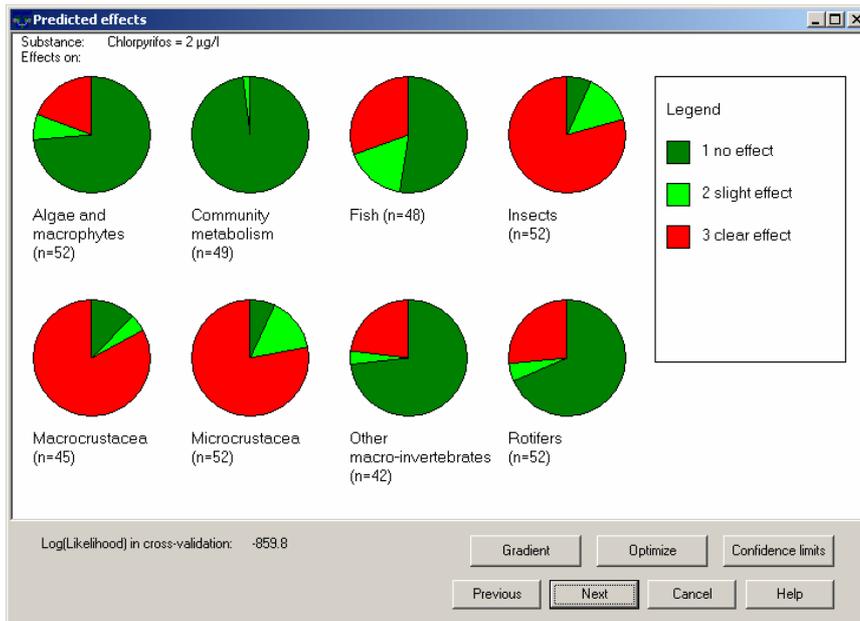


Fig. 3.5. The predicted effects screen.

Below the figure, the following items are visible:

- **Log(likelihood)** – loglikelihood is a goodness-of-fit measure that is determined by cross-validation (may take some time to appear).
- **Gradient button** – Here you can create a plot of the effects of a concentration gradient.
- **Optimize button** - click this button to optimize the method of prediction. See also: CRS dialog box.
- **Confidence limits button** - view the prediction dialog box, in which the results are presented as table and a bootstrap estimate of the confidence limits is given here.

3.2.5 Browse analogous cases

After pressing the “next” button, the “Brows cases analogous with ...” screen appears (Fig 3.6).

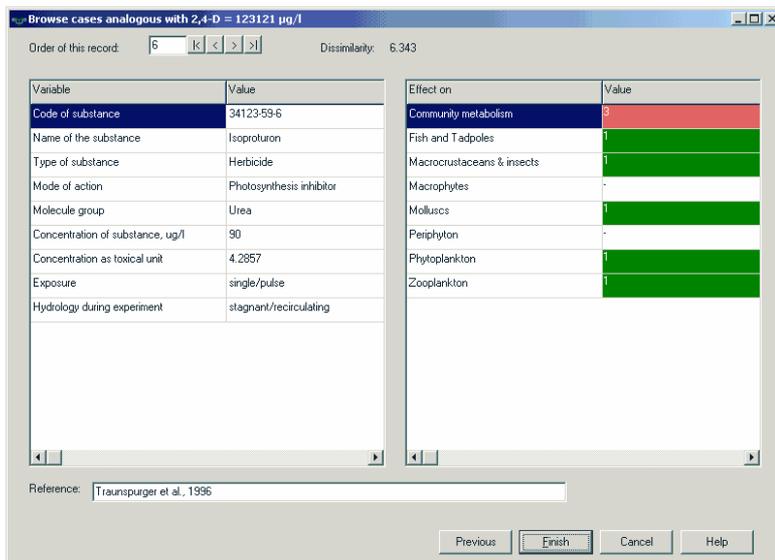


Fig. 3.6. The Browse cases analogous with (question case) screen

This dialog box makes it possible to view the details of the 10 most similar experiments. The cases are sorted in order of similarity. The first case (order number 1) is the most similar case. The left panel shows the conditional variables of that experiment and the right panel the values of the response variables.

Press the > button to view the next case and the < button to move backwards. Pressing the >| button moves to the last most dissimilar case. The |< button restores the first case.

Press *Finish* to close the dialog box. Before you return to the first screen, you get the opportunity to save your session (all settings are saved to a file that you can load in the Substance data dialog box (§ 3.2)

3.3 Optimizing the prediction

With this option, the weights and some of the parameters can be optimized. To start optimization click on the *Optimize* button in the Predicted effects dialog box (see: § 3.2.4). The next dialog box appears (Fig. 3.7):

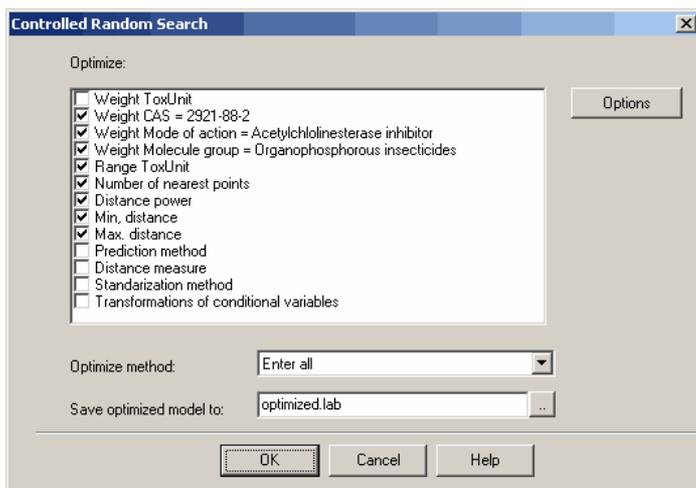


Fig. 3.7. The controlled Random Search dialog box. Use this screen to select the way of optimization and the parameters that must be optimized.

This dialog box has the following components:

1. *Optimize*: Use this box to select which parameters should be optimized. The following items can be (de)selected:
 - *Weights of conditional variables*. This item should be checked to optimize the weights of conditional variables. If there is only one conditional variable, changing the weight is useless. Therefore, then this item is disabled.
 - *Range of conditions*. If there is a filter with relative ranges defined, the relative range can be optimized. If there is no relative range, this option is useless and disabled.
 - *Number of nearest points*. Check this option to optimize the number of nearest points.
 - *Distance power*. When using the inverse distance prediction method, the distance power is an important parameter, which determines how the influence of the cases declines with the dissimilarity. This parameter can be optimized. When using other prediction methods, this option is grayed.
 - *Min, and max. distance* When using the inverse distance prediction method, the minimum and maximum distance are important parameters, that may prevent that nearby cases are weighted too strongly. Both parameter are optimized if this option is checked. When using other prediction methods, this option is grayed.
 - *Prediction method*. Use this option to find the optimal prediction method. Note: this is a nominal parameter and therefore the CRS optimization method may fail; it is probably better to optimize the different methods separately.
 - *Distance measure*. Use this option to optimize the distance measure. Note: this is a nominal parameter and therefore the CRS optimization method may fail; it is probably better to optimize models with different measures separately.
 - *Standardization method*. Note: this is a nominal parameter and therefore the CRS optimization method may fail.

- *Transformations of conditional variables.* Note: this is a nominal parameter and therefore the CRS optimization method may fail.
2. *Optimize method:* There are two ways of optimization:
 - *Enter all.* Just optimize the model with all conditional variables.
 - *Stepwise.* Enter the best conditional variable in a similar way as described with stepwise prediction (see: § 3.2.3), but each step is optimized first. While this is the ‘best’ optimization method, it may be very time consuming.
 3. *Save optimized model to:* Type here the file name to save the optimized model.
 4. *Options button:* If you press this button, the options dialog box is displayed (with the optimize tab). You can change the optimization ranges and other parameters here (see: § 3.2.3)

After the OK button is pressed, optimization starts. The progress of the optimization process is showed in a window (Fig. 3.8). In this screen the following information is showed:

- *Goodness of fit.* This is the goodness-of-fit of the last set of parameters.
- *Best goodness of fit.* This is the best goodness-of-fit so far.
- *Convergence.* This value is empty while the ‘vase’ is being filled (see Controlled Random Search). Thereafter it shows the relative difference between the best and the worst parameter set in the ‘vase’.
- *Table with parameters.* In this table all parameters that are being optimized are showed. The Minimum, Maximum and the Best value in the ‘vase’ is displayed. The last column (Current) shows the last value of this parameter that has been evaluated.
- *Close button.* Press this button to stop the optimization and proceed with the currently best parameter set. It is not recommended to do this because there is a chance that it might fail.
- *Stop CRS button.* Press this button to stop the optimization process temporarily. Press the button again to proceed.

Parameter	Min	Max	Best	Current
Weight CAS = 94-75-7	0.047282	9.966	7.56	9.862
Weight Mode of action = Auxine simulator	0.035726	9.9854	8.052	3.023
Weight Molecule group = Aryloxyalkanoic	0.035281	9.9627	9.956	9.958
Range ToxUnit	8.4069	9.9609	9.956	9.501
NNearestPoints	35	155	118	58
DistPower	-4.9879	-0.51661	-1.891	-0.5216
MinDistance	0.046862	9.9774	2.443	0.3025
MaxDistance	0.10245	9.9817	6.654	2.475

Fig. 3.8. The progress of the optimizing process.

If the convergence criterion is reached or if the user has pushed the *Close* button, the CRS results dialog is displayed. In this dialog, the best parameter set is displayed, and you are prompted if you want to use the new parameter set now. It is always saved to the *.lab file that is indicated in the first screen.

3.4 Creating concentration gradients

In the *Predicted effects* dialog box (see: § 3.2.4) you can predict concentration gradients (Fig. 3.9) by pressing the *Gradient* button. The concentration gradient dialog appears.

3.4.1 Concentration gradient dialog

In this figure the effects of different concentrations on all endpoints are plotted. The effect classes are stacked and shown as coloured areas. At default the gradient is logarithmic from 0.0125 to 6.4 toxic units.

Right-clicking on the figure brings up a popup-menu with the following items:

Copy to clipboard – Copies the figure to the clipboard (as metafile). You can paste the figure in Word or another program (example: Fig. 3.9).

Toxic units – Toggles between concentrations ($\mu\text{g/l}$) and toxic units.

Change Concentration Range – Opens the concentration range dialog to change the concentration range or to add observed effects in new studies in the figure.

Tables – Shows the data as tables that can be copied to other applications (e.g. Excel).

Properties – Change the colours, axes and titles of the plot.

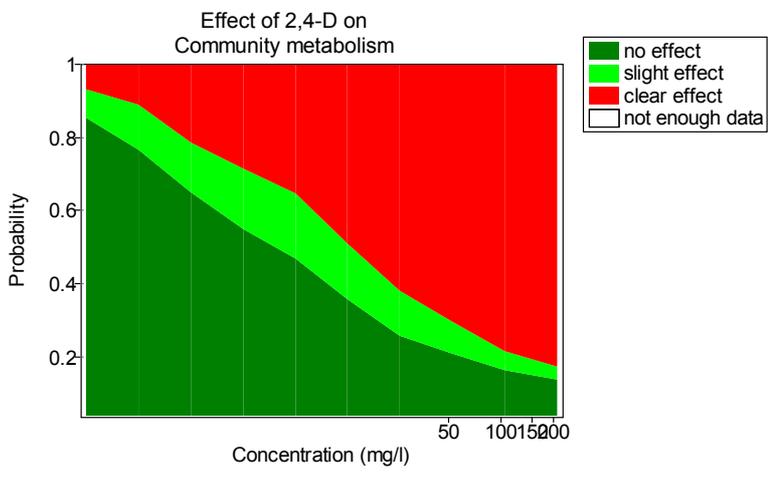


Fig. 3.9. Example of a concentration gradient.

3.4.2 Concentration range dialog

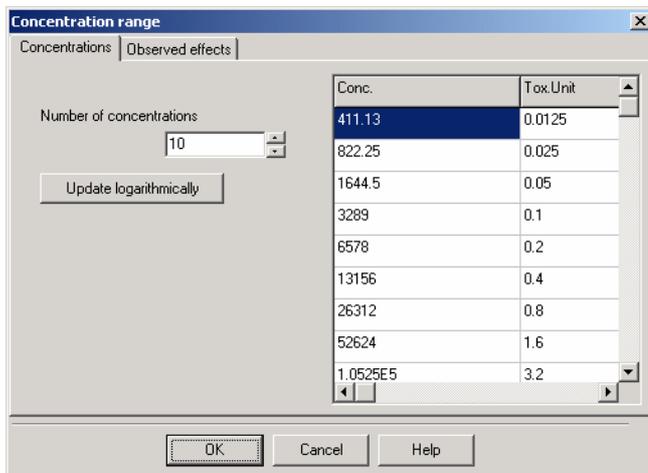


Fig. 3.10. The concentration range dialogue.

Use this dialog box to change the concentration range or to add observed effects in the concentration gradient figure (Fig. 3.10).

This screen has two tab sheets:

Concentrations – In this tab sheet you can enter the number of concentrations in the plot (default 10). If this number is changed, the concentration range is updated logarithmic. You can also change the concentrations or toxic units separately. If you press the **Update Logarithmically** button, the concentration range is updated logarithmically (doubled) with the last changed concentration as basis.

Observed effects – In this tab sheet you can enter results from your own experiments to compare the predicted values with.

3.4.3 Gradient data dialog

The data of the concentration gradient graphs are displayed as tables here. There are two buttons to save the data to the clipboard:

To Clipboard button – copy the current table to the Windows clipboard. You can paste these data in Excel or Word.

All to Clipboard button – copy all tables to the Windows clipboard (This may take some time).

3.4.4 Graph properties dialog

Use this dialog box to change several features of the concentration gradient figure.

The screen has the following tab sheets:

Series – Change the colour and legend title of each series.

Legend – Change the font and the position of the legend.

Axes – Select on the left-hand side the axis that you want to adjust. On the right side, you can edit the title, font and scaling of each axis.

Titles – Edit the graph title and font here.

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Appendix I Supported transformations

Before standardization, a non-linear transformation can be used to shrink certain parts of the scale and to stretch other parts. The following transformations are available:

1. *Logarithmic transformation*

Commonly used transformation to change a log-normally-distributed variable into a normal distribution or to give less weight to large quantities.

$$y_{ki}^* = \ln(y_{ki})$$

2. *Log(x+1) transformation*

Like logarithmic transformation but scaled for variables that can be zero.

$$y_{ki}^* = \ln(y_{ki} + 1)$$

3. *Log(x/(100-x)) transformation*

Special transformation to bring data of percentages as close as possible to a normal distribution.

$$y_{ki}^* = \ln\left(\frac{y_{ki}}{100 - y_{ki}}\right)$$

4. *Square root transformation*

Square root transformation, applied when analyzing Poisson-distributed variables.

$$y_{ki}^* = \sqrt{y_{ki}}$$

5. *Inverse transformation*

Used, e.g., to make the relation between Secchi depth and extinction approximately linear:

$$y_{ki}^* = \frac{I}{y_{ki}}$$

6. *Inverse (x+1) transformation*

Like the inverse transformation but scaled for variables that can be zero.

$$y_{ki}^* = \frac{I}{y_{ki} + 1}$$

7. *Angular Percentages transformation*

Special transformation to bring data of percentages as close as possible to a normal distribution. Alternative for *Log(x/(100-x))* transformation.

$$y_{ki}^* = \sqrt{\arcsin\left(\frac{y_{ki}}{100}\right)}$$

8. *Angular transformation*

Special transformation to bring data of fractions as close as possible to a normal distribution.

$$y_{ki}^* = \sqrt{\arcsin(y_{ki})}$$

9. *No transformation*

Use unchanged data.

Symbols:

y_{ki} = value of the variable k in case i

y^*_{ki} = transformed value of the variable k in case i

Appendix II Supported standardization methods

The different variables need to be standardized to give equal weight to different scaled variables.

4. *Normalization*

By this method the relative position of an observation within a distribution is described. The normalized value (also called *standard* or *Z score*) shows how many times the standard deviation an observation deviates from the mean of the population. The mean of the normalized values is 0 and the standard deviation is 1. It is obtained by subtracting the mean from a value and dividing this difference by the standard deviation.

$$y_{ki}^* = \frac{y_{ki} - \bar{y}_k}{s.d.}$$

5. *MinMax standardization*

By this method the variables are scaled between the minimum and maximum values in the database. The minimum gets value 0 and the maximum gets value 1.

$$y_{ki}^* = \frac{y_{ki} - \text{MIN}_i(y_{ki})}{\text{MAX}_i(y_{ki}) - \text{MIN}_i(y_{ki})}$$

6. *No standardization*

Do not change data. Use this option only if the data are already standardized.

Symbols:

y_{ki}^*	transformed value of the variable k in case i
y_{ki}	value of the variable k in case i
$\text{MIN}_i(y_{ki})$	minimal value of the variable k in the database
$\text{MAX}_i(y_{ki})$	maximal value of the variable k in the database
\bar{y}_k	mean of variable k in the database
$s.d.$	standard deviation of variable k in the database
n	number of variables

Appendix III Supported dissimilarity measures

The distance between the 'question case' and all other cases is calculated by a dissimilarity index. The following gives a list of the supported indices.

1. *Euclidean distance* (default). The Euclidean Distance (ED) is the most frequently used index. It is the distance in the n-dimensional space constrained by the conditional variables (Each variable is one dimension of the space).

$$ED = \sqrt{\sum_{k=1}^n (y_{ki} - y_{kj})^2}$$

2. *City Block distance* (also called the Manhattan Distance). The City Block Distance (CB) is the sum of the differences between all variables. It weights the variables that are far out stronger than the Euclidean Distance does.

$$CB = \sum_{k=1}^n |y_{ki} - y_{kj}|$$

3. *Cord Distance*. The Cord Distance (CD) is geometrically represented by the distance between points where the sample vectors intersect a unit sphere (see: Jongman et al., 1995). It gives more weight to qualitative aspects than the other indices of the program.

$$CD = \sqrt{\sum_{k=1}^n \left[\frac{y_{ki}}{\sqrt{\sum_{k=1}^n y_{ki}^2}} - \frac{y_{kj}}{\sqrt{\sum_{k=1}^n y_{kj}^2}} \right]^2}$$

4. *Chebychev Distance*. The Chebychev Distance (ChD) is the maximum difference between variables. It weights one variable that is far out even stronger than the City Block Distance.

$$ChD = \text{MAX}_k |y_{ki} - y_{kj}|$$

Symbols:

- y_{ki} transformed and standardized value of the variable k in case i multiplied with the weight of the variable (default weights are 1).
 n number of variables

The properties of the Euclidean Distance and the Cord Distance are discussed by Jongman, *et al.*, (1995). Optionally the dissimilarity coefficients can be scaled between the minimum and maximum dissimilarity, which is especially useful with noisy data:

$$D^* = \text{MinDist} + \frac{D - \text{MIN}(D)}{\text{MAX}(D) - \text{MIN}(D)} (\text{MaxDist} - \text{MinDist})$$

Appendix IV Supported validation measures

The following indices are used as goodness-of-fit measures. In case of a model with more than one response variables, these measures are combined in a single value (see: § 2.4)

Adjusted R²

R² (sometimes called coefficient of determination) is the same statistic that is commonly used in linear regression. The sample R² usually is an optimistic estimate of how well the model fits the reality. The statistic adjusted R² attempts to correct R² to reflect more closely the goodness of fit of the model in the population.

Formula:

$$adj. R^2 = 1 - \frac{\text{residual sum of squares}/(N - p - 1)}{\text{total sum of squares}/(N - 1)}$$

N = sample size, p = number of parameters.

If the adjusted R² equals 1, the model fits perfectly, if the adjusted R² is negative, the mean value of the response variables is a better prediction than the model.

Log(likelihood)

For binary data the adjusted R² is not suitable. For these data two other measures are implemented: The likelihood is the probability that the observed data occur if the model is correct. As this is usually an extremely low probability, the logarithm of this value is taken, resulting in a negative number. In our case the log likelihood (L) is calculated as follows:

$$L = \sum_{obs=0} \ln(1 - p) + \sum_{obs=1} \ln(p)$$

Symbols:

p Prediction

$\sum_{obs=0}$ Sum of the cases where the observed conditional variable equals 0

Percentage correctly predicted

This simple measure is less accurate as the log(likelihood), but is also suited for binary variables only. It simply gives the percentage of the responses that is predicted correctly.

