**Step 5: Filling data gap - Predict missing data by read-across, trend analysis or QSAR models**

Select a data gap by clicking in the corresponding empty cell in the data matrix, select one of the three data gap filling methods:

- **Read-across:** for “qualitative” endpoints (skin sensitisation or mutagenicity e.g. positive, negative, equivocal) or for “quantitative endpoints” (e.g., 96h-LC50 for fish) if only very few analogues with experimental results are identified.
- **Trend analysis** for “quantitative endpoints” if many analogues with experimental results are identified.
- **(Q)SAR models** if no analogue with experimental results is identified or to build a weight of evidence case.

The resulting graph proposes a prediction based on the available results for the analogues (or training set and test set in case of (Q) SAR models)

Once you are satisfied with a prediction, click **Accept prediction** and **Return to Matrix**.

**Step 6: Report – Obtain a detailed report for your prediction**

To obtain a report, select a prediction

Visit [www.qsartoolbox.org](http://www.qsartoolbox.org) for more detailed guidance documents.
Step 2: Profiling - Retrieve information based on the identity of the substance or its structure

Select profilers by ticking the corresponding boxes (consult Manual for Getting Started to identify the most relevant profilers for any given endpoint) → . The program establishes a "profile" of the chemical based on its structure.

Step 3: Endpoint - Retrieve experimental results from the resident databases

Select databases by ticking the corresponding databases → . The retrieved information is displayed according to four sub-sections:

Step 4: Category definition - Identify chemicals which could form a category with the "target" chemical

Select one grouping method according to the profile of your target chemical in the window Grouping methods and then click Define. You are prompted to confirm the query details, name of the category and retrieval of experimental data. Press OK each time.

If in the selected databases some experimental results are available more than once, the system identifies those multiple entries in a separate window. To keep only one result for multiple entries → Select one → OK.

To refine the category, repeat the procedure by clicking on Subcategory and selecting other grouping methods. In the subcategorisation procedure, the function deletes chemicals with the highlighted profiles (i.e. by default chemicals that have profiles different from the target chemical).