

A.B.O.S.

Toolbox to analyse omic data



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Rapid detection, classification and evaluation of biological characteristics or processes in complex data sets

Today's technology platforms for the detection of biological processes (expression, transcription, regulation, modification, etc.) generate vast amounts of data. The evaluation and assessment of this data is a major task that can frequently encounter difficulties, above all when the desired information cannot be read out directly from the individual data. A.B.O.S. solves this problem and enables a quick and efficient evaluation of complex data sets. The compilation and classification of measured values is rendered fully possible through the use of self-learning algorithms. Alongside, differentiated templates for pattern recognition are generated via system-based learning processes. Extensive measurement data are then evaluated on the basis of the identified templates before being assigned to a corresponding group.

As an efficient, fast and cost-effective evaluation method, A.B.O.S. purposefully employs a visually reduced presentation of results. These findings can then be immediately utilised for further evaluation runs.

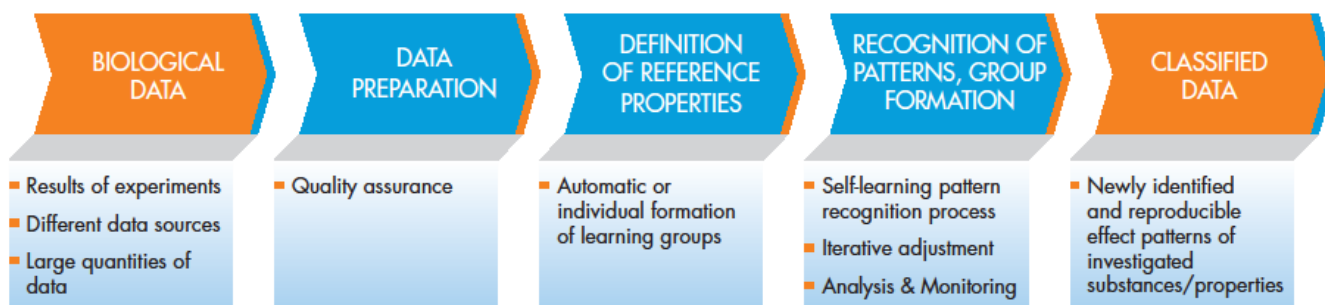
Applicable for:

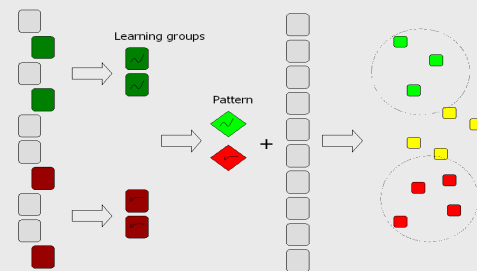
- transcriptomic data
- metabolomic data
- mass spectrometric data
- impedance data
- infrared spectroscopic data
- in each case also from different sources

Cost and time optimisation through standardisation

The described procedure differs from others on the market with respect to its design and implementation, and care has been taken to avoid existing and standard approaches. Critical to the procedure is the ability to weigh captured parameters in terms of their contribution to group differentiation and in this way separate relevant from non-relevant declarative parameters.

In connection with in vitro-based test procedures, A.B.O.S. provides a functional tool for the assessment of toxicity endpoints as well as general physiological effects. >





An important feature of A.B.O.S. is the option to consider either known biological (previous-) knowledge in the choice of learning groups, or for these to be defined by the tool without any previous knowledge. This represents a crucial difference to the majority of software tools already available on the market.

Performance features:

- In just a few steps, A.B.O.S. can supply substantial statements on non-obvious relationships in complex biological measurement data.
- Existing knowledge of group affiliations is fully integrated, while the tool establishes new group members on the basis of common effects.
- Attributes are worked out for the identification of group affiliations (marker search), enabling cost reduction in subsequent experiments.
- The integrated QA module secures the input quality of data.
- The customisable QA module gives due consideration to necessary tolerance thresholds and can work simultaneously with various data sources.
- High-performance evaluations and fast work in iterations enables the verification of hypotheses at any time.
- The tool is complemented by extensive support from decision-making aids, flexibility, automatic evaluations and the integration of expert knowledge.
- The greatly reduced complexity of the display underpins the efficient evaluation of results and provides insights for further evaluation runs.
- The option of a detailed overview of relevant parameters enables a high reproducibility of results.
- The procedure is available as a stand-alone application and can be straightforwardly integrated into existing processes.

***Everything starts with a first step.
Don't hesitate to contact us to discuss your requirements.***