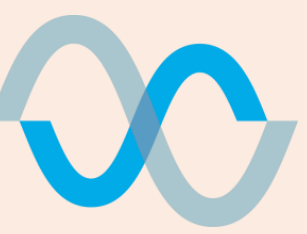


AUTOMATIC WORKFLOW FOR IN VITRO HIGH-THROUGHPUT SCREENING DATA FAIRIFICATION, PREPROCESSING AND SCORING: A CASE STUDY ON NANOMATERIALS



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MOTIVATION

- Address safety challenges of new chemical substances and materials, including advanced nanomaterials.
- Regulatory agencies are interested in using safety data generated through New Approach Methodologies (NAM).
- Data management based on FAIR guiding principles helps with consistent curation and reusing of accumulated data.
- Nanosafety, cheminformatics, and bioinformatics communities can benefit from this data management approach.
- The high-throughput screening (HTS) biological data is used for efficient clustering, ranking, prioritization of NMs and read across.

CHALLENGES

- Difficulty in consistently assessing and validating multiple agent effects simultaneously in HTS data.
- Challenges in linking large experimental datasets with descriptive metadata and harmonizing terminology.
- Ensuring data is machine-readable, findable, accessible, and reusable (FAIR principles) is complex.
- Traditional HTS results documentation approaches, such as using spreadsheets for data collecting and preprocessing are time-consuming and error prone.
- Integrating external tools like ToxPi [1] adds complexity, especially due to limited preprocessing capabilities and output options.

RESULTS

- ✓ **ToxFAIRy** [2] is a Python package that provides faster data preprocessing, scoring, hierarchical clustering, and data FAIRification. ToxFAIRy minimizes the possibility of errors through automation and improves on the original ToxPi software in terms of data visualization, flexibility, and easier data export.
- ✓ **Orange3-ToxFAIRy** [2] is an Orange3 add-on that makes composition of complex workflows much easier for the users through a visual programming interface.
- ✓ **HTS_METADATA template** developed as part of the Template Wizard supports data annotation and harmonization in a reproducible manner
- ✓ Extending the eNanoMapper FAIRification workflow [3] by facilitating FAIRification of HTS data. The resulting FAIR data includes both raw and interpreted data (scores) in machine readable format serialized in NeXus format that can be integrated into the eNanoMapper database [4].

Case study on NANOMATERIALS

The example raw data and filled out HTS_METADATA templates are available in <https://doi.org/10.5281/zenodo.13683162>

Index	Description	Cell	populat
1	A1	219	8.029E+1
2	A2	276	6.997E+1
3	A3	147	9.728E+1
4	A4	0	0.000E+0
5	A5	222	9.836E+1
6	A6	342	8.367E+1
7	A7	217	9.852E+1
8	A8	248	8.438E+1
9	A9	143	9.497E+1
10	A10	2	5.628E+1
11	A11	3	1.791E+1
12	A12	265	9.234E+1
13	A13	173	8.902E+1
14	A14	40	3.734E+1
15	A15	224	8.902E+1
16	A16	319	1.862E+1
17	A17	319	1.862E+1
18	A18	319	1.862E+1
19	A19	319	1.862E+1
20	A20	319	1.862E+1

Well Address	Sample name	Assessment	Concentration (μg/ml)
A1	TOX5	TOX5	1
A2	TOX5	TOX5	1
A3	TOX5	TOX5	1
A4	TOX5	TOX5	1
A5	TOX5	TOX5	1
A6	TOX5	TOX5	1
A7	TOX5	TOX5	1
A8	TOX5	TOX5	1
A9	TOX5	TOX5	1
A10	TOX5	TOX5	1
A11	TOX5	TOX5	1
A12	TOX5	TOX5	1
A13	TOX5	TOX5	1
A14	TOX5	TOX5	1
A15	TOX5	TOX5	1
A16	TOX5	TOX5	1
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A18	TOX5	TOX5	1
A19	TOX5	TOX5	1
A20	TOX5	TOX5	1

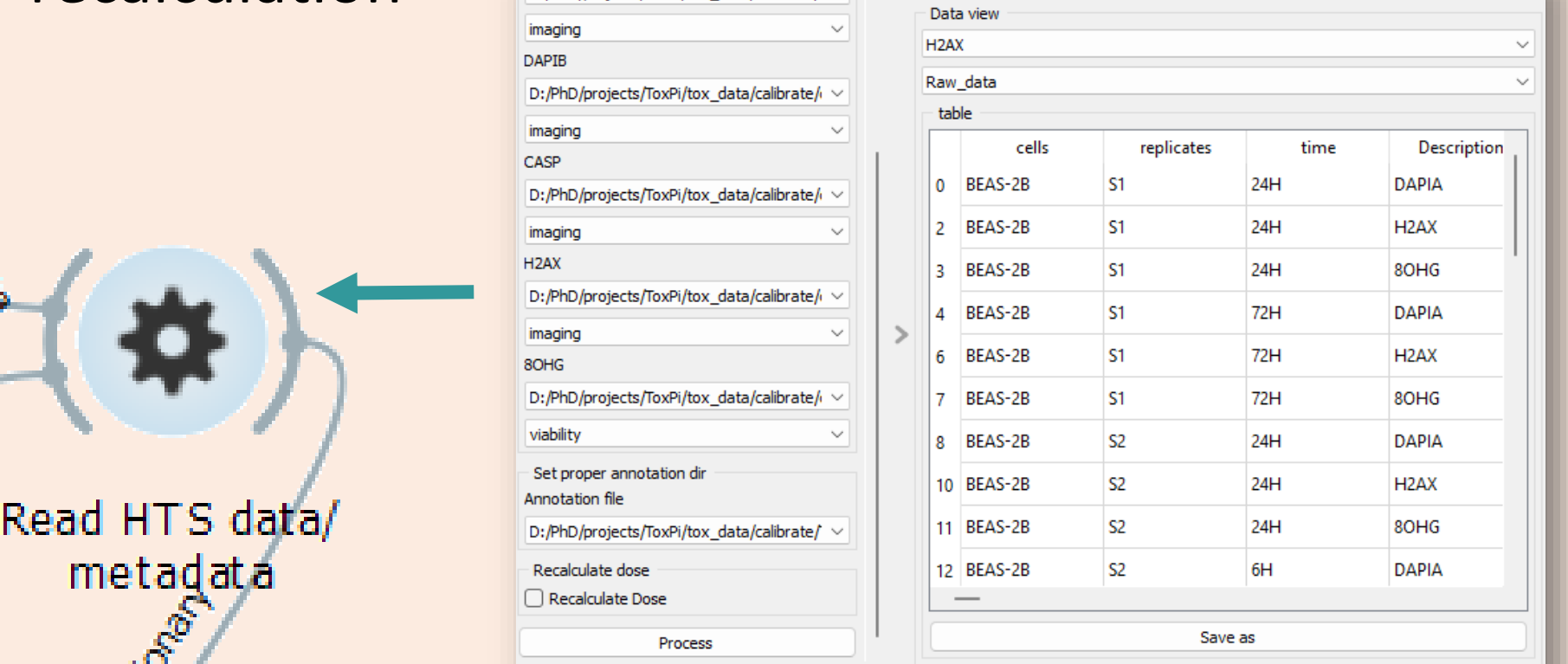
Index	Material	HTS score	HTS rank	HTS score	HTS rank
1	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
2	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
3	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
4	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
5	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
6	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
7	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
8	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
9	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
10	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
11	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
12	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
13	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
14	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
15	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
16	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
17	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
18	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
19	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27
20	4-Nitroquinoline 1-oxide	0.2668	27	0.2668	27

Material	HTS score	HTS rank	HTS score	HTS rank
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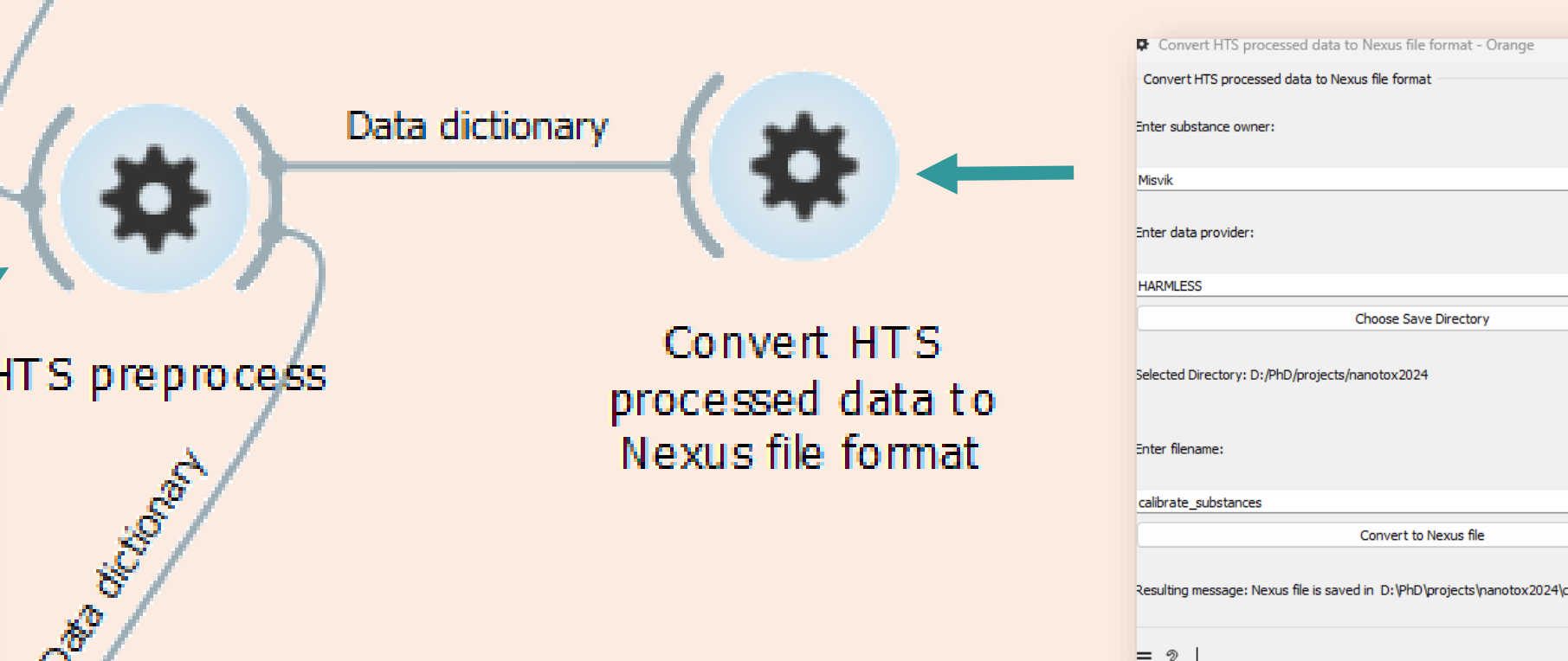


- Marvel, S.W., et al. BMC Bioinformatics 19, 80, 2018 <https://doi.org/10.1186/s12859-018-2089-2>
- <https://github.com/ideconsult/orange3-toxfairy>
- Kochev, N et al. *Nanomaterials*, 10, 2020, <https://doi.org/10.3390/nano10101908>
- Jeliakzova, N et al. *Nat. Nanotechnol.* 16, 2021, 644–654 <https://doi.org/10.1038/s41565-021-00911-6>
- Nymark, P; Hongisto, V et al. *Toxicology Letters*, 314, 2019, <https://doi.org/10.1016/j.toxlet.2019.09.002>
- Demsar, J et al, *Journal of Machine Learning Research*, 2013, 2349–2353.

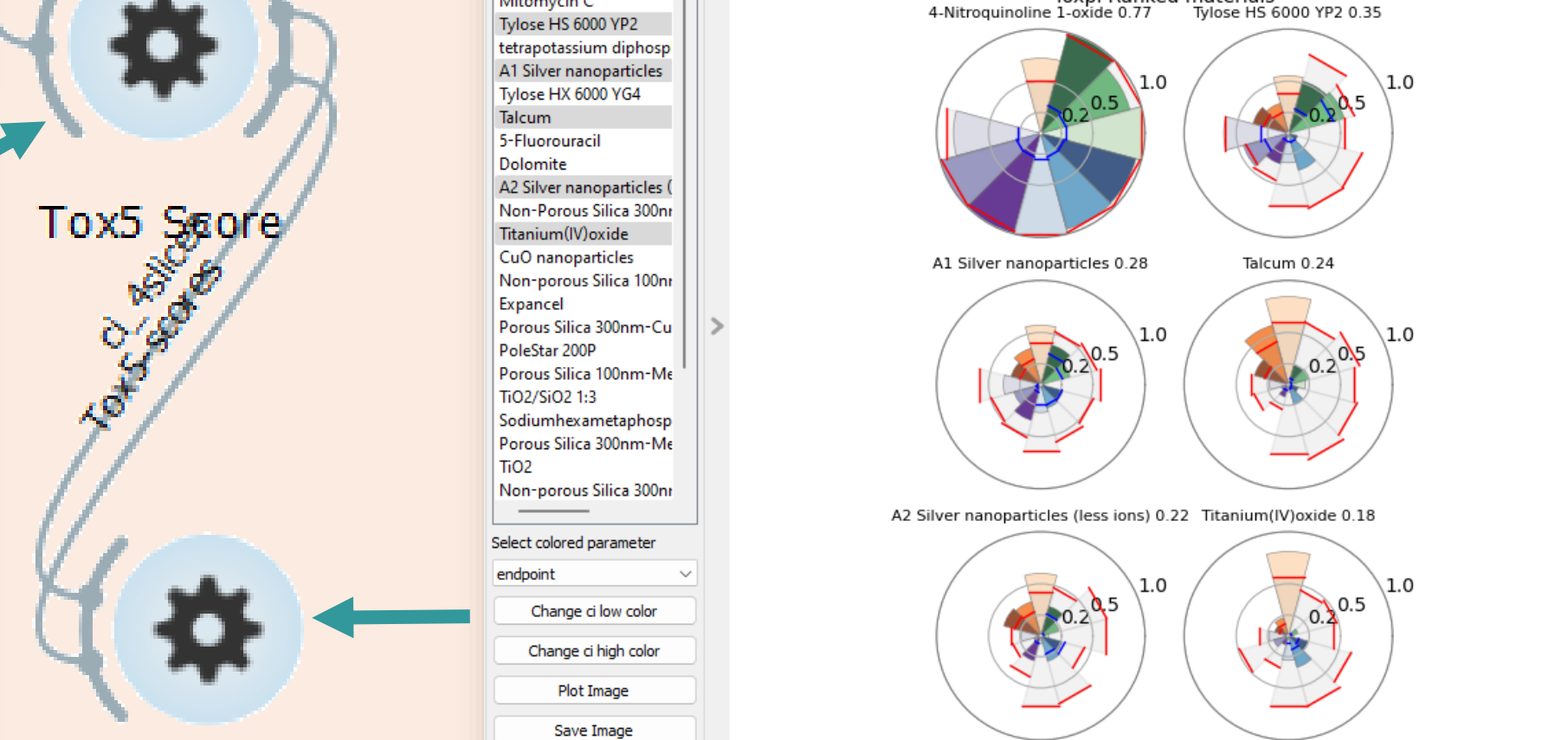
Read and annotate HTS data with option for dose recalculation



Make the processed data FAIR by converting to an eNanoMapper data model and serialize in NeXus format.



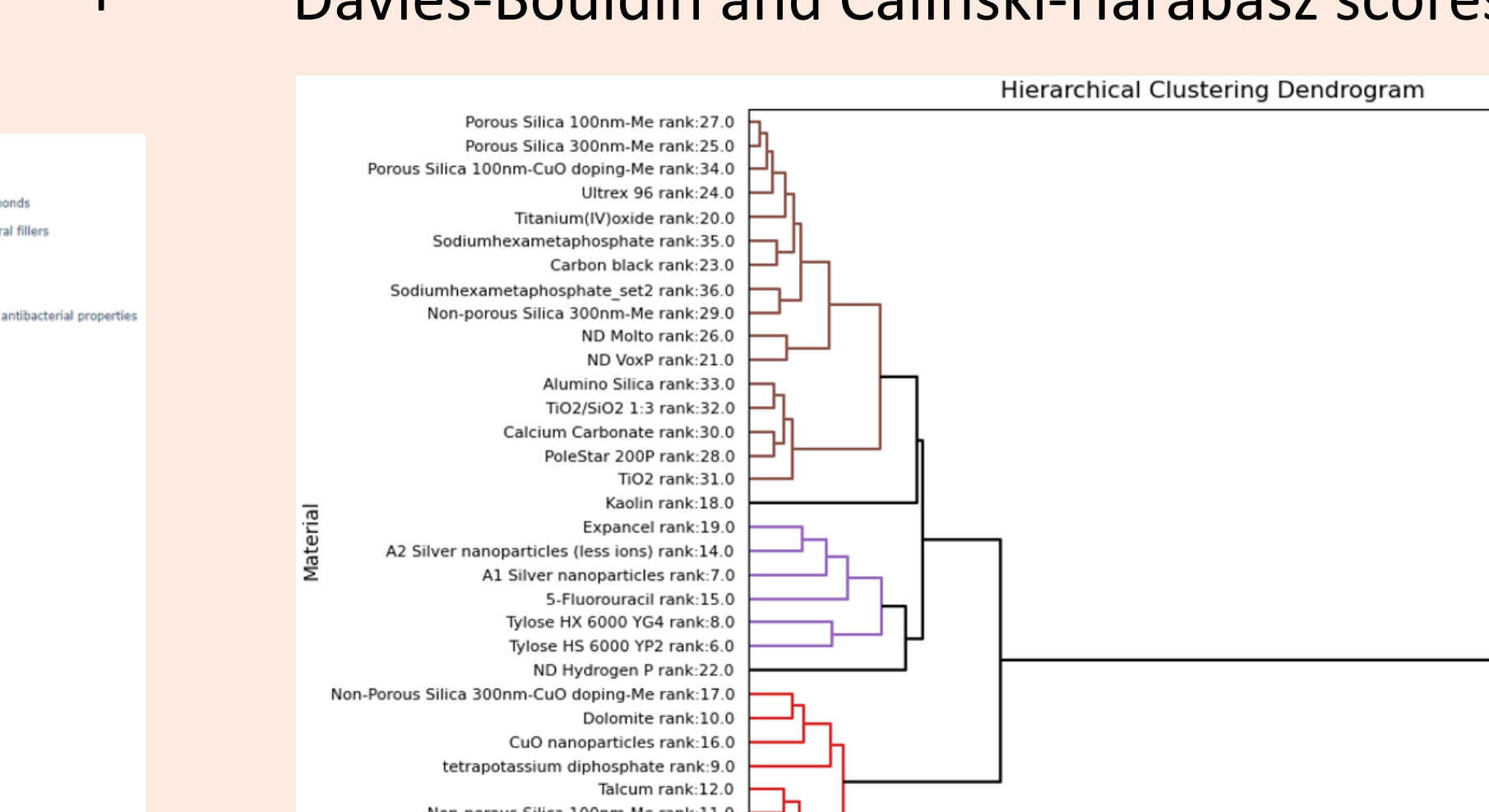
Visualize NeXus file from: <https://myhdf5.hdfgroup.org/>



Pie view of toxicity scores of selected materials with upper and lower bounds of confidence intervals.

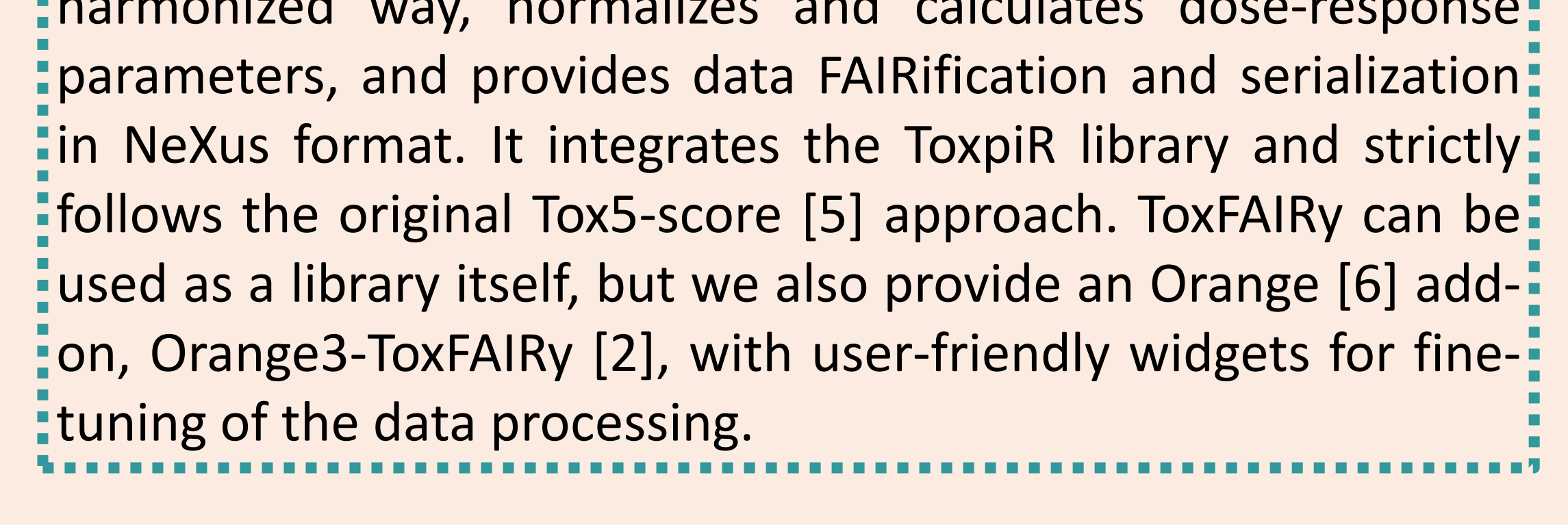
The pie chart is available as an interactive HTML graphic, featuring slice markers that display additional information on hover, along with zoom functionality for enhanced exploration.

Hierarchical clustering methods integrated in ToxFAIRy

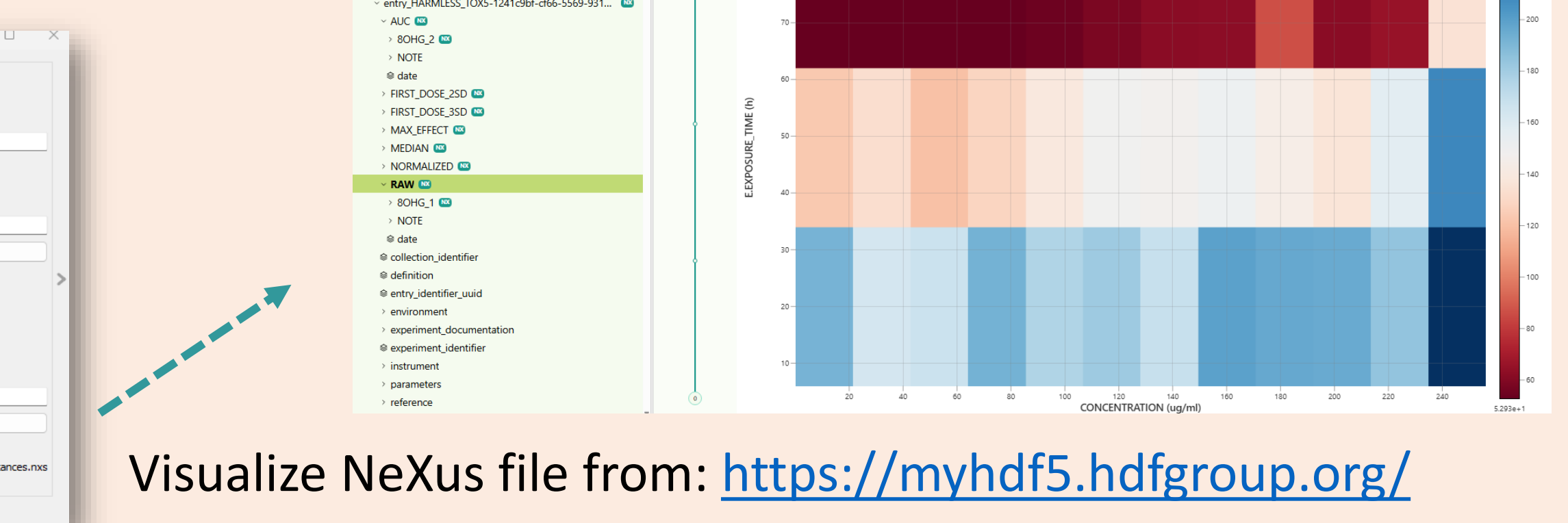


Hierarchical clustering, utilizing euclidean distance as the metric and clustering method – ward and optimal number of clusters by elbow method. Automatically calculated cluster significance metrics Silhouette, Davies-Bouldin and Calinski-Harabasz scores.

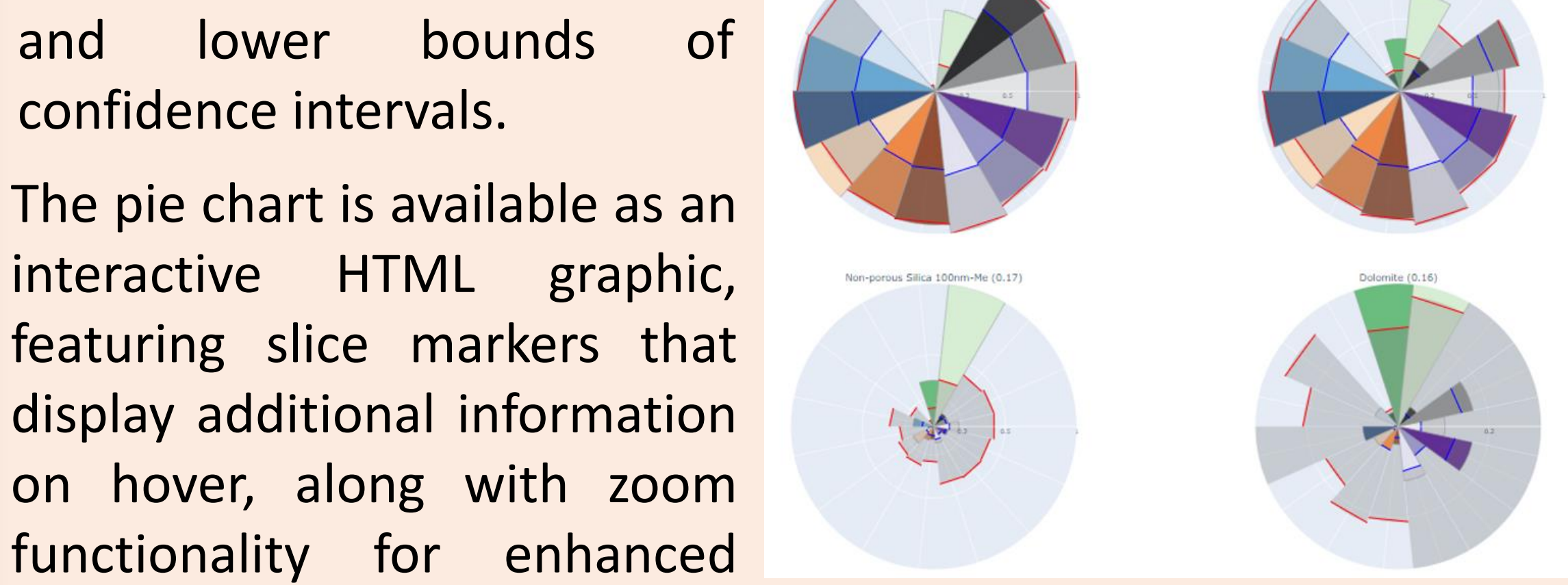
ToxFAIRy [2] collects and annotates raw HTS data in a harmonized way, normalizes and calculates dose-response parameters, and provides data FAIRification and serialization in NeXus format. It integrates the ToxPi library and strictly follows the original Tox5-score [5] approach. ToxFAIRy can be used as a library itself, but we also provide an Orange [6] add-on, Orange3-ToxFAIRy [2], with user-friendly widgets for fine-tuning of the data processing.



Normalize and calculate dose-response metrics for each endpoint separately.



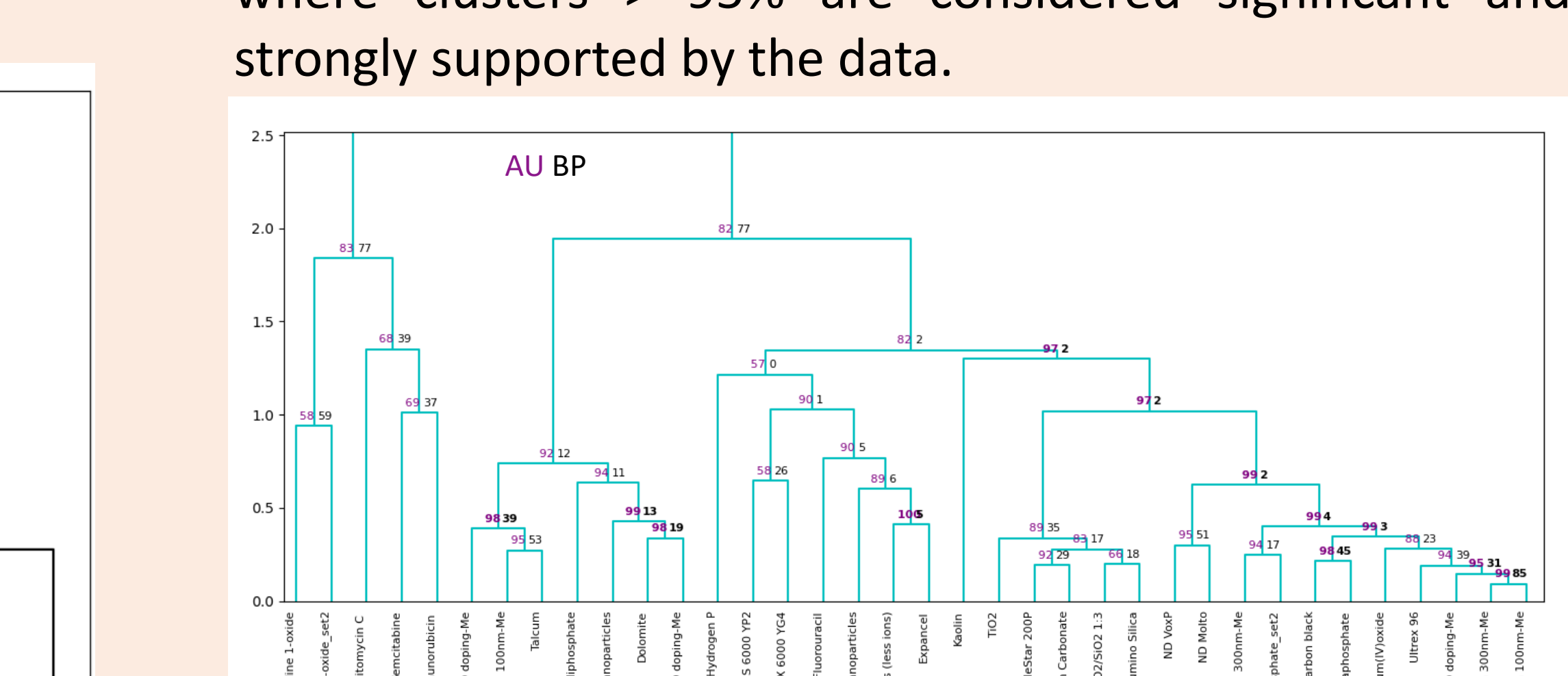
Create slices automatically or manually for selected cell lines. Transform data with chosen functions, add specific weight for selected metrics and calculate scores with Bootstrap confidence intervals.



Resulting tables with Tox5-scores, ranks, specific slices scores and confidence intervals

Ranked materials and controls with bootstrap confidence interval from resulting table

Multiscale bootstrap resampling to the hierarchical clustering, by reintegrated pcluster python package. Approximately Unbiased p-value (AU) and Bootstrap Probability (BP) report the significance of each cluster where clusters > 95% are considered significant and strongly supported by the data.



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