Intelligent workflows for automated analysis of mass spectrometry-based proteomics data

Güler, A.T.

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**Intelligent Workflows for Automated Analysis of
Mass Spectrometry-based Proteomics Data**

1. Automated literature analysis gives an extensive overview of the domain even when some terms are used ambiguously in publications. (this thesis)

2. To promote the reusability of components in modular scientific workflows, inputs and outputs of the modules should be open data formats. If there is any need, non- standard data formats should only be used inside the modules. (this thesis)

3. Tools that use metadata should be flexible to traverse between different levels of ontological hierarchies to be widely applicable for different experimental setups. (this thesis)

4. Systematic bias in mass spectrometry measurements can be corrected automatically with the help of appropriate metadata. (this thesis)

5. It is impossible to turn poor-quality data into good-quality data, but good-quality data can be wasted in suboptimal analysis workflows.

6. It is data hoarding, not data keeping, unless you make it FAIR.

7. Good quality data without metadata is like a high-end instrument without a user's manual.

8. The field of proteomics does not exist in a vacuum; multi-omics integration is crucial to understanding underlying biological mechanisms.

9. If a picture is worth a thousand words, then an interactive one is worth ten thousand words.

10. The good thing about computer programming is that the computers do what you ask them to do; the bad thing about computer programming is that the computers do what you ask them to do.

11. Make it work first, you can make it better afterwards!