The handle http://hdl.handle.net/1887/28508 holds various files of this Leiden University dissertation.

**Author:** Peironcely Miguel, Julio Eduardo  
**Title:** Automated de novo metabolite identification with mass spectrometry and cheminformatics  
**Issue Date:** 2014-09-03
Stellingen
Behorende bij het proefschrift

Automated de novo metabolite identification with mass spectrometry and cheminformatics

1. The canonical augmentation path method can be applied to molecules and it generates all possible non-duplicated chemical structures for a given elemental composition (this thesis, chapter 2).

2. Metabolite-likeness differentiates human and non-human metabolites and it can be accurately calculated (this thesis, chapter 3).

3. The combination of a reference database of spectra, fragment information and good algorithms using only mass spectrometry allows in many cases the de novo metabolite identification resulting in only a few possible structures (this thesis, chapter 4).

4. Pruning early on the search space using chemical constraints speeds up the generation of molecules and provides a better list of results (this thesis, chapter 5).

5. In addition to these trends towards better or more comprehensive metabolite identification, it is also expected that the growing movement towards open-source software, open-access databases and freely available web servers will stimulate the development of even better, more user-friendly tools for metabolite identification (Wishart DS et al, 2009, Bioanalysis, p. 1954). However, incentives for scientists are not yet aligned with the “open” movement.
6. Metabolites were found to occupy a typical compact continuous chemical space well carved in the broader chemical space of available chemicals (Gupta S and Aires-de-Sousa J 2007, *Molecular Diversity*, p. 32). In addition, measuring metabolite-likeness is done with higher accuracy by using simple molecular descriptors instead of complex molecular descriptors.

7. Process cheap tests first, that is, tests that consume least computation time. Process selective tests first, that is, tests that eliminate most intermediates (Meringer M 2009, In Handbook of Chemoinformatics Algorithms, p. 251). The former requires computational knowledge, the latter chemistry knowledge. Therefore the proper use of cheminformatics for metabolite identification can accelerate identification processes significant.

8. The maximum common substructure from a list of structures that have the most similar fragmentation trees appears to be a valuable tool to identify unknown metabolites (Rojas-Chertó M et al. 2012, Analytical Chemistry, p. 10). An even more useful approach would be to find common subtrees in a database of annotated fragmentation trees.

9. Predictive models teach you valuable life lessons: everything is a trade-off, and garbage in, garbage out.

10. All what you should expect from your PhD is to preserve correct knowledge and pass it on for the next generation.

11. Also for a PhD, the saying is true: the journey (doing the PhD) matters more than the destination (PhD title).