

**Algorithms in Genome Research  
Winter 2010/2011**

**Exercises**

**Number 6, Discussion: 2010 December 10**

1. Find out which peak detection algorithms exist that may be used in the analysis of GC-MS and GCxGC-MS experiments. How do they work? Discuss the pros and cons.
2. Consider the mass decomposition algorithm that we discussed in proteomics, in order to calculate all compomers for a given parent mass. Which additional effects do we have to consider when we apply this to metabolites?