Composition module

# Create composition library

## Input:

1. Dictionary of peptideObjects  
   {‘PEPTIDECK’: <peptideObject>, ….}
2. settings

### (Relevant) Attributes of peptideObject:

**sequence**

The full peptide sequence

**charge**

The charge of the precursor

**includedPeaks**

The MS1 peaks that are isolated

**fragments**

A dictionary of the m/z of all peaks. Keys have the format ‘y3 h1++’.

## Output:

Dictionary of compensationObjects

{‘PEPTIDECK’: <compensationObject>, ….}

### Attributes of the compensationObject:

**sequence**

The full peptide sequence

**charge**

The charge of the precursor

**includedPeaks**

The MS1 peaks that are isolated

**fragments**

A list of peaks in the format ‘y3 h1++’.

**compensationConstants**

A dictionary of what to multiply each peak intensity with in order to compensate for redistribution.

**overlappingPeaks**

Dictionary of which peaks overlap with which:

{'y10 l2+': 'y10 h0+', 'y4 l1++': None, 'y2 h0+': 'y2 l2+', …}

## Workflow