Since the discovery of the first antibiotic, penicillin, in 1928, countless lives have been saved by the drugs. Despite being an essential part of modern medicine

```
(peptide)
string <- peptide+peptide
Subpeptides(0) <- peptide
n <- |peptide|-1
O  i <- 0
     i <- 0 to |peptide|
       sub <- string(i to i+n)
       add sub to subpeptides
   n <- n-1
```

The theoretical spectrum is created from a list of the masses of all subpeptides, the mass of the original peptide, and 0. Masses of each string in the list subpeptide are found by adding the known integer masses of each amino that make up the subpeptide. The function returns the mass value of each amino acid in the peptide as it is entered into a dictionary. Once all masses are added to the list spectrum, the list is ordered from smallest to largest mass.

```
spectrum (0) <-0
          i <- 0 to |subpeptides|
            subpeptideM
```

experimental spectrum. Alternatively, we can design a faster and more efficient branch-and-bound algorithm. This approach begins with a list, Peptides, consisting of an empty peptide. Each iteration, the list of peptides is rewritten with a new set of peptides by adding each amino acid to a peptide that was previously found to be consistent with the experimental spectrum with (peptide). If the mass of the peptide is equal to the mass of the tested peptide, ParentMass, and the cyclospectrum of the peptide matches the input spectrum the peptide is added to a list of final peptides. The linear spectrum of the peptide is also checked against the theoretical spectrum. If the peptide does not pass these tests, it is removed from the list, therefore, limiting the number of peptides tested in the next iteration.

```
                    (Spectrum)
ParentMass <- maximum value in spectrum
Peptides ћ a set containing only the empty peptide
FinalPeptides ћ empty list of strings
GЋ ıÑd Peptides is nonempty
        Peptides ћ Expand(Peptides)
            each peptide Peptide in Peptides
                Mass(Peptide) = ParentMass
                    ıHcreateSpectrum(Peptide) = Spectrum
                        add Peptide to FinalPeptides
                    remove Peptide from Peptides
                    Peptide is not consistent with Spectrum
                    remove Peptide from Peptides
        FinalPeptides
```

Using this program we can sequence cyclopeptides from the experimental spectrum of masses like that produced by a mass spectrometer. Creating a program helps us reconstruct these peptides is useful for the identification and research of various א