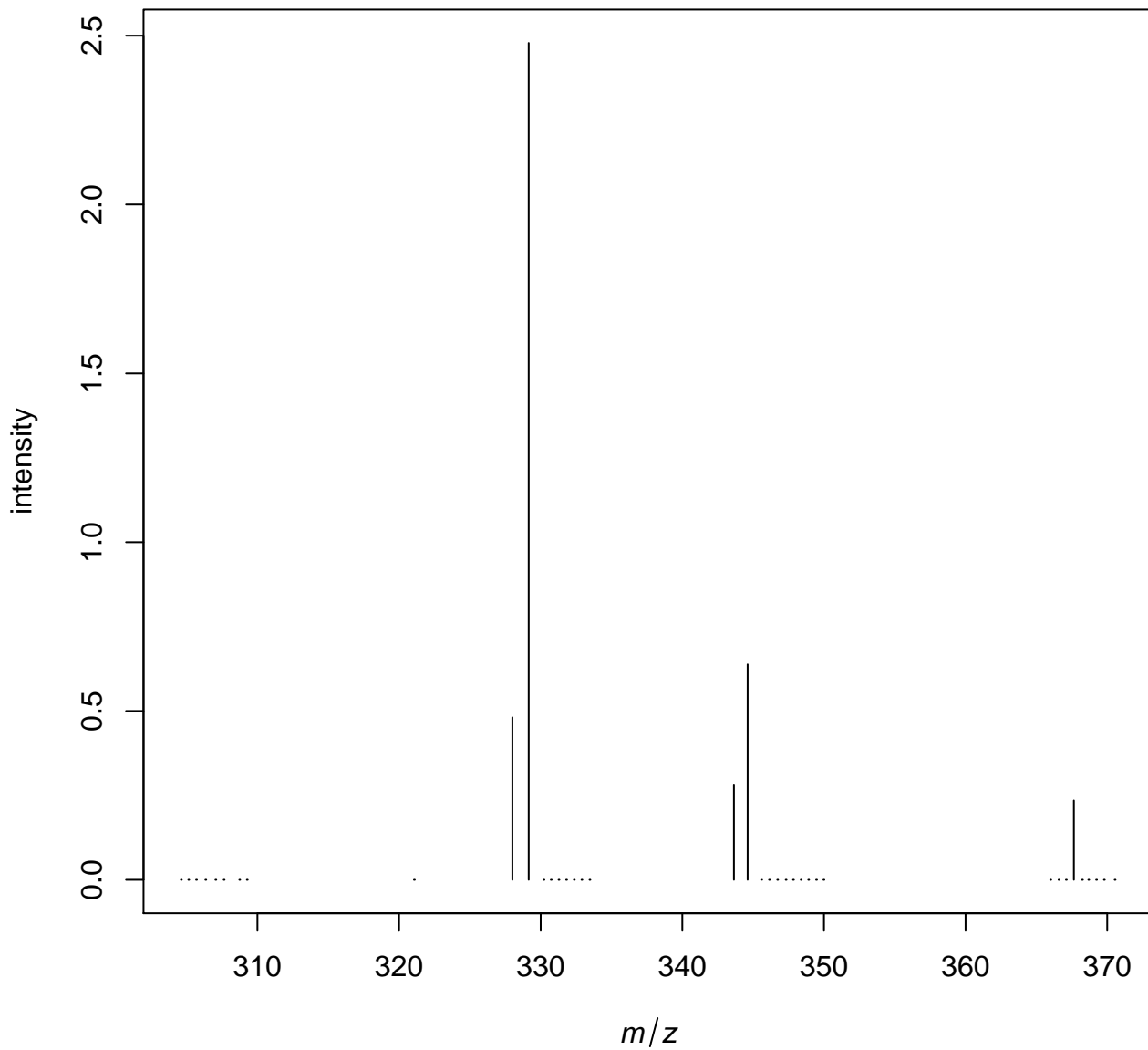
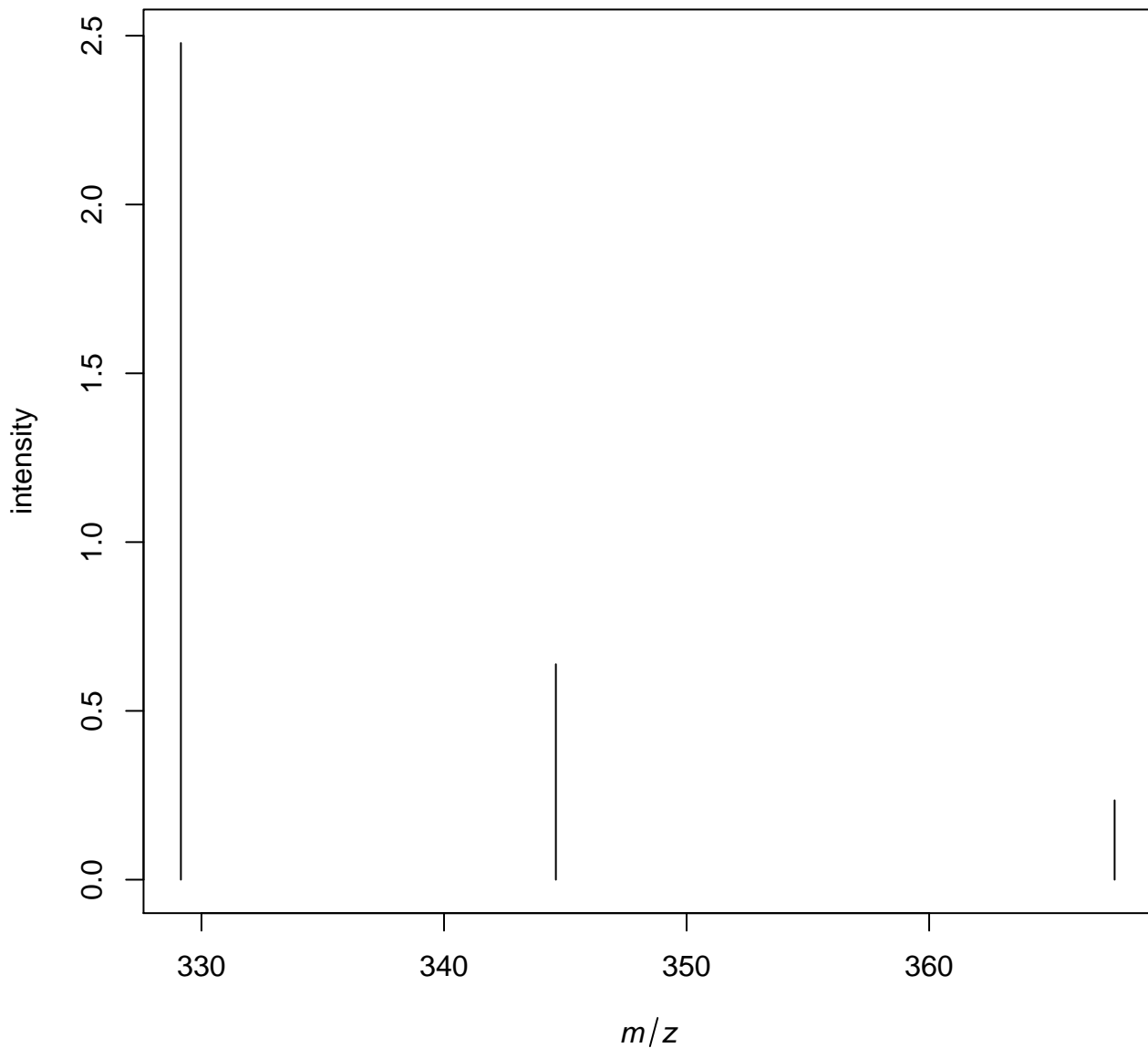


**masspeaks3\_forinput.tabular**

# First spectrum of input file



# First spectrum after monoisotopic peaks detection



	<b>min m/z</b>	<b>max mz</b>	<b># features</b>	<b>median intensity</b>
<i>inputdata</i>	304.5953	396.9167	33	0
<i>monoisotopes</i>	308.2667	394.7917	2.11	0.2