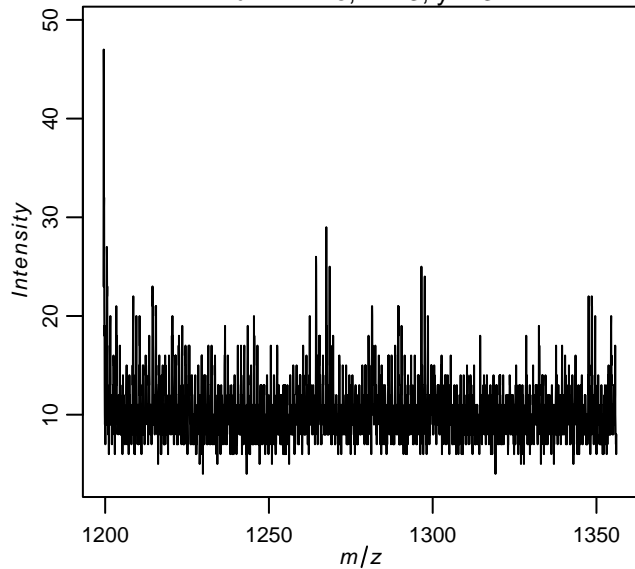


Quality control during preprocessing

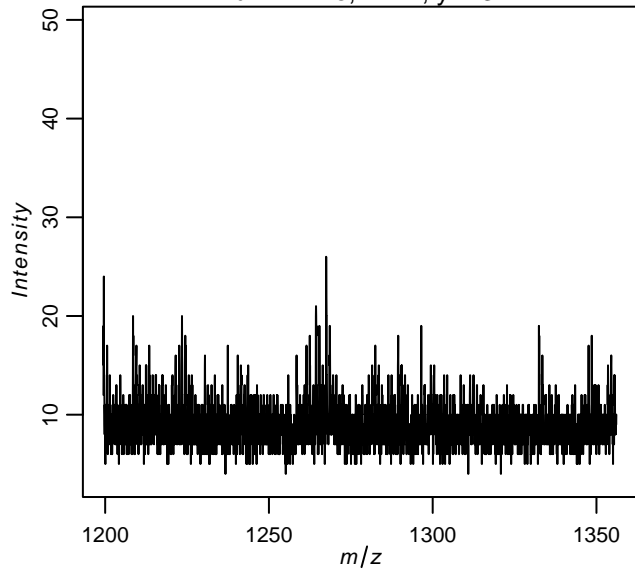
Filename: files_

Input spectra

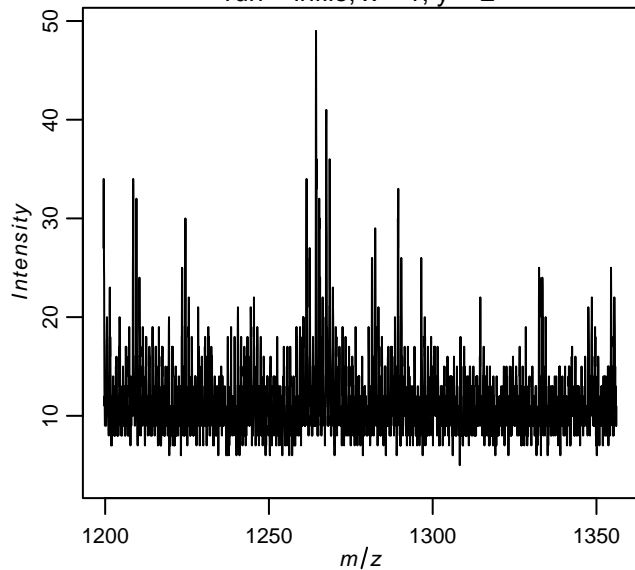
run = infile, x = 3, y = 3



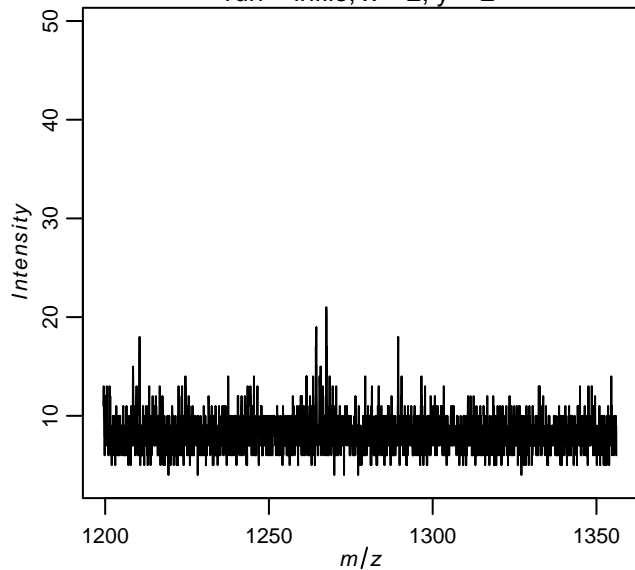
run = infile, x = 2, y = 3



run = infile, x = 1, y = 2

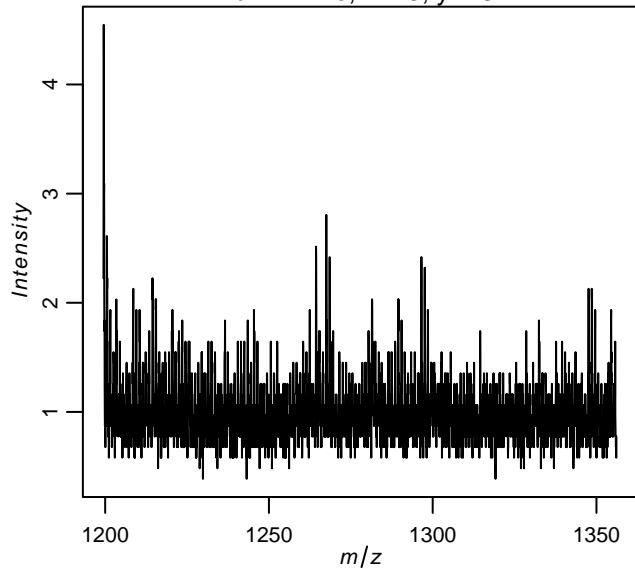


run = infile, x = 2, y = 2

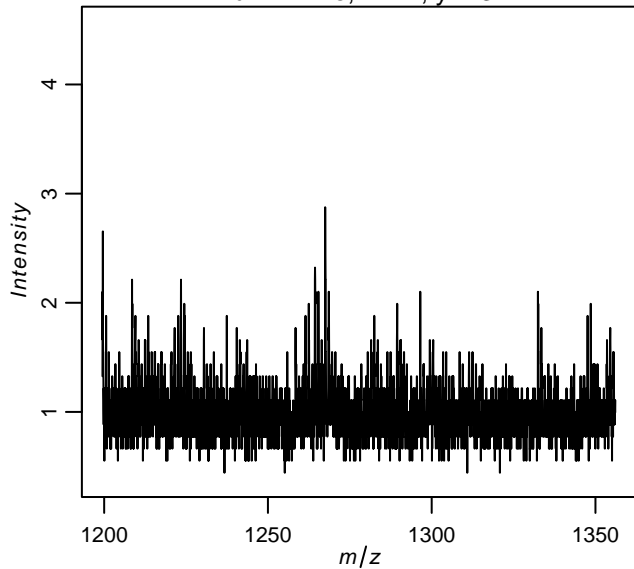


Spectra after normalization

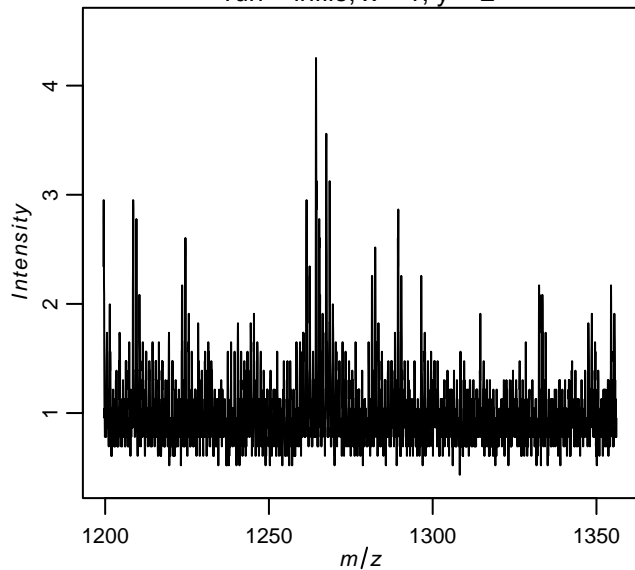
run = infile, x = 3, y = 3



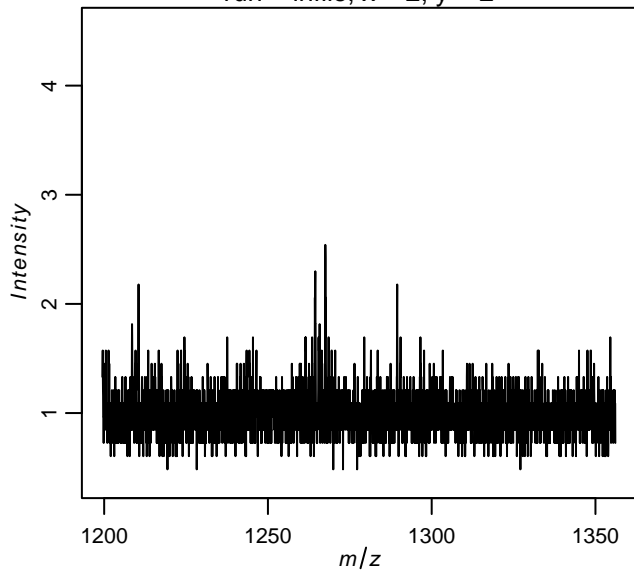
run = infile, x = 2, y = 3



run = infile, x = 1, y = 2

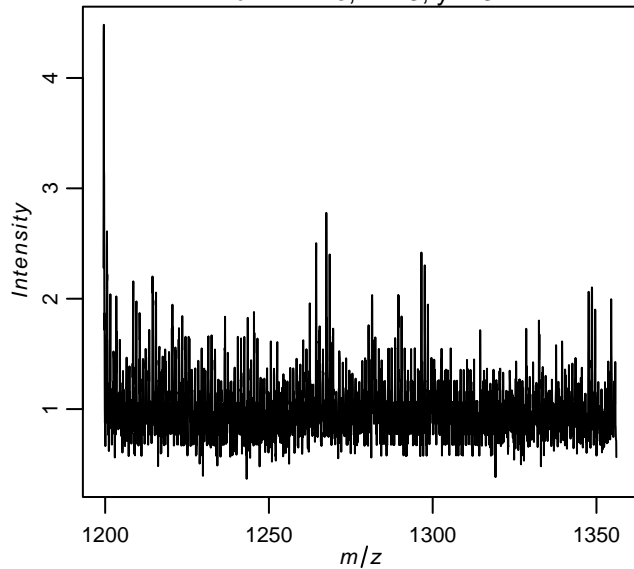


run = infile, x = 2, y = 2

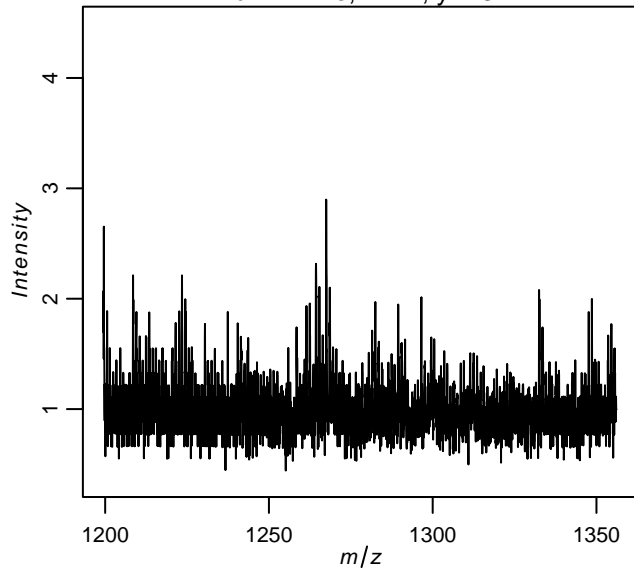


Spectra after m/z alignment

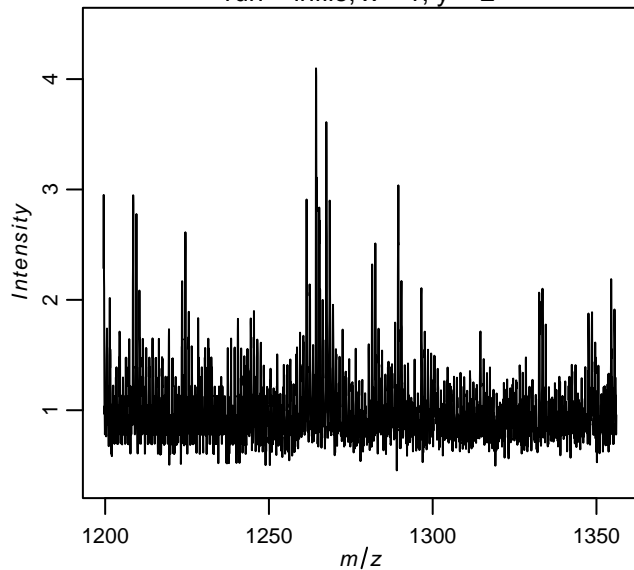
run = infile, x = 3, y = 3



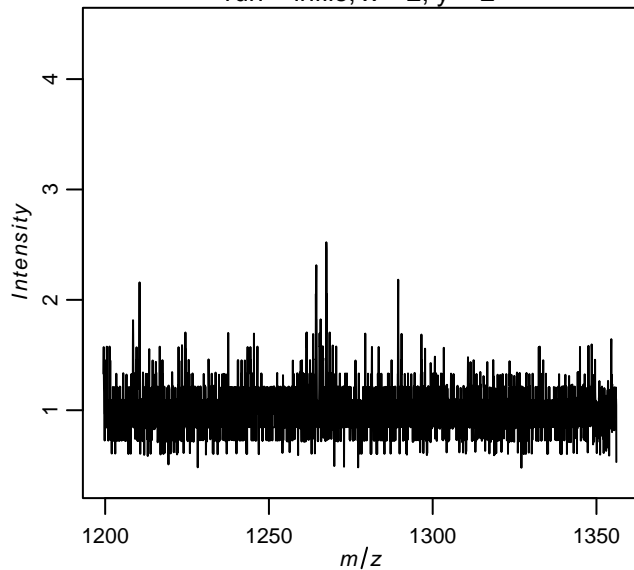
run = infile, x = 2, y = 3



run = infile, x = 1, y = 2

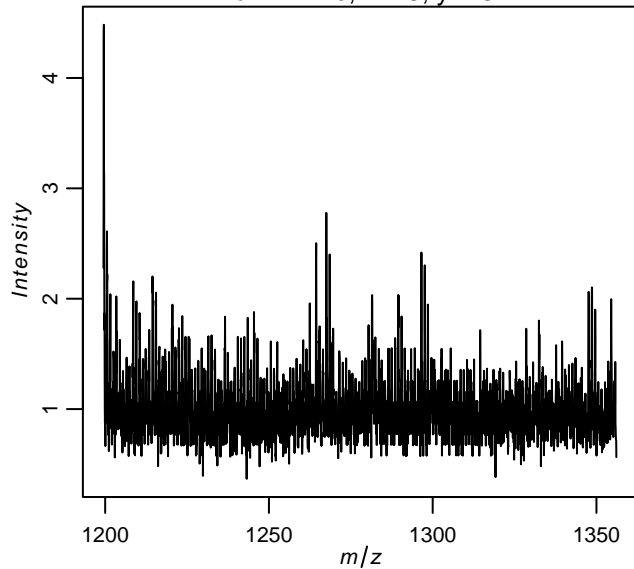


run = infile, x = 2, y = 2

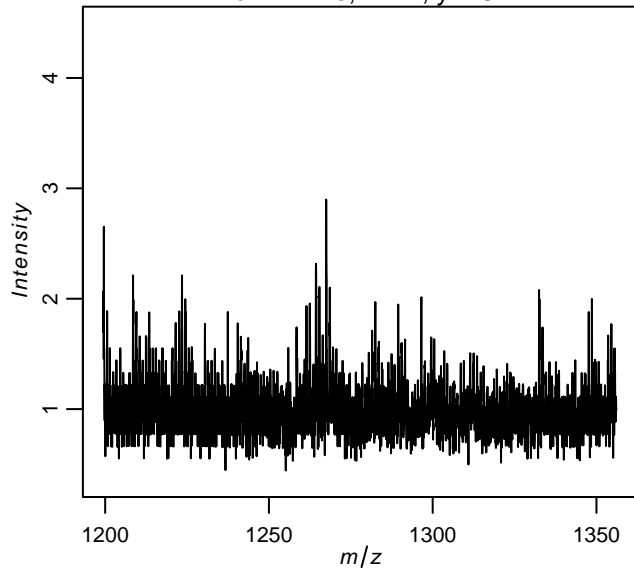


Spectra after m/z recalibration

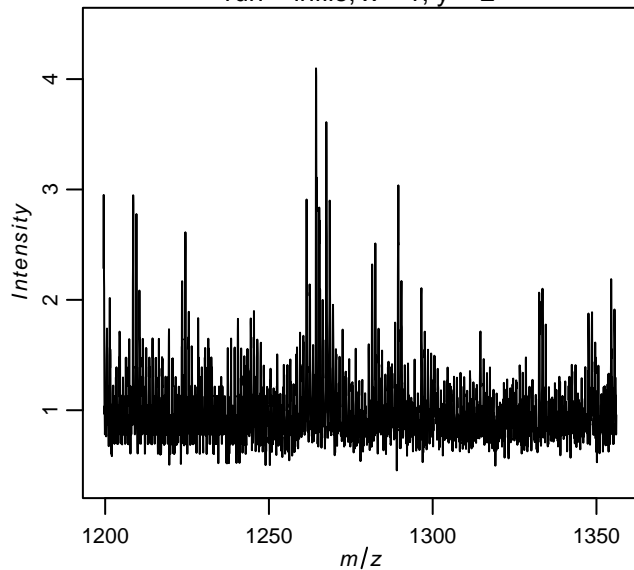
run = infile, x = 3, y = 3



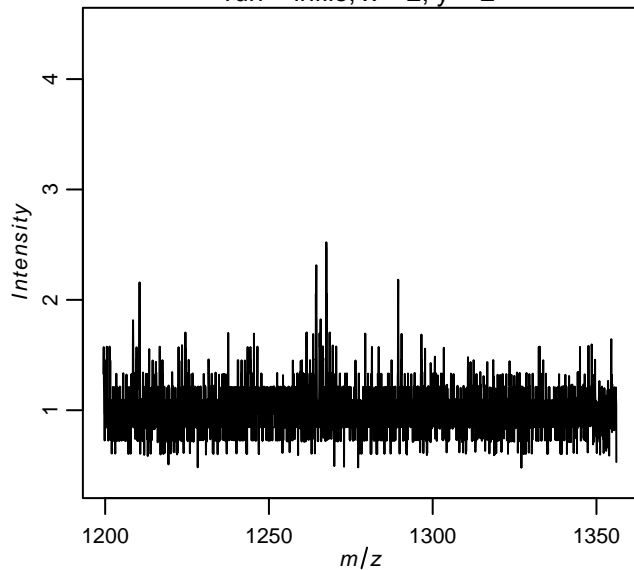
run = infile, x = 2, y = 3



run = infile, x = 1, y = 2

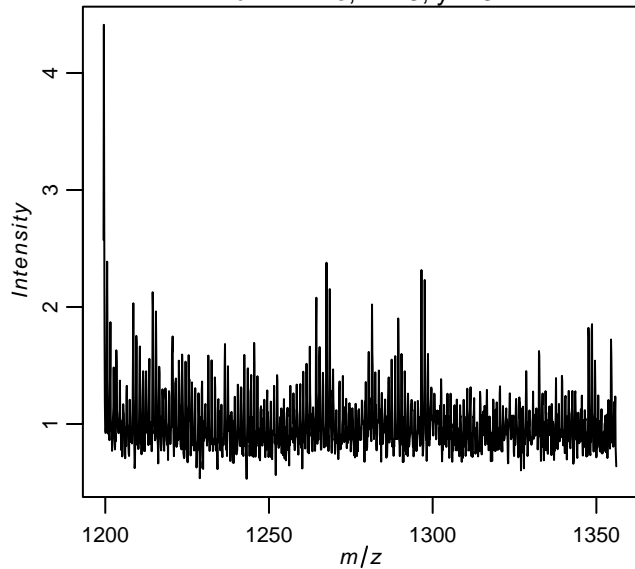


run = infile, x = 2, y = 2

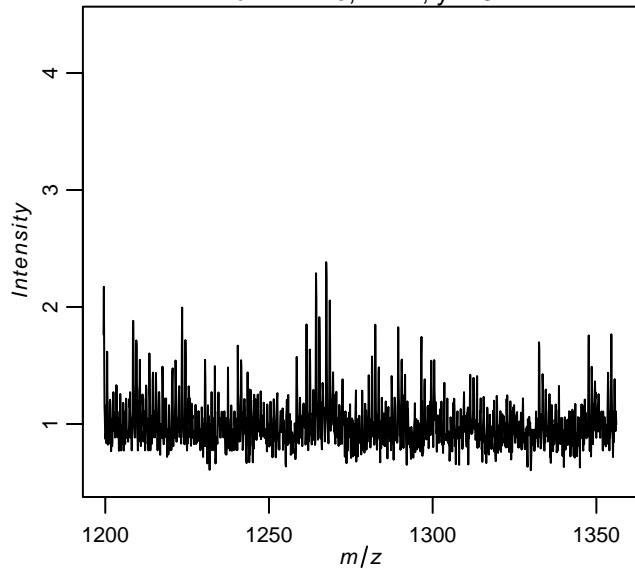


Spectra after m/z binning

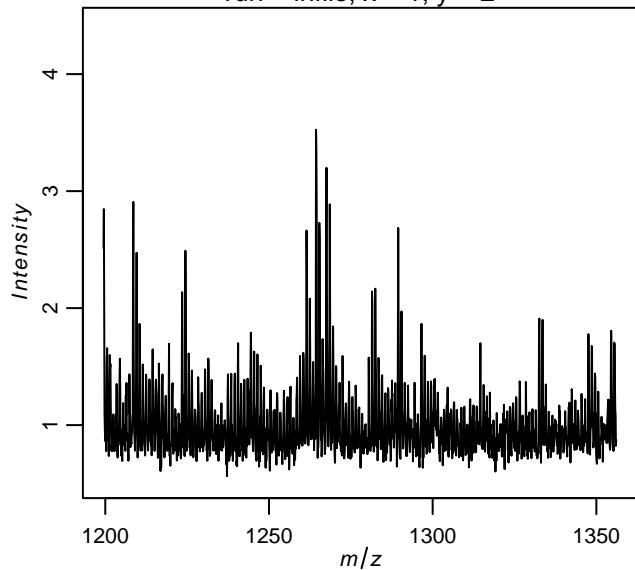
run = infile, x = 3, y = 3



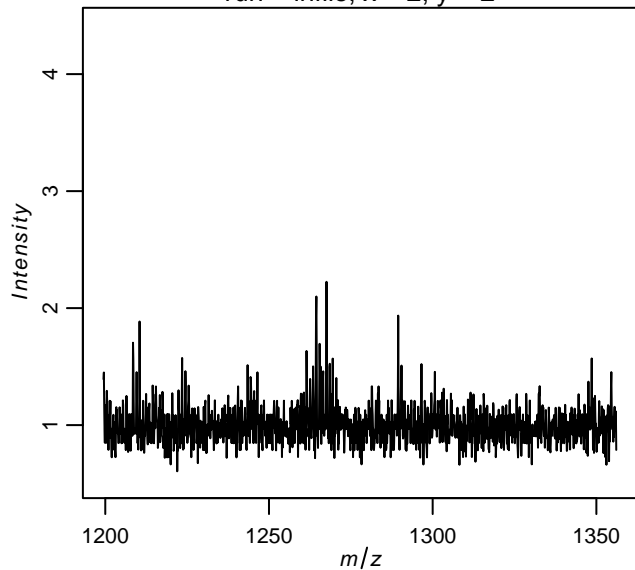
run = infile, x = 2, y = 3



run = infile, x = 1, y = 2



run = infile, x = 2, y = 2



	min m/z	max mz	# features	# spectra
<i>inputdata</i>	1199.47	1356.08	3672	9
<i>normalized</i>	1199.47	1356.08	3672	9
<i>mz_aligned</i>	1199.47	1356.08	3672	9
<i>mz_recal</i>	1199.47	1356.08	3672	9
<i>reduced</i>	1199.47	1356.07	1567	9