Purpose: As more techniques to monitor or compensate for patient respiratory motion before or during radiation treatment are used, analyzing the motion also becomes important. The starting point to analyze the respiratory motion data is breaking it into individual respiratory cycles to obtain the information on the motion, such as peak-to-trough distance and period. The purpose of this study was to develop a robust algorithm to separate patient respiratory motion data into individual respiratory cycles and to test it with a large dataset of patient respiratory tumor motion.

Method and Materials: The 3D tumor motion data from 160 treatment fractions for 46 thoracic and abdominal cancer patients treated with Cyberknife Synchrony system was used. From the filtered motion data, smoothed curve (smoothed by moving average of 25 points) and a baseline (smoothed by moving average of 200 points) were generated and the intersections between these two curves were searched. Starting from the intersection where breathing is from a trough to a peak, a peak point was determined as a maximum point between adjacent intersections, and a trough point was determined as a minimum point between next adjacent intersections. Peak-to-trough distance and peak-to-peak period was calculated.

Results and discussion: By using the smoothed data and a baseline, even very irregular respiratory tumor motion was correctly separated into individual cycles. However, there are some outliers where the algorithm failed to determine correct peak and trough points. For 160 treatment fractions, mean, minimum, and maximum values of mean respiratory peak-to-trough distance were 0.47 cm, 0.02 cm, and 1.44 cm, and those of mean respiratory peak-to-peak period were 3.79 sec, 2.18 sec, and 6.37 sec.

Conclusions: This robust, general algorithm is useful to break patient respiratory tumor motion data into individual cycles, thus enables us to obtain the information on the respiratory tumor motion.