As we could see, the majority of dataset are normal points, besides, the others abnormal points have only about 176 points. Therefore, in this case, all the normal points have the common features and of course, along with their mass number, the data closer to the center of Gaussian distribution are likely to be normal points so we just need to use GMM with K = 1 component. All the abnormal points obviously have smaller likelihoods compared to normal point, then we can easily detect the abnormal points if those likelihood are smaller than the threshold.