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Kinematic Features Extraction

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According to the refined whole-body pose estimation stage mentioned above, we obtain the Clinical Rating Scale for Tremor (CRST) task pose sequence. Given the video frames sequence , our goal is to estimate accurate keypoints of the whole-body in each image. We define the CRST task pose sequence  of *T* video frames, where  represents the keypoints in the  frame; each keypoint contains Cartesian coordinates in both *x* and *y* directions. Further, the *K* denotes the number of keypoints of each motion, and the *C* means the extracted motion feature vectors. By default, the number of whole-body is 133 [21], and the original motion features are the coordinates of the keypoint, thus the *C*=2. We can further define the kinematic features, e.g., amplitude, velocity, acceleration, and frequency. Specifically, the amplitude  can be derived as

 (S1)

where  and  represent the *x* and *y* coordinate values of the  keypoint corresponding to the  frame, respectively. Similarly, the velocity  and acceleration  are calculated by differential operations:

 (S2)

 (S3)

Moreover, in signal processing, frequency domain analysis gives more intuitive parameter characteristics than time-domain analysis.  is the complex conjugate of , and  denotes the discrete Fourier transform of the expressed power signal , which can be calculated from Eq. (4):

 (S4)

Further from Eq. (5) we can calculate power spectral density (PSD) :

 (S5)

Finally, the nonlinear features of this study include approximate entropy (ApEn). ApEn is a technique to quantify the degree of irregularity and unpredictability of time series data fluctuations. In this study, For the acceleration sequence , use a window truncation of length  to obtain the embedded sequence , the similarity tolerance is (SD is the serial standard deviation), and ApEn is defined as

 (S6)

where  represents a continuous 3 s sequence fragment,  denotes the average similarity rate for all *m*-length subfragments of the entire sequence under the similarity criterion *r*, the calculation formula is as follows:

 (S7)

where  satisfy .

The entropy feature characterizing the sequence complexity can sufficiently improve the tremor quantization model's performance, so it is all altogether estimated in this study.