# Appendices

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### **APPENDIX A THE SUMMARY OF THE CONTEXT AND MOTION DATA**

This study was approved by the Institutional Review Board of the University of Hong Kong / Hospital Authority Hong Kong West Cluster (IRB number: UW 19-516). Informed written consent was obtained from the parents of the participants. The context and motion features are summarized in TABLE 1. In tabular data, each feature has one numerical or categorical value [1]. Time series refers to sequences of values ordered by time [2]. The Body Mass Index (BMI) was calculated using height and weight. Specifically, the data are collected across the worldwide prevalence of the COVID-19 pandemic, which has greatly influenced children's daily activities since many schools in Hong Kong have experienced temporary closures and adopted different learning modes [3]. Therefore, we also incorporate learning modes as an important input feature. We also present the missing ratio of data. The highest ratio of missing values is 2.99% (socioeconomic status). It is suggested that a missing rate of 5% or less is inconsequential [4].



TABLE 1: Description of the context and motion features used in this study.

As for the reliability of data, the highest ratio of missing values for context features is 2.99% (socioeconomic status). It is suggested that a missing rate of 5% or less is inconsequential [4]. As for the reliability of acceleration data, the devices used for acceleration data collection are ActiGraph wGT3X-BT accelerometers, which are very sensitive and accurate within +/- 0.5% of the data collected [3]. Children's demographics (e.g., height and weight) are measured by researchers, so we think they are highly reliable. For those rating scales used to derive the six indicators, i.e., the physical functioning (*PHYF*) and psychosocial functioning (*PSYF*) from PedsQL, health confidence (*VVAS*) from EQ5D, resilience (*RESI*) from CD-RISC, and connectedness (*CONN*) from RSCS, they have been widely used in clinics and research. We also use Cronbach's  $\alpha$ [5] to measure the scale reliability. As shown in TABLE 2, Cronbach's *alpha* of all scales is above 0.7, meaning that they have high reliability [6]. Specifically, to validate the *VVAS* score from EQ5D, we use the score of the five dimensions from EQ5D (i.e., mobility, self-care, usual activities, pain/discomfort, and anxiety/depression) and the *VVAS* score to measure the criterion-related validity [7]. We conduct Spearman's rank correlation analysis between the five-dimension score and *VVAS* score, and the results of T0-T3 are -0.402, -0.466, -0.397, and -0.385, respectively, with p-value<0.001. Since a higher

TABLE 2: The Cronbach's  $\alpha$  for the rating scales.

 $\overline{a}$  $\overline{a}$ 



five-dimension score indicates worse health, we can find that the *VVAS* scores are significantly positively related to the participants' health status, showing the reliability of *VVAS*. Since the self-reported information from rating scales is highly reliable, we presume that other self-reported contextual characteristics (e.g., electronic device usage patterns and sleep patterns) are also reliable. Before the participants filled out the questionnaire, we emphasized that they must answer all questions truthfully. The contact information has also been collected for double-checking. The questionnaire collection strictly follows ethics. Informed written consent was obtained from the parents of the participants. Therefore, we consider the data collected in this work reliable.

#### **APPENDIX B THE ALGORITHM FOR FINDING THE MAXIMAL AVERAGE IMPORTANCE WITH CUSTOMIZED TIME WINDOW**

The motion pattern  $m_i$  with a shape of  $3 \times 10080$  is input into Algorithm 1 as matrix M to find the maximal average importance with time window W. The number of channels  $C$  is three, and the overall time length  $T$  is 10080. In the visualization system, users can select the time window (denoted by  $W$ ) to customize the measurement of feature importance for the motion pattern. In the algorithm, the three sequences of  $m_i$  are first combined into one (with size  $1 \times 10080$ ) using the Root Mean Square (RMS). After that, an algorithm with  $O(T)$  time complexity is used to find the time slot with the length of  $W$  that has the maximal average importance. The above steps will be repeated to find the second, third, ... most important time slot. The previous most important time slots are removed from the sequence and conduct the algorithm iteratively. After that, we can get the importance of the input motion pattern during specific time points with a customized time window.

**Algorithm 1:** The algorithm for finding the maximal average importance with time window W for motion pattern.

```
Input: M: The C \times T raw feature importance for the motion pattern of an individual, where C is the number of channels.
          W: The time window for importance assessment selected by users.
          T: The overall time length.
  Output: v: The max average importance with time window W.
          max_i, max_j: The start and end points of the time window.
   // Combine the multi-channel sequences using RMS.
1 for 0 \le t \le T - 1 do
 2 A[t] = \sqrt{\sum_{i=0}^{C-1} M[i, t]^2 / C}3 end for
4 i \leftarrow 0, j \leftarrow 0, s \leftarrow 0, v \leftarrow 0, max_i \leftarrow 0, max_j \leftarrow 0// Find the max sum subarray with length W.
5 while j < T do
6 s \leftarrow s + A[j]7 if (j − i + 1 < W) do
8 j \leftarrow j + 19 end if
10 else if (j − i + 1 == W) do
11 v \leftarrow max(s, v), max_i \leftarrow i, max_i \leftarrow j12 s \leftarrow s - A[i], i \leftarrow i + 1, j \leftarrow j + 113 end else if
14 end while
15 v \leftarrow v/W16 return v, max_i, max_j
```
## **APPENDIX C EXPERT INTERVIEW PROCEDURES AND QUESTION LIST**

The procedures and question list for expert interviews are detailed in TABLE 3.

## TABLE 3: Procedures and question list for expert interviews.



#### **APPENDIX D THE CONFIGURATION OF THE HEALTH PROFILING MODEL**

The detailed configuration of the health profiling model is shown in TABLE 4.

TABLE 4: The configuration of the health profiling model.

<b>Parameters Setting</b>
$CONV1D(1, 1, 1)$ , Sigmoid
$CONVID(3, 3, 1)$ , Sigmoid
(50×128, Dropout, ReLU), (128×64, Dropout, ReLU), (64×64, Dropout, ReLU)×2
GroupNorm(1, 3), CONV1D(3, 32, 10), MaxPool1D(3), (CONV1D(32, 32, 5), MaxPool1D(3)) $\times$ 2, Group-
Norm(4, 32), GRU(32, 64)
$(128\times128,$ Dropout, ReLU), $(128\times64,$ ReLU), $(64\times64,$ ReLU), $(64\times32,$ Dropout, ReLU), $(32\times32,$ Dropout,
ReLU), $(32\times16$ , Dropout, ReLU), $(16\times16)$ , Dropout, ReLU), $(16\times1)$ , Dropout, ReLU)
Sigmoid

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