

Article

Implicit Measurement of Sweetness Intensity and Affective Value Based on fNIRS

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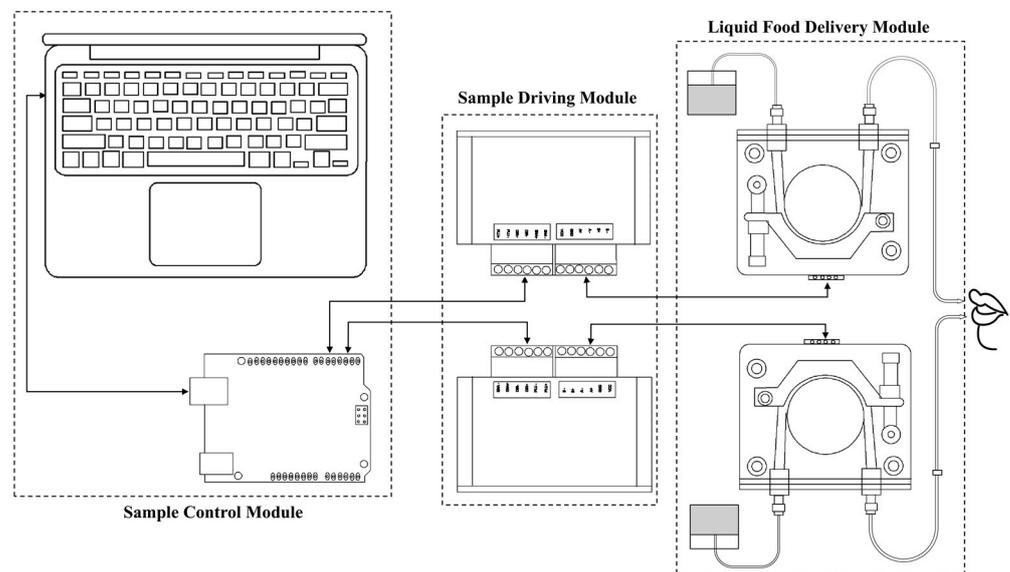


Figure S1. Overview of the taste solution delivery apparatus setup.

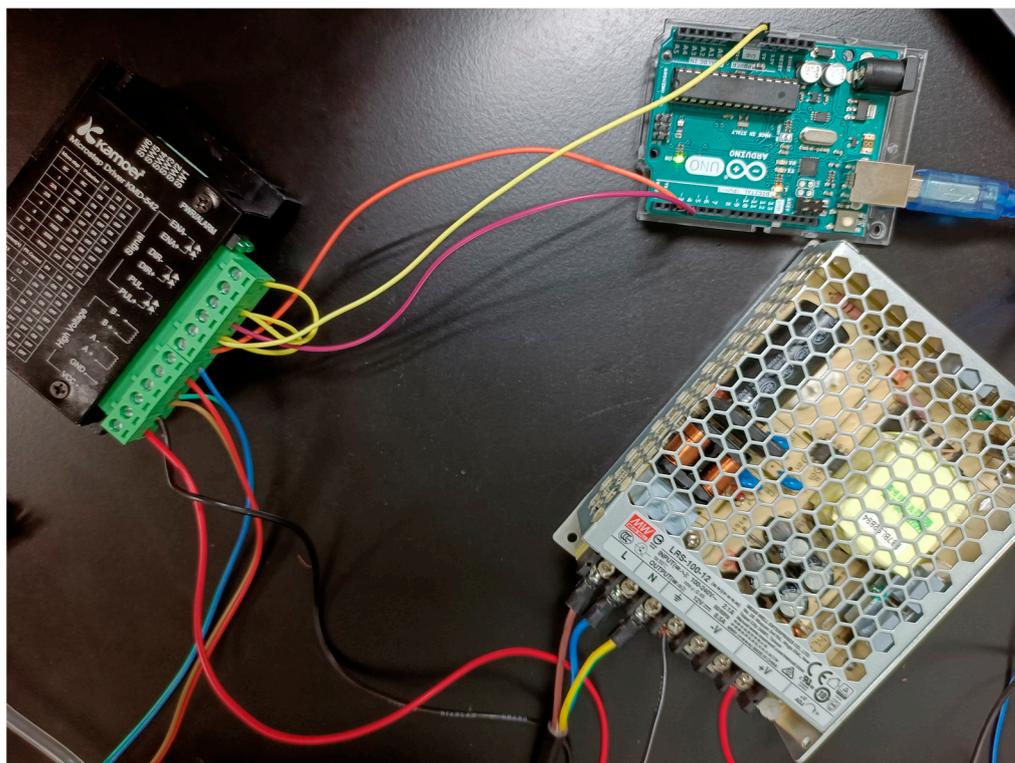


Figure 2. Hardware configuration of the taste solution delivery apparatus.

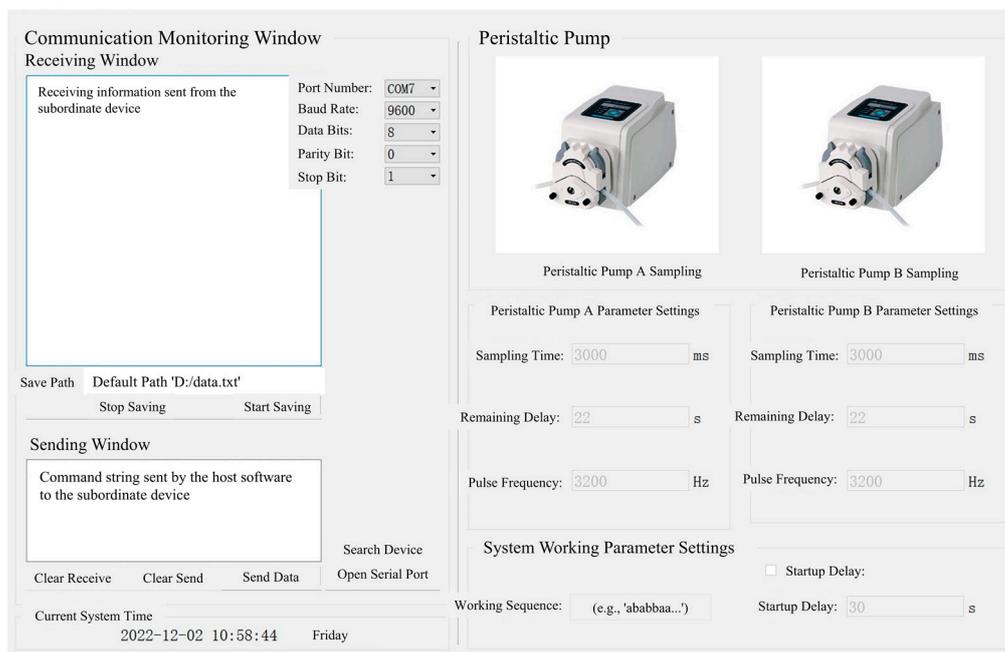


Figure 3. Software control panel of the taste solution delivery apparatus.

Explanation of the Modified Beer–Lambert Law (MBLL):

The modified Beer–Lambert Law (MBLL) is used in fNIRS to calculate the changes in the concentrations of oxygenated hemoglobin (HbO) and deoxygenated hemoglobin (HbR) from the changes in the detected light intensity. It is an adaptation of the classical Beer–Lambert Law, modified to account for light scattering in biological tissues.

The classical Beer–Lambert Law describes the relationship between light absorbance and the concentration of absorbing molecules in a uniform medium, as in the following equation:

$$A = \log \frac{I_0}{I} = \epsilon \cdot c \cdot L$$

where:

A : Absorbance (optical density);

I_0 : Incident light intensity;

I : Detected light intensity;

ϵ : Molar extinction coefficient of the chromophore;

c : Concentration of the chromophore;

L : Optical pathlength.

In fNIRS, the MBLL incorporates a differential pathlength factor (DPF) to account for the increased pathlength caused by scattering. The equation is expressed as follows:

$$\Delta A = \epsilon \cdot \Delta c \cdot L \cdot DPF$$

where:

ΔA : Change in absorbance (optical density);

Δc : Change in concentration of the chromophore (HbO or HbR);

L : Mean pathlength of light through the tissue;

DPF : Differential pathlength factor, a scaling factor to correct for scattering effects.

Mathematical Definitions and Calculations of Features:

Maximum Value (Max): The maximum value of the HbO concentration curve is defined as the highest point reached by the signal within the 0–20-second post-stimulus window. This feature reflects the peak neural activation, which is often related to the magnitude of sensory intensity (such as sweetness intensity).

$$Max = \max(HbO(t))$$

where $t \in [0,20]$ seconds.

Mean Value (Mean): The mean value represents the average concentration of HbO over the 0–20-second post-stimulus window. It serves as an indicator of the overall baseline level of the neural response.

$$Mean = \frac{1}{T} \sum_{t=1}^T HbO(t)$$

where T is the number of timepoints within the 0–20-second window.

Area Under the Curve (AUC): The area under the curve quantifies the total neural response over the entire 0–20-second post-stimulus time window. It is computed as the integral of the HbO signal over this window, providing a measure of the sustained response to the stimulus.

$$AUC = \int_0^{20} HbO(t) dt$$

Standard Deviation (SD): The standard deviation quantifies the variability of the HbO signal during the post-stimulus window. It reflects the degree of fluctuations in the neural response, which can be related to how sensitive or variable the response is across trials.

$$SD = \sqrt{\frac{1}{T} \sum_{t=1}^T (HbO(t) - Mean)^2}$$

Left Slope (2–7 seconds): The left slope measures the rate of change in the HbO signal between 2 and 7 seconds after the onset of the stimulus. This period corresponds to the rapid initial neural processing phase, where the brain begins to integrate sensory information.

$$Slope = \frac{HbO(t_2 - HbO(t_1))}{t_2 - t_1}$$

where $t_1 = 2$ seconds and $t_2 = 7$ seconds. This slope reflects the steepness of the initial neural response.

Sample Entropy (SampEn): Sample entropy measures the complexity of the time series by assessing the likelihood that similar patterns of signal values will repeat over time. A lower SampEn value indicates a more predictable or regular signal, while a higher value indicates a more complex or unpredictable signal.

Sample entropy is defined by the following formula:

$$SampEn(m, r) = -\ln\left(\frac{A_m(r)}{B_m(r)}\right)$$

where $A_m(r)$ and $B_m(r)$ are the counts of similar patterns for the length m and tolerance r , respectively. m is the length of the signal segment being compared. r is the tolerance threshold used to define similarity between patterns.

Approximate Entropy (ApEn): Approximate entropy quantifies the likelihood that a pattern of length m in the signal will repeat itself, helping assess the unpredictability of the signal over time. A higher ApEn value indicates greater unpredictability and complexity in the response. Approximate entropy is given by the following:

$$SampEn(m, r) = \lim_{N \rightarrow \infty} \frac{1}{N} \sum_{i=1}^N \ln\left(\frac{A_m(r)}{B_m(r)}\right)$$

where $A_m(r)$ and $B_m(r)$ are similar to those in SampEn, but ApEn computes this over all possible patterns.

Autoregressive Model Parameters (AR): Autoregressive (AR) models are used to capture the temporal dynamics of the signal, representing how the neural response evolves over time. The AR parameters reflect the brain's predictive processing, helping to model the future state of the response based on past values. An AR model is represented by the following equation:

$$HbO(t) = \alpha_0 + \sum_{i=1}^p \alpha_i HbO(t - i) + \epsilon(t)$$

where α_0 is the intercept, α_i is the autoregressive coefficient, p is the order of the AR model, and $\epsilon(t)$ is the error term.

Benjamini–Hochberg Procedure:

Sort the p-values: The raw p-values from all the paired t-tests were sorted in ascending order: $p_{(1)}, p_{(2)}, \dots, p_{(m)}$, where m is the total number of tests.

Determine the adjusted threshold: For each p-value $p_{(i)}$ at rank i in the sorted list, the BH threshold is calculated as follows:

$$\alpha_{(i)} = \frac{i}{m} \cdot \alpha$$

where α is the chosen significance level (0.05), i is the rank of the p-value, and m is the total number of tests.

Compare p-values to the thresholds: Starting from the smallest p-value, each p-value is compared to its corresponding threshold $\alpha_{(i)}$. The largest $p_{(i)}$ that satisfies $p_{(i)} \leq \alpha_{(i)}$ is considered significant, and all p-values smaller than this are also declared significant.

Control the FDR: By this method, we control the proportion of false discoveries (Type I errors) among the rejected hypotheses (Supplementary Material).

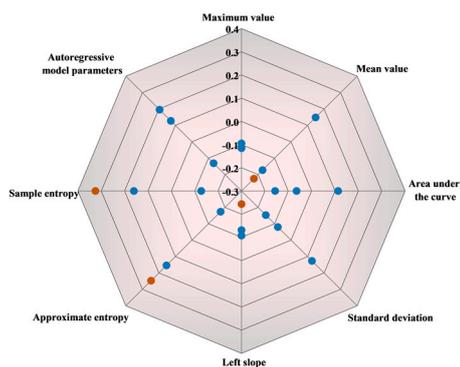


Figure S4. Correlation coefficients between explicit and implicit measures of sweetness intensity across various features.

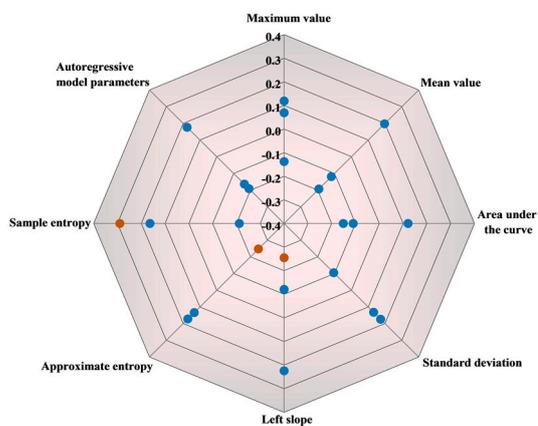


Figure S5. Correlation coefficients between explicit and implicit measures of affective value across various features.