On the modeling and deconvolution of blood or breath alcohol concentration (BrAC/BAC) from biosensor-measured transdermal alcohol concentration (TAC)

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New technology has produced biosensors that measure transdermal alcohol concentration (TAC) in naturalistic settings. However, due to several physiological and environmental factors, no direct conversion from TAC to BAC/BrAC exists. The skin's transport and filtering of alcohol is physiologically complex and is affected by numerous factors that vary across individuals (e.g., skin layer thickness, porosity, tortuosity) and drinking episodes within individuals (e.g., skin surface, ambient temperature, hydration, vasodilation). TAC readings also depend on the particular device used to collect the data. In earlier work, we developed a mathematical framework and protocol for calibrating BrAC and TAC data for a single drinking episode that captured the dynamics of the forward process and then inverted the resulting fit model by deconvolving estimated BrAC from TAC for subsequent drinking episodes. In this study, we compare three methods for implementing this approach. Method_1 is frequency domain-based wherein the forward convolution filter is taken to be the low pass filtered inverse Fourier transform of the quotient of the Fourier transforms of the calibration TAC and BrAC. In Method_2, the convolution filter is determined as the impulse response function of an auto regressive/moving average (ARMA) model fit to the calibration episode[1]. In Method_3, the filter is determined via finite dimensional approximation of the linear semigroup-based mild solution of a distributed parameter model with unbounded input and output fit to the calibration data. In tests using clinical and field contemporaneous TAC and BrAC collected by one of the authors, we examined model fit indices and summary BrAC scores and curves. Results indicated Method_2 yielded the most accurate estimate of peak BrAC and Method_3 yielded the best estimate of time of peak BrAC. Method_1 had the smallest variance across episodes, in particular for estimating ascending and descending slopes, but had slightly larger bias. Method_1 is computationally efficient but theoretically is estimating infinitely many parameters. Method_3 estimates only two parameters but required more computational time to fit the data. Method_2 was between Method_1 and Method_3 in terms of computational efficiency and degrees of freedom. The next step including the incorporation of the methods into learning algorithms and comparison studies using data drawn from a larger population will be discussed.

References

1. M. H. Perrott, R. J. Cohen, "An efficient approach to ARMA modeling of biological systems with multiple inputs and delays", *IEEE Trans. Biomed. Eng.*, vol. 43, no. 1, p. 1, 1996. DOI: 10.1109/10.477696.