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**Rayanne A. Luke\*** (rluke3@jhu.edu), **Anthony J. Kearsley**, **Nora Pisanic**, **Yukari C. Manabe**, **David L. Thomas**, **Christopher Heaney** and **Paul N. Patrone**. *Improving diagnostic testing accuracy by moving to higher dimensional probability models with applications to saliva-based SARS-CoV-2 assays*. Preliminary report.

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic has called attention to the importance and difficulty of correctly interpreting antibody test results. Identification of positive and negative samples requires a classification strategy with low error rates, which can be hard to achieve if positive and negatives overlap. The classification is further complicated when the data exhibit complex structure or the disease prevalence is unknown; this can lead to an increased error rate. We address these problems using multidimensional probability models and optimal decision theory. We show that by increasing the dimension of the measurement space, we can better separate positive and negative data, which allows us to build models that are well-suited to the structure of the populations. This ability to represent the data is not possible by traditional methods such as confidence intervals (CIs) and receiver operating characteristics. The fidelity of our models to the data divides the two populations and allows for a highly accurate binary classification. This procedure is applied to a saliva-based SARS-CoV-2 dataset; we outperform CI methods, halving classification errors on average. Our work showcases the power of modeling in diagnostic classification. (Received January 25, 2022)