Semiquantification Limitations: FMTVDM©℗ Demonstrates Quantified Tumor Response to Treatment with Both Regional Blood Flow and Metabolic Changes

TO THE EDITOR: True quantification (*1–6*) is the actual measurement of material within a tested region. In molecular imaging, the ability to accurately measure isotope accumulation is dependent on the demonstration that the measuring device, be it a SPECT or PET camera, is accurately calibrated, is measuring the correct isotope, and can be counted and reproduced serially.

The publication by Humbert et al. (*7*) is important because it raises the question of whether PET cameras can detect actual changes in disease after treatment. To accurately measure changes in regional blood flow and metabolism it is necessary to rely on a truly quantified (*1–6*) method and not on a method that produces only a calculated value. The Humbert et al. (*7*) method makes 2 flawed presumptions. First, it applies the wrong pharmacologic kinetic model that the isotope absent from the arterial bed traveled only to the site of interest. Second, it uses a matrix setting, which has been demonstrated to produce a loss of signal data, which produces a significant error rate (*2–6*). This method produces a *semi*quantified value derived from "first-pass extraction," not an accurate measurement of the amount of isotope within the tissue of interest.

We have demonstrated that using a true quantification method provides an actual measurement of change in regional blood flow and metabolism, which is useful in assessment of treatment response.

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Published online ••••••••••••.
DOI: 10.2967/jnumed.118.217018

JNM-217018-pm ■ 9/8/18