progress slices of the single-shot over time interval [0,t]. The result he quotes follows. However, we do not find this point of view particularly useful in dealing with the specific problems of clearance determination.

What is important in this regard is the problem of extrapolating the synthesized response function to equilibrium. This is ideally equivalent to extrapolating the single-shot response function to zero, if you adopt Dr. Unsworth's point of view. This is what we have called the "truncation" problem.

We say these are ideally equivalent, but do not regard them to be practically equivalent. This belief hinges upon our finding that the synthesis method with the priming dose as the adjustable, extrapolation parameter is *superior* in situations of high noise (i.e., variability) to techniques such as exponential fitting where the exponential function parameters are adjusted for extrapolation. These findings are experimental based upon the application of our method to both simulated data, which we reported in our paper and real data, which we have not yet reported.

Finally, we do not understand and must reject his assertion that our method of using a priming dose is "scientifically invalid" and that it "makes assumptions ... about extrapolated plasma activities" which the alternative (exponential fitting and total urine collection) he proposes do not. Our use of "priming dose" replicates precisely what the physiologist in the laboratory does. *Only* the information within the single-shot response function is used, and then in a natural way. Our belief is that the weaknesses we have experienced using the exponential fitting method lie primarily in its bias toward the two (or multi) compartment model, especially under "high-noise" (data variability) condition. Also, we pointed out in our paper [c.f. discussions surrounding pgs. (3) and (4)] where the assumptions involving the application of that method lie. We reject the notion that older methods are invariably and inherently better simply because of their longer history and suggest that objective comparison of results will be of greater service in understanding the concepts we utilize.

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Detection of Melanomas In Vivo with Indium-111 Monoclonal Antibody

TO THE EDITOR: Murray and co-workers studied 21 patients with melanomas and documented the ability to detect tumors in terms of both tumor size and percent of known tumor sites visualized (*1*). A further analysis can be carried out by examining the percent of tumors imaged as a function of the quantity of monoclonal antibody administered (in mg, Table 1). We recognize that the situation is complex, depending upon blood flow, number of sites, and binding affinities. A simplified analysis however may suggest more sophisticated approaches.

Visualization depends upon the quantity of radiolabeled antibody bound to the tumor. We assume that the reaction between antibody (A) and tumor (T) can be represented as:

$$A + T \rightleftharpoons AT \rightarrow (AT) \qquad (1)$$

Here AT is the antibody attached to tumor; this can then dissociate back to A and T or form a stable or internalized complex (AT). Visualization (V) of the tumor can then be described as follows.

$$V = \frac{C \cdot A}{K + A} \qquad (2)$$

A is the quantity of labeled antibody, and C and K are constants descriptive of the system. From this Michaelis-Menten type analysis, equation (2) is placed in reciprocal form (Lineweaver-Burk).

$$\frac{1}{V} = \frac{K}{C} \cdot \frac{1}{A} + \frac{1}{C} \qquad (3)$$

A plot of the data in Table 1 of Murray and co-workers is shown here as Figure 1. The reciprocal of the percent visualized is shown as a function of the reciprocal of dose administered. The calculated equation (with a correlation coefficient of 0.91) was:

$$\frac{1}{V} = 0.0295 \cdot \frac{1}{A} + 0.01339 \qquad (4)$$

In the heterogenous system present in the patients, the equation predicts a maximum detectability of 1/0.01339 or 74.7%. The constant K calculates to be 2.20, and the quantity of antibody required to detect half the tumor sites as 4.5 mg. More detailed analysis, as a function of clusters of tumor sites of the same size may be a logical initial approach.

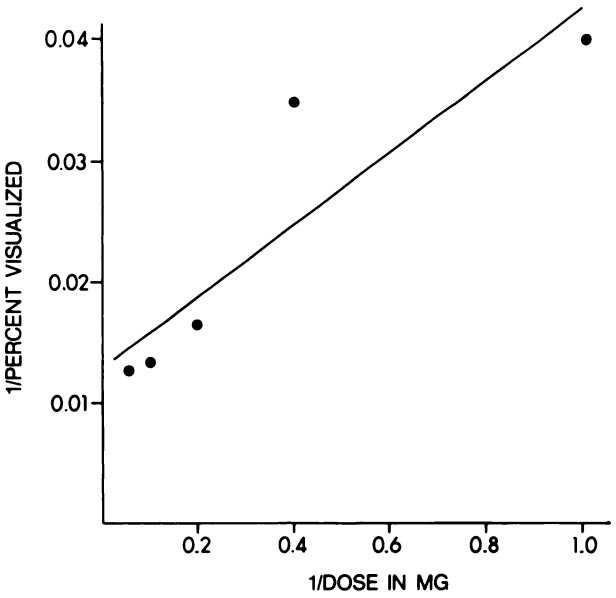

FIGURE 1
Data from Table 1 of Murray et al. is presented as a Lineweaver-Burk plot (1/percent visualized as a function of 1/dose in mg).

ACKNOWLEDGMENT

This work was supported by USPHS CA 17802 from the National Cancer Institute.

References

1. Murray JL, Rosenblum MG, Lamki L, et al. Clinical parameters related to optimal tumor localization of in-

dium-111-labeled mouse antimelanoma monoclonal antibody ZME-018. *J Nucl Med* 1987; 28:25–33.

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REPLY: Dr. Spencer proposes a unique and presumably useful method of evaluating the percentage of tumors imaged as a function of the quantity of antibody administered. This is done using a Michaelis Menten type analysis. There are concerns about the formula $A + T \rightleftarrows AT \rightarrow (AT)$, in addition to those mentioned by Dr. Spencer.

1. The formula indicates that the antibody can dissociate back and forth to form a stable or internalized complex. However, it is possible that the degree to which each individual antibody is in equilibrium is dependent on its affinity, whether the antigen is shed from the surface and to what degree, and the extent to which internalization and/or modulation occurs. It is uncertain whether this formula would hold in all cases—for example, there are studies, such as the use of T 101 in leukemia, in which other variables may influence this hypothesis.

2. ^{111}In may dissociate to a small or great extent after antibody binding and is in equilibrium with transferrin in the serum (~5% of the indium per day is in equilibrium with this protein). With ^{131}I, there is considerable dehalogenation over time. This will affect calculation of actual uptake of the antibody isotope/complex.

Thus, this equation is an oversimplification of what is actually happening at the cell surface, although, as Dr. Spencer suggests, it may lead to useful approaches.

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Monitoring of Radioactive "Dirty Linen" After Iodine-131 Therapy

TO THE EDITOR: In Los Angeles County, trash that is to be dumped into sanitary landfills is routinely monitored at the site for radioactive contamination (1). Generally speaking, waste from patients who have had nuclear medicine diagnostic procedures is not intense enough to cause a detector external to the dumpster to register a count rate warranting investigation (ten times background). The Los Angeles County Division of Radiation Management will permit the trash to be dumped if after investigation detected radioactivity is related to nuclear medicine patient excreta.

Many hospitals have purchased radiation detector systems to monitor trash bins before they leave the hospital grounds, in order to prevent unnecessary incidents at landfills. Recently, however, a problem occurred when linens, contaminated with I-131 from a therapy patient dose (20 mCi), were sent to a laundry service. En route the laundry truck was stopped by the California Highway Patrol at a weighing station and radiation detectors detected a count rate greater than 20 times background. The hospital health physicist was notified and the radioactive linen was brought back to the hospital to be stored for decay.

It is suggested that hospitals monitor laundry that leaves the hospital grounds just as they do with trash. Radioactive linen from therapy patients should be monitored and held for radioactive decay, although in the vast majority of cases the types and quantities of radioactive material involved will not constitute a risk to the public health.

References

1. Ketchum L. LA nuclear medicine community improves radiation monitoring at landfills. *J Nucl Med* 1985; 26:336–337.

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Correction: Design, Preparation, and Biodistribution of a Technetium-99m Triaminedithiol Complex to Assess Regional Cerebral Blood Flow.

TO THE EDITOR: In the article by Lever, Burns, and Kervitsky et al. appearing in *J Nucl Med* 1985; 26:1287–1294, Figure 4 should be replaced with the one shown below. Intermediate **2**, the fraction isolated from the crude reaction mixture, was incorrectly characterized as the monocyclic diamine. The correct structure is the bicyclic diamine, which resulted from an intramolecular ring closure during sodium borohydride reduction. Spectroscopic experiments on **2** permit the unambiguous assignment of the methine carbon. An Insensitive Nuclei Enhanced by Polarization Transfer (INEPT) sequence assigns the peak at 91.5 ppm to C6 in the carbon NMR spectrum and the heteronuclear 2D chemical shift correlation spectrum assigns the singlet at 3.53 ppm to C6-H

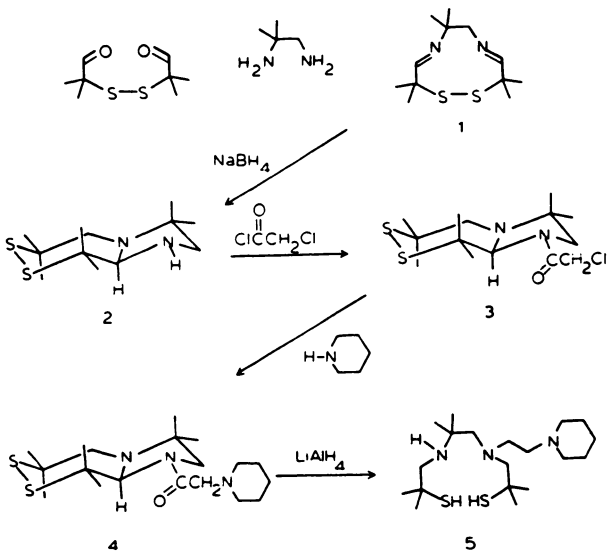

FIGURE 4
Triaminedithiol ligand synthesis.