are assumed to be too fast (essentially always at a pseudoequilibrium) or too slow to influence greatly the observed response. By using black-box techniques equivalent to the traditional approach to the control of chemical processes, it is possible to generate transfer functions that can represent the dynamic response of a culture. An example of the results from such an approach are given in Fig. 6.13. However, it should be recognized that such approaches are limited to cultures with similar growth histories and subjected to qualitatively similar perturbations.

6.3.3.2. Chemically structured models. A much more general approach with much greater a priori predictive power is a model capturing the important kinetic interactions among cellular subcomponents. Initially, chemically structured models were based on two components, but at least three components appear necessary to give good results. More sophisticated models with 20 to 40 components are being used in many laboratories. A schematic of one such model is given in Fig. 6.14.

Writing such models requires that the modeler understand the physical system at a level of greater detail than that at which the model is written, so that the appropriate assumptions can be made. A detailed discussion of such models is appropriate for more advanced texts. However, two important guidelines in writing such models should be understood by even the beginning student. The first is that all reactions should be expressed in terms of *intrinsic* concentrations. An *intrinsic* concentration is the amount of a compound per unit cell mass or cell volume. *Extrinsic* concentrations, the amount of a compound per unit reactor volume, cannot be used in kinetic expressions. Although this may seem self-evident, all the early structured models were flawed by the use of *extrinsic*

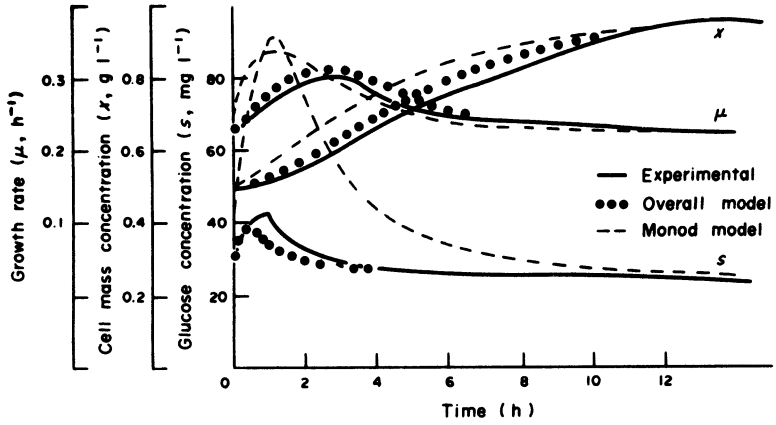

Figure 6.13. Comparison of predictions from a model derived from a system-analysis perspective, predictions from a Monod model, and experiment. The experimental system was a chemostat for a glucose-limited culture of *Saccharomyces cerevisiae* operating at a dilution rate of 0.20 h^{-1}. In this particular experiment, the system was perturbed with a stepwise increase in feed glucose concentration from 1.0 and 2.0 g l^{-1}. *X* is biomass concentration, μ is growth rate, and *S* is substrate concentration. (With permission, from T. B. Young III and H. R. Bungay, "Dynamic Analysis of a Microbial Process: A Systems Engineering Approach," *Biotechnol. Bioeng. 15*:377, 1973, and John Wiley & Sons, Inc., New York.)