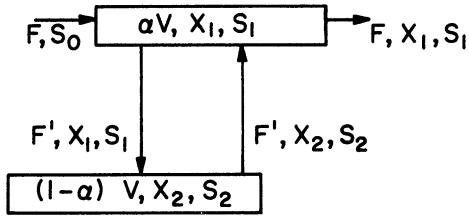

Figure 6.20. Simple two-compartmental model for an incompletely mixed "chemostat."

	Substrate balance	Biomass balance
Region 1	$X_1 = Y(S_0 - S_1)$	$X_2 + \alpha D' \mu_m \dfrac{S_1}{K_s + S_1} X_1 = (1 + DD')X_1$
Region 2	$X_2 - X_1 = Y(S_1 - S_2)$	$X_1 + (1-\alpha)D' \mu_m \dfrac{S_2}{K_s + S_2} X_2 = X_2$

In an imperfectly mixed chemostat with a stagnant biotic phase, the dilution rate can exceed μ_m without washout. The washout dilution rate is obtained by setting $S_0 = S_1 = S_2$ and is

$$D_{wo} = \frac{\mu_m S_0}{K_m + S_0}\left[\frac{(1-\alpha)^2 \mu_m S_0}{K_s + S_0 - (1-\alpha)D' \mu_m S_0} + 1\right]$$

where D_{wo} is the washout dilution rate.

6.5. SUMMARY

During batch cultivation, a population of cells typically exhibits several different growth phases. During the lag phase, the cell builds the biosynthetic pathways necessary for maximal growth rates in the fresh medium. During *exponential growth*, cell replication is maximal, and the chemical composition of the cell population is nearly constant (e.g., balanced growth). When substrate is nearly exhausted or when toxic metabolic by-products have built to a critical level, the growth rate begins to drop rapidly, causing significant changes in biosynthetic pathways. In the *stationary phase*, there is no net growth; cells now reorient their metabolic machinery to increase the probability of long-term survival. At some point, some cells can no longer obtain enough energy from their reserves or enough of another critical resource, and the culture enters the *death phase*. Dead cells do not have an energized membrane and often lyse (or break apart). Nutrients released by lysed cells can be utilized by survivors, allowing cryptic growth.

Products formed by cells can be related to this batch-culture growth cycle. Primary products are growth associated. Secondary products are nongrowth associated and are made in the stationary phase. Some products have both growth-associated and nongrowth-associated components.

Cell-growth kinetics can be modeled. Models that are *structured* break the population into distinct subcomponents. *Unstructured* models quantify cell mass as a single