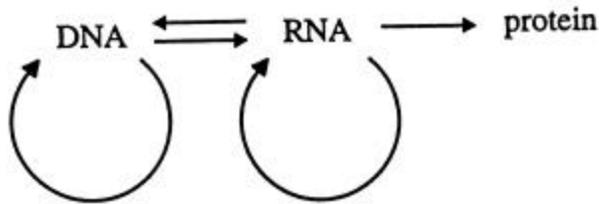


NUCLEIC ACIDS

1. **DNA** is a long polymer strand whose monomers (nucleotides) are either A, T, C and G.
2. Double-stranded DNA is composed of two polymers weakly bonded to each other along their lengths. A on one strand is always bonded to T on the other strand, and C on one strand is always bonded to G on the other. Thus, one polymer of DNA has the information for the construction of the other strand.
3. **RNA** has four somewhat different monomers (nucleotides) and can also be either single- or double-stranded, and like DNA can code for its own replication.
4. RNA and DNA can code for each other.
5. RNA can code for proteins.

FLOW OF GENETIC INFORMATION



Note that:

1. DNA and RNA can code for their own self-replication.
2. DNA and RNA can code for one another.
3. RNA can code for proteins.
4. Proteins may be structural, e.g. muscle or viral envelope, or they may be catalytic, e.g., enzymes.
5. Research over the past decade has shown that RNA and DNA, under certain conditions, may have catalytic functions. Such forms are called ribozymes and DNAzymes, resp.

BIOCHEMICAL REACTIONS

1. Reversible biochemical reactions in cells usually have an equilibrium lying far to one side:



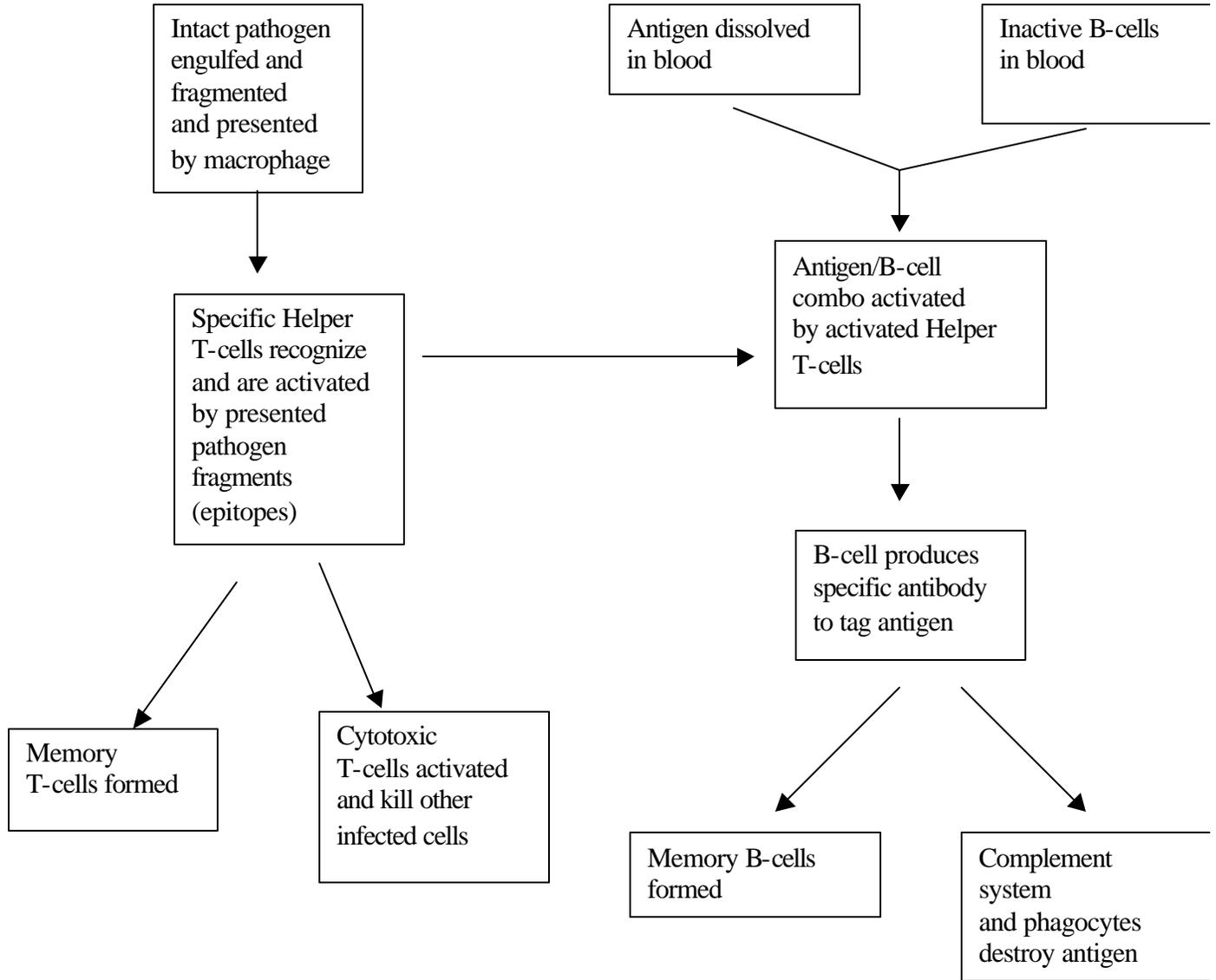
In this reaction the equilibrium will lie toward the left, i.e., at equilibrium there will be more A and B than C and D, normally because A and B are simpler than, and require energy to form, C and D.

2. Useful biomolecules in a cell generally are the ones AWAY from the equilibrium side, i.e., to the right in the scheme above. Thus, their availability to the cell requires that C and D be removed as fast as they are made, which forces the reaction toward the right, **or** that an excess of A and B be added, which also forces the reaction toward the right.
3. Reactions in cells are almost always facilitated by a very specific catalyst, called an **enzyme** (usually a protein). Each reaction in a cell requires its own specific enzyme.

FLOW SHEET FOR SPECIFIC IMMUNE RESPONSES

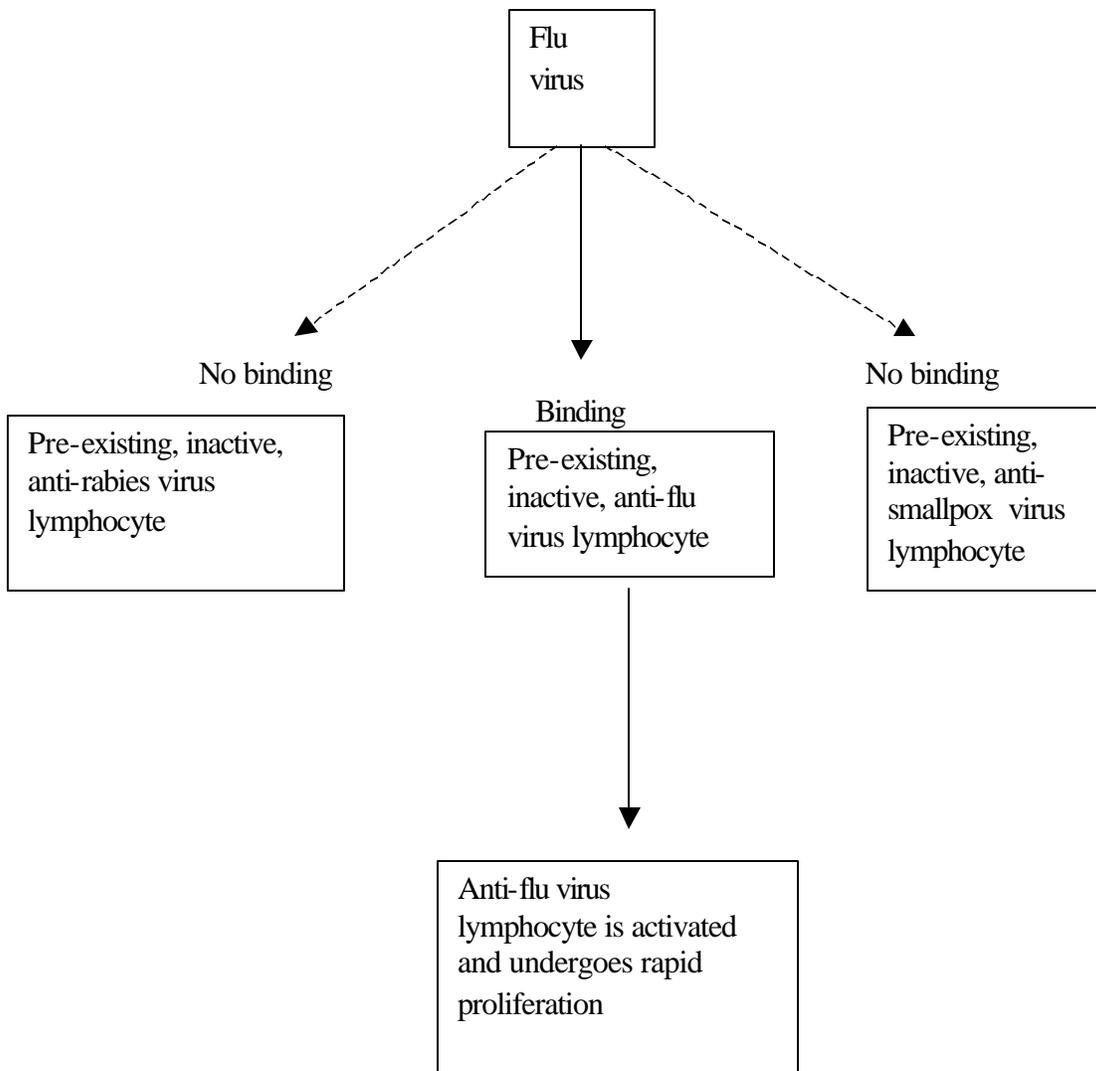
Cell-mediated

Humoral



CLONAL SELECTION MODEL FOR LYMPHOCYTE ACTIVATION

A SIMILAR MODEL IS APPLICABLE TO T-CELLS AND B-CELLS, BOTH OF WHICH ARE LYMPHOCYTES



THE HUMAN IMMUNODEFICIENCY VIRUS

HIV has a somewhat spherical lipid covering, which is imbedded with gp120 sugar-protein projections. The virus contains 2 identical pieces of s.s. RNA and some proteins.

The gp120 projections recognize and bind to CD4 protein on Helper T-cells and macrophages.

The HIV RNA is inserted into the attached cell.

Inside the cell, HIV RNA information is converted to HIV DNA information (“provirus”) and inserted into the cell’s own DNA.

The HIV DNA provirus contained in the cell’s DNA directs the cell’s metabolic machinery to make gp120 proteins on the cell surface and to make new HIV RNA, which buds off the cell’s surface, taking some of the gp120 sugar-protein with it.

HIV triggers the specific immune/antibody responses, which are found clinically and are used for diagnosis. Like all RNA viruses, HIV is highly mutable and requires a completely new response for each new mutant. Some parts of the virus mutate very frequently and some parts seldom do (they are conserved).

Gradually the infection kills all the Helper T-cells in the body, but the exact mechanisms are not understood. The main clinical complication is that killing the Helper T-cells shuts down both the cell-mediated and the humoral specific immune responses.

