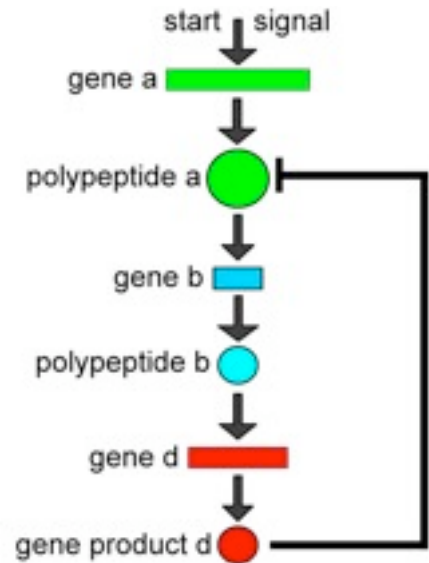
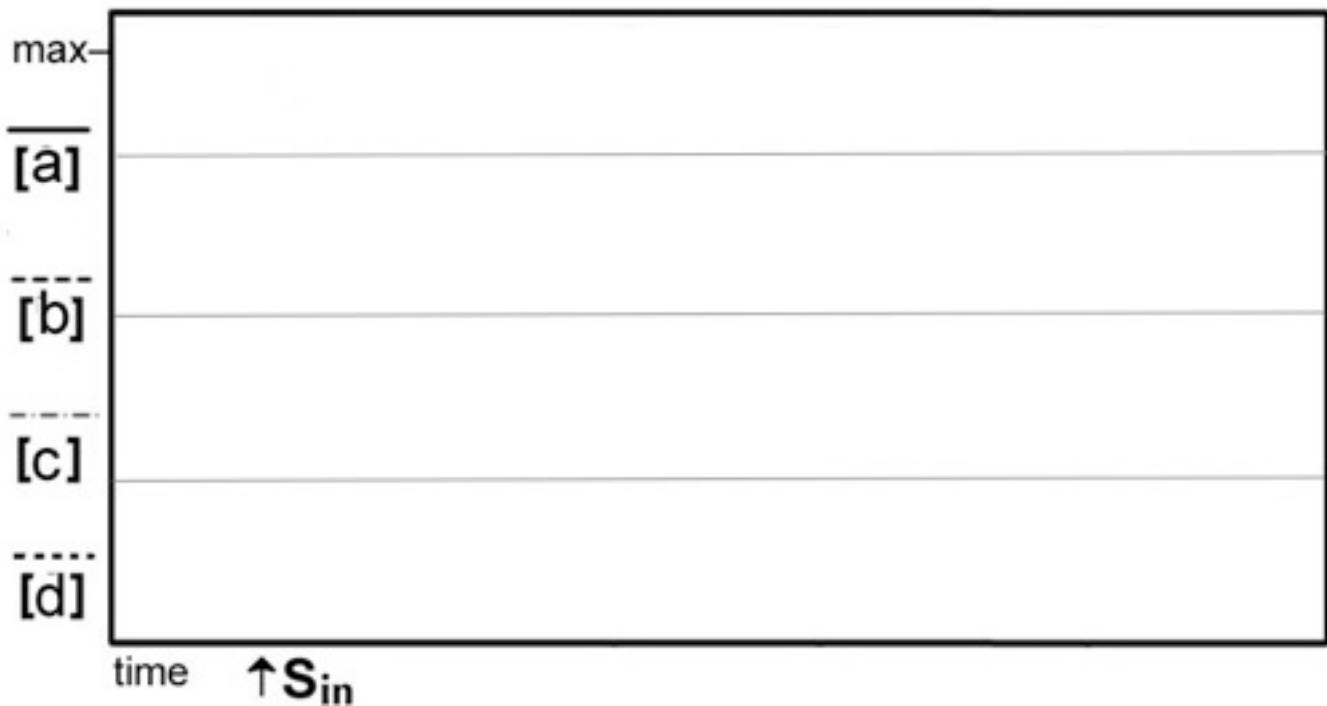
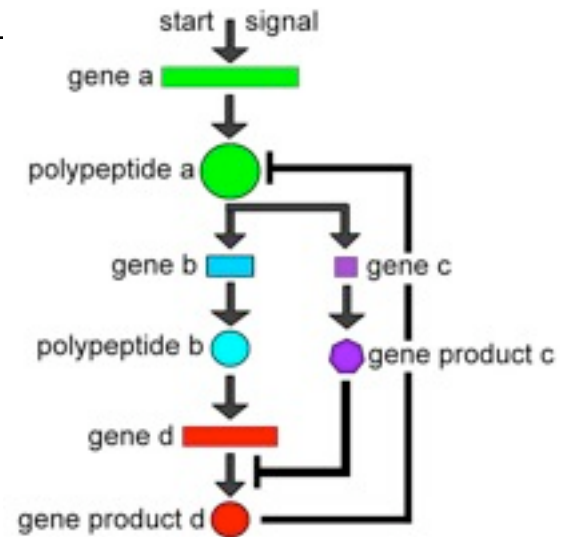


Question I) Let us consider the behavior of gene regulatory networks, beginning with a relatively simple network (on the right) and then a more complex network (next page). Genes are represented by rectangles and polypeptides by circles; positive interactions are indicated by arrows, while negative interactions are indicated by bars.

At time zero, the level of all gene products is zero. Adding a start signal (the chemical S) initiates expression of gene a. The maximum level that any polypeptide can reach is indicated on the graph as “max”. Your task is to graph the levels of the polypeptides a, b, and d over time. Before you begin working on the graph, would you please **outline your assumptions** (use extra sheet if necessary):



Question II. Now, here is a more complicated network that contains an undefined gene product (c) marked by a heptagon. As before, at time zero, the levels of all gene products are zero and the expression of gene **a** is initiated by the addition of S. Map the levels of the polypeptides a, b, and d and gene product c on the graph below. Again, before you begin on the graph, please indicate **what additional assumptions you are making.**



Question III: How would your graph change if the half-life of polypeptide b were short and the its concentration was low?