C Formal models

C.1 Sticker systems

C.1.a Basic operations

The *sticker model* was developed by Rosweis et al. in the mid-1990s. It depends primarily on separation by means of hybridization and makes no use of strand extension and enzymes. It implements a sort of random-access binary memory. Each bit position is represented by a substrand of length m. A *memory strand* comprises k contiguous substrands, and so has length $n = km$ and can store k bits. *Sticker strands* or *stickers* are strands that are complementary to substrands representing bits. When a sticker is bound to a bit, it represents 1, and if no sticker is bound, the bit is 0. Such a strand, which is partly double and partly single, is called a *complex* strand.

Computations begin with a prepared *library* of strings. A (k, l) library uses the first $l \leq k$ bits as inputs to the algorithm, and the remaining $k-l$ for output and working storage. Therefore, the last $k - l$ are initially 0. There are four basic operations, which act on multi-sets of binary strings:

Merge: Creates the union of two *tubes* (multi-sets).

Separate: The operation separate(N, i) separates a tube N into two tubes: $+(N, i)$ contains all strings in which bit i is 1, and $-(N, i)$ contains all strings in which bit i is 0.

Set: The operation set(N, i) produces a tube in which every string from N has had its ith bit set to 1.

Clear: The operation clear(N, i) produces a tube in which every string from N has had its ith bit cleared to 0.

C.1.b Set cover problem

The *set cover problem* is a classic NP-complete problem. Given a finite set of p objects S, and a finite collection of subsets of S $(C_1, \ldots, C_q \subset S)$ whose union is S, find the *smallest* collection of these subsets whose union is S. For an example, consider $S = \{1, 2, 3, 4, 5\}$ and $C_1 = \{3, 4, 5\}, C_2 = \{1, 3, 4\}, C_3 = \{1, 2, 5\}, C_4 = \{3, 4\}$. In this case there are three minimal solutions: $\{C_1, C_3\}, \{C_3, C_4\}, \{C_2, C_3\}$.

algorithm Minimum Set Cover:

Data representation: The memory strands are of size $k = p + q$. Each strand represents a collection of subsets, and the first q bits encode which subsets are in the collection; call them *subset bits*. For example 1011 represents $\{C_1, C_3, C_4\}$ and 0010 represents $\{C_3\}$. Eventually, the last p bits will represent the union of the collection, that is, the elements of S that are contained in at lease one subset in the collection; call them *element bits*. For example, 0101 10110 represents $\{C_2, C_4\}$ $\{1, 3, 4\}$.

Library: The algorithm begins with the $(p + q, q)$ library, which must be initialized to reflect the subsets' members.

Step 1 (initialization): For all strands, if the i subset bit is set, then set the bits for all the elements of that subset. Call the result tube N_0. This is accomplished by the following code:

Initialize $(p + q, q)$ library in N_0
for $i = 1$ **to** q **do**
  separate$(+(N_0, i), -(N_0, i))$ //separate those with subset i
  for $j = 1$ **to** $|C_i|$ **do**
    set$(+(N_0, i), q + c_i^j)$ //set bit for jth element of set i
  end for
  $N_0 \leftarrow$ merge$(+(N_0, i), -(N_0, i))$ //recombine
end for

Step 2 (retain covers): Retain only the strands that represent collections that cover the set. To do this, retain in N_0 only the strands whose last p bits are set.

for $i = q + 1$ **to** $q + p$ **do**
  $N_0 \leftarrow +(N_0, i)$ //retain those with element i
end for

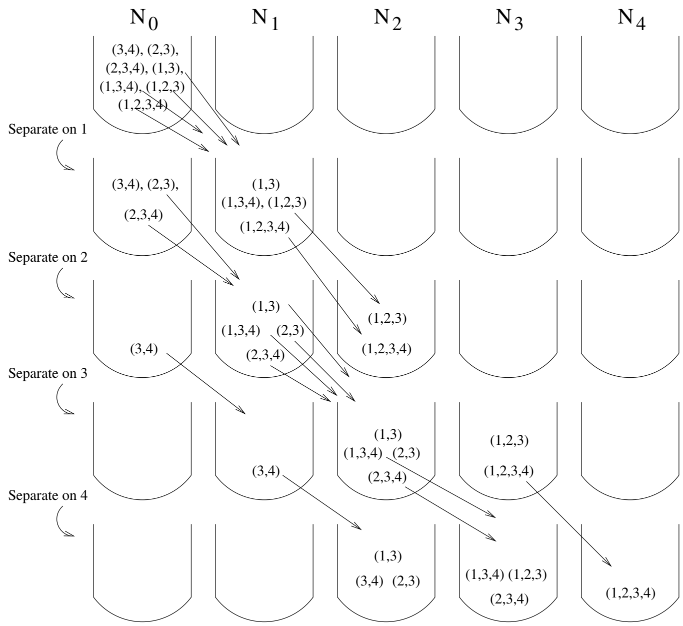

Figure IV.11: Sorting of covers by repeated separations. [source: Amos, Fig. 3.4]

Step 3 (isolate minimum covers): Tube N_0 now holds all covers, so we have to somehow sort its contents to find the minimum cover(s). Set up a row of tubes $N_0, N_1, \ldots, N_q$. We will arrange things so that N_i contains the covers of size i; then we just have to find the first tube with some DNA in it.

Sorting: For $i = 1, \ldots, q$, "drag" to the right all collections containing C_i, that is, for which bit i is set (see Fig. IV.11). This is accomplished by the following code:[10]

for $i = 0$ **to** $q - 1$ **do**
  for $j = i$ **down to** 0 **do**
    separate$(+(N_j, i+1), -(N_j, i+1))$ //those that do & don't have i

[10]Corrected from Amos p. 60.

$N_{j+1} \leftarrow \text{merge}(+(N_j, i+1), N_{j+1})$ //move those that do to N_{j+1}
$N_j \leftarrow -(N_j, i+1)$ //leave those that don't in N_j
end for
end for

Detection: Find the minimum i such that N_i contains DNA; N_i contains the minimum covers.
$\square$

The algorithm is $\mathcal{O}(pq)$.

C.2 Splicing systems

It has been argued that the full power of a TM requires some sort of string editing operation. Therefore, beginning with Tom Head (1987), a number of *splcing systems* have been defined. The splicing operations takes two strings $S = S_1S_2$ and $T = T_1T_2$ and performs a "crossover" at a specified location, yielding S_1T_2 and T_1S_2. *Finite extended splicing systems* have been shown to be computationally universal (1996).

The *Parallel Associative Memory (PAM) Model* was defined by Reif in 1995. It is based on a restricted splicing operation called *parallel associative matching* (PA-Match) operation, which is named *Rsplice*. Suppose $S = S_1S_2$ and $T = T_1T_2$. Then,

$$\text{Rsplice}(S, T) = S_1T_2, \quad \text{if } S_2 = T_1,$$

and is undefined otherwise. The PAM model can simulate nondeterministic TMs and parallel random access machines.