

Figure IV.7: Graph  $G_2$  for Lipton's algorithm (with two variables, x and y). [source: Lipton (1995)]

## B.2 Lipton: SAT

This lecture is based on Richard J. Lipton (1995), "DNA solution of hard computational problems," *Science* **268**: 542–5.

- B.2.a REVIEW OF SAT PROBLEM
  - ¶1. Boolean satisfiability: The first problem proved to be NP-complete.
  - ¶2. Use conjunctive normal form with n variables and m clauses.
  - ¶3. Example:

$$(x_1 \lor x_2' \lor x_3') \land (x_3 \lor x_5' \lor x_6) \land (x_3 \lor x_6' \lor x_4) \land (x_4 \lor x_5 \lor x_6),$$

where, for example,  $x'_2 = \neg x_2$ .

## B.2.b DATA REPRESENTATION

- ¶1. Solutions: Solutions are *n*-bit binary strings.
- ¶2. These are thought of as paths through a particular graph  $G_n$  (see Fig. IV.7). For vertices  $a_k, x_k, x'_k, k = 1, ..., n$ , and  $a_{n+1}$ , there are edges from  $a_k$  to  $x_k$  and  $x'_k$ , and from  $x_k$  and  $x'_k$  to  $a_{k+1}$ .
- ¶3. Binary strings are represented by paths from  $a_1$  to  $a_{n+1}$ . A path through  $x_k$  encodes the assignment  $x_k = 1$  and through  $x'_k$  encodes  $x_k = 0$ .

¶4. The DNA encoding is essentially the same as in Adleman's algorithm.

## B.2.c Algorithm

- ¶1. Suppose we have an instance (formula) to be solved:  $I = C_1 \wedge C_2 \wedge \cdots \wedge C_m.$
- ¶2. Step 1 (initialization): Create a "test tube" (reaction vessel) of all possible *n*-bit binary strings, encoded as above. Call this test tube  $T_0$ .
- ¶3. Step 2 (clause satisfaction): For each clause  $C_k$ , k = 1, ..., m: Extract from  $T_{k-1}$  only those strings that satisfy  $C_k$ , and put them in  $T_k$ .

The goal is that for every string  $\forall x \in T_k \forall 1 \leq j \leq k : C_j(x) = 1$ . This is done as follows.

- ¶4. Extract operation: Let E(T, i, a) be the operation that extracts from test tube T all (or most) of the strings whose *i*th bit is a.
- ¶5. For k = 0, ..., m 1: *Precondition:* The strings in  $T_k$  satisfy clauses  $C_1, ..., C_k$ . Let  $\ell = |C_k|$ , and suppose  $C_{k+1}$  has the form  $v_1 \lor \cdots \lor v_\ell$ , where the  $v_i$ are literals (plain or complemented variables). Let  $\overline{T}_k^0 = T_k$ . Do the following for literals  $i = 1, ..., \ell$ .
- ¶6. Positive literal: Suppose  $v_i = x_j$  (some positive literal). Let  $T_k^i = E(\overline{T}_k^{i-1}, j, 1)$  and let a = 1. These are the paths that satisfy this positive literal.
- ¶7. Negative literal: Suppose  $v_i = x'_j$  (some negative literal). Let  $T_k^i = E(\overline{T}_k^{i-1}, j, 0)$  and let a = 0. These are the paths that satisfy this negative literal.
- ¶8. In either case,  $T_k^i$  are the strings that satisfy literal *i*. Let  $\overline{T}_k^i = E(\overline{T}_k^{i-1}, j, \neg a)$  be the remaining strings (which do not satisfy this literal).

Continue until all literals are processed.

## **B.** FILTERING MODELS

- ¶9. Combine  $T_k^1, \ldots, T_k^\ell$  into  $T_{k+1}$ . *Postcondition:* The strings in  $T_{k+1}$  satisfy clauses  $C_1, \ldots, C_{k+1}$ .
- ¶10. Step 3 (detection): At this point, the strings in  $T_m$  satisfy  $C_1, \ldots, C_m$ , so do a *detect* operation to see if there are any strings left. If there are, the formula is satisfiable; if not, not.
- ¶11. **Performance:** If the number of literals is fixed (as in 3SAT), then performance is linear in m.
- ¶12. Errors: The main problem is the effect of errors. But imperfections in extraction are not fatal, so long as there are enough copies of the desired sequence.
- ¶13. "A much larger (20 variable) instance of 3-SAT was successfully solved by Adlemans group in an experiment described .... This is, to date, the largest problem instance successfully solved by a DNA-based computer; indeed, as the authors state, 'this computational problem may yet be the largest yet solved by nonelectronic means'."<sup>5</sup> This was in 2002.  $2^{20} \approx 10^{6}$ . It had 24 clauses.

 $^{5}$ Amos 140.