

# Syndrome and Transition Count are Uncorrelated

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**Abstract**—In the testing of logic circuits, two of the proposed data compression methods are the number of ones (syndrome) and the number of sequence changes (transition count). An enumeration  $N(m, k, t)$  of the number of length- $m$  binary sequences having syndrome value  $k$  and transition count  $t$  is developed. Examination of this result reveals that the parallel compression of these two methods has small overlap in error masking. An asymptotic expression for  $N(m, k, t)$  is developed.

## I. INTRODUCTION

DATA compression has made built-in testing feasible in very large scale integration (VLSI). Several compression or compaction methods have been proposed. These methods can be broadly classified into two approaches: 1) signature analysis (SA) [1]–[4] based on linear feedback shift register compression, and 2) counting-based methods like syndrome testing (ST) [5], [6], transition count (TC) [7], [8], accumulator compression testing (ACT) [9], and Walsh coefficient testing (WCT) [10], [11]. In addition to presenting a unified view of the various compression methods, the authors in [12] have emphasized the need to match one or more compression methods to the function under test to obtain optimal fault coverage. Investigation of new compression functions or study of the combination of two or more compression functions (parallel compression) is therefore worthwhile. A desirable property in parallel compression is orthogonality between the compression functions. This property ensures minimum overlap in error masking. In [13], signature analysis and counting-based methods are shown to be orthogonal under certain conditions.

It is shown here that syndrome and transition count are uncorrelated. A function  $N(m, k, t)$  is defined as the number of length- $m$  binary sequences having syndrome and transition count values  $k$  and  $t$ , respectively. A  $2 \times 2$  matrix generating function is derived which enumerates  $N(m, k, t)$ . The covariance of  $k$  and  $t$  as random variables is shown to be zero. An asymptotic formula for  $N(m, k, t)$  is obtained.

This work was motivated by the interest in the combined use of ST and TC shown in [14]. An experimental study on the combination of ST and TC was done in [12].

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In [15] only a special case for ST and TC was considered. Results indicate that if TC is augmented to output data modification [16], then error masking can be further reduced.

## II. COMBINATORIAL EXPRESSION

The test situation we wish to examine is indicated in Fig. 1. For simplicity, we assume a single output function. At test time an input sequence is applied to the unit under test (UUT). The syndrome is analogous to the integral of the test data, while the transition count is analogous to the integral of the absolute value of the derivative. The output test data are compressed, and the two attributes of syndrome ( $k$ ) and transition count ( $t$ ) are compared to those of a correctly functioning unit. Error masking is possible if more than one length- $m$  sequence has the same values of  $k$  and  $t$ . We will count the number of such sequences.  $N(m, k, t)$  is the number of length- $m$  binary sequences having syndrome value  $k$  and transition count  $t$ .

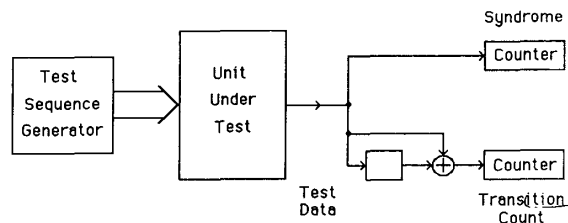


Fig. 1. Test compression block diagram.

From the definition of transition count [7], [8],  $t$  is one less than the number of runs in the sequence. The ranges of  $k$  and  $t$  are

$$\begin{aligned} 0 &\leq k \leq m \\ 0 &\leq t \leq m - 1. \end{aligned}$$

For a particular sequence, let  $R_0$  be the number of runs of zeros and  $R_1$  be the number of runs of ones. Thus

$$t = R_0 + R_1 - 1.$$

Since the type of run alternates,

$$|R_0 - R_1| \leq 1.$$

The number of ones,  $k$ , is an upper bound on  $R_1$ , and the number of zeros,  $m - k$ , is an upper bound on  $R_0$ . The

transition count  $t$  is thus bounded

$$t \leq 2 \min(k, m - k).$$

This last expression implies that about half of the points in the joint space of  $m^2 + m$  pairs  $k, t$  have  $N(m, k, t) = 0$  (see Figs. 2 and 3). The development of  $N$  for the rest of the space treats the cases of  $t$  even and  $t$  odd separately.

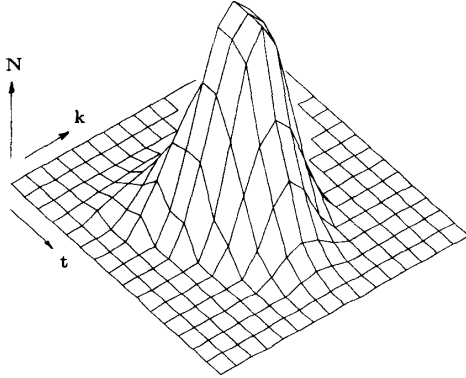


Fig. 2.  $N(16, t, k)$ .

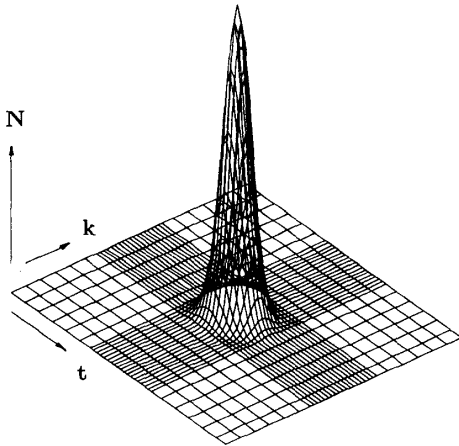


Fig. 3.  $N(128, t, k)$ .

*Case 1:  $t = 2\beta + 1$ :* In this case  $R_0 = R_1 = \beta + 1$ . The smallest possible  $k$  and  $m$  would be for a sequence of alternate ones and zeros;  $k = \beta + 1$ ,  $m = 2\beta + 2$ . Since we could start with either a zero or a one, two such sequences exist and

$$N(2\beta + 2, \beta + 1, 2\beta + 1) = 2.$$

Next we consider extending this basic alternating sequence so that  $m$  and possibly  $k$  are larger but keeping the same value of  $t$ . The additional number of ones would be  $k - R_1$ . These "extra" ones can be distributed next to any of the basic ones without changing  $t$ . This can be done in

$$\binom{k-1}{R_1-1} = \binom{k-1}{\beta}$$

ways. In the same manner, the  $m - k - R_0$  "extra" zeros can be independently distributed in

$$\binom{m-k-1}{R_0-1} = \binom{m-k-1}{\beta}$$

ways. The product of these two coefficients yields the number of patterns starting with either a one or a zero; thus an additional factor of 2 results, and

$$N(m, k, 2\beta + 1) = 2 \binom{m-k-1}{\beta} \binom{k-1}{\beta}. \quad (1)$$

*Case 2:  $t = 2\beta + 2$ :* For even  $t$ , there must be an odd number of runs and two subcases result. The first has sequences starting with a zero.

*Case 2a:  $R_0 = \beta + 2$ ,  $R_1 = \beta + 1$ :* Using the same arguments as in Case 1, a total of

$$\binom{m-k-1}{\beta+1} \binom{k-1}{\beta}$$

sequences start with a zero. For sequences starting with a one, we have the following.

*Case 2b:  $R_0 = \beta + 1$ ,  $R_1 = \beta + 2$ :* Repeating the Case 1 reasoning, a total of

$$\binom{m-k-1}{\beta} \binom{k-1}{\beta+1}$$

sequences start with a one. Combining the last two expressions yields

$$N(m, k, 2\beta + 2) = \binom{m-k-1}{\beta} \binom{k-1}{\beta} \binom{m-2\beta-2}{\beta+1}. \quad (2)$$

Expressions (1) and (2) assume  $\beta$  is at least zero. For the particular case  $t = 0$ , which is not covered, the sequence must be all ones or all zeros, and clearly,

$$N(m, k, 0) = \begin{cases} 1, & \text{for } k = 0 \text{ and } k = m; \\ 0, & \text{otherwise.} \end{cases}$$

For large values of  $m$ ,  $k$ , and  $t$  an approximate expression can be obtained using the following limit form for the binomial coefficient [17]:

$$\binom{m}{n} \approx 2^m \left( \frac{2}{\pi m} \right)^{1/2} \exp - \left[ \frac{(m-2n)^2}{2m} \right]. \quad (3)$$

Fig. 2 is a representation of  $N(16, k, t)$  for various pairs  $k$  and  $t$ . For even  $m$  the counts are clearly symmetric about  $k = m/2$  since  $t$  is preserved under complementation. Note that there are already suggestions of the Gaussian shape of limit form (3). Fig. 3 is a similar plot for  $m = 128$ . Note that both figures demonstrate the symmetry inherent in expressions (1) and (2). Substituting the limiting form (3) into (1), assuming  $m$ ,  $k$ , and  $t$  are large, results in

$$N(m, k, t) \approx \frac{2^m}{\pi} \frac{1}{\sqrt{(m-k)k}} \cdot \exp - \left[ \frac{(m-k-t)^2}{2(m-k)} + \frac{(k-t)^2}{2k} \right]. \quad (4)$$

### III. EQUIVALENT LENGTH

Counting-based compression techniques, which include syndrome [5], transition count [7], and spectral coefficients [11], exhibit variable masking. That is, the number of sequences which give the same compressed result as correct operation depends on the particular function being compressed. Signature compression, on the other hand, is a linear operation having a fixed number of sequences with the same signature. A signature compressor can be realized using a linear feedback shift register (LFSR). The number of sequences resulting in the same signature is exactly  $2^{m-L}$  for a LFSR with length  $L$ . As  $L$  is increased, the number of masking patterns decreases exponentially. We define the equivalent length  $L_e$  for a compression method as that value of  $L$  which has the same number of masking patterns. Thus

$$L_e = m - \log_2 N.$$

We consider noninteger  $L_e$  for comparison purposes; of course, a real LFSR has integer length. Let  $L_e(k) = L_e$  for syndrome compression,  $L_e(t) = L_e$  for transition count, and  $L_e(k, t) = L_e$  for simultaneous syndrome and transition count. Using the approximation (3) for these three cases (assuming  $m$ ,  $k$ , and  $t$  are large with respect to 1), we obtain

$$L_e(k) = \frac{1}{2} \text{Lg}(\pi m/2) + (\text{Lg } e) \left[ \frac{(m/2 - k)^2}{m/2} \right] \quad (5)$$

$$L_e(t) = \frac{1}{2} \text{Lg}(\pi m/2) + (\text{Lg } e) \left[ \frac{(m/2 - t)^2}{m/2} \right] \quad (6)$$

$$L_e(k, t) = \frac{1}{2} \text{Lg}(\pi^2(m-k)k/4) + (\text{Lg } e) \left[ \frac{(m-k-t)^2}{2(m-k)} + \frac{(k-t)^2}{2k} \right] \quad (7)$$

where Lg represents the logarithm to the Base 2.

As has been noted, (5) and (6) indicate that the equivalent length grows as the square of the difference between  $k$  or  $t$  and their midvalues. The incremental benefit of using syndrome and transition count together over the use of either syndrome, transition count, or signature alone can be estimated from (5)-(7). Table I illustrates some values for  $m = 256$ .

TABLE I  
EQUIVALENT LENGTHS FOR VALUES OF  $k$  AND  $t$  WHEN TEST LENGTH  
 $m = 256$

$k$ Weight	$t$ Transition Count	$L_e(k)$ Syndrome	$L_e(t)$ TC	$L_e(k, t)$ Both
128	128	4.3	4.3	7.4
128	64	4.3	50.6	73.6
64	128	50.6	4.3	69.5
160	96	15.9	15.9	26.1

Note for the cases in Table I that an eight-stage counter is sufficient to calculate  $k$  or  $t$ . The first row is the worst case for counting where an eight-stage LFSR would have fewer masking sequences. As  $k$  and  $t$  differ from  $m/2$ , the equivalent length becomes larger.

### IV. RECURRENCE RELATIONS

In this section we present some recurrence relations on  $N(m, k, t)$ . Two subfunctions are defined as follows:

- $N_0(m, k, t)$  number of length- $m$  binary sequences having syndrome  $k$  and transition count  $t$  with the restriction that the first term in all these sequences is always zero;
- $N_1(m, k, t)$  number of length- $m$  binary sequences having syndrome  $k$  and transition count  $t$  with the restriction that the first term in all these sequences is always one.

From the definitions of subfunctions we have the following relation:

$$N(m, k, t) = N_0(m, k, t) + N_1(m, k, t).$$

Next we develop recurrence relationships  $N_0$  and  $N_1$ . These functions are illustrated in Fig. 4. Expressions (8) and (9) clearly follow:

$$N_0(m, k, t) = N_0(m-1, k, t) + N_1(m-1, k, t-1) \quad (8)$$

$$N_1(m, k, t) = N_1(m-1, k-1, t) + N_0(m-1, k-1, t-1). \quad (9)$$

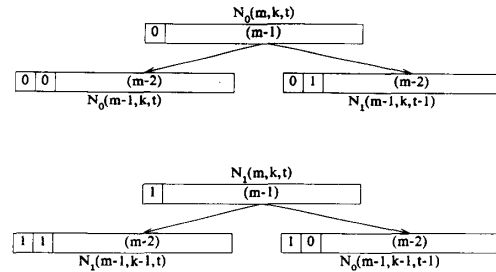


Fig. 4. Recursion forms.

The following are base conditions for (8) and (9):

$$N_0(1, 0, 0) = 1 \text{ and } N_0(1, k, t) = 0,$$

for all  $(k, t) \neq (0, 0)$

$$N_1(1, 1, 0) = 1 \text{ and } N_1(1, k, t) = 0,$$

for all  $(k, t) \neq (1, 0)$ .

The base conditions are for length-one sequences. The TC for a length-one sequence is always zero.  $N(m, k, t)$  is defined for positive values of  $m$  with  $k$  and  $t$  satisfying the boundary conditions  $0 \leq k \leq m$  and  $0 \leq t \leq m-1$ , respectively.  $N(m, k, t)$  is zero when  $k$  or  $t$  do not satisfy the boundary conditions. The function  $N(m, k, t)$  may be interpreted for null sequence ( $m = 0$ ) or for negative values of  $m$ , but then we may have to redefine  $k$  and  $t$  because

the boundary conditions will not make sense. This interpretation is important because if we consider  $N_0(1,0,0)$  and apply (2) backwards, then we have  $N_0(0,0,0) + N_1(0,0,-1) = 1$ , which implies that at least one of the function terms with  $m = 0$  is a positive quantity. A similar argument can be made for cases where  $m$  is negative.

## V. GENERATING FUNCTIONS AND ASYMPTOTIC RESULTS

In the previous section we obtained recurrence relations on  $N(m, k, t)$ . The enumeration can be easily done for small values of  $m$ . However, our interest is in examining the behavior of this function when  $m$ ,  $k$ , and  $t$  are large. The problem of enumerating  $N(m, k, t)$  is formulated in terms of probability generating functions and an asymptotic formula is derived. The following definitions and notations will be used:

$\mu_x$	mean value of random variable $k$ ,
$\mu_y$	mean value of random variable $t$ ,
$\sigma_x^2$	variance of $k$ ,
$\sigma_y^2$	variance of $t$ ,
$A(m, k)$	number of length- $m$ sequences with syndrome $k$ ,
$B(m, k)$	number of length- $m$ sequences with transition count $t$ ,
$r_m(x)$	generating function for $A(m, k)$ ,
$s_m(y)$	generating function for $B(m, k)$ ,
$g_m(x, y)$	generating function for $N_0(m, k, t)$ ,
$f_m(x, y)$	generating function for $N_1(m, k, t)$ ,
$h_m(x, y)$	generating function for $N(m, k, t)$ ,
$\mu_{xy}$	mean value of the product $kt$ ,
$r$	coefficient of correlation.

$A(m, k)$  is the same as the number of different ways of arranging  $k$  ones in length- $m$  binary sequence.  $A(m, k)$  is simply  $\binom{m}{k}$ . Thus  $r_m(x)$  can be expressed as

$$r_m(x) = \sum_{k=0}^m A(m, k)x^k = \sum_{k=0}^m \binom{m}{k} x^k = (1+x)^m \quad (10)$$

$$r_m(1) = 2^m.$$

Let  $r(x) = r_m(x)/r_m(1)$ . It follows that  $r(1) = 1$ , and  $r(x)$  behaves as a probability density function. Therefore, we have

$$\mu_x = r'(1)$$

$$\sigma_x^2 = r''(1) - r'(1)^2 + r'(1).$$

Differentiating (10) and substituting  $x = 1$ , we get

$$\mu_x = \frac{m}{2} \quad (11)$$

and

$$\sigma_x^2 = \frac{m}{4}. \quad (12)$$

From [7] we have  $B(m, t) = 2\binom{m-1}{t}$ . Therefore, we have

$$s_m(y) = 2(1+y)^{m-1}. \quad (13)$$

In a manner similar to  $A(m, k)$  we can show

$$\mu_y = \frac{m-1}{2} \quad (14)$$

$$\sigma_y^2 = \frac{m-1}{4}. \quad (15)$$

The following identities can be proved from the definitions of  $N_0$ ,  $N_1$ , and  $N$ :

$$g_m(x, y) = \sum_{k=0}^m \sum_{t=0}^{m-1} N_0(m, k, t)x^k y^t \quad (16)$$

$$f_m(x, y) = \sum_{k=0}^m \sum_{t=0}^{m-1} N_1(m, k, t)x^k y^t \quad (17)$$

$$\begin{aligned} h_m(x, y) &= \sum_{k=0}^m \sum_{t=0}^{m-1} N(m, k, t)x^k y^t \\ &= g_m(x, y) + f_m(x, y). \end{aligned} \quad (18)$$

Substituting (8) and (9) in the previous identities and applying boundary conditions, we can show that

$$g_m(x, y) = g_{m-1}(x, y) + yf_{m-1}(x, y) \quad (19)$$

$$f_m(x, y) = xyg_{m-1}(x, y) + xf_{m-1}(x, y). \quad (20)$$

From base conditions, we have

$$g_1(x, y) = 1 \quad f_1(x, y) = x.$$

We can represent the generating functions more compactly in a  $2 \times 2$  matrix closed form in (21):

$$\begin{bmatrix} g_m(x, y) \\ f_m(x, y) \end{bmatrix} = \begin{bmatrix} 1 & y \\ xy & x \end{bmatrix}^{m-1} \begin{bmatrix} 1 \\ x \end{bmatrix}. \quad (21)$$

Using (19) and (20), we can obtain

$$g_3(x, y) = 1 + xy + xy^2 + x^2y$$

$$f_3(x, y) = xy + x^2y^2 + x^2y + x^3$$

and, therefore,

$$h_3(x, y) = 1 + 2xy + 2x^2y + xy^2 + x^2y^2 + x^3.$$

The coefficient of  $x^2y$  in  $h_3(x, y)$  will be the same as  $N(3, 2, 1)$ , namely, two. There are two length-3 sequences, (011, 110), with  $k = 2$  and  $t = 1$ .

To derive the asymptotic result, we consider the joint distribution of  $k$  and  $t$ :

$$h_m(x, y) = \sum_{k=0}^m \sum_{t=0}^{m-1} N(m, k, t)x^k y^t$$

$$h_m(1, 1) = 2^m.$$

Let us define  $h(x, y) = h_m(x, y)/h_m(1, 1)$ .

$h(1, 1) = 1$  and  $h(x, y)$  can be considered as a joint probability distribution density function. The covariance

of the random variables  $k$  and  $t$  is  $\mu_{xy} - \mu_x \mu_y$ :

$$\begin{aligned}\mu_{xy} &= \frac{1}{2^m} \sum_{k=0}^m \sum_{t=0}^{m-1} ktN(m, k, t) \\ &= \frac{1}{2^m} \left. \frac{\partial^2 h_m}{\partial x \partial y} \right]_{x=1, y=1} \\ &= \frac{1}{2^m} \left. \frac{\partial^2 g_m}{\partial x \partial y} + \frac{\partial^2 f_m}{\partial x \partial y} \right]_{x=1, y=1}.\end{aligned}$$

To compute  $\mu_{xy}$ , we need to find the following at  $x=1$ ,  $y=1$ :

$$\frac{\partial g_m}{\partial x}, \frac{\partial g_m}{\partial y}, \frac{\partial f_m}{\partial x}, \frac{\partial f_m}{\partial y}, \dots$$

Taking the partial derivative of  $g_m$  and  $f_m$ , we have

$$\begin{aligned}\frac{\partial g_m}{\partial x} &= \frac{\partial g_{m-1}}{\partial x} + y \frac{\partial f_{m-1}}{\partial x} \\ \frac{\partial f_m}{\partial x} &= y g_{m-1} + xy \frac{\partial g_{m-1}}{\partial x} + f_{m-1} + x \frac{\partial f_{m-1}}{\partial x} \\ \frac{\partial g_m}{\partial y} &= \frac{\partial g_{m-1}}{\partial y} + f_{m-1} + y \frac{\partial f_{m-1}}{\partial y} \\ \frac{\partial f_m}{\partial y} &= xy g_{m-1} + xy \frac{\partial g_{m-1}}{\partial y} + x \frac{\partial f_{m-1}}{\partial y}.\end{aligned}$$

We will use the following notation for ease in representation:

$$\begin{aligned}a_m &= \left. \frac{\partial g_m}{\partial x} \right]_{x=1, y=1} \\ b_m &= \left. \frac{\partial f_m}{\partial x} \right]_{x=1, y=1} \\ u_m &= \left. \frac{\partial g_m}{\partial y} \right]_{x=1, y=1} \\ v_m &= \left. \frac{\partial f_m}{\partial y} \right]_{x=1, y=1} \\ c_m &= a_m + b_m \\ z_m &= u_m + v_m.\end{aligned}$$

With  $x=1$  and  $y=1$  the partial differential recurrence relations can be written as

$$a_m = a_{m-1} + b_{m-1} = c_{m-1} \quad (22)$$

$$\begin{aligned}b_m &= a_{m-1} + g_{m-1}(1,1) + f_{m-1}(1,1) + b_{m-1} \\ &= h_{m-1}(1,1) + c_{m-1}\end{aligned} \quad (23)$$

$$u_m = u_{m-1} + f_{m-1}(1,1) + v_{m-1} = z_{m-1} + f_{m-1}(1,1) \quad (24)$$

$$\begin{aligned}v_m &= g_{m-1}(1,1) + u_{m-1} + v_{m-1} \\ &= g_{m-1}(1,1) + z_{m-1}\end{aligned} \quad (25)$$

$$h_{m-1}(1,1) = 2^{m-1} \quad g_{m-1}(1,1) = f_{m-1}(1,1) = 2^{m-2}.$$

Adding (22) and (23), we have

$$c_m = 2c_{m-1} + 2^{m-1}.$$

Since  $c_1 = 1$ , we can show that  $c_m = m2^{m-1}$ . Thus we have

$$\begin{aligned}a_m &= \left. \frac{\partial g_m}{\partial x} \right]_{x=1, y=1} = c_{m-1} = (m-1)2^{m-2} \\ b_m &= \left. \frac{\partial f_m}{\partial x} \right]_{x=1, y=1} = c_{m-1} + 2^{m-1} = (m+1)2^{m-2}.\end{aligned}$$

Similarly, we can show that

$$\begin{aligned}u_m &= \left. \frac{\partial g_m}{\partial y} \right]_{x=1, y=1} = (m-1)2^{m-2} \\ v_m &= \left. \frac{\partial f_m}{\partial y} \right]_{x=1, y=1} = (m-1)2^{m-2}.\end{aligned}$$

Taking second derivatives and forming linear recurrence yields

$$\begin{aligned}\left[ \frac{\partial^2 g_m}{\partial x \partial y} + \frac{\partial^2 f_m}{\partial x \partial y} \right]_{x=1, y=1} &= 2^{m-1} \binom{m}{2} \\ \mu_{xy} &= \frac{1}{2} \binom{m}{2}.\end{aligned}$$

Thus

$$\text{covariance} = \mu_{xy} - \mu_x \mu_y = \frac{m(m-1)}{4} - \frac{m(m-1)}{4} = 0.$$

Since the covariance is zero, the correlation coefficient  $r$  will also be zero. Fitting this in the bivariate normal distribution, we obtain the following asymptotic result:

$$N(m, k, t) = \frac{2^{m+1}}{\sqrt{m(m-1)}} \exp \left[ -2 \left[ \frac{(k-m/2)^2}{m} + \frac{(t-(m-1)/2)^2}{m-1} \right] \right].$$

Enumeration by this asymptotic formula closely follows the value of  $N(m, k, t)$  in the neighborhood of the maximum. We conjecture that generalized syndromes presented in [12] will exhibit similar orthogonal characteristics. It is conceivable that  $m$  complete and orthogonal generalized syndromes similar to  $2^m$  spectral coefficients could be defined. These syndromes, besides being useful in built-in testing, might find application in digital signal processing.

## VI. CONCLUSION

We have developed an expression  $N(m, k, t)$  for the number of length- $m$  binary sequences having syndrome value  $k$  and transition count  $t$ . This count, which serves as a measure of the error masking for logic test data compression, has a strong dependence on the values of  $k$  and  $t$ . Differences between  $k$  and  $t$  and their respective midrange values of  $m/2$  and  $(m-1)/2$  reduce this count exponentially as the square of these differences.

The value of  $k$  is just the weight of the data sequence compressed and is independent of the order of the data. For many real logic functions,  $k$  is significantly larger or smaller than  $m/2$ .

The parameter  $t$  depends strongly on the order of the data. In testing logic circuits, it may be worthwhile to examine various test pattern sequences to minimize possible error masking by maximizing or minimizing  $t$ . Particularly for built-in testing, it may be advantageous to match the test pattern generator to the functions under test. The counter used to compute  $k$  could be time multiplexed to compute  $t$  as well.

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