

De Bruijn Sequences : Generation, Reproduction and Applications

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Abstract

De Bruijn sequences had been well investigated in 70s-80s. In the past, most of the approaches used to generate de Bruijn sequences were based upon either finite field theory or combinatorial theory. This paper describes a simple approach for generating de Bruijn sequences as “seeds”, and then based upon the “seeds”, a simple procedure is presented to reproduce a class of de Bruijn sequences. Numerical results of the distribution of reproduced sequences are provided. Additionally, this paper also reports some recent applications of de Bruijn sequences in psychology and engineering.

1. De Bruijn sequences

Given m symbols which, without loss of generality, it is assumed that $1, 2, \dots, m-1, m$, with the nature order $1 < 2 < \dots < m-1 < m$. An m -symbol n -tuple de Bruijn sequence (or (m, n) de Bruijn sequence), is a string of m^n symbols $s_0 s_1 \dots s_{m^n-1}$ such that each substring of length n ,

$$s_{i+1} s_{i+2} \dots s_{i+n}, \quad (1)$$

is unique with subscripts in (1) taken modulo m^n . For example, sequence 123133221 is a $(3, 2)$ de Bruijn sequence produced by the symbol set $\{1, 2, 3\}$, since each substring of length 2, namely, 12, 23, 31, 13, 33, 32, 22, 21, 11, is unique over the symbol set $\{1, 2, 3\}$. For $m \geq 2$ and $n \geq 2$, according to Fredricksen's account that there are $N = [(m-1)!]^{m^{n-1}} \cdot m^{m^{n-1}-n}$ of (m, n) de Bruijn sequences (Fredricksen [3]).

In the 70s-80s, de Bruijn sequences had been well studied and several algorithms had been proposed for generating such sequences, e.g., Fredricksen and Kessler [4], Fredricksen and Maiorana [5], and Ralston [9] etc. However, most of the proposed algorithms are based upon either finite field theory or combinatorial theory to generate a single (m,n) de Bruijn sequence rather than a class of sequences. An excellent survey is referred to Fredricksen [3].

The purpose of this paper is multiple. Firstly, a simple algorithm directly based upon de Bruijn digraphs is described for generating (m,n) de Bruijn sequences as “seeds” for $m \geq 2$ and $n \geq 2$. As shown, this algorithm is much simpler than the other aforementioned approaches. Secondly, using the generated “seeds”, a simple procedure is proposed to generate a class of (m,n) de Bruijn sequences. Numerical results are reported to show the distribution of the class of de Bruijn sequences. Finally, two recent applications of de Bruijn sequences in reaction time experiment problems (psychology) and 3D pattern recognition problems (engineering) are presented.

2. The generation of de Bruijn sequences

It is well known that each (m,n) de Bruijn sequence corresponds to an Eulerian circuit in the so-called de Bruijn digraph $D_{m,n}$ in which the vertex set of $D_{m,n}$ is the set of all distinct m^{n-1} words of length $n-1$ over the symbol set $\{1,2,\dots,m\}$ (Chartrand and Oellermann [1]). Given m and n , generating an (m,n) de Bruijn sequence is equivalent to finding an Eulerian circuit in its corresponding digraph $D_{m,n}$. Based upon the set of vertices and the set of arcs, one may represent the de Bruijn digraph $D_{m,n}$ by an $m^{n-1} \times m^{n-1}$ square adjacency matrix A . Next, throughout the paper, it is defined that the value of arc (i,j) in $D_{m,n}$ is $r_{ij} = 1 + \{[(m-1) + j \bmod m^{n-1}] \bmod m\}$.

Example 1. For $(m,n)=(3,3)$, the de Bruijn digraph $D_{3,3}$ is shown in Figure 1, and its corresponding adjacency matrix A is shown in Figure 2.

In the adjacency matrix A , $A_{ij}=1$ indicates that there is an arc (i,j) from the i th vertex to the j th vertex and its arc value is r_{ij} (see Figure 1 and Figure 2). Generally, for an (m,n) de Bruijn sequence, its corresponding adjacency matrix A is given by :

$$A_{ij} = \begin{cases} 1 & \text{if } 1 \leq j - [(i-1)m \bmod m^{n-1}] \leq m \\ 0 & \text{otherwise} \end{cases} \quad i, j \in \{1,2,\dots,m^{n-1}\} \quad (2)$$

Thus, for this example, finding an Eulerian circuit in the de Bruijn digraph $D_{3,3}$ is equivalent to assigning numbers of $1,2,\dots,3^3 (=m^n)$ into 27 cells $(i,j) \in \Theta \equiv \{(i,j) \mid A_{ij}=1\}$ of the adjacency matrix A , where $1,2,\dots,3^3$ indicating the ordering of arcs

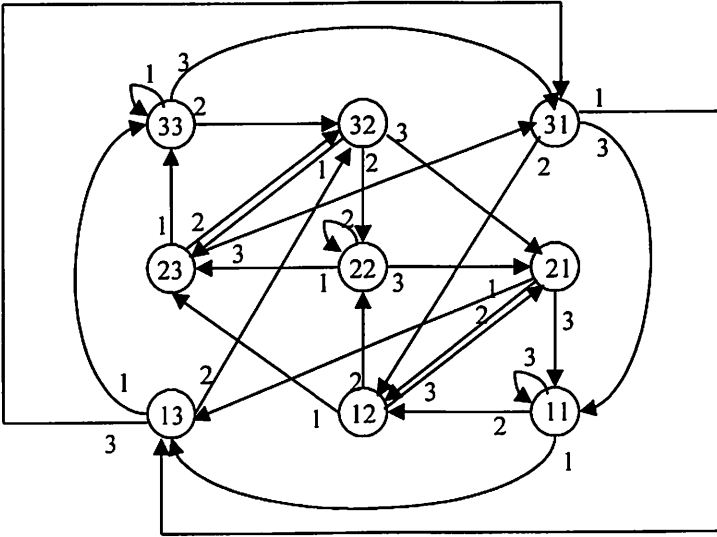


Figure 1. The de Bruijn digraph for $D_{3,3}$.

arc value $r_{ij} \Rightarrow$	1	2	3	1	2	3	1	2	3
vertex \Rightarrow	33	32	31	23	22	21	13	12	11
\bar{ij}	1	2	3	4	5	6	7	8	9

33	1	1	1						
32	2			1	1	1			
31	3						1	1	1
23	4	1	1	1					
22	5				1	1	1		
21	6						1	1	1
13	7	1	1	1					
12	8				1	1	1		
11	9						1	1	1

Figure 2. The adjacency matrix A for the de Bruijn digraph $D_{3,3}$.

to be traveled in the de Bruijn digraph $D_{3,3}$ in Figure 1. In general, if t is assigned to cell (i,j) , then the next positive integer $t+1$ must be assigned to an unassigned cell of row j . For this example, one possible ordering of assignments for an Eulerian circuit is shown in Figure 3.

arc value $r_{ij} \Rightarrow$	1	2	3	1	2	3	1	2	3	
vertex \Rightarrow	33	32	31	23	22	21	13	12	11	
	ij	1	2	3	4	5	6	7	8	9
33	1	27	20	1						
32	2				25	21	17			
31	3							15	9	2
23	4	26	24	14						
22	5				23	22	11			
21	6							18	12	6
13	7	19	16	8						
12	8				13	10	5			
11	9							7	4	3

Figure 3. One possible assignment of Eulerian circuit for the de Bruijn digraph $D_{3,3}$.

In Figure 3, following the ordering of arcs to be traveled and appending its corresponding arc values r_{ij} a (3,3) de Bruijn sequence is given by 33323 31322 32131 23112 22121 11.

Based upon the same idea of this example, Hsieh [7] proposed the following simple algorithm for generating an (m,n) de Bruijn sequence. In the algorithm, $L(S)$ denotes the length of sequence S .

Algorithm A: (input : (m,n) ; output : S =an (m,n) de Bruijn sequence)

0. $i \leftarrow 1, I \leftarrow (m,m,\dots,m) \in R^{m^{n-1}}$, and S is an empty sequence.

1. While $L(S) < m^n$ do

begin

$$j \leftarrow I[i] + [(i-1)m \bmod m^{n-1}] \tag{3a}$$

$$\text{Append } 1 + [(m-1+j) \bmod m^{n-1}] \bmod m \text{ to } S \tag{3b}$$

$$I[i] \leftarrow I[i] - 1 \tag{3c}$$

$$i \leftarrow j \tag{3d}$$

end (while)

Noted that this algorithm is much simpler to implement than those typical approaches by Fredricksen and Kessler [4], Fredricksen and Maiorana [5], and Ralston [9]; and it has several computational advantages over those typical approaches, such as : (i) this algorithm does not require to generate additional necklaces (substrings), (ii) this algorithm does not require to test whether additional necklaces had been previously generated or not, and (iii) this algorithm does not require to test that additional necklaces are periodic or aperiodic

3. The reproduction of de Bruijn sequences

In this section, we will present a simple procedure to generate a class of de Bruijn sequences by using the “seed” sequence generated by Algorithm A.

Firstly, we note that each de Bruijn sequence S can be represented by a sequence C (or C -sequence) which is constructed by the coordinates of orderings in the adjacency matrix A . Consider Example 1. The de Bruijn sequence is $S=33323 31322 32131 23112 22121 11$, and its corresponding C -sequence is $C=(1)39986 97385 68437 26712 55424 11$ (the preamble within parentheses is identical to the final integer of the sequence). Since, in Figure 3, the first substring of C , i.e., (1,3), corresponds to the first integer 3 ($=r_{13}$) in S , and the second substring in C , i.e., (3,9), corresponds to the second integer 3 ($=r_{39}$) in S . Similarly, the fourth substring of C , i.e., (9,8), corresponds to the fourth integer 2 ($=r_{98}$) in S and so on. For a C -sequence, one observes that :

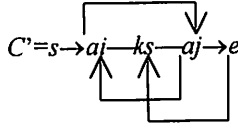
- (i) $L(C)=L(S)$, i.e., the length of C -sequence is equal to that of de Bruijn sequence;
- (ii) for any n , it only requires a substring of length 3 to identify two adjacent vertices in a C -sequence, while it requires $n+1$ for de Bruijn sequence S ; and
- (iii) any de Bruijn sequence can be converted to a C -sequence by the above process in the example, and vice versa.

By (i) there is no additional storage required, by (ii), for a given C -sequence, we may easily generate the other new C -sequence (Theorem 2, see below), and by (iii) we may convert the new C -sequence to a new de Bruijn sequence. Next we will introduce the main result for the reproduction of de Bruijn sequences. For simplicity, we omit the preamble in the parentheses of C -sequence throughout the paper.

Let $\Phi \equiv \bigcup_{i=1}^{m-1} \Phi_i$ be the set of substrings of length 2 in C , where Φ_i is the set of coordinates of orderings $(i,j) \in \Phi, 1 \leq j \leq m-1$. For example, in Figure 2 we have $\Phi_1 = \{(1,1)(1,2)(1,3)\}$, $\Phi_2 = \{(2,4)(2,5)(2,6)\}, \dots$, and $\Phi_9 = \{(9,7)(9,8)(9,9)\}$.

Lemma 1. Suppose that $C = s \rightarrow ai \rightarrow ks \rightarrow aj \rightarrow e$ is a C -sequence, i.e., there exists an leading element s between two coordinates $(a,i) \in \Phi_a$ and $(a,j) \in \Phi_a$.

Then



is a new C-sequence.

Theorem 2. For each given C-sequence, Lemma 1 can be used to generate a distinct C-sequence for $m \geq 2$ and $n \geq 2$.

Proof. The proof is based upon the following procedure.

Procedure (Input: a C-sequence; Output: a new C-sequence)

1. Choose $a \in \{1, 2, \dots, m^{n-1}\}$ randomly, and select any two distinct substrings

$p_1 = (a, i_1)$ and $p_2 = (a, i_2)$ from the given C-sequence, $p_1, p_2 \in \Theta$.

2. If there is no element between these two chosen substrings, then go to Step 1, otherwise, randomly choose b ($b \neq a$) between p_1 and p_2 .

3. **IF** b appears exactly n times between p_1 and p_2 , **THEN** choose any two substrings $p_1 = (b, j_1)$ and $p_2 = (b, j_2)$, and then go to Step 2;

ELSE there must exist at least one b which is not included between p_1 and p_2 , and the C-sequence would appear as :

either $(s \dots b \dots a_{i_1} \dots b \dots a_{i_2} \dots e)$ or $(s \dots a_{i_1} \dots b \dots a_{i_2} \dots b \dots e)$,

where s is the leading element and e is the ending element.

4. Shifting the sequence such that b is the leading element. The C-sequence appears as

either $(b \dots a_{i_1} \dots b \dots a_{i_2} \dots es \dots)$ or $(b \dots es \dots a_{i_1} \dots b \dots a_{i_2} \dots)$.

Thus one may directly apply Lemma 1 to obtain a new C-sequence.

Note that because the length of each C-sequence is finite, the procedure is valid.

Example 2. Consider Example 1 again.

- (i) Suppose that $p_1 = (a, i) = (5, 6)$ and $p_2 = (a, j) = (5, 4)$ are selected in Step 1, and $3 (= b = s)$ is randomly selected in Step 2 of the above procedure. Thus

$$C = 3998697385)(684372671255)(42411$$

$s \qquad \qquad a \ i \ ks \qquad \qquad a \ j \ e$

where “)” indicates the position of the selected substrings. Directly using Lemma 1, we obtain a new $C' = 39986 \ 97385 \ 42411 \ 37267 \ 12556 \ 84$ which corresponds to the new distinct de Bruijn sequence $S' = 33323 \ 31322 \ 12111 \ 31231 \ 12223 \ 21$.

- (ii) Suppose that substrings (2,6) and (2,4) are chosen in Step 1, and 7 is randomly selected in Step 2 of the procedure, then the C-sequence is :

$$C = 3998697385684372)(67125542)(411$$

$s \qquad \qquad b \qquad \qquad a \ i \ b \qquad \qquad a \ j \ e$

Thus, by the shifting of Step 3 we have

$$\begin{array}{cccc} 7385684372)(67125542)(411399869. \\ b & a & i & b & a & j & e & s \end{array}$$

By Lemma 1, the new $C'=73856\ 84372)(4113998697125542)(6$ which corresponds to the new distinct de Bruijn sequence $S'=13223\ 21312\ 11133\ 32331\ 12221\ 23$.

- (iii) Suppose substrings (3,9) and (3,7) are chosen in Step 1 and 8 is randomly selected in the Step 2 of the procedure. The C -sequence is as 3)(9986 97385 6843)(7 26712 55424 11. Since element 8 appears 3 times ($=n$) between these two chosen substrings, one may randomly choose (8,6) and (8,4) as the new chosen substrings in Step 3 and then go to Step 2. Suppose element 7 is selected in Step 2, the C -sequence is now as :

$$3998)(69738568)(437267125542411.$$

Similarly, by the shifting of Step 3, we have :

$$71255424113998)(69738568)(43726.$$

By Lemma 1 again, the new $C'=71255\ 42411\ 39984\ 37267\ 38568\ 69$ which corresponds to the new distinct de Bruijn sequence $S'=11222\ 12111\ 33321\ 31231\ 32232\ 33$.

Therefore, given a "seed" sequence, one may repeat this similar procedure to reproduce a class of de Bruijn sequences. To evaluate the quality (distribution) of sequences generated by the proposed procedure, we perform the following experiments.

- (i) If $N \leq 500$, where N =the total number of distinct (m,n) de Bruijn sequences, we use Algorithm A to generate a "seed" sequence. Using the seed sequence, $100N$ continuous (m,n) de Bruijn sequences are reproduced by the proposed procedure. And then these generated sequences are classified into these N cells and the counts are recorded.
- (ii) If $N > 500$, then based upon the "seed" sequence by Algorithm A , 500 continuous (m,n) de Bruijn sequences are reproduced by the proposed procedure. And then we compute the percentage of different (m,n) de Bruijn sequences. Of course, if the percentage is higher, then it might be assured that this procedure can reproduce (m,n) de Bruijn sequences efficiently.

Since $N=1$ for $(m,n)=(2,2)$ and $N=2$ for $(m,n)=(2,3)$, the experiments for these two cases are omitted. For $(m,n)=(2,4)$ and $(3,2)$, we have $N=16$ and $N=24$, respectively. Thus experiment (i) is executed for these two cases. For more accuracy, 20 experiments are performed for each case and each experiment generates $100N$ de Bruijn sequences. Since the length of (m,n) de Bruijn sequence increases drastically, experiment (ii) only tests cases of $(m,n)=(2,5)$, $(3,3)$, $(3,4)$, $(3,5)$, $(4,2)$, $(4,4)$, $(4,5)$, $(5,2)$, $(5,3)$, $(5,4)$, and $(5,5)$. Similarly, 20 experiments are performed for each case. The results of experiment (i) are given in Table 1 and Table 2, and the results of experiment (ii) are shown in Table 5.

Table 1. Results of frequencies for 1600 continuous generated sequences for $(m,n)=(2,4)$. (20 experiments)

No.	Sequence	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	2211112112212122	81	75	60	90	65	70	71	65	82	61	71	78	78	75	79	74	69	65	73	84
2	2211112121122122	68	75	69	82	90	79	73	64	73	57	73	69	74	70	77	87	68	69	73	78
3	2211112122121122	118	137	134	120	144	128	128	134	120	126	124	127	127	136	124	129	116	134	120	129
4	2211112212112122	140	141	120	131	120	117	110	143	130	111	132	118	134	129	127	136	139	123	128	109
5	2211211112212122	57	70	73	71	70	70	58	77	78	71	64	85	78	69	64	76	84	75	81	73
6	2211212111122122	63	82	82	75	67	66	70	79	74	74	84	79	75	66	68	70	92	64	75	67
7	2211212212111122	132	122	115	126	122	119	122	144	132	131	129	115	120	118	120	125	130	129	128	129
8	2211221211112122	113	144	113	131	128	131	125	135	123	125	144	131	144	125	114	155	136	123	116	132
9	2212111121221122	127	114	119	121	112	123	111	116	120	136	114	116	123	122	128	111	128	119	138	134
10	2212111122112122	132	116	124	133	129	153	127	118	127	132	140	128	125	123	125	128	123	125	138	140
11	2212112122111122	136	121	143	115	116	119	133	129	128	143	134	118	109	120	124	110	121	124	129	125
12	2212112211112122	133	128	118	130	146	132	127	115	112	111	125	147	126	143	134	117	125	135	105	124
13	2212122111121122	73	80	81	64	65	78	102	65	72	90	71	84	71	87	82	56	70	83	84	59
14	2212122112111122	68	68	98	57	81	70	87	71	71	79	59	63	64	73	77	78	65	85	71	75
15	2212211112121122	77	61	85	76	72	62	80	68	64	65	61	74	84	74	84	75	64	68	72	59
16	2212211212111122	82	66	66	78	73	83	76	77	94	88	75	68	68	70	73	73	70	79	69	83

Table 2. Results of frequencies for 2400 continuous generated sequences for $(m, n)=(3, 2)$. (20 experiments)

No.	Sequence	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	331121322	91	83	92	78	89	97	80	77	85	89	102	103	87	84	89	75	97	88	98	91
2	331122132	74	85	98	80	88	75	91	67	83	106	78	88	96	89	80	96	90	83	88	73
3	331122321	81	83	73	99	84	106	92	93	89	93	77	95	82	109	110	76	92	81	74	93
4	331123221	129	110	97	106	121	131	113	109	101	120	137	134	111	111	135	130	133	100	127	116
5	331132122	81	80	94	90	86	86	80	75	87	102	54	95	95	79	69	83	85	87	83	78
6	331132212	105	100	119	96	119	85	100	108	108	111	98	107	137	103	118	92	101	110	116	104
7	331211322	132	120	126	122	110	107	128	127	122	121	131	114	112	107	114	123	134	122	133	135
8	331221132	122	123	133	135	126	115	123	119	139	113	112	110	121	115	88	109	108	120	114	122
9	331223211	96	115	103	128	88	100	116	109	128	89	114	107	101	133	106	108	92	108	92	101
10	331232211	100	89	89	87	87	76	96	92	90	89	91	77	69	81	91	99	107	101	95	94
11	331321122	81	106	96	103	95	87	91	89	101	85	103	71	77	83	67	81	89	103	82	84
12	331322112	129	107	112	93	93	120	103	119	87	111	111	108	97	104	112	98	130	107	134	120
13	332112231	107	125	106	127	102	121	123	128	126	107	113	119	119	139	119	115	119	119	115	109
14	332113122	108	117	119	117	117	106	113	105	120	116	115	86	108	89	97	99	95	115	95	114
15	332122311	118	110	124	121	113	133	104	126	110	112	120	112	116	136	145	109	88	115	92	124
16	332131122	84	70	85	74	90	99	82	78	78	112	64	110	101	90	78	84	73	91	70	67
17	332211231	82	89	76	87	85	91	85	66	86	84	87	80	76	88	76	97	115	80	96	86
18	332211312	94	85	98	85	105	77	86	128	78	82	82	84	102	75	67	91	85	84	95	92
19	332212311	95	96	72	84	98	97	92	92	75	76	87	101	84	71	98	87	84	80	95	87
20	332213112	117	126	127	103	130	102	105	120	121	134	124	113	133	112	127	129	115	122	134	117
21	332231121	106	102	96	112	108	117	114	89	96	112	110	111	107	110	124	121	131	94	98	118
22	332231211	89	77	75	87	72	80	83	79	92	61	95	84	78	78	70	97	101	101	94	68
23	332311221	107	108	94	100	104	129	117	113	95	92	99	116	107	131	126	113	65	108	97	120
24	332312211	72	94	96	86	90	63	83	92	103	83	96	75	84	83	94	88	71	81	83	87

Table 3. The probability distribution based upon 20 experiments for $(m,n)=(2,4)$.
(1600 generations for each experiment)

Sequence No.	Probability
1	0.045625
2	0.045625
3	0.080000
4	0.079375
5	0.045000
6	0.046250
7	0.078125
8	0.080625
9	0.076250
10	0.080625
11	0.078125
12	0.079375
13	0.047500
14	0.047500
15	0.044375
16	0.047500
Interchange	Probability
1,16	0.093125
2,14	0.093125
3,11	0.158125
4,7	0.157500
5,6	0.091250
8,10	0.161250
9,12	0.155625
13,15	0.091875
Interchange+Reverse	Probability
1,2,14,16	0.186250
3,4,7,11	0.315625
5,6,13,15	0.183125
8,9,10,12	0.316875

Table 4. The probability distribution based upon 20 experiments for $(m,n)=(3,2)$.
(2400 generations for each experiment)

Sequence No.	Probability
1	0.037083
2	0.035416
3	0.037083
4	0.049583
5	0.034583
6	0.044583
7	0.050833
8	0.049166
9	0.044583
10	0.037500
11	0.037083
12	0.045833
13	0.049166
14	0.045000
15	0.048333
16	0.035000
17	0.035833
18	0.037083
19	0.036666
20	0.050416
21	0.045416
22	0.034583
23	0.044583
24	0.035416
Interchange	Probability
1,3,11,18,19,24	0.220414
2,5,10,16,17,22	0.212915
4,7, 8, 13,15,20	0.297497
6,9,12,14,21,23	0.269998
Interchange+Reverse	Probability
1,2,3,5,10,11,16,17,18,19,22,24	0.43
4,6,7,8,9,12,13,14,15,20,21,23	0.57

Table 1 and Table 2 count the frequencies of observations for each possible de Bruijn sequence. The mean probability of distribution for each possible sequence is reported in Table 3 and Table 4, respectively. Table 3 indicates that these 16 possible sequences are not equally generated. For example, sequences 3,4,7,8,9,10,11,12 have higher probabilities to appear than sequences 1,2,5,6,13,14,15,16. Moreover, if the interchange of elements 1 and 2 are allowed for each sequence, one can classify these 16 sequences into only 8 sequences. For example, interchanging 1 and 2 in sequence 1 (=22111 12112 21212 2), we have 11222 21221 12121 1. And after a simple shift, we have 22122 11212 11112 2 which is exactly the same as sequence 16. Thus, it means that sequence 1 and sequence 16 are indeed identical if interchange is allowed. Similar results are also shown in Table 3. Furthermore, if reverse is also allowed for each possible sequence, these 8 sequences can be reduced to only 4 sequences. For example, reversing sequence 1, we have 22121 22112 11112 2 which is exactly identical to sequence 14. It means that if both interchange and reverse are allowed, there are only 4 basic de Bruijn sequences for $(m,n)=(2,4)$. Table 3 presents the distribution of reproduction for these 4 basic sequences. Similar results are reported in Table 4 for $(3,2)$ de Bruijn sequences. In general, if both interchange and reverse are allowed, there are

$$[(m-1)!]^{m^{n-1}} \cdot m^{m^{n-1}-n} / 2(m!) = [(m-1)!]^{m^{n-1}-1} \cdot m^{m^{n-1}-n-1} / 2$$

basic de Bruijn sequences. Though the probabilities are not even for each cell of possible de Bruijn sequence, the proposed procedure still has certain large probability to generate all possible de Bruijn sequences.

Table 5 shows the percentages of different de Bruijn sequences among 500 continuous reproductions for 20 experiments with various (m,n) . The results are summarized in Table 6. We observe that :

1. when m is fixed, the percentage increases with the increase of n .
2. when n is fixed, the percentage increases with the increase of m .
3. except for the case of $(m,n)=(2,5)$, the percentages are all above 95%. Especially, for the cases of $m+n > 7$, the percentage is 100%.

Limited numerical results indicate that the proposed procedure seems efficient to generate a class of distinct (m,n) de Bruijn sequences, especially when m and n are large.

4. Recent applications of de Bruijn sequences

In this section we will present two recent practical applications of de Bruijn sequences in psychology and engineering. Owing to the special properties of de Bruijn sequences, it is expected that they will be widely applied to various fields in the future.

Table 5. The percentage of different de Bruijn sequences for 20 experiments with various (m,n) .
(500 de Bruijn sequences for each experiment)

(m,n)	(2,5)	(3,3)	(3,4)	(3,5)	(4,2)	(4,3)	(4,4)	(4,5)	(5,2)	(5,3)	(5,4)	(5,5)
1	0.856	0.984	1.000	1.000	0.974	0.996	1.000	1.000	0.994	1.000	1.000	1.000
2	0.848	0.992	1.000	1.000	0.948	1.000	1.000	1.000	0.998	1.000	1.000	1.000
3	0.868	0.992	0.998	1.000	0.952	0.998	1.000	1.000	0.994	1.000	1.000	1.000
4	0.818	0.982	0.998	1.000	0.958	1.000	1.000	1.000	0.994	1.000	1.000	1.000
5	0.824	0.982	1.000	1.000	0.964	0.998	1.000	1.000	0.998	1.000	1.000	1.000
6	0.846	0.992	1.000	1.000	0.958	0.998	1.000	1.000	0.998	1.000	1.000	1.000
7	0.844	0.990	1.000	1.000	0.958	1.000	1.000	1.000	0.994	1.000	1.000	1.000
8	0.858	0.988	0.998	1.000	0.954	0.998	1.000	1.000	0.990	1.000	1.000	1.000
9	0.856	0.996	1.000	1.000	0.952	1.000	1.000	1.000	0.994	1.000	1.000	1.000
10	0.854	0.980	0.998	1.000	0.958	1.000	1.000	1.000	0.998	1.000	1.000	1.000
11	0.848	0.992	1.000	1.000	0.954	0.998	1.000	1.000	0.998	1.000	1.000	1.000
12	0.858	0.988	1.000	1.000	0.974	0.998	1.000	1.000	0.990	1.000	1.000	1.000
13	0.832	0.988	1.000	1.000	0.956	0.998	1.000	1.000	0.994	1.000	1.000	1.000
14	0.870	0.978	1.000	1.000	0.958	1.000	1.000	1.000	0.994	1.000	1.000	1.000
15	0.860	0.994	0.998	1.000	0.952	1.000	1.000	1.000	0.998	1.000	1.000	1.000
16	0.854	0.982	1.000	1.000	0.964	1.000	1.000	1.000	0.998	1.000	1.000	1.000
17	0.852	0.988	0.998	1.000	0.958	0.998	1.000	1.000	0.994	1.000	1.000	1.000
18	0.858	0.980	1.000	1.000	0.974	1.000	1.000	1.000	0.994	1.000	1.000	1.000
19	0.844	0.973	0.998	1.000	0.952	0.998	1.000	1.000	0.998	1.000	1.000	1.000
20	0.832	0.994	1.000	1.000	0.958	0.998	1.000	1.000	0.990	1.000	1.000	1.000
mean	0.849	0.987	0.999	1.000	0.959	0.999	1.000	1.000	0.995	1.000	1.000	1.000

Table 6. The mean percentage of different de Bruijn sequences for 20 experiments with various (m,n) .
(500 de Bruijn sequences for each experiment)

$m \setminus n$	2	3	4	5
2	—	—	*	0.849
3	*	0.987	0.999	1.000
4	0.959	0.999	1.000	1.000
5	0.995	1.000	1.000	1.000

* : results of experiment (i) are shown in Tables 1-4.

1. *Reaction time experiment problems* (Emerson and Tobias [2] and Sohn et al. [10]).

In Psychology, a so-called reaction time experiment is made to evaluate the effects of various stimuli. In a reaction time experiment, various stimuli are typically presented a number of times to subjects following a predetermined or randomly generated sequence. Then, the mean/median, variance, and error rates etc. of reaction times for each of various stimuli can be computed for further analysis (Sohn et al. [10]). To reduce the potential possible noises (e.g., learning effects) in reaction time experiments, experimenters generally present each stimulus equally often in a sequence of trials. Recently, Emerson and Tobias [2] presented a computer code (C program) to generate random sequences of trials such that each stimulus appears equally often and is preceded equally often by itself and by other stimulus. For example, sequence 332312211 is a valid 3-stimulus sequence of trials, where 1, 2 and 3 represent three distinct stimuli. It is clear that this sequence is one of $(3,2)$ de Bruijn sequences.

2. *3D pattern recognition problems* (Griffin et al. [6], Yee and Griffin [11], Yee [12] and Hsieh [7 · 8]).

3-Dimensional range data is a set of points (x,y,z) for surface points of an object. Range data can be used to 3D matching, object recognition, and dimensional/geometric measurement (Yee and Griffin [11]). Recently, Yee and Griffin [11] developed a new system that acquires 3D range data using a single camera with a structured light pattern. The structured light pattern (see Figure 4) is encoded to provide unique correspondence with a single image and, hence, the approach is applicable in dynamic environments such as in robot guidance, manufacturing, or medical imaging. Note that Figure 4 is constructed by $S_1 = a(4,3)$ de Bruijn sequence and $S_2 = a(4,2)$ de Bruijn sequence using the following procedure. (i) The first row of W is S_1 , and (ii) for $2 \leq i \leq 4^2 + 1$ and $i \leq j \leq 64$, $W_{i,j} = ([W_{i-1,j} + S_2[i-1] \bmod 4])$. It should be noted that $(4 \bmod 4)$ is defined to 4 here. Thus, each 5-tuple word, e.g., $(2,1,4,1,3)$, is unique in Figure 4.

44434424414333432431423342224214134124111333233132232131231122212111
444344244143343243142342224214134124111333333132232131231122212111
44434424414334324314234224214134124111333233132232131231122212111
3332331334322321324312311314342341344222122421121424124411141444
33323313343223213243123113143423413442221224211214241124411141444
111411311214414314213413313212412312244434424343242342233323222
111411311214414314213413313212412312244434424343242342233323222
2221224223211214213241244243231234223111411314414313413344434333
1114113112144143142134133132124123122444344243343242342233323222
444344244143343243142334224214134124111333233132232131231122212111
22212242232112142132412442432312342233114111314414313413344434333
1114113112144143142134133132124123122444344243343242342233323222
22212242232112142132412442432312342233114111314414313413344434333
444344244143343243142334224214134124111333233132232131231122212111
44434424414334324314234224214134124111333233132232131231122212111

Figure 4. The structured light pattern W .

5. Conclusions

In this paper :

1. we have studied the generation, reproduction and applications of (m, n) de Bruijn sequences. The algorithm is both simpler and more efficient than the other typical approaches.
2. we have proposed a simple procedure to reproduce a class of (m, n) de Bruijn sequences. Numerical results show the performance of the distribution of the reproduced de Bruijn sequences.
3. we have provided two recent applications of de Bruijn sequences.
Owing to the special properties of de Bruijn sequences, it is expected that (m, n) de Bruijn sequences can be widely applied to various fields in the future.

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