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Re:	IEEE P802.16e Preamble
Abstract	
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# GCL-based Preamble Design for 1024,512 and 128 FFT Sizes in the OFDMA PHY Layer

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## 1. Introduction

This contribution proposes preamble designs for the 1024, 512 and 128 FFT OFDMA modes. The proposed preambles are based on a particular family of polyphase sequences, i.e., the Generalized Chirp Like or GCL sequences.

The proposed preambles have very low PAPR (lower than the PN sequence based preambles in IEEE C80216e-04/125 and IEEE C80216e-04/164) and better cross correlation between any pair of the preambles (see Section 4 for simulation results). The design also allows a fast cell search to identify the sequences very easily in a one-step processing (see Appendix A for simulation results). The optimal cross correlation property also allows more reliable estimation of the channels to the desired BS (see Section 4 for simulation results), as well as the interfering BSs that are occupying the same subcarriers. This knowledge of the interference channel can be used for handover or advanced receive processing (e.g., interference suppression). A complexity comparison of GCL and PN is also shown in Appendix A that the GCL is only slightly more complex, but both are well within the comfortable complexity range, to meet the goal of fast access to the network after power-up with low power consumption.

## 2. Basis of the Proposed Preamble

### Sequence design

The sequence design methodology for any desired sequence length  $N_d$  is described first. We first choose a prime number  $N_G$  that is the smallest prime number larger than  $N_d$ . Then, the sequences is generated according to

$$s_u(k) = \exp\left\{-j2\pi u \frac{k(k+1)}{2N_G}\right\}, k=0 \cdots N_G-1, \text{ and } u=1 \cdots N_G-1 \quad (1)$$

The integer “ $u$ ” is referred to as class index. We will have  $N_G-1$  sequences that have the optimal cyclic cross correlation between any pair of them. The sequences will be truncated to  $N_d$  and be applied to  $N_d$  subcarriers. After truncation, the cross correlation still holds well. Due to the oversampling introduced in OFDM with null subcarriers, the PAPR will be degraded to different degrees for different “ $u$ ” from the theoretical 0dB value (at Nyquist sampling rate), we can choose the indices that have the best PAPR among  $N_G-1$  candidates. The preambles used by different sectors/cells are obtained from different “classes” of this generalized chirp like (GCL) sequences [2] (unit-amplitude complex-valued sequences). A different “ $u$ ” will also act as a cell ID.

**Sequence properties** (See more background information of polyphase sequence in Appendix B)

The time domain waveforms of the GCL-modulated OFDM signals have low PAPR. In addition, because of the use of different “classes” of GCL sequences, any pair of the sequences will have low cross correlation at all time lags, which greatly improves the code detection and CIR estimation. The GCL sequence has the following important properties:

*Property 1:* The GCL sequence has constant amplitude, and its  $N_G$ -point DFT has also constant amplitude.

*Property 2:* The GCL sequences of any length have an “ideal” cyclic autocorrelation (i.e., the correlation with the circularly shifted version of itself is a delta function)

*Property 3:* The absolute value of the cyclic cross-correlation function between any two GCL sequences is constant and equal to  $1/\sqrt{N_G}$ , when  $|u_1-u_2|$ ,  $u_1$ , and  $u_2$  are all relatively prime to  $N_G$  (a condition that can be easily guaranteed if  $N_G$  is a prime number).

The cross-correlation  $1/\sqrt{N_G}$  at all lags (Property 3) actually achieves the minimum cross-correlation value for any two sequences that have the ideal autocorrelation property (meaning that the theoretical minimum of the maximum value of the cross-correlation over all lags is achieved). The minimum is achieved when the cross correlations at all lags equal to  $1/\sqrt{N_G}$ . The cross correlation property allows the impact of an interfering signal be evenly spread in the time domain after correlating the received signal with the desired sequence in the time domain. Hence, at least the significant taps of the desired channel can be detected more reliably (see more in the simulation section). A simple tap-selection or “de-noising” strategy can be used to take advantage of the cross-correlation property. Tap selection simply means that the channel taps below some threshold are set to zero. Thanks to the cross correlation property, the interference channels will be evenly spread over the IFFT window after correlating with the desired preamble, so at least the significant channel tap will be estimated more reliably. Tap selection is especially effective for relatively sparse channels by attempting to match the channel estimator to the instantaneous power delay profile.

Compared with BPSK or even QPSK preambles, the complex-valued GCL sequences can be systematically constructed with guaranteed good PAPR and good correlation.

**One-Step Fast Cell Search for GCL Sequences** (See Appendix for simulation results)

The one-step fast cell search is to determine directly the class indices “u” from the received signal. The process is described as in the following.

After a rough timing estimate has been found (e.g., using the 1/3 symmetry of the preamble and/or other techniques such as the common sync symbol), a block of  $N$  received time-domain data is transformed to the frequency domain using the usual FFT process. Denote the frequency domain data on a particular segment as  $Y(m)$  for  $m = 1$  to  $N_p$  (ignoring the unused subcarriers) and  $S_G(m)$  is the GCL sequences used at those reference subcarriers, a vector of “differential-based” values is then computed based on the pairs of reference subcarriers. These values are conveniently collected into vector format (e.g., a differential-based vector) for efficient FFT-based processing. The differential-based vector is computed as

$$Z(m) = Y(m) * \text{conj}(Y(m+1)), m = 1, \dots, N_p - 1 \quad (2)$$

where “conj()” denotes conjugation.

Assuming the channel between two adjacent reference subcarriers does not change drastically, which is normally satisfied as long as the spacing of reference subcarriers is not too large,  $Y(m+1)/Y(m)$  is approximately equal to

$$Y(m+1)/Y(m) \approx S_G(m+1)/S_G(m) = \exp\left\{-j2\pi u \frac{k+1+q}{N_G}\right\}, m = 1, \dots, N_p - 1 \quad (5)$$

Thus, the class index (or sequence index) information “u” is carried in the differential-based vectors. By processing the differential-based values and identifying a prominent frequency component of the vector, we can detect “u”. To obtain the frequency domain components, a commonly used tool is to take an IFFT (say T-point,  $T \geq N_p - 1$ ) on  $\{Z(m)\}$  to get

$$\{z(n)\} = \text{IFFT}_T(\{Z(m)\}), m = 1, \dots, N_p - 1, n = 1, \dots, T \quad (6)$$

The peak position (say  $n_{\max}$ ) of  $\{z(n)\}$  gives information about  $u$ , i.e., the mapping between the identified prominent frequency component at  $n_{\max}$  to a corresponding transmitted sequence index is determined as

$$\frac{u}{N_G} = \frac{n_{\max}}{T} \quad (7)$$

In summary, the sequence index (and therefore the Cell ID) is identified in a “one-step” cell search without searching over all of the possible preamble sequences. Instead, only one set of differential multiplications and one IFFT are needed, enabling the cell ID detection within one or two OFDMA symbol periods (note that differential multiplication is already used in the legacy 1/3 symmetry detection process, and has also been assumed in the common sync symbol proposals.)

### 3. Proposed Text Changes

[Change paragraph in page 556 IEEE802.16d-2004. Change the table 307 to 307a]

-----Start from here -----

The preambles used for 1024, 512, and 128 modes are defined by

$$s_u(k) = \exp\left\{-j2\pi u \frac{k(k+1)}{2N_G}\right\}, \quad k=0 \cdots N_G-1 \quad \text{and} \quad u(\text{"class index"})=1 \cdots N_G-1 \quad (2)$$

where  $N_G$  is the length of the sequence that is pre-determined according to the FFT size and  $u$  is referred to as the sequence class index that is an integer between 1 and  $N_G-1$ . The preamble, which depends on the segment used and IDcell parameter, is defined by  $N_G$  and  $u$  in Table 307b-d (PAPR comparisons are given for information only). If the specified value of  $N_G$  is larger than is needed for the sequence, then the sequence of length  $N_G$  is truncated from the end until it is the needed length.

Table 307b. 1024-point FFT

Index	ID cell	Segment	Sequence index: "u" ( $N_G=293$ )	PAPR (mean=2.99 dB)	PAPR in C802.16e- 04/125 (mean=4.12 dB)
0	0	0	147	2.58	3.65
1	1	0	146	2.58	4.09
2	2	0	292	2.64	3.93
3	3	0	1	2.64	3.94
4	4	0	117	2.78	4.14
5	5	0	176	2.78	4.13
6	6	0	220	2.9	4
7	7	0	73	2.9	4.01
8	8	0	49	2.95	4.1
9	9	0	244	2.95	4.02
10	10	0	98	3.11	4.05
11	11	0	195	3.11	3.98
12	12	0	42	3.12	4.05
13	13	0	251	3.12	4.14
14	14	0	205	3.17	4.08
15	15	0	88	3.17	4.2
16	16	0	45	3.19	4
17	17	0	248	3.19	4.2
18	18	0	185	3.2	4.15

19	19	0	108	3.2	4.26
20	20	0	224	3.22	4.25
21	21	0	69	3.22	4.11
22	22	0	179	3.25	4.17
23	23	0	114	3.25	3.96
24	24	0	21	3.26	4.12
25	25	0	272	3.26	4.27
26	26	0	228	3.27	4.26
27	27	0	65	3.27	4.04
28	28	0	149	3.33	4.25
29	29	0	144	3.33	4.14
30	30	0	39	3.33	4.2
31	31	0	254	3.33	4.26
32	0	1	292	2.31	3.96
33	1	1	1	2.31	3.96
34	2	1	146	2.41	3.97
35	3	1	147	2.41	3.97
36	4	1	73	2.63	3.97
37	5	1	220	2.63	3.98
38	6	1	49	2.71	3.98
39	7	1	244	2.71	3.99
40	8	1	42	2.77	3.99
41	9	1	251	2.77	3.99
42	10	1	117	2.77	3.99
43	11	1	176	2.77	3.99
44	12	1	98	2.83	3.99
45	13	1	195	2.83	4
46	14	1	179	2.88	4
47	15	1	114	2.88	4
48	16	1	185	2.99	4
49	17	1	108	2.99	4.01

50	18	1	248	3	4.01
51	19	1	45	3	4.01
52	20	1	224	3	4.02
53	21	1	69	3	4.02
54	22	1	40	3.03	4.02
55	23	1	253	3.03	4.02
56	24	1	272	3.04	4.02
57	25	1	21	3.04	4.02
58	26	1	39	3.05	4.02
59	27	1	254	3.05	4.02
60	28	1	238	3.06	4.03
61	29	1	55	3.06	4.03
62	30	1	110	3.14	4.03
63	31	1	183	3.14	4.03
64	0	2	292	2.28	4.27
65	1	2	1	2.28	4.36
66	2	2	73	2.51	4.35
67	3	2	220	2.51	4.29
68	4	2	98	2.58	4.37
69	5	2	195	2.58	4.2
70	6	2	146	2.63	4.35
71	7	2	147	2.63	4.37
72	8	2	42	2.84	4.21
73	9	2	251	2.84	4.12
74	10	2	244	2.85	4.11
75	11	2	49	2.85	4.23
76	12	2	183	2.86	4.06
77	13	2	110	2.86	4.19
78	14	2	117	2.94	4.12
79	15	2	176	2.94	4.18
80	16	2	39	2.98	4.22

81	17	2	254	2.98	4.15
82	18	2	21	3.03	4.19
83	19	2	272	3.03	4.17
84	20	2	253	3.06	4.14
85	21	2	40	3.06	4.24
86	22	2	179	3.06	4.21
87	23	2	114	3.06	4.29
88	24	2	69	3.07	4.27
89	25	2	224	3.07	4.31
90	26	2	228	3.12	4.25
91	27	2	65	3.12	4.29
92	28	2	157	3.2	4.13
93	29	2	136	3.2	4.23
94	30	2	51	3.21	4.15
95	31	2	242	3.21	4.15
96	0	0	83	3.34	4.26
97	1	1	171	3.17	4.03
98	2	2	55	3.22	4.2
99	3	0	210	3.34	4.1
100	4	1	122	3.17	4.04
101	5	2	238	3.22	4.25
102	6	0	122	3.35	4.22
103	7	1	65	3.18	4.05
104	8	2	82	3.23	4.2
105	9	0	171	3.35	4.28
106	10	1	228	3.18	4.05
107	11	2	211	3.23	4.35
108	12	0	238	3.35	4.37
109	13	1	205	3.22	4.06
110	14	2	83	3.26	4.35
111	15	0	55	3.35	4.13



112	16	1	88	3.22	4.06
113	17	2	210	3.26	4.23

Table 307c. 512-point FFT

Index	ID cell	Segment	Sequence index: "u" ( $N_G=149$ )	PAPR ( <u>mean=3.18</u> <u>dB</u> )	PAPR in C802.16e- 04/125 ( <u>mean=3.60</u> <u>dB</u> )
0	0	0	74	2.59	3.83
1	1	0	75	2.59	3.65
2	2	0	112	2.83	3.79
3	3	0	37	2.83	3.63
4	4	0	1	2.88	3.63
5	5	0	148	2.88	3.83
6	6	0	99	2.97	3.83
7	7	0	50	2.97	3.58
8	8	0	25	3.18	3.85
9	9	0	124	3.18	3.84
10	10	0	30	3.25	3.91
11	11	0	119	3.25	3.49
12	12	0	27	3.28	3.83
13	13	0	122	3.28	3.76
14	14	0	23	3.31	3.83
15	15	0	126	3.31	3.88
16	16	0	121	3.34	3.75
17	17	0	28	3.34	3.88
18	18	0	47	3.42	3.85
19	19	0	102	3.42	3.6
20	20	0	15	3.45	3.83
21	21	0	134	3.45	3.79
22	22	0	78	3.5	3.7
23	23	0	71	3.5	3.49
24	24	0	117	3.5	3.81

25	25	0	32	3.5	3.67
26	26	0	58	3.51	3.67
27	27	0	91	3.51	3.88
28	28	0	24	3.52	3.9
29	29	0	125	3.52	3.86
30	30	0	82	3.55	3.55
31	31	0	67	3.55	3.83
32	0	1	74	2.3	3.46
33	1	1	75	2.3	3.46
34	2	1	148	2.34	3.46
35	3	1	1	2.34	3.46
36	4	1	37	2.71	3.46
37	5	1	112	2.71	3.46
38	6	1	50	2.78	3.46
39	7	1	99	2.78	3.46
40	8	1	119	2.92	3.46
41	9	1	30	2.92	3.46
42	10	1	23	2.98	3.46
43	11	1	126	2.98	3.46
44	12	1	124	3.04	3.47
45	13	1	25	3.04	3.47
46	14	1	15	3.04	3.47
47	15	1	134	3.04	3.47
48	16	1	35	3.2	3.47
49	17	1	114	3.2	3.47
50	18	1	27	3.25	3.48
51	19	1	122	3.25	3.48
52	20	1	10	3.27	3.48
53	21	1	139	3.27	3.48
54	22	1	82	3.31	3.49
55	23	1	67	3.31	3.49

56	24	1	58	3.35	3.49
57	25	1	91	3.35	3.49
58	26	1	117	3.36	3.49
59	27	1	32	3.36	3.5
60	28	1	36	3.41	3.5
61	29	1	113	3.41	3.5
62	30	1	33	3.42	3.5
63	31	1	116	3.42	3.5
64	0	2	74	2.3	3.5
65	1	2	75	2.3	3.5
66	2	2	148	2.34	3.5
67	3	2	1	2.34	3.5
68	4	2	37	2.71	3.5
69	5	2	112	2.71	3.51
70	6	2	50	2.78	3.51
71	7	2	99	2.78	3.51
72	8	2	119	2.92	3.51
73	9	2	30	2.92	3.51
74	10	2	23	2.98	3.51
75	11	2	126	2.98	3.51
76	12	2	124	3.04	3.51
77	13	2	25	3.04	3.51
78	14	2	15	3.04	3.51
79	15	2	134	3.04	3.52
80	16	2	35	3.2	3.52
81	17	2	114	3.2	3.52
82	18	2	27	3.25	3.52
83	19	2	122	3.25	3.53
84	20	2	10	3.27	3.53
85	21	2	139	3.27	3.53
86	22	2	82	3.31	3.54

87	23	2	67	3.31	3.54
88	24	2	58	3.35	3.54
89	25	2	91	3.35	3.54
90	26	2	117	3.36	3.54
91	27	2	32	3.36	3.54
92	28	2	36	3.41	3.54
93	29	2	113	3.41	3.54
94	30	2	33	3.42	3.54
95	31	2	116	3.42	3.54
96	0	0	56	3.57	3.9
97	1	1	71	3.48	3.54
98	2	2	71	3.48	3.54
99	3	0	93	3.57	4.01
100	4	1	78	3.48	3.54
101	5	2	78	3.48	3.54
102	6	0	10	3.58	3.93
103	7	1	102	3.53	3.54
104	8	2	102	3.53	3.54
105	9	0	139	3.58	3.85
106	10	1	47	3.53	3.54
107	11	2	47	3.53	3.54
108	12	0	135	3.61	3.98
109	13	1	125	3.56	3.55
110	14	2	125	3.56	3.55
111	15	0	14	3.61	4
112	16	1	24	3.56	3.55
113	17	2	24	3.56	3.55

Table 307d. 128-point FFT

Index	ID cell	Segment	Sequence index: "u" ( $N_G=41$ )	PAPR ( <u>mean=4.23</u> dB)	PAPR in C802.16e- 04/125 ( <u>mean=3.22</u> dB)
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0	0	0	40	2.74	2.24
1	1	0	1	2.74	2.27
2	2	0	20	2.74	2.31
3	3	0	21	2.74	2.32
4	4	0	14	3.16	2.35
5	5	0	27	3.16	2.38
6	6	0	7	3.24	2.38
7	7	0	34	3.24	2.39
8	8	0	10	3.3	2.41
9	9	0	31	3.3	2.42
10	10	0	9	3.56	2.42
11	11	0	32	3.56	2.42
12	12	0	6	3.6	2.42
13	13	0	35	3.6	2.42
14	14	0	24	3.94	2.43
15	15	0	17	3.94	2.44
16	16	0	8	4.03	2.44
17	17	0	33	4.03	2.45
18	18	0	15	4.13	2.47
19	19	0	26	4.13	2.48
20	20	0	39	4.2	2.49
21	21	0	2	4.2	2.49
22	22	0	37	4.45	2.49
23	23	0	4	4.45	2.49
24	24	0	5	4.47	2.5
25	25	0	36	4.47	2.5
26	26	0	23	4.7	2.5
27	27	0	18	4.7	2.5
28	28	0	38	5.02	2.5
29	29	0	3	5.02	2.5
30	30	0	12	5.02	2.5

31	31	0	29	5.02	2.5
32	0	1	1	2.76	3.64
33	1	1	40	2.76	3.64
34	2	1	10	3.14	3.64
35	3	1	31	3.14	3.42
36	4	1	20	3.59	3.64
37	5	1	21	3.59	3.64
38	6	1	7	3.68	3.19
39	7	1	34	3.68	3.35
40	8	1	14	3.71	3.25
41	9	1	27	3.71	3.64
42	10	1	6	3.81	3.64
43	11	1	35	3.81	3.64
44	12	1	33	3.82	3.64
45	13	1	8	3.82	3.64
46	14	1	37	4.21	3.14
47	15	1	4	4.21	3.29
48	16	1	18	4.3	3.19
49	17	1	23	4.3	3.35
50	18	1	32	4.32	3.64
51	19	1	9	4.32	3.64
52	20	1	24	4.37	3.64
53	21	1	17	4.37	3.64
54	22	1	36	4.45	3.62
55	23	1	5	4.45	2.7
56	24	1	29	4.51	3.34
57	25	1	12	4.51	3.64
58	26	1	26	4.59	3.32
59	27	1	15	4.59	3.64
60	28	1	2	4.6	3.39
61	29	1	39	4.6	3.48

62	30	1	38	4.77	3.6
63	31	1	3	4.77	3.37
64	0	2	33	3.23	4.13
65	1	2	8	3.23	3.56
66	2	2	6	3.38	4.19
67	3	2	35	3.38	4.19
68	4	2	4	3.7	3.93
69	5	2	37	3.7	4.69
70	6	2	9	3.77	2.75
71	7	2	32	3.77	2.75
72	8	2	40	3.87	3.41
73	9	2	1	3.87	3.86
74	10	2	7	4.01	3.86
75	11	2	34	4.01	3.56
76	12	2	14	4.12	3.25
77	13	2	27	4.12	4.08
78	14	2	10	4.2	3.79
79	15	2	31	4.2	3.44
80	16	2	26	4.27	3.56
81	17	2	15	4.27	3.25
82	18	2	22	4.34	3.19
83	19	2	19	4.34	3.3
84	20	2	20	4.61	3.3
85	21	2	21	4.61	3.3
86	22	2	11	4.75	4.69
87	23	2	30	4.75	4.14
88	24	2	5	4.8	3.34
89	25	2	36	4.8	3.53
90	26	2	17	4.8	3.5
91	27	2	24	4.8	4.69
92	28	2	38	4.97	3.88

93	29	2	3	4.97	4.1
94	30	2	23	4.98	3.47
95	31	2	18	4.98	3.86
96	0	0	22	5.2	2.56
97	1	1	19	4.79	3.22
98	2	2	29	4.98	3.93
99	3	0	19	5.2	2.57
100	4	1	22	4.79	3.57
101	5	2	12	4.98	4.69
102	6	0	28	5.21	2.57
103	7	1	11	4.83	3.52
104	8	2	2	5.36	4.01
105	9	0	13	5.21	2.57
106	10	1	30	4.83	3.41
107	11	2	39	5.36	4.03
108	12	0	30	5.48	2.57
109	13	1	16	5.01	3.64
110	14	2	16	5.75	4.02
111	15	0	11	5.48	2.58
112	16	1	25	5.01	2.86
113	17	2	25	5.75	3.46

-----End here -----

#### 4. Additional Information

##### PAPR and Cross Correlation Comparison

In addition to the low PAPR properties, the cross correlation properties of the proposed preambles are much better than PN-based BPSK sequences such as those proposed in IEEE C80216e-04/125 and IEEE C80216e-04/164, as can be seen in the following Figure 1-3 where the cross correlation of all pairs of preambles that are used for segment 0 is plotted (similar correlation for segment 1 and 2).



In IEEE C80216e-04/125, there are a few sequences used twice for segment 0, but for different cellIDs (e.g., for the 512 mode and for segment 1, preamble #1 = preamble #2, #8 = #9, #12 = #13, #15 = #16; for the 128 mode and for segment 2, preamble #1 = preamble #2, #6 = preamble #16, and there are more. But the problem only occurs for 512 and 128 modes). We believe there may be some errors in IEEE C80216e-04/125, and these cross correlation are already excluded from the plot.

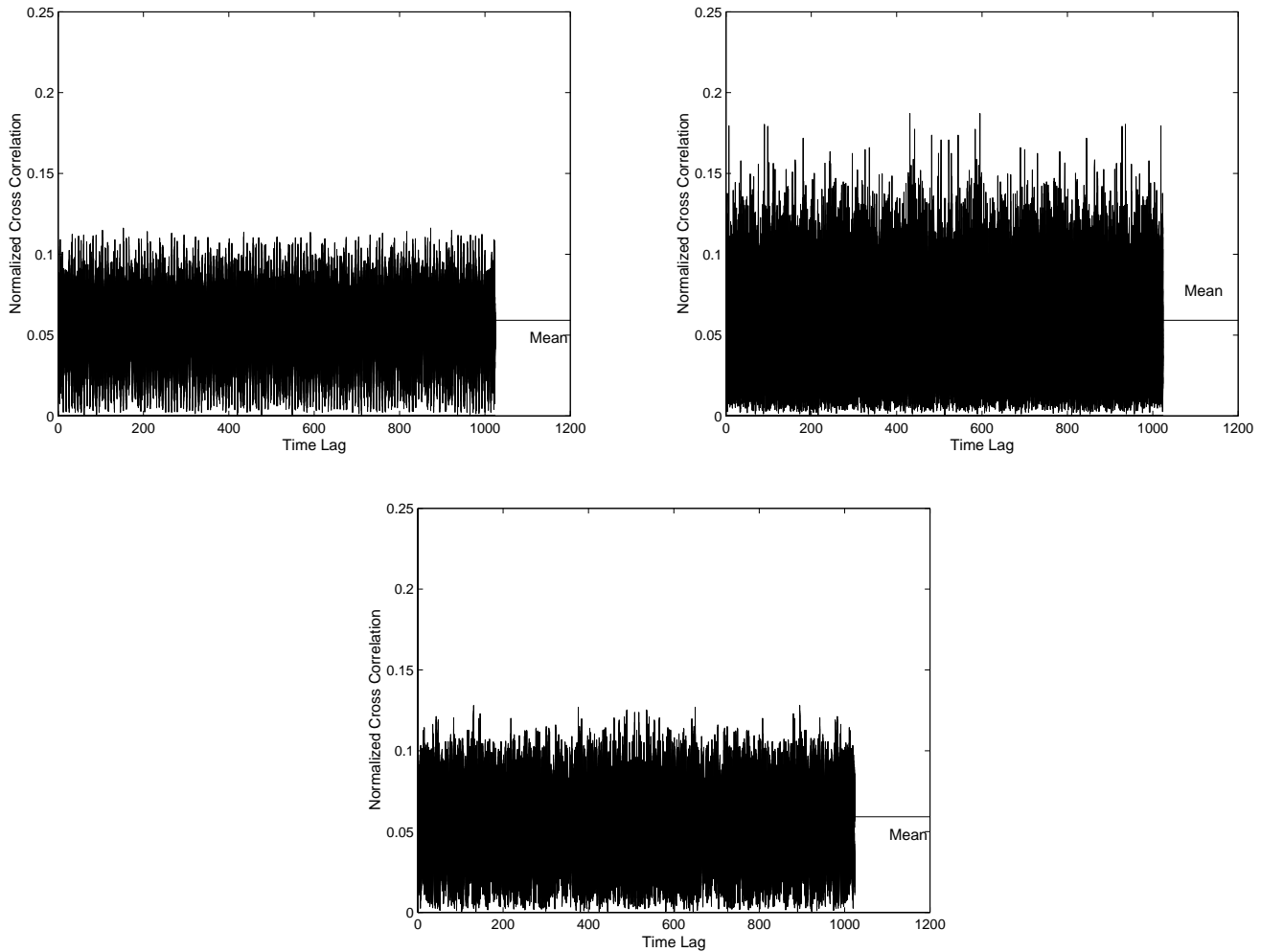


Figure 1. Cross- correlation characteristics of the proposed **GCL-based** preamble (top left, **PAPR 2.58-3.26dB** with mean 2.99dB) and the BPSK PN ranging sequence from IEEE C80216e-04/125 (top right, **PAPR 3.65-4.37 dB** with mean 4.12dB) and IEEE C80216e-04/164 (bottom middle, **PAPR 4.96-5.94dB** with mean 5.54dB) (1024 mode)

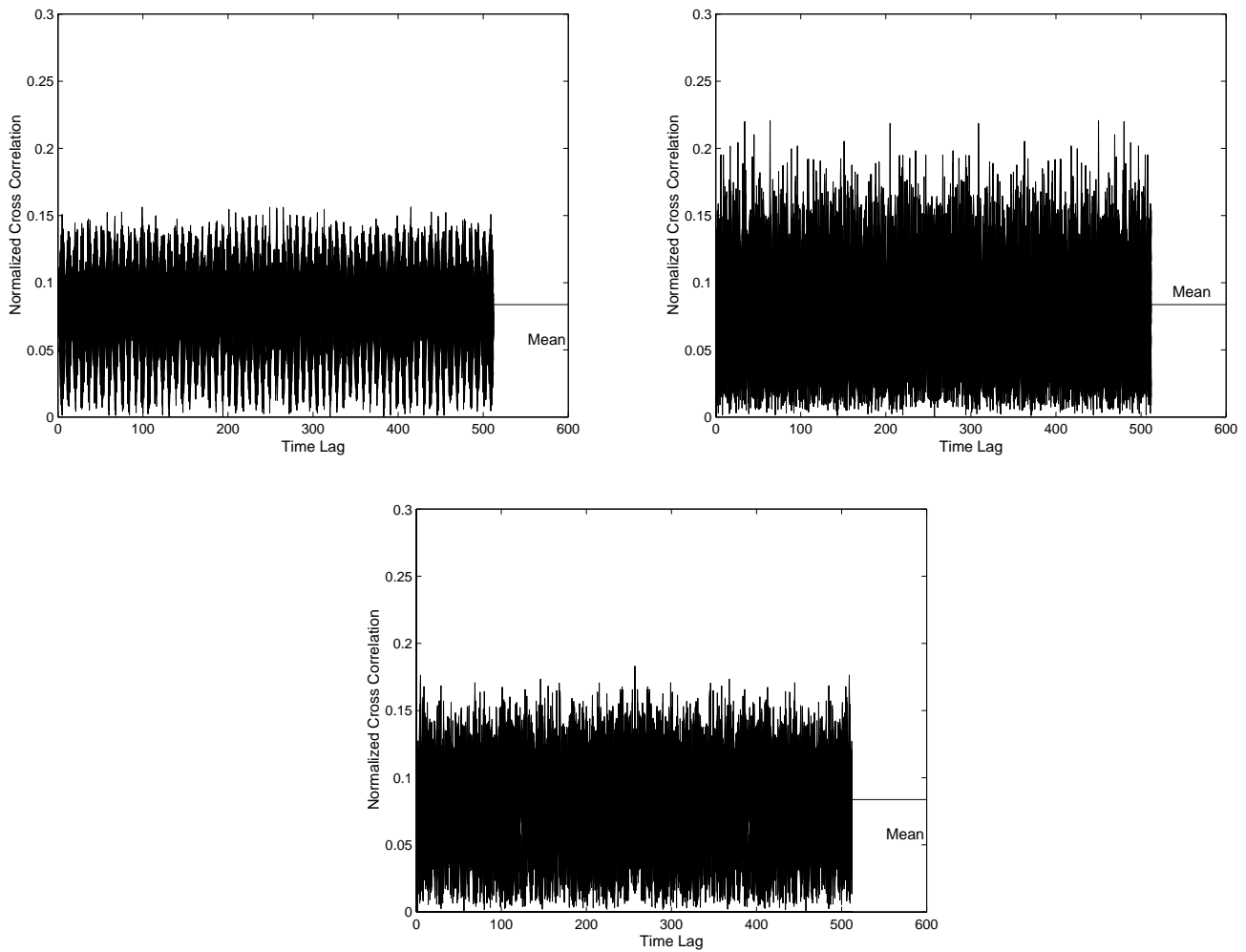


Figure 2. Cross- correlation characteristics of the proposed **GCL-based** preamble (top left, **PAPR 2.59-3.56dB** with mean 3.18dB) and the BPSK PN ranging sequence from IEEE C80216e-04/125 (top right, **PAPR 3.46-4.00 dB** with mean 3.60dB) and IEEE C80216e-04/164 (bottom middle, **PAPR 4.96-5.94dB** with mean 5.54dB) (512 mode)

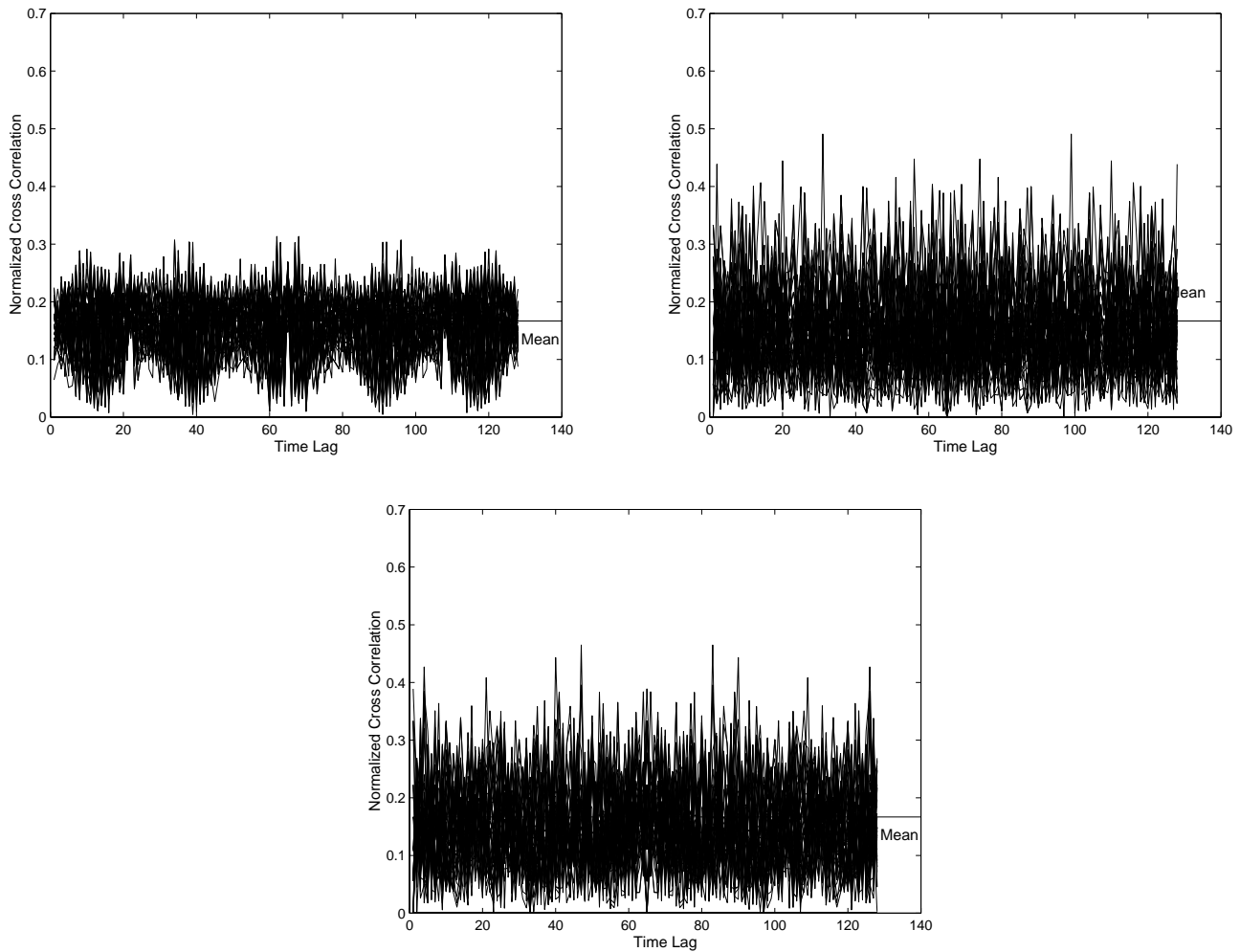


Figure 3. Cross- correlation characteristics of the proposed **GCL-based** preamble (top left, **PAPR 2.74-5.75dB** with mean 4.23dB) and the BPSK PN ranging sequence from IEEE C80216e-04/125 (top right, **PAPR 2.24-4.69 dB** with mean 3.22dB) and IEEE C80216e-04/164 (bottom middle, **PAPR 3.93-6.03dB** with mean 4.82dB) (128 mode)

### Channel Estimation Comparison

This cross advantage translates into improved channel estimation performance, as can be seen in the following figure, especially for low SINR (but with decent SNR, which is 7dB in the figure). Two base stations are simulated in the figure (one desired and one interfering). The comparison is made between GCL design and random BPSK design in which a random BPSK sequence is used in each Monte Carlo trial (similar overall cross correlation to that for sequences in IEEE C80216e-04/125). As we can see that even for very low SINR, the channel estimation performance is still reasonable, especially when the delay spread is relatively small. If this SINR is rather for the interference signal, it means that the channel to the weaker interference base station can

be monitored reasonably well (which is good for hard- or soft- handover, potential interference suppression, BS-cooperative scheduling, etc.).

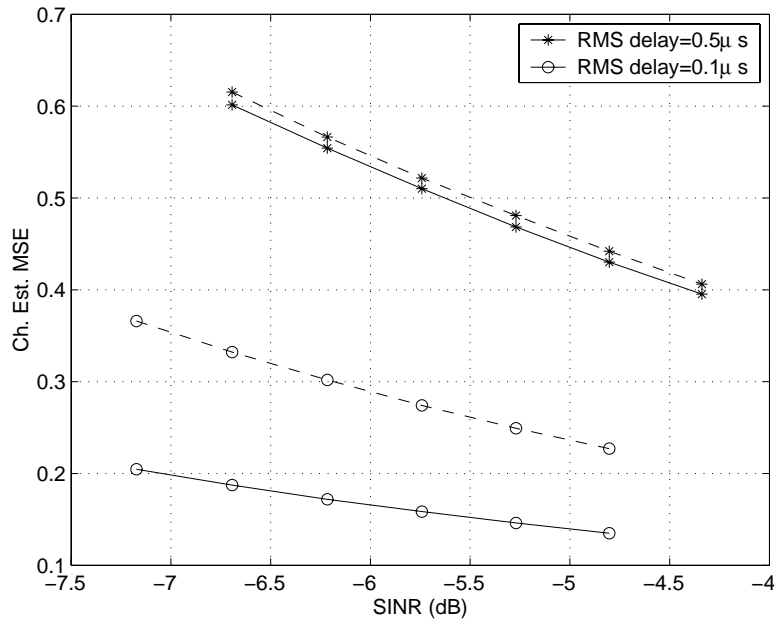


Figure 4. Channel estimation error under different delay spread with proposed design (solid lines) and a random BPSK preamble design (dashed lines) for the 1024 mode.

**Try GCL design for 2048 FFT (Information Only)**

In fact, we can see from the 1024, 512, and 128 modes that the longer the GCL sequence, the better the cross correlation and the easier to choose a subset of sequences with very good PAPR. In addition, the approximation due to truncation can also be made nearly negligible if the sequence is long. Although the 2048 mode is not under the scope of the proposed change, but just to show how easy and effective the GCL-based preamble design can be, we show in the below a quick design for the 2048 mode and an average 1.4dB PAPR reduction is obtained with additional benefit of good cross correlation.

Table YYYa. 2048-point FFT (just to show the easiness and effectiveness of GCL design)

Index	ID cell	Segment	Sequence index: “u” (N <sub>G</sub> =569)	PAPR (mean=2.91 dB)	PAPR in C802.16e-04/125 (mean=4.62 dB)
0	0	0	1	2.75	4.34
1	1	0	568	2.75	4.29

2	2	0	190	2.75	4.31
3	3	0	379	2.75	4.49
4	4	0	284	2.8	4.39
5	5	0	285	2.8	4.53
6	6	0	95	2.84	4.4
7	7	0	474	2.84	4.49
8	8	0	427	2.86	4.56
9	9	0	142	2.86	4.39
10	10	0	71	2.87	4.52
11	11	0	498	2.87	4.44
12	12	0	114	2.97	4.58
13	13	0	455	2.97	4.47
14	14	0	512	3	4.46
15	15	0	57	3	4.59
16	16	0	244	3.03	4.48
17	17	0	325	3.03	4.54
18	18	0	253	3.03	4.6
19	19	0	316	3.03	4.5
20	20	0	38	3.03	4.6
21	21	0	531	3.03	4.58
22	22	0	394	3.04	4.6
23	23	0	175	3.04	4.44
24	24	0	539	3.1	4.63
25	25	0	30	3.1	4.59
26	26	0	561	3.11	4.49
27	27	0	8	3.11	4.53
28	28	0	362	3.12	4.63
29	29	0	207	3.12	4.65
30	30	0	271	3.12	4.65
31	31	0	298	3.12	4.63
32	0	1	1	2.54	4.45

33	1	1	568	2.54	4.46
34	2	1	284	2.56	4.46
35	3	1	285	2.56	4.46
36	4	1	190	2.63	4.46
37	5	1	379	2.63	4.47
38	6	1	427	2.64	4.48
39	7	1	142	2.64	4.49
40	8	1	455	2.71	4.5
41	9	1	114	2.71	4.5
42	10	1	95	2.71	4.5
43	11	1	474	2.71	4.5
44	12	1	498	2.76	4.51
45	13	1	71	2.76	4.51
46	14	1	531	2.8	4.51
47	15	1	38	2.8	4.51
48	16	1	512	2.84	4.52
49	17	1	57	2.84	4.52
50	18	1	253	2.87	4.52
51	19	1	316	2.87	4.52
52	20	1	325	2.89	4.52
53	21	1	244	2.89	4.52
54	22	1	30	3.01	4.53
55	23	1	539	3.01	4.54
56	24	1	175	3.03	4.54
57	25	1	394	3.03	4.54
58	26	1	207	3.06	4.55
59	27	1	362	3.06	4.55
60	28	1	388	3.11	4.55
61	29	1	181	3.11	4.55
62	30	1	274	3.12	4.55
63	31	1	295	3.12	4.55

64	0	2	1	2.5	4.63
65	1	2	568	2.5	4.69
66	2	2	427	2.51	4.71
67	3	2	142	2.51	4.74
68	4	2	71	2.65	4.79
69	5	2	498	2.65	4.68
70	6	2	379	2.67	4.78
71	7	2	190	2.67	4.47
72	8	2	455	2.67	4.74
73	9	2	114	2.67	4.7
74	10	2	284	2.72	4.79
75	11	2	285	2.72	4.63
76	12	2	95	2.74	4.67
77	13	2	474	2.74	4.77
78	14	2	325	2.84	4.72
79	15	2	244	2.84	4.7
80	16	2	175	2.86	4.61
81	17	2	394	2.86	4.71
82	18	2	30	2.86	4.83
83	19	2	539	2.86	4.83
84	20	2	57	2.87	4.76
85	21	2	512	2.87	4.81
86	22	2	316	2.9	4.85
87	23	2	253	2.9	4.83
88	24	2	531	2.91	4.85
89	25	2	38	2.91	4.71
90	26	2	207	2.95	4.78
91	27	2	362	2.95	4.77
92	28	2	19	2.98	4.84
93	29	2	550	2.98	4.83
94	30	2	91	3.07	4.84

95	31	2	478	3.07	4.82
96	0	0	388	3.21	4.84
97	1	1	298	3.15	4.66
98	2	2	388	3.11	4.82
99	3	0	181	3.21	4.87
100	4	1	271	3.15	4.69
101	5	2	181	3.11	4.87
102	6	0	19	3.22	4.91
103	7	1	564	3.16	4.71
104	8	2	332	3.11	4.88
105	9	0	550	3.22	4.87
106	10	1	5	3.16	4.71
107	11	2	237	3.11	4.85
108	12	0	194	3.27	4.75
109	13	1	550	3.17	4.74
110	14	2	5	3.13	4.88
111	15	0	375	3.27	4.82
112	16	1	19	3.17	4.75
113	17	2	564	3.13	4.94

## 5. References:

- [1] Yossi Segal, "Preambles design for OFDMA PHY layer, FFT sizes of 1024,512 and 128," IEEE C802.16e-04/125, June 2004
- [2] B.M. Popovic, "Generalized Chirp-like Polyphase Sequences with Optimal Correlation Properties," IEEE Trans. Info. Theory, vol. 38, pp. 1406-1409, July 1992

## Appendix I: Complexity Analysis (GCL vs. PN)

### Single Channel Estimation:

Assuming the processing is: Take N-point FFT, Multiply the sequence at  $N_u/3$  subcarriers (not needed for PN), Take N/2-point IFFT back to time.



MMSE frequency domain channel estimation is also possible without transforming back to time domain. But if the full band channel is needed, the additional complexity of getting time domain channel is not too much (comparable to using  $\log_2 N$  filter taps in MMSE channel estimation).

The only difference between PN and GCL sequence is the additional complexity for GCL on complex multiplication at every third subcarriers.

Table 2. Comparison of Complex Multiplication Counts (Simple Channel Estimation)

	PN sequences	GCL sequences
1024 (850)	$7.42 \times 10^3$	7.70
512 (425)	3.33	3.47
128 (105)	0.64	0.68
2048 (1702)	16.39	16.95

#### Cell search for PN sequences:

Processing steps:

1. Obtain a rough timing synchronization point  
The complexity analysis below does NOT include the complexity of this step. The complexity involved in this step will be the same for both GCL and PN sequences. Runcom stated that this coarse synchronization point is derived from a time domain correlation, exploiting the repetitive structure obtained from fact that every third subcarriers is used.
2. Take a  $N$ -point FFT to the received data to get the frequency domain data at  $N_u$  subcarriers, starting from a timing synchronization point ( $N/2 \log_2 N$  complex multiplications)
3. For each possible channel delay, apply a “phase ramp” on  $N_u$  subcarriers. Sum every third subcarriers (i.e,  $N_u/3$ ) for each segment, after changing the signs of the frequency data according to the PN sequence of that segment. The result corresponds to the time-domain channel at that delay for that segment. Up to  $L_{CP}$  channel taps may need to be searched. If the phase ramping is implemented as a complex multiplication, ignoring the additions, there are  $L_{CP}N$  complex multiplications in this step. Assuming  $L_{CP}=N/8$  in the following comparison.

Total multiplications:  $N/2 \log_2 N + N_u N/8$

#### One-step Fast cell search for GCL sequences:

Processing steps (GCL sequences with fast cell search)

1. Obtain a rough timing synchronization point  
Same as PN sequences (the complexity is not counted)

2. Take a  $N$ -point FFT to the received data to get the frequency domain data at  $N_u$  subcarriers, starting from a timing synchronization point ( $N/2 \log_2 N$  complex multiplications, same as PN sequences)
3. For each of the three segments, compute the differential-based vector for every third subcarrier. Take an  $N/2$ -point IFFT from which prominent peak(s) are identified. ( $[N/4(\log_2 N - 1) + N_u/3] * 3$ )
4. For the desired cell/segment, multiply the GCL sequence at  $N_u/3$  subcarriers and take an  $N/2$ -point IFFT to obtain the time-domain channel estimate.

Total multiplications:  $N/2 \log_2 N + 4[N/4(\log_2 N - 1) + N_u/3]$

Table 1. Comparison of Complex Multiplication Counts (GCL with fast cell search )

	PN sequences	GCL sequences
1024 ( $N_u=850$ )	$11.4 \times 10^4$	1.55
512 (425)	2.95	0.70
128 (105)	0.21	0.14
2048 (1702)	44.7	3.4

After we presented our “differential-based” cell search idea, Runcom indicated they can do a similar thing, by changing the step to “For each of the three segments, compute the differential-based vector for every third subcarrier. Sum over all possible PN’s, by using a modified sequence which is the output of xoring the PN sequence for every two adjacent PN samples (No operation of multiplication, as these are ignored in this calculation). The results will give estimation about the energy over all PN’s. Therefore only  $3 * N_u/3$  operations of multiplication. And then, for the desired cell/segment, multiply the PN sequence at  $N_u/3$  subcarriers and take an  $N/2$ -point IFFT to obtain the time-domain channel estimate.” This results in a total complexity of  $\frac{N}{2} \log_2 N + N_u + \frac{N}{2} (\log_2 N - 1)$ , which is still slightly better than GCL with fast cell search. Our response was:

- 1) **Now the complexity of PN and GCL approaches is pretty close.**

The complexity for cell search with either sequence is well within the comfortable complexity range, to meet the goal of fast access to the network after power-up with low power consumption. **Thus, the PAPR and cross correlation advantages of GCL sequences make them a clear choice.**

- 2) **Using the differential based processing/energy detection (for fast cell search) with PN sequences appears less reliable than with GCL sequences.** (See included simulation results below)

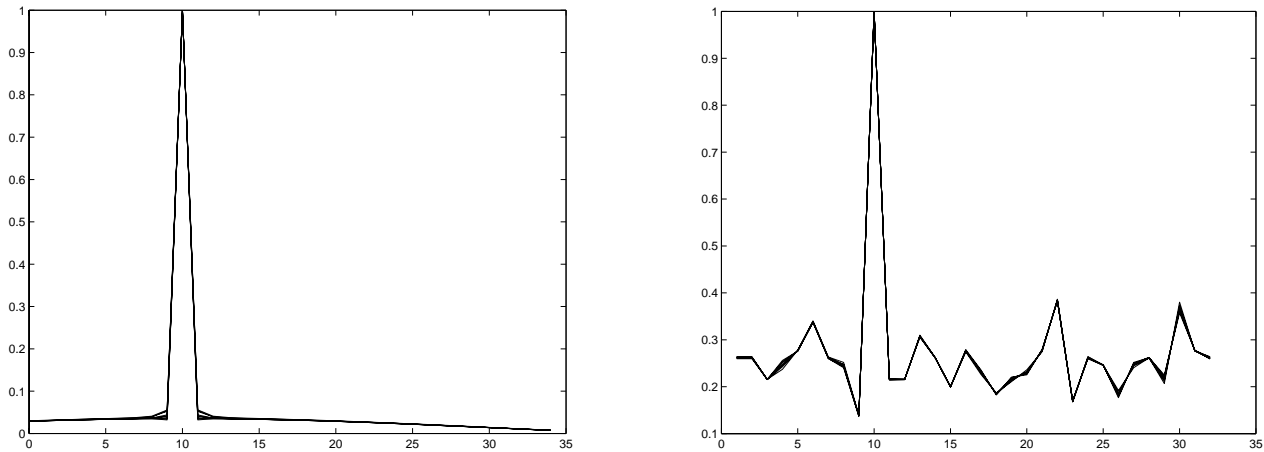


Figure 5. Cell identification performance (ID=10,segment 0) for GCL (left, only the first 35 sequence indices are shown) and PN (right, energy detection on 32 Runcom sequences for segment 0), **flat channel, no noise, 1024-FFT.**

(For all simulation results: 200 Monte-Carlo runs, each time with a random channel, Peaks are always normalized to “1” in each run)

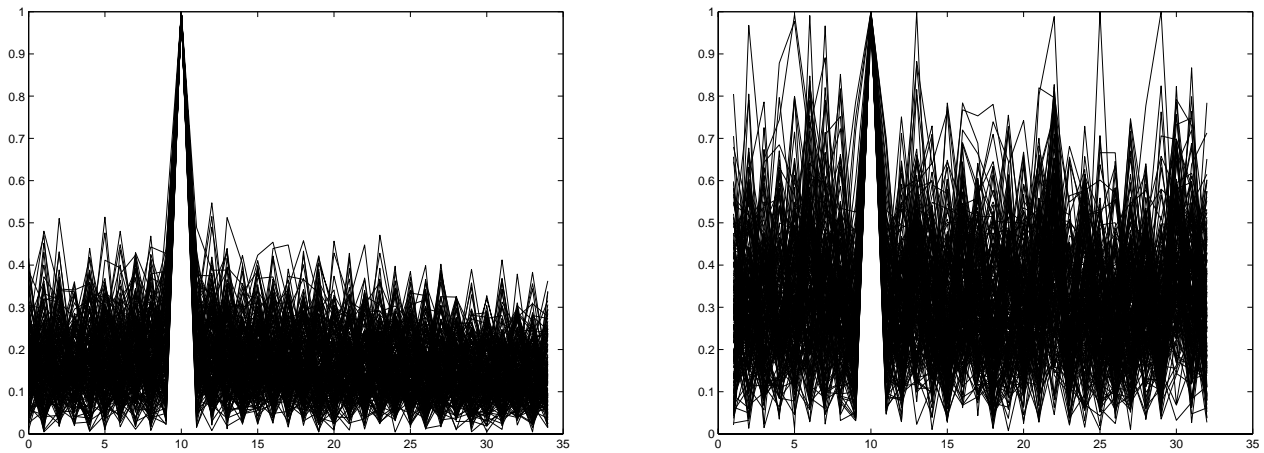


Figure 6. Cell identification (ID=10) for GCL (left) and PN (right, multiple false peaks), **RMS Delay Spread =2us, SNR= -1dB, 1024-FFT**

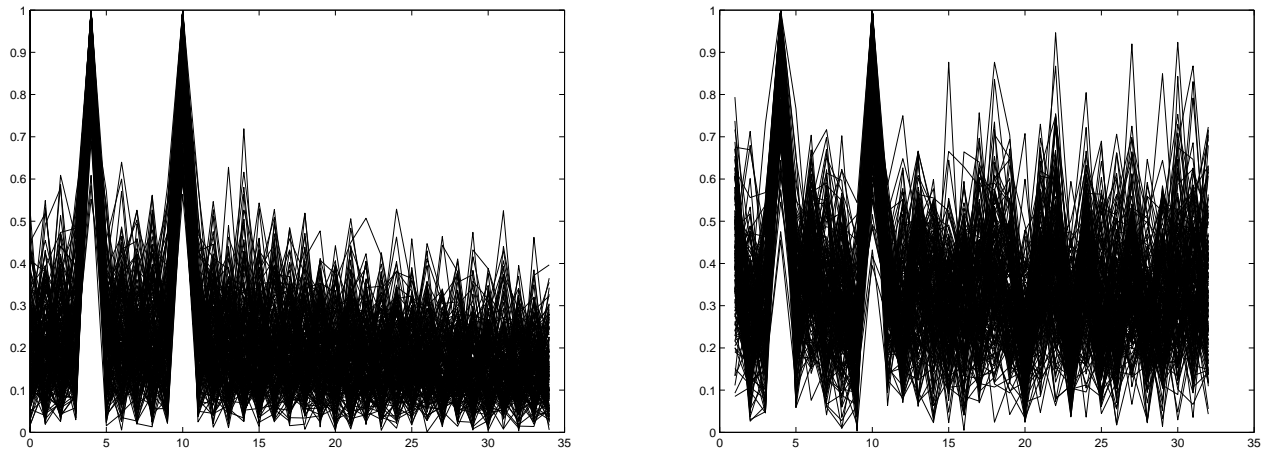


Figure 7. **Two cell** identification (ID=10 and ID=4, same received power, each has SNR= 2dB), GCL (left) and PN (right, several peaks in addition to the two expected peaks), RMS = 2us, 1024-FFT (Note: For PN, in addition to the false detection, the relative amplitude of the two expected peaks are often incorrect, meaning one can pick the wrong cell if we want to pick the best cell when there is a power difference. On the other hand, the peaks for GCL are clearer)

#### Brute-force cell search (for information only):

Processing steps (GCL sequences with fast cell search)

1. Obtain a rough timing synchronization point  
Same as PN sequences (the complexity is not counted)
2. Take a N-point FFT to the received data to get the frequency domain data at  $N_u$  subcarriers, starting from a timing synchronization point ( $N/2 \log_2 N$  complex multiplications, same as PN sequences)
3. Multiply with the GCL conjugate on each of the  $N_u/3$  subcarriers (for each preamble, assuming P of them in total). Take an IFFT to get the time domain channel (since there are only  $N_u/3$  non-zero subcarriers, we can take an  $N/2$ -point IFFT). The complexity for this step is  $N/4(\log_2 N - 1) + N_u/3$ .

Total multiplications:  $N/2 \log_2 N + P[N/4(\log_2 N - 1) + N_u/3]$

Table 3. Comparison of Complex Multiplication Counts (Brute Force Cell Search)

	PN sequences	GCL sequences			
		P=114(19cellx6sec)	78(13cellx6sec)	42(7cellx6sec)	6(1cellx6sec)
1024 ( $N_u=850$ )	$11.4 \times 10^4$	30.0	20.7	11.4	2.1
512 (425)	3.0	13.5	9.3	5.1	0.93
128 (105)	0.21	2.6	1.8	1.0	0.18
2048 (1702)	44.7	66.0	45.5	25.0	4.5

## Appendix B: A Few Facts of GCL and Polyphase Sequences

### GCL sequence definition:

- Official definition of Generalized Chirp Like (GCL) sequence is

$$a(k) = s(k)b(k \bmod m), \quad k = 0 \cdots N_G - 1, \quad N_G = cm^2$$

where  $\{b(i)\}, i=0, \dots, m-1$  is any sequence of  $m$  complex numbers with unit amplitude and  $\{s(k)\}$  is a Zadoff-Chu sequence

$$s_u(k) = \begin{cases} \exp\left\{-j2\pi u \frac{k(k+1) + qk}{2N_G}\right\}, & \text{for odd } N_G \\ \exp\left\{-j2\pi u \frac{k^2 + qk}{2N_G}\right\}, & \text{for even } N_G \end{cases} \quad k=0 \cdots N_G - 1, \quad q \text{ any integer, and } u=1 \cdots N_G - 1$$

- A particular GCL family we like:

In order to come up a maximal number of sequences with low PAPR and good cross correlation, we choose a prime number  $N_G$  because any ‘‘class index’’  $u$  will be relatively prime to  $N_G$ , which results in optimal cross correlation between any two sequences with different class indices (we also choose  $b=1, q=0$  for simplicity). Note that a prime number  $N_G$  means that in the first equation  $c=N_G$  and  $m=1$ .

Any desired length is obtained by picking the smallest prime number that is larger than the desired length, then truncate the sequences. The good sequences characteristics are approximated reasonably well.

GCL is one type of CAZAC (constant amplitude zero auto-correlation). But GCL is also optimal in terms of cross correlations (the best among all CAZAC). If you need one sequence, we can get away with any of the CAZAC sequence below, if the sequence length provided happens to meet you need.

### Relationship to other polyphase sequences:

- Frank-Zadoff sequence: (one type of CAZAC)

$$s_u(k = p + q\sqrt{N_G}) = \exp\left\{-j\pi \frac{pq}{\sqrt{N_G}}\right\}, \quad p, q = 0 \cdots \sqrt{N_G} - 1, \quad N_G = x^2$$

was extended by Chu to any code length to what is known as Zadoff-Chu sequence. Frank-Zadoff sequence is also related to the ‘‘modulatable orthogonal sequence’’ proposed by Suehiro for  $N_G=x^2$ . This sequence has  $\sqrt{N_G}$  phases, which is the minimal number of phases required. In the original polyphase literature, the sequences were used in time domain for applications like radar signal detection and channel training, so the length  $N_G = 2^{2n}$  was often used mainly to facilitate FFT processing.

- Milewski extended to length  $t^{2n+1}$  with  $t^{n+1}$  phases (one example is  $t=2$ )

$$s_u(k = p + qt^n) = \exp \left\{ -j\pi \frac{pq}{\sqrt{t^{2n+1}}} \right\}, \quad p = 0 \dots t^n - 1, q = 0 \dots t^{n+1} - 1, \quad N_G = t^{2n+1}$$

- “Chu” sequence used in ZTE’s proposal: (I cannot find it from Chu’s publication. I have seen a paper referred to this as the “Newman” sequence.)

$$s_u(k) = \exp \left\{ -j\pi \frac{k^2}{N_G} \right\}, \quad k = 0 \dots N_G - 1, \quad N_G \text{ is even}$$

It can be obtained as a special case of GCL ( $u=1, q=0$  of Zadoff-Chu)

### Some Properties:

- GCL sequences are circular, i.e.,  $s(k) = s(k \bmod N_G)$

A cyclic shift of the sequence is equivalent to applying a phase ramp (denoting the circularly shifted sequence of  $\{s(k)\}$  as  $\{s(k+z)\}$ ):

$$s(k+z) = s(k) e^{-j2\pi u \frac{2zk+z+z^2}{2N_G}} = e^{-j2\pi u \frac{z+z^2}{2N_G}} e^{-j2\pi u \frac{zk}{N_G}} s(k)$$

- When a cyclically shifted GCL sequences is used in the frequency domain, it is equivalent to cyclically shift the time sequence by some amount, as can be seen from this time domain cross correlation of the two time-domain sequences:

$$IFFT \left\{ \frac{s(k+z)}{s(k)} \right\} = IFFT \left\{ e^{-j2\pi u \frac{2zk+z+z^2}{2N_G}} \right\} = e^{-j2\pi u \frac{z+z^2}{2N_G}} IFFT \left\{ e^{-j2\pi u \frac{zk}{N_G}} \right\}$$

This means that in time domain, the second sequence is a cyclically delayed replica of the first sequence (by  $uzN/N_G$  samples, and up to a constant phase rotation). So, if another base uses the second sequence, we want to make sure that its signal will not be confused with a delayed multipath of the first sequence.