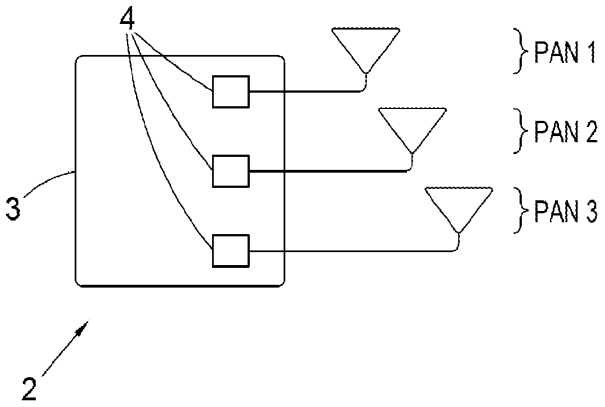


FIG. 1

time slot

ID:	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
1	21	91	77	75	123	93	11	59	15	41	95	89	71	17	57	69	37	45	107	13	67	61	5	115	63	83	7	35	25	103	119	73
2	11	63	37	29	19	119	5	17	9	15	81	23	55	51	21	103	105	35	13	61	45	85	33	115	79	47	65	87	123	49	75	111
3	43	79	17	9	81	91	127	67	27	45	31	21	51	19	25	69	11	39	123	95	3	5	53	63	85	61	23	101	47	99	35	89

time slot

ID:	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63
1	79	49	99	81	27	51	19	121	113	125	87	85	31	97	127	9	105	55	117	39	65	23	109	111	3	53	101	1	47	33	43	29
2	93	71	25	97	77	109	7	107	127	1	99	89	73	117	57	69	39	125	91	3	67	41	31	43	113	121	83	101	95	27	59	53
3	49	65	41	73	117	29	97	13	113	83	105	111	87	71	125	7	103	109	115	33	57	121	59	93	15	55	1	107	75	77	37	119

FIG. 2

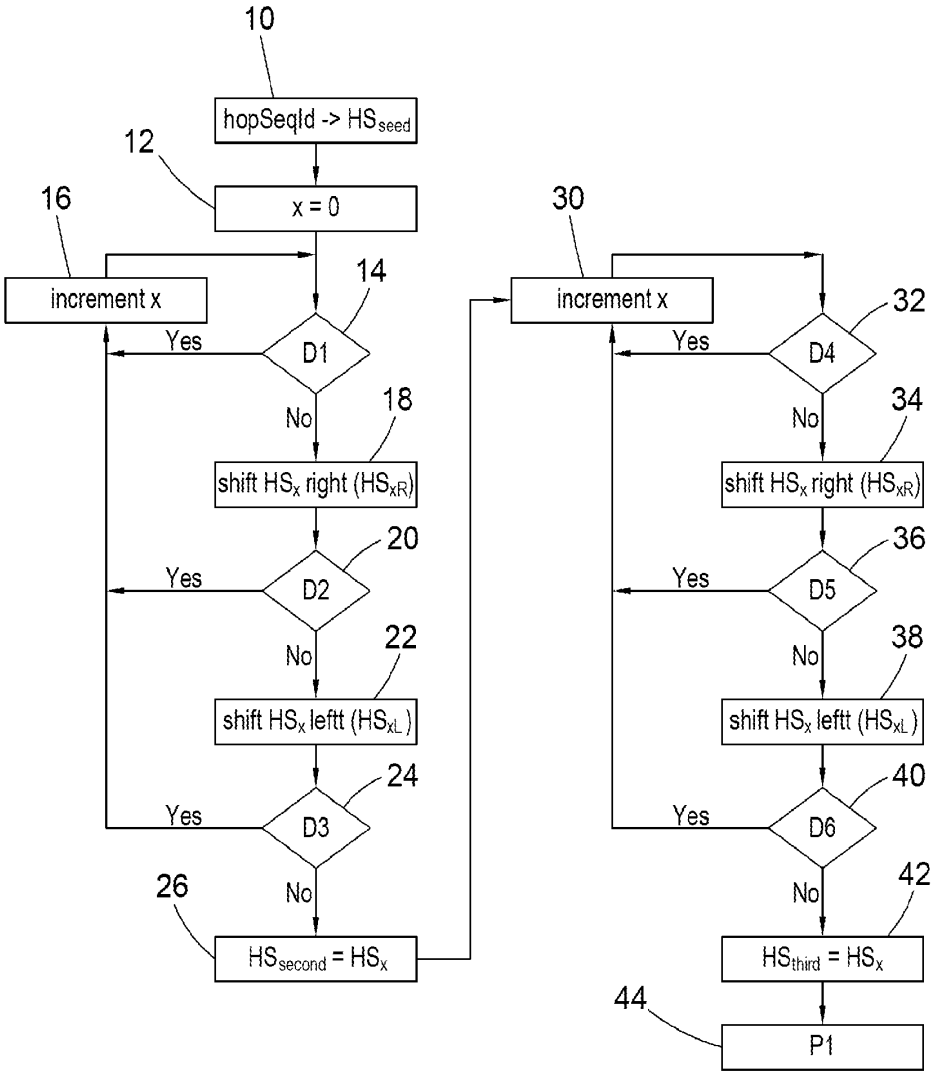

10
hopSeqId -> HSseed
12
x = 0
16
increment x
14
D1
Yes
No
18
shift HSx right (HSxR)
20
D2
Yes
No
22
shift HSx leftt (HSxL)
24
D3
Yes
No
26
HSsecond = HSx
30
increment x
32
D4
Yes
No
34
shift HSx right (HSxR)
36
D5
Yes
No
38
shift HSx leftt (HSxL)
40
D6
Yes
No
42
HSthird = HSx
44
P1

FIG. 3

hopSeqId: 19, list: set([(19, 69, 121)])

hopSeqId: 25, list: set([(25, 26, 207)])

hopSeqId: 28, list: set([(28, 110, 154)])

hopSeqId: 29, list: set([(29, 203, 228), (29, 203, 205)])

hopSeqId: 38, list: set([(7, 38, 167)])

hopSeqId: 50, list: set([(38, 50, 106), (38, 50, 140)])

hopSeqId: 69, list: set([(19, 69, 121), (69, 121, 205)])

hopSeqId: 95, list: set([(95, 156, 195)])

hopSeqId: 119, list: set([(83, 119, 252)])

hopSeqId: 121, list: set([(19, 69, 121), (69, 121, 205)])

FIG. 4

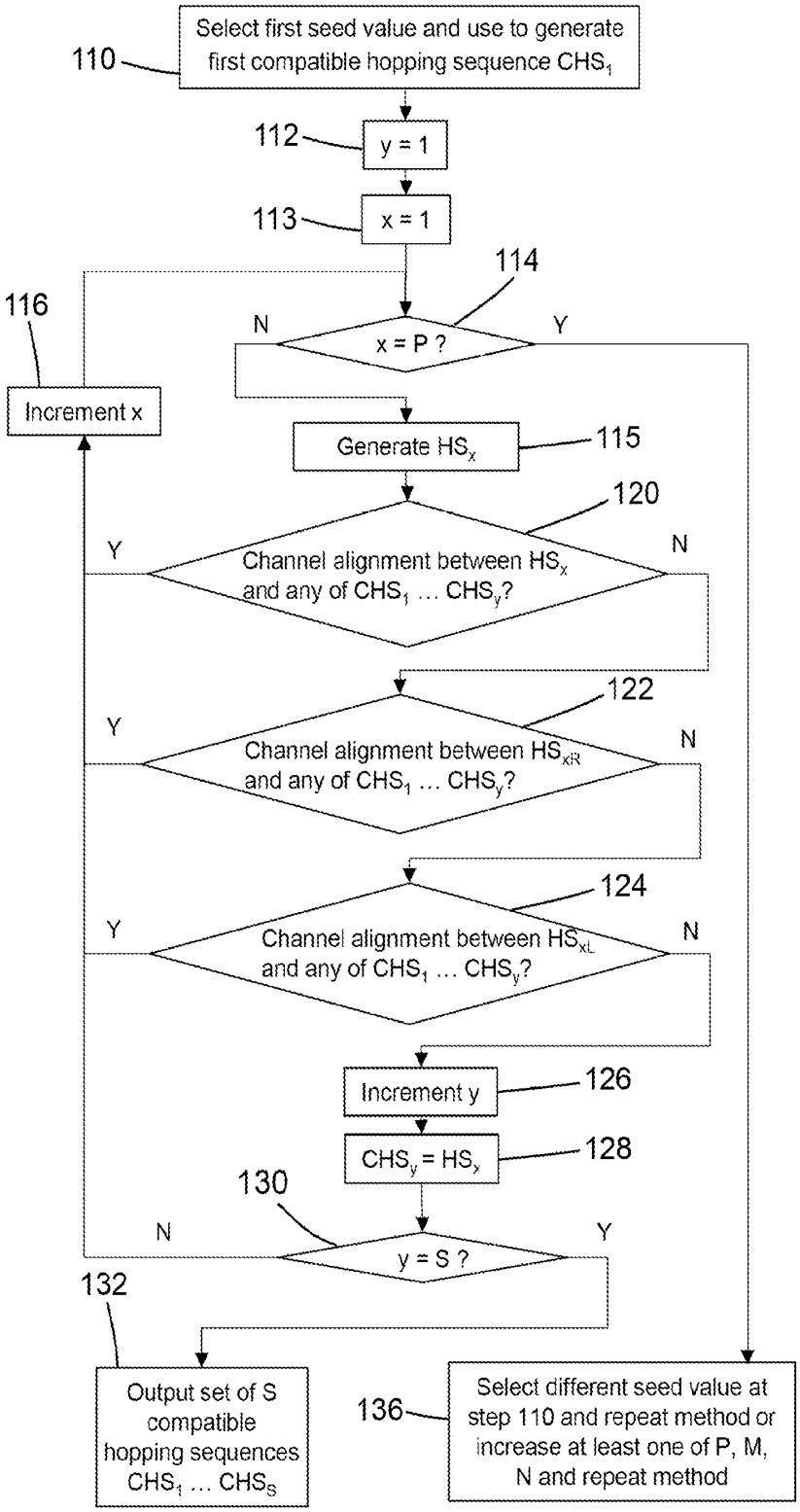

Select first seed value and use to generate first compatible hopping sequence CHS1
110
y = 1
112
x = 1
113
114
x = P ?
N
Y
116
Increment x
Generate HSx
115
120
Channel alignment between HSx and any of CHS1 … CHSy?
Y
N
122
Channel alignment between HSxR and any of CHS1 … CHSy?
Y
N
124
Channel alignment between HSxL and any of CHS1 … CHSy?
Y
N
Increment y
126
CHSy = HSx
128
130
y = S ?
N
Y
132
Output set of S compatible hopping sequences CHS1 … CHSS
136
Select different seed value at step 110 and repeat method or increase at least one of P, M, N and repeat method

FIG. 5

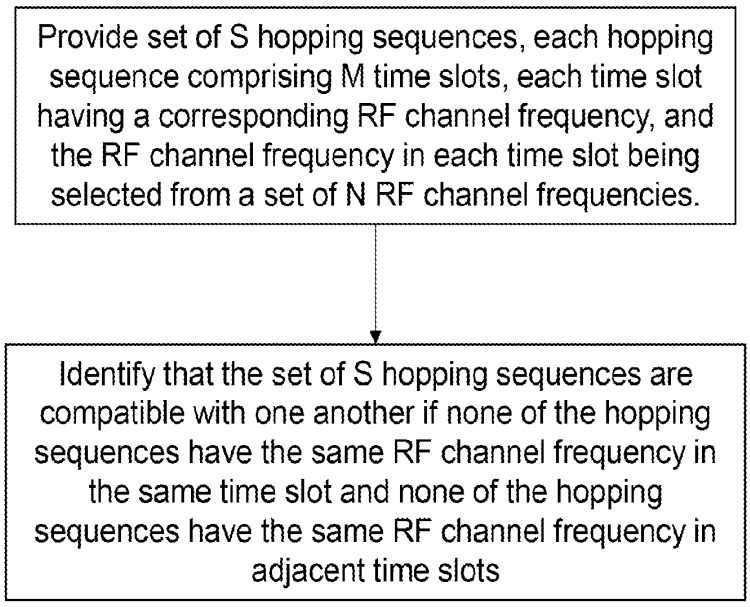


FIG. 6

IDs 1 and 2 channel alignment = ['115']
IDs 1 and 2 channel adjacency = ['13', '15', '101']

IDs 2 and 3 channel alignment = []
IDs 2 and 3 channel adjacency = ['51']

IDs 1 and 3 channel alignment = ['69', '113']
IDs 1 and 3 channel adjacency = ['05', '63', '49', '01']

FIG. 7