

*

40

60

가

가

가

: , , ,

I.

가

가

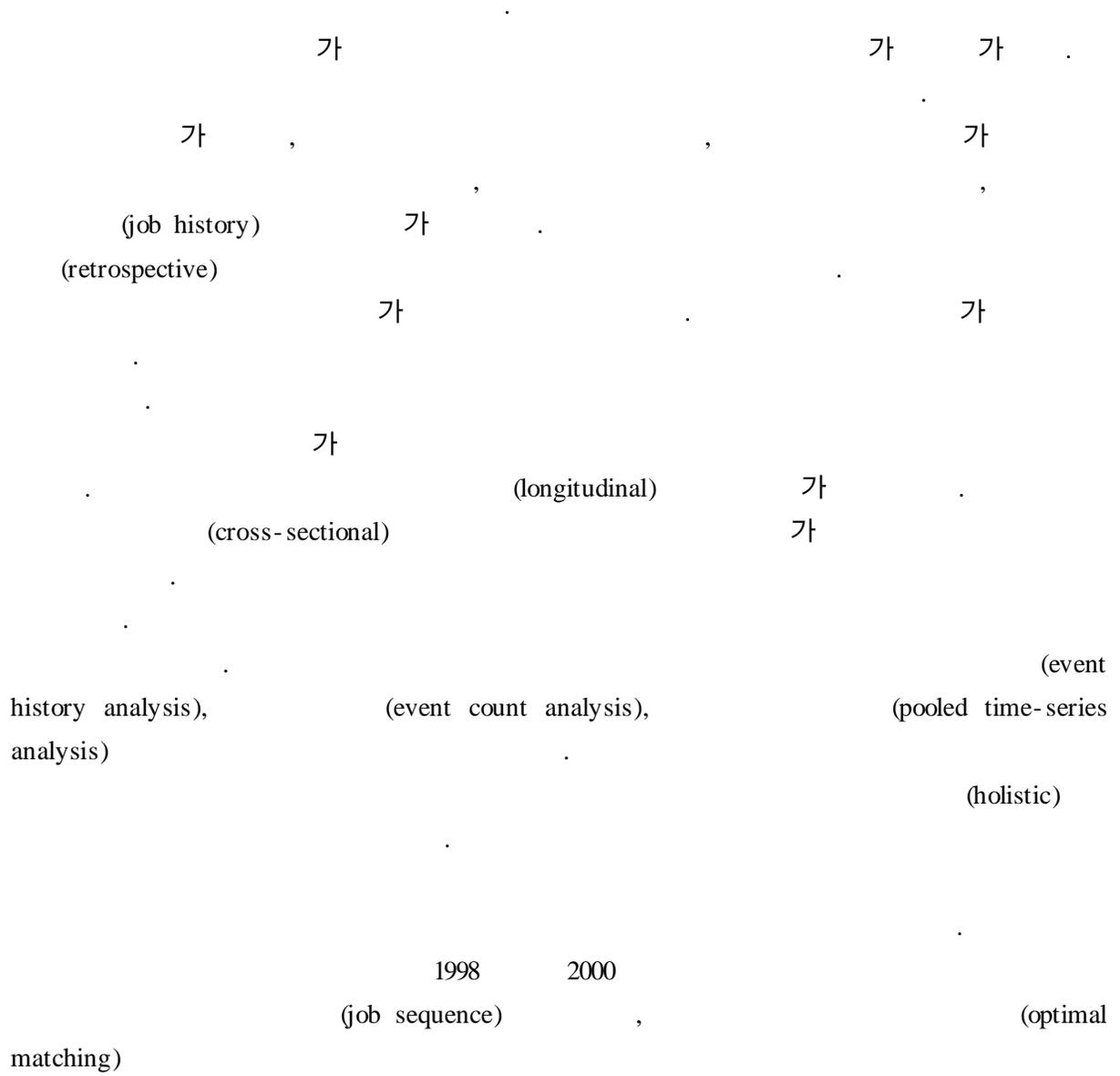
가 가

가

가

가

*



II.

1.

(optimal matching)

DNA

(가

Kruskal(1983) .)

Andrew

Abbott .
가

(Abbott 1983; 1984; 1988; 1990)

. Abbott

. Ginsberg Baum(1994)

, Levitt Nass(1989)

. Stovel,
가

Savage Bearman(1996)

Lloyd

, Blair-Loy(1999)

가

. Han

Moen(1999)

Chan(1995) Halpin and Chan(1998)

가(Stovel, Savage and Bearman, 1996

Blair-Loy, 1999)

Chan(1995) Halpin and Chan(1998)

가

. 가

가

20 21 22 23 24 25

1:

2:

(substitution),

(insertion),

(deletion)

, 1 2

2가 1

(가)
. 1 21

가

24

, 2 20

가 23

, (3), (4)
 . , ,
 (2).
 (substitution cost)

0.1 , 0.1 가 .
 ,
 0.2가 ,
 0.3 , 가 가 0.4가 .
 0.1
 X 'XABC'
 'ABCC' 'AABC' 가 .
 가 가 , 가
 가

Chan(1995)

1.

0.0	0.1	0.2	0.3	0.3	0.4	0.3	0.3	0.4	0.0
	0.0	0.2	0.3	0.3	0.4	0.3	0.3	0.4	0.1
		0.0	0.1	0.2	0.3	0.2	0.2	0.3	0.1
			0.0	0.1	0.2	0.1	0.1	0.2	0.1
				0.0	0.2	0.1	0.1	0.2	0.1
					0.0	0.2	0.2	0.1	0.1
						0.0	0.1	0.2	0.1
							0.0	0.2	0.1
								0.0	0.1

3.

가
 가 n
 n(n-1)/2
 n
 10 100 , n 100 10,000

Abbott (州)
 가
 Stovel, Savage Bearman(1996) Blair-Loy(1999)

Scherer(2001)
 (가 British Household Panel Survey (BHPS)
 German Socio-Economic Panel (SOEP)) 1,000 가
 Halpin Chan(1998)

Scherer (reference sequence)
 n
 n(n-1)/2 m × n (m < n)
 가 가 m
 가?

(analogically) (mobility table)
 (diagonal cell)
 m

n n
m m × n

4.

가
(cluster analysis)

가
(MDS: multi-dimensional scaling)

가,
가

assumption)

(explore)

가
(explain)

가 (parametric

가 -

가

가

가

가

가

(landscape of opportunity structure)
Halpern Chan(1998)

가

가

(life course)

가 가

III.

1998 1
 5,000 가
 421
 13,317 가
 15 가
 2000 3
 가
 9
 40
 40
 40 , 50 , 60 1951 -60
 1941 -50 , 1931 -1040
 가 (,
 2001)
 가
 1897 가
 , 가 가 ,
 40 가 923 , 41 -50 50 가 599 , 31 -40
 60 가 375
 (episode) 가
 (sequence)
 TDA(Transition Data Analysis) 6.2
 15 40 9
 -1
 0

TDA 가 (average linkage groups) . TDA 가 (agglomeration)

IV.

1.

1951 -60 923

가 < 2>

< 2> 51 -60

	8	18	3 4 5 7
	37	9	3 7
	62	28	4 5 7
	47	46	(3 7) 1 3 5
	67	49	4 7 4 8
	31	25	7
	151	34	6 9
		67	5 8 5 8
	57	49	6 7 5 7
	20	23	(5 7) 5
		42	
		53	
	480	443	

: 1, 2, 3

: 51-60 가 923

923 가 480 , 가 443

3), 가

. 443 12

. 9

3) 가 (aggregation bias)가

가 ,

가

가

< 3> - () : 51 -60

1	4.11	3.67	1.67	1.50	1.67	0.01	0.89	0.50	0.11	2.83	9.05	26.00
2	3.00	10.56	1.00	0.56	0.44	0.00	1.44	0.00	0.00	0.11	8.89	26.00
3	0.36	0.00	12.86	1.57	0.82	0.11	0.64	0.18	0.01	1.18	8.28	26.00
4	2.09	0.15	2.85	8.35	0.98	0.11	0.70	1.30	0.28	0.74	10.41	26.00
5	0.00	0.00	0.00	4.24	10.04	0.31	2.10	0.90	0.20	1.43	6.77	26.00
6	0.00	0.04	0.00	0.20	0.60	11.52	2.04	0.72	6.24	1.36	3.28	26.00
7-(1)	0.00	0.00	0.00	0.41	1.82	4.56	6.00	2.88	2.91	1.21	6.21	26.00
7-(2)	0.00	0.04	0.27	0.19	1.73	0.27	14.42	1.45	0.39	1.43	5.80	26.00
8	0.00	0.00	0.00	0.37	1.04	0.47	2.67	13.49	0.39	1.37	6.20	26.00
9	0.00	0.00	0.35	0.48	1.26	3.00	1.00	0.96	8.83	2.09	8.04	26.00
0	0.00	0.05	0.26	0.74	3.19	0.14	3.21	3.57	0.48	7.40	6.95	26.00
	0.25	0.19	1.32	0.70	0.79	0.30	5.55	1.30	0.34	1.32	13.94	26.00
	0.29	0.42	1.44	1.80	2.35	1.35	4.48	2.78	1.28	1.93	7.86	26.00

: < 2>

< 3>

< 2>

< 2>

(1)

(9)

9

15

40

26

가

13

14

4 , 8

2.

51 -60 10 20

40

가 가
가

51 -60

41 -50

31 -40

가 < 4> < 5>

< 4> 41 -50

	10	13	2 4 6	
	17			
	30	13	4 7	(4 7)
		8	4	
	33			
	60	27	6 7 8	
	74	25		5 7
		15		7 9
	84	36	8	5
	37	29	4 5	
	34	20	5	5
		9		
		25		
	379	220		

: 1, 2, 3

: 41 -50

599

< 5> 31 -40

8			
8	2	3	
	2	4	4
17	4	5	
26	14	5 6	
25	5	6 7 8	
94	14		9
	28		7 8
42	22	(5) 6	(5)
23			
20			
	5		
	14		
	265	110	

: 1, 2, 3

: 31 -40

375

< 2>, < 4>, < 5>

가 . 31
-40 51

-60 가 가 가 .

(retrospective)

가 .

가 .

가
31 -40

, 41 -50

51 -60

가 .

가

가 , 51 -60

가

가

가

가

가

< 3>, < 6> < 7>
가

가 31 -40

가 (17.4) , 41 -51

가 (5.93)

가 51 -60

(10)

가

< 6> - () : 41 -50

1	6.08	3.62	0.46	2.62	0.08	0.46	0.85	0.38	0.00	1.38	10.08	26.00
3-(1)	0.00	0.00	6.15	3.92	1.15	0.15	3.15	1.15	0.15	0.62	9.54	26.00
3-(2)	0.00	0.00	11.13	0.88	0.00	0.38	0.50	0.88	0.00	1.38	10.88	26.00
5	0.00	0.00	0.00	1.30	5.93	3.74	1.41	4.41	1.41	1.74	6.07	26.00
6-(1)	0.00	0.00	0.08	0.00	2.40	7.96	7.12	0.80	1.72	2.32	3.60	26.00
6-(2)	0.00	0.00	0.00	0.53	0.20	10.93	1.20	0.00	6.00	1.60	5.53	26.00
7	0.00	0.00	0.03	0.08	1.89	0.39	11.47	3.42	0.36	2.61	5.75	26.00
8	0.00	0.00	0.14	5.59	4.76	0.52	0.59	5.93	0.00	1.86	6.62	26.00
9	0.00	0.00	0.10	0.50	1.00	4.70	1.60	0.85	6.35	0.70	10.20	26.00
0	0.00	0.00	0.56	1.44	1.89	0.22	2.22	1.67	0.78	11.56	5.67	26.00
	0.00	0.00	0.44	0.68	1.24	1.00	4.24	1.76	1.16	1.44	14.04	26.00
	0.36	0.21	0.91	1.55	2.33	2.84	3.99	2.44	1.59	2.13	7.65	26.00

: < 4>

< 7> - () : 31 -40

2	1.50	12.50	2.25	1.00	0.00	0.00	0.00	0.00	0.00	0.00	8.75	26.00
3	0.00	0.00	10.30	0.00	4.75	0.25	1.00	0.00	0.00	1.00	8.70	26.00
4	0.00	0.00	0.29	7.71	2.21	1.71	0.21	4.93	0.29	1.36	7.29	26.00
5	0.00	0.00	0.00	0.00	17.40	0.40	0.80	1.80	0.20	1.20	4.20	26.00
6-(2)	0.00	0.00	0.11	0.54	1.64	10.50	2.96	0.57	2.43	2.11	5.15	26.00
6-(1)	0.00	0.00	0.00	0.00	0.00	11.90	0.36	0.00	7.86	1.07	4.81	26.00
7	0.00	0.00	0.27	0.14	2.05	1.59	12.60	0.23	0.55	2.27	6.31	26.00
0	0.00	0.00	0.00	4.00	1.20	1.20	0.40	0.60	2.00	11.40	5.20	26.00
	0.00	0.36	1.00	1.64	1.07	1.71	2.07	0.00	1.07	1.14	15.94	26.00
	0.29	0.42	1.44	1.80	2.35	1.35	4.48	2.78	1.28	1.93	7.86	26.00

: < 5> .

V.

(. , 2000; , 2001)

가

가

(reference sequence)

가

가

(immobility)

가

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Sequence Analysis of Occupational Mobility Paths

Han Joon

In this study, I have tried to find the trajectories of intra-generational occupational mobility by applying optimal matching method to the job sequence data from Korean males with ages between 40s and 70s. The results from the study show that the job sequences with mobility experience can be meaningfully classified with the help of both optimal matching method and cluster analysis. I extended the study by comparing the results from analysis of a set of successive cohorts of males between 40s and 70s. The differences across cohorts in the results from sequence analysis can be attributed to the changing context of opportunity structure under the influence of structural transformation of society. Methodologically this study showed how we can save the enormous computing burden in sequencing big data set by relying on comparison with limited numbers of reference sequences.