

Matched-Pair Algorithm

Detailed overview

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Step 1: Calculate the Hazard Ratio for each patient record

Patient Record

Patient Record	Dysplasia Present	Invasive Code >1	Depth Code >1	ENE	Perineural	LVI	Sum	Hazard Ratio
#1	Yes; 2.0	No; 0.0	Yes; 1.8	Yes; 1.4	No; 0.0	Yes; 1.3	2.0+0.0+1.8+1.4+0.0+1.3	6.5
#2	No; 0.0	Yes; 2.0	Yes; 1.8	No; 0.0	Yes; 1.4	No; 0.0	0.0+2.0+1.8+0.0+1.4+0.0	5.2
#3	Yes; 2.0	No; 0.0	Yes; 1.8	No; 0.0	Yes; 1.4	No; 0.0	2.0+0.0+1.8+0.0+1.4+0.0	5.2
...

Hazard values are same as those used in the algorithm.

Step 2: Separate patient records into SLNB list, ELND list

SLNB Records

Patient Record	Hazard Ratio
#2	6.0
#8	5.2
#12	5.8
...	...

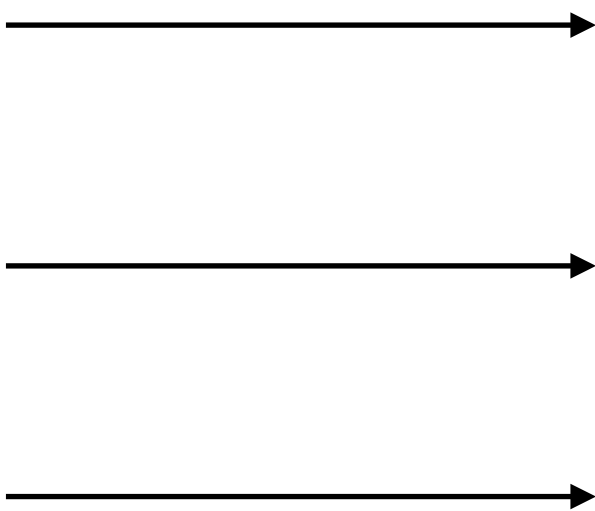
ELND Records

Patient Record	Hazard Ratio
#1	5.8
#3	5.0
#4	4.2
...	...

Step 3: For each SLNB record, produce a ranked priority list of closest ELND records

SLNB Records

Record	Hazard Ratio
#2	6.0
#8	5.2
#12	5.8
...	...



Ordered List of ELND Records
(ranked according to closest match)

1st closest	2nd closest	3rd closest	4th closest	...
#11 Hazard=6.0	#29 Hazard=6.0	#62 Hazard=6.1	#36 Hazard=5.8	...
#41 Hazard=5.2	#04 Hazard=5.3	#71 Hazard=5.0	#07 Hazard=5.6	...
#36 Hazard=5.8	#55 Hazard=5.7	#13 Hazard=5.7	#07 Hazard=5.6	...
...

Note: Identical Histopathological variables are ranked higher than identical Hazard Ratios (this produces more ‘perfect’ matches)

SLNB Records

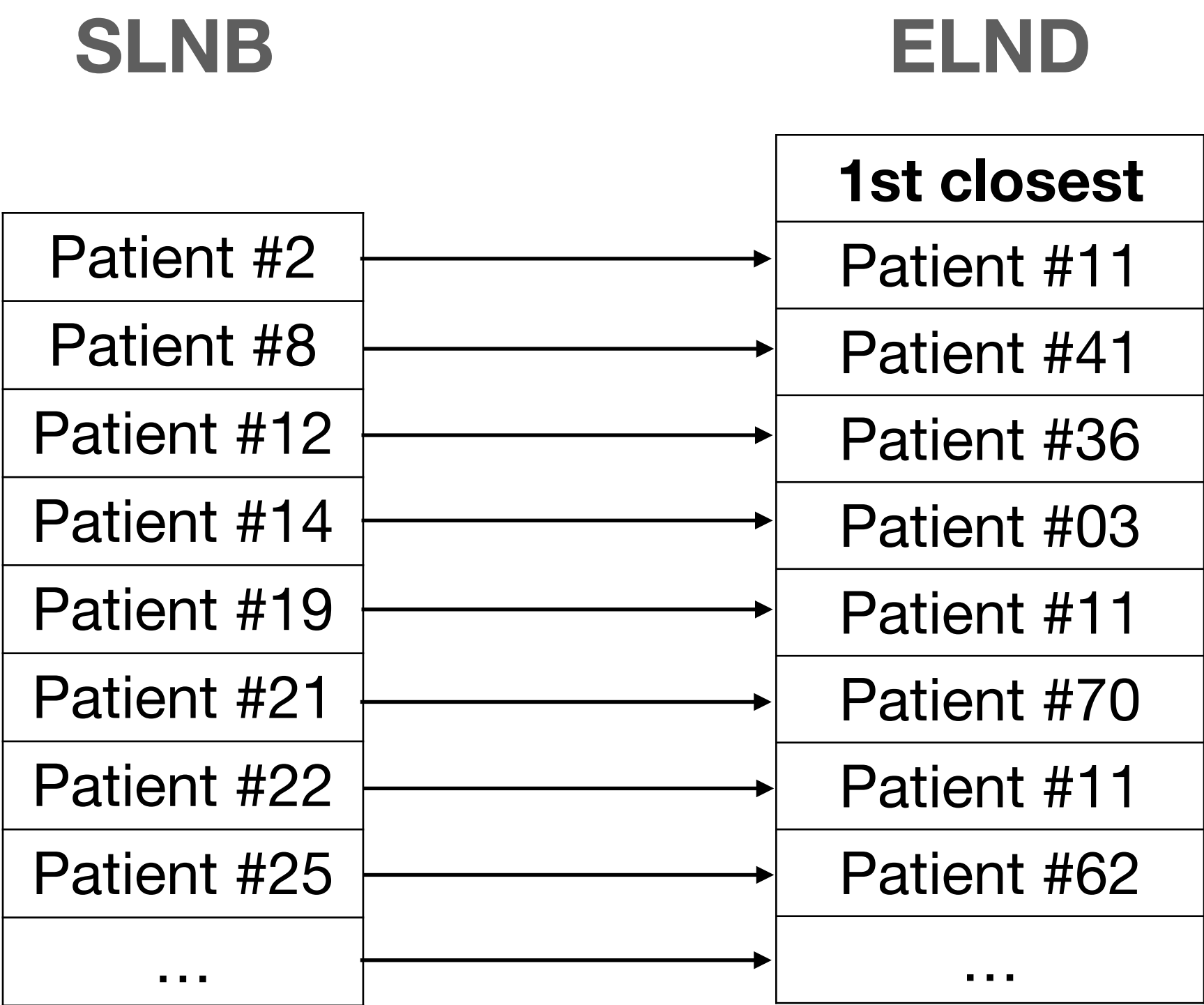
Record	Variables	Hazard Ratio
...	< ... >	...
#69	Dysplasia: TRUE INV Code: 2 Depth Code: 1 ENE: FALSE Perineural: FALSE LVI: TRUE	5.5
...	< ... >	...



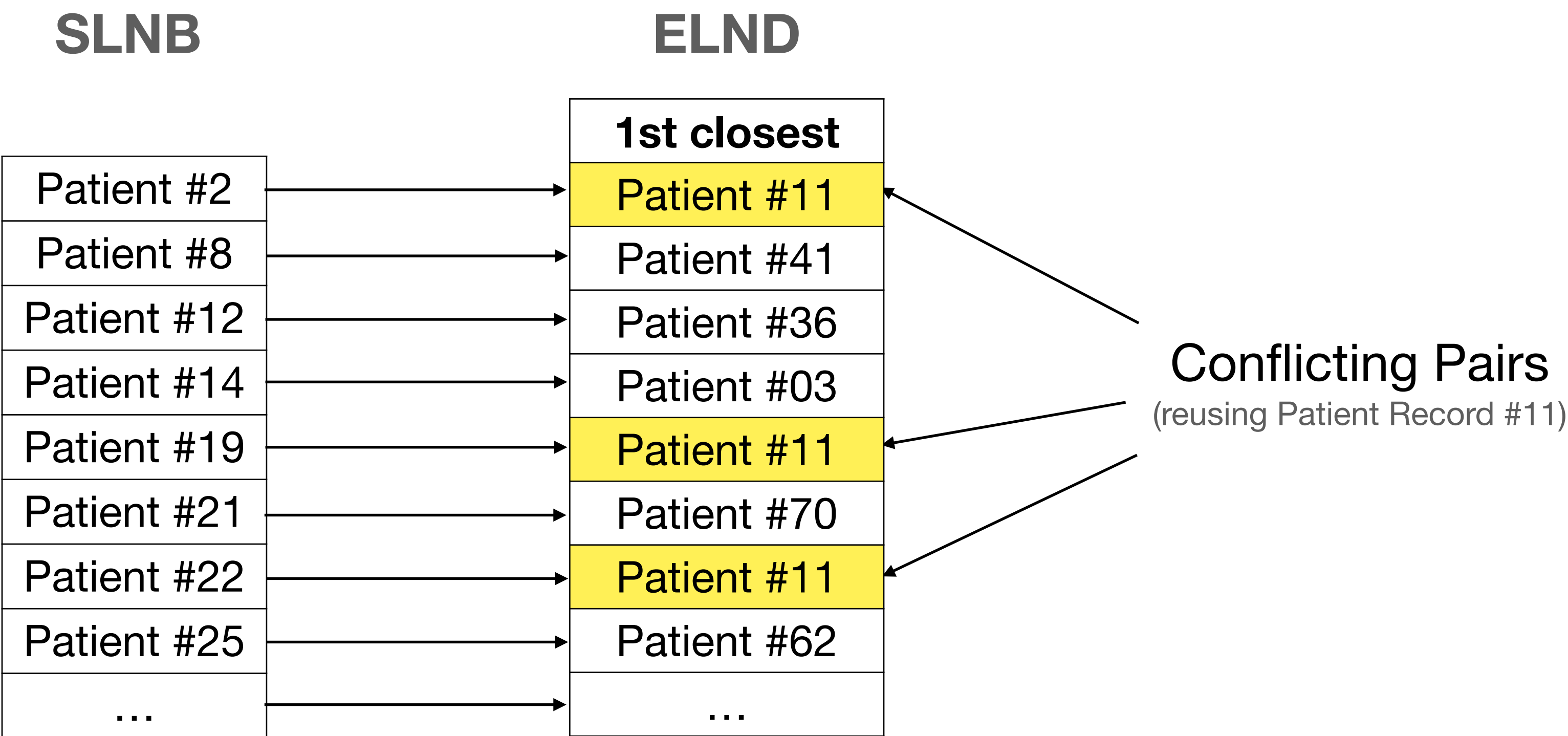
Ordered List of ELND Records
(ranked according to closest match)

1st closest	2nd closest	3rd closest	4th closest	...
...
Dysplasia: TRUE INV Code: 2 Depth Code: 1 ENE: FALSE Perineural: FALSE LVI: TRUE	5.5	5.4
...

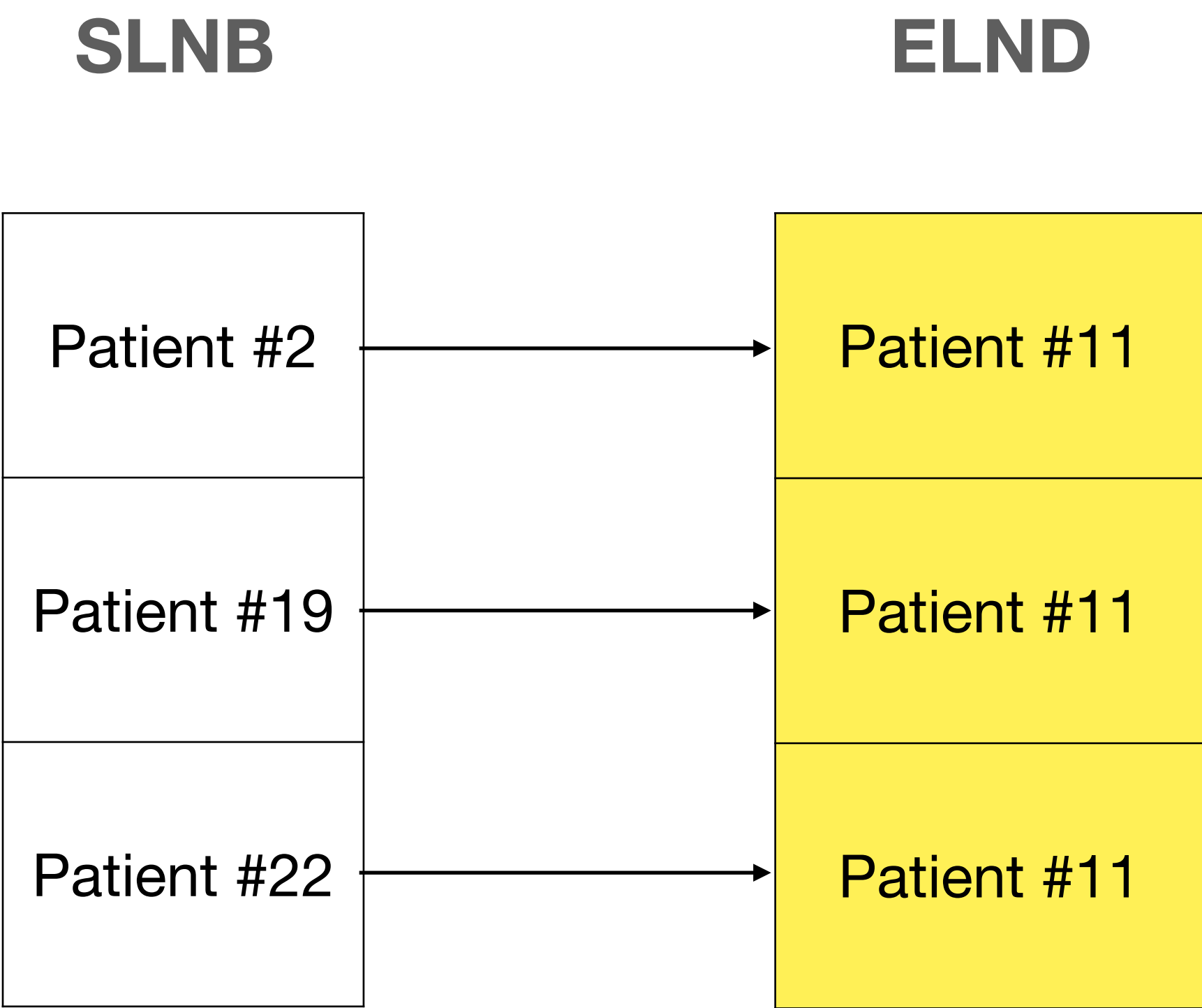
Step 4: Naïvely pair each SLNB record with top ELND match



Step 5: Identify conflicting pairings



Step 6: Isolate each group of conflicts to resolve



Step 7: Consider the next closest matches for each conflicting pair

Conflicting SLNB Records

Patient Record	Hazard Ratio
#2	6.0
#19	5.8
#22	6.0



Next best ELND matches

1st	2nd	3rd
#11 Hazard=6.0	#29 Hazard=6.1	#62 Hazard=6.1
#11 Hazard=6.0	#36 Hazard=5.3	#71 Hazard=5.0
#11 Hazard=6.0	#29 Hazard=6.1	#62 Hazard=6.1

Step 8: Try each set of alternative next-best pairings, calculating Hazard Ratio differences

Patient Record	Hazard Ratio
#2	6.0
#19	5.8
#22	6.0

1st		2nd		3rd
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1
#11 Hazard=6.0		#36 Hazard=5.3		#71 Hazard=5.0
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1

#2 <-> #29, H.R. difference = 0.1
#19 <-> #36, H.R. difference = 0.5
#22 <-> #11, H.R. difference = 0.0
Total Hazard Ratio difference = 0.6

Step 8: Try each set of alternative next-best pairings, calculating Hazard Ratio differences

Patient Record	Hazard Ratio
#2	6.0
#19	5.8
#22	6.0

1st		2nd		3rd
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1
#11 Hazard=6.0		#36 Hazard=5.3		#71 Hazard=5.0
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1

#2 <-> #11, H.R. difference = 0.0
#19 <-> #36, H.R. difference = 0.5
#22 <-> #29, H.R. difference = 0.1
Total Hazard Ratio difference = 0.6

Step 8: Try each set of alternative next-best pairings, calculating Hazard Ratio differences

Patient Record	Hazard Ratio
#2	6.0
#19	5.8
#22	6.0

1st		2nd		3rd
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1
#11 Hazard=6.0		#36 Hazard=5.3		#71 Hazard=5.0
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1

#2 <-> #62, H.R. difference = **0.1**
#19 <-> #11, H.R. difference = **0.2**
#22 <-> #29, H.R. difference = **0.1**
Total Hazard Ratio difference = 0.4

Step 8: Try each set of alternative next-best pairings, calculating Hazard Ratio differences

Patient Record	Hazard Ratio
#2	6.0
#19	5.8
#22	6.0

1st		2nd		3rd
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1
#11 Hazard=6.0		#36 Hazard=5.3		#71 Hazard=5.0
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1

#2 <-> #29, H.R. difference = **0.1**
#19 <-> #36, H.R. difference = **0.5**
#22 <-> #11, H.R. difference = **0.0**
Total Hazard Ratio difference = 0.6

Step 8: Try each set of alternative next-best pairings, calculating Hazard Ratio differences

Patient Record	Hazard Ratio
#2	6.0
#19	5.8
#22	6.0

1st		2nd		3rd
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1
#11 Hazard=6.0		#36 Hazard=5.3		#71 Hazard=5.0
#11 Hazard=6.0		#29 Hazard=6.1		#62 Hazard=6.1

#2 <-> #29, H.R. difference = 0.1
#19 <-> #11, H.R. difference = 0.2
#22 <-> #62, H.R. difference = 0.1
Total Hazard Ratio difference = 0.4

Step 8: Try each set of alternative next-best pairings, calculating Hazard Ratio differences

...

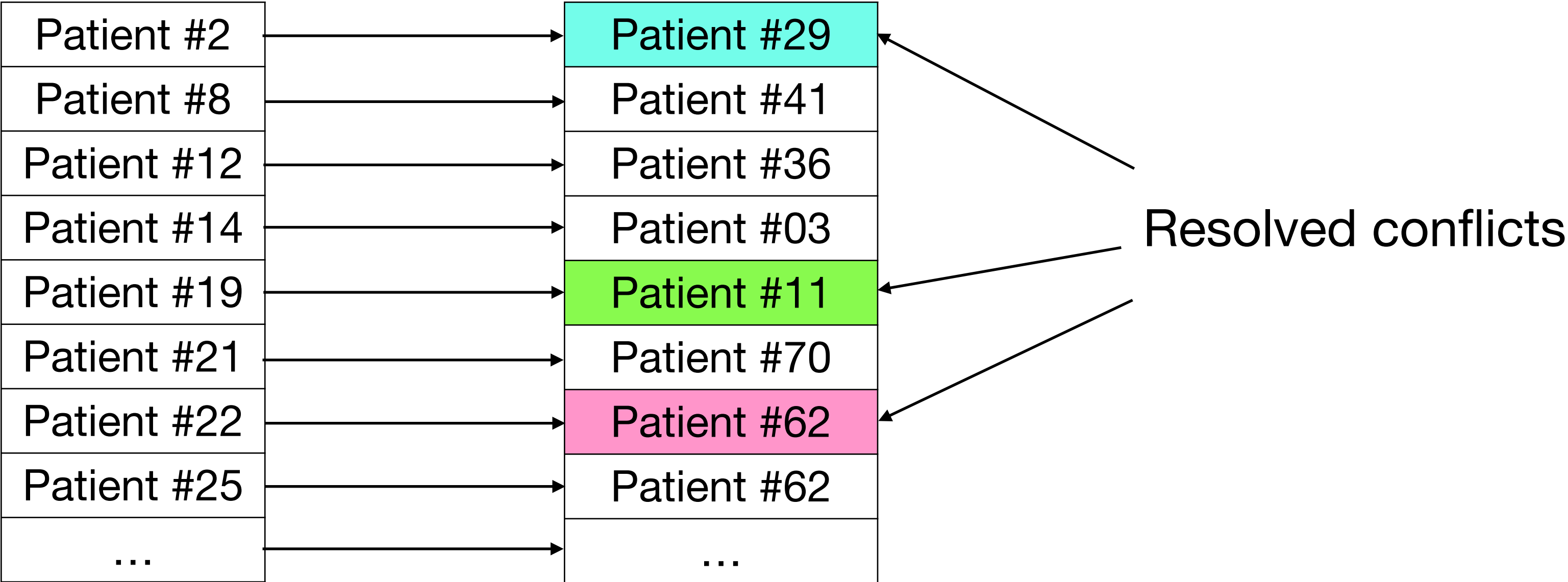
Step 9: Select the combination of pairings with the lowest Total Hazard Ratio difference

Patient Record	Hazard Ratio		
#2	6.0	→	#29 Hazard=6.1
#19	5.8	→	#11 Hazard=6.0
#22	6.0	→	#62 Hazard=6.1

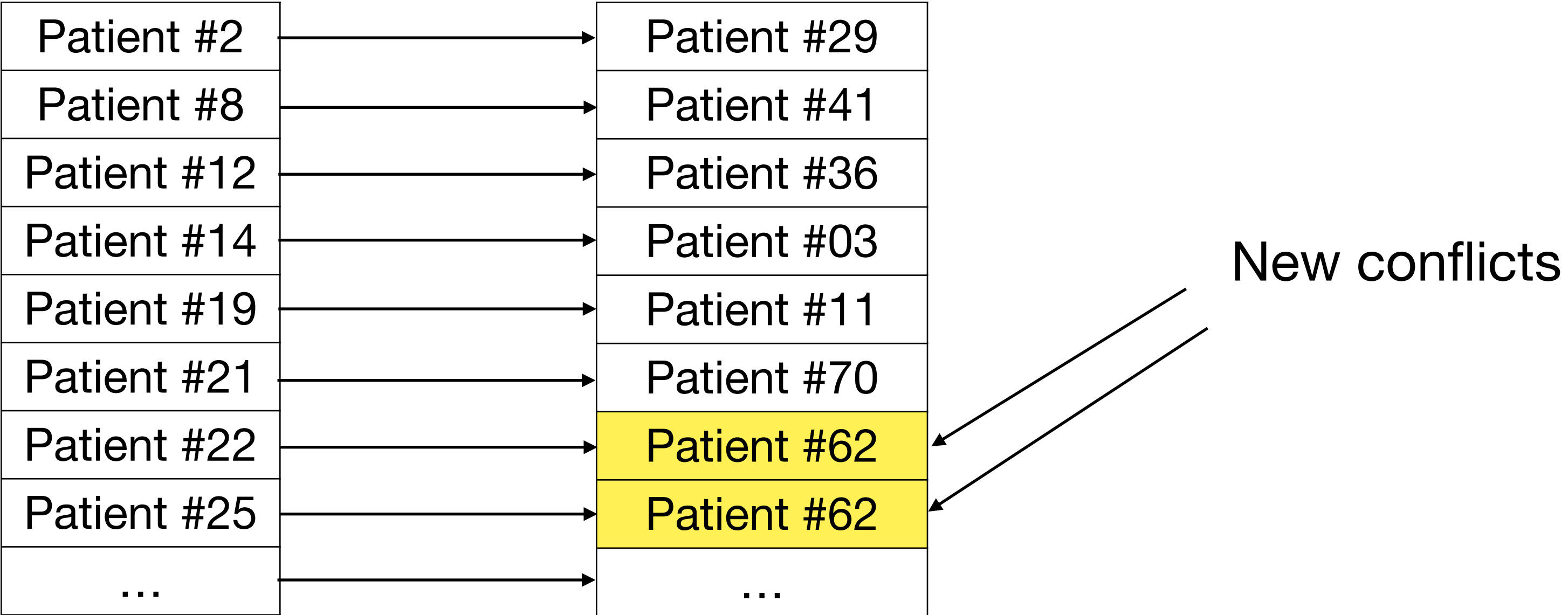
Total Hazard Ratio difference = **0.4**

There may be multiple combinations that produce a difference of 0.4 - the choice is ephemeral

Step 11: Reintroduce the resolved pairings back into the list

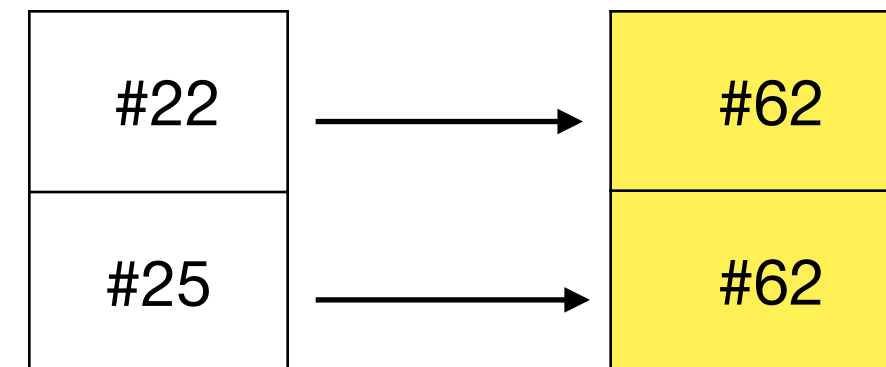


Reintroduction may cause new conflicts!



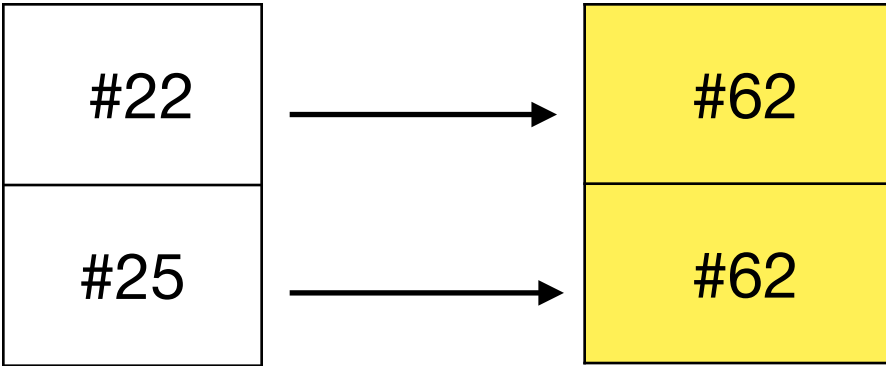
Repeat Steps 6 to 11 until no conflicts remain...

- **Identify & isolate conflicts**



Repeat Steps 6 to 11 until no conflicts remain...

- Identify & isolate conflicts

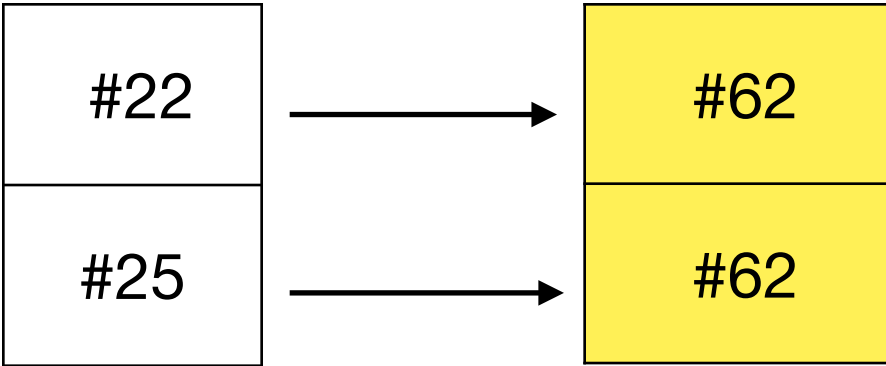


- Consider next closest matches

Patient		1st	2nd
#22	→	#62 Hazard=6.0	#88 Hazard=6.3
#25	→	#62 Hazard=5.7	#72 Hazard=5.3

Repeat Steps 6 to 11 until no conflicts remain...

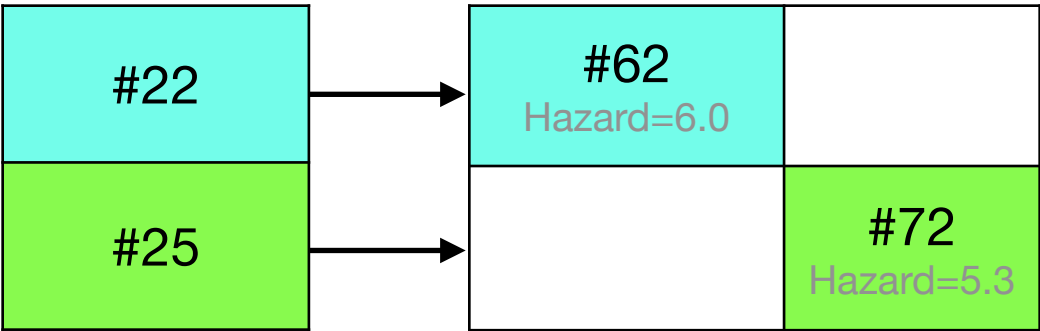
- Identify & isolate conflicts



- Consider next closest matches

Patient	1st	2nd
#22	#62 Hazard=6.0	#88 Hazard=6.3
#25	#62 Hazard=5.7	#72 Hazard=5.3

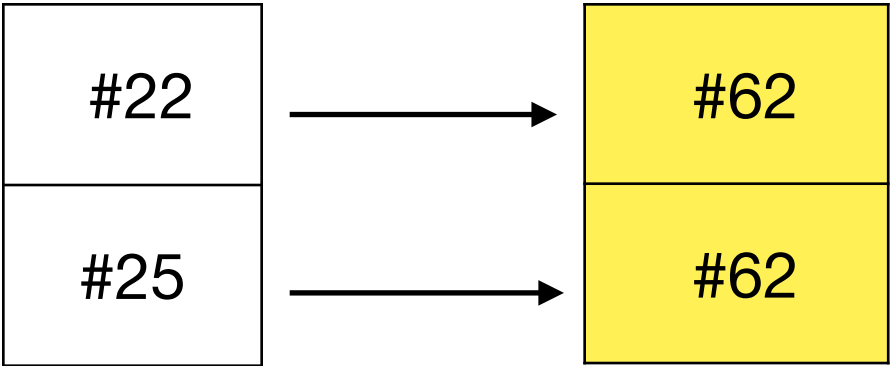
- Select combination with lowest difference



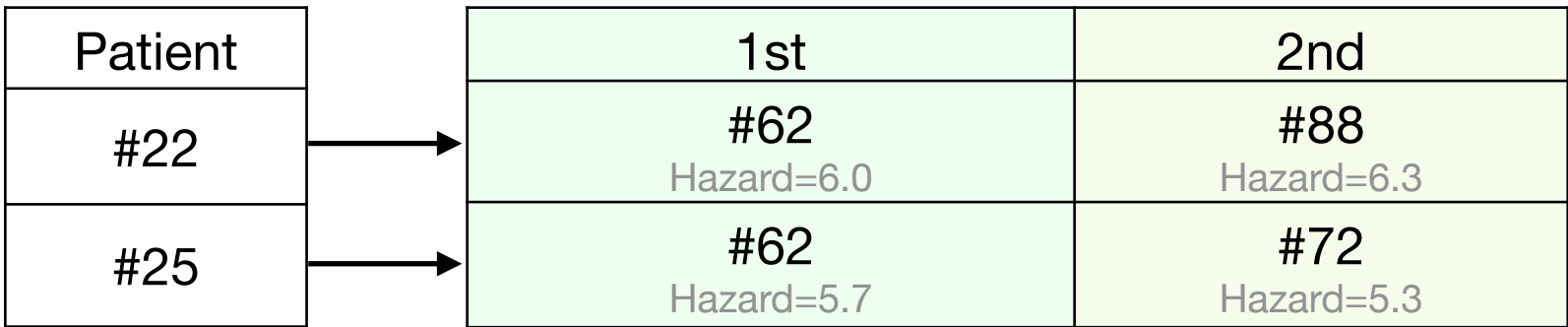
#22 <-> #62, H.R. difference = 0.1
#25 <-> #72, H.R. difference = 0.4
Total Hazard Ratio difference = 0.5

Repeat Steps 6 to 11 until no conflicts remain...

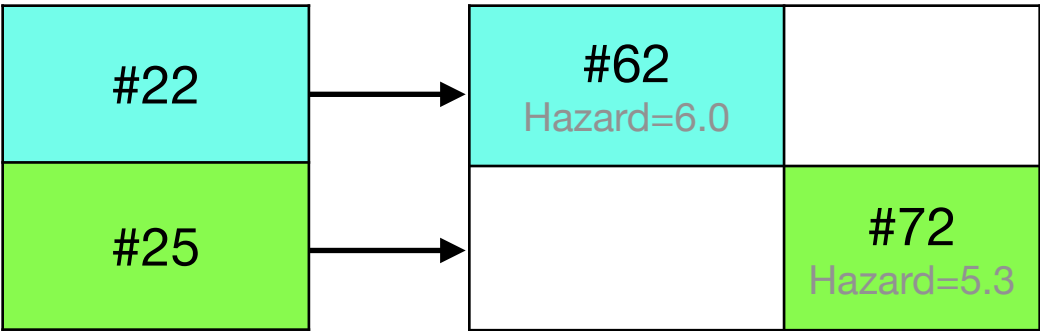
- Identify & isolate conflicts



- Consider next closest matches

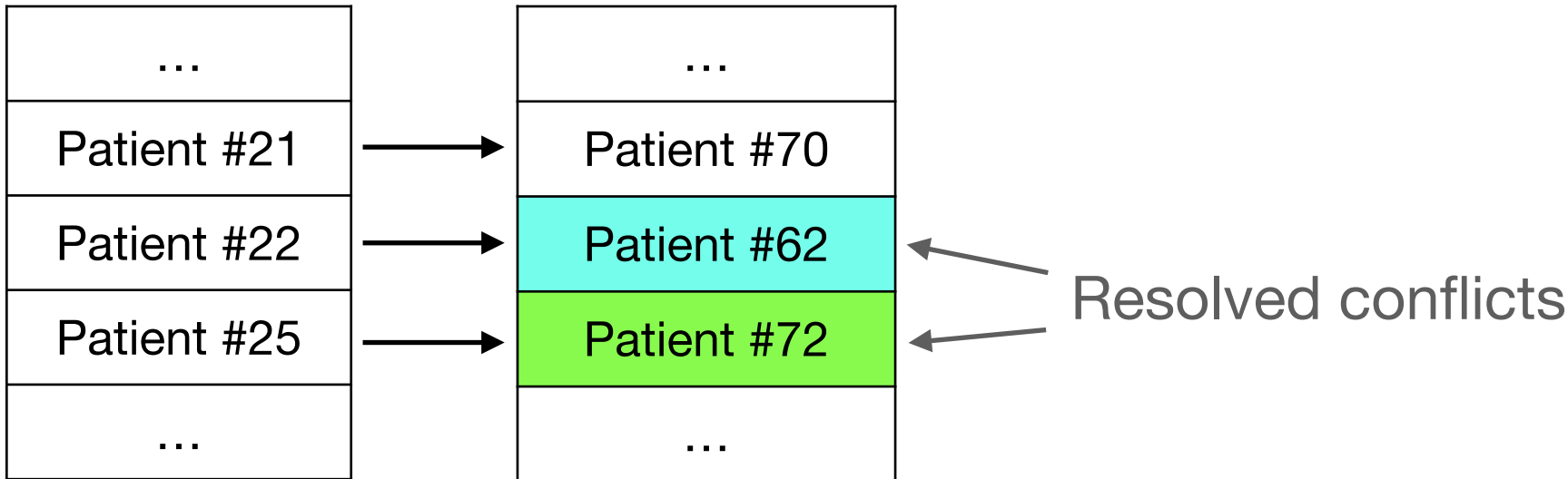


- Select combination with lowest difference



#22 <-> #62, H.R. difference = 0.1
#25 <-> #72, H.R. difference = 0.2
Total Hazard Ratio difference = 0.3

- Reintroduce pairings



Finish: No conflicts remain; all pairings are unique with lowest possible sum of Hazard Ratio differences

Patient #2	→	Patient #29
Patient #8	→	Patient #41
Patient #12	→	Patient #36
Patient #14	→	Patient #03
Patient #19	→	Patient #11
Patient #21	→	Patient #70
Patient #22	→	Patient #62
Patient #25	→	Patient #72
...	→	...

=
=
=
=
=
=
=
=

H.R. Difference
0.1
0.0
0.0
0.0
0.2
0.0
0.1
0.2
...
Total = 0.7