ANALYSIS OF CHARM AND DOHMPI MATCHING

19TH ANNUAL EARLY HEARING DETECTION & INTERVENTION MEETING

KANSAS CITY, MO MARCH 9, 2020

# INTRODUCTIO N

- In public health care, federated or integrated data systems can provide
  - Authorized users with access to data from multiple sources
  - Timely alerts about unusual situations
  - Opportunities to validate data or to fill-in missing pieces of information
- The success of a federated or integrated data system involving person-centric data depends on accurately matching person records across its data sources
- In Utah, EHDI is a data source for two different federated data systems:
  - Child-health Advanced Record Management (CHARM)
  - Department of Health Master Patient Index (DOPMPI)

# THE MATCHING QUALITY PROBLEM

- As with most federated or integrated data systems with person-centric data, CHARM and DOHMPI both include software components for matching person records
- Problem: How can the CHARM or DOHMPI teams measure the quality of their matchers
- Three common approaches
  - Match rates
  - Manual review of a sampling of matching decisions
  - Run matchers against known testbeds

# THE MATCHING QUALITY PROBLEM

- Approach #I Match rates
  - Measure the number of records from one data source that match records from another
  - Track the measurements over time, looking at
    - Whether they are close to the expected overlap in the data source's population
    - Whether there are any sudden increases or decreases
  - Pros:
    - Easy to automate
  - Cons
    - Does not measure matching quality directly
    - Significant changes are only indication of potential changes in matching quality that warrant further investigation

# BACKGROUND

### Matching Rates

### Given two data sources: A and B

# BACKGROUND

Classification Analysis of Matching Decisions Classification of pairs of records between A and B:

Matcher's	True Classification			
Classification	Match (P)	Non-Match (N)		
Match	True Positive (TP)	False Positive (FP)		
Non-Match	False Negative (FN)	True Negative (TN)		

Metric	Equation
Sensitivity (recall, hit rate, or true positive rate)	TP / P
Specificity (selectivity or true negative rate)	TN / N
Precision	TP / (TP + FP)
Accuracy	(TP + TN) / (P + N)

# THE MATCHING QUALITY PROBLEM

- Approach #2 Manual review of sample matching decisions
  - Select a set of sample matching decisions
  - For each selected matching decision, manually determine if is a true match (TP), false match (FP), true non-match (TN), or missed match (FN)
  - Use TP, FP, TN, TN to compute
    - Sensitivity How well the matcher is finding TP's and avoiding FN's
    - Specificity How well the matcher is finding TN's and avoiding FP's
    - Precision How well the matcher is finding TP's while avoiding FP's
    - Accuracy How well the matcher is doing in make correct decisions, i.e., finding TP's and TN's, while avoiding FP's or FN's
  - Pros
    - Can provide excellent indicators of matching quality
  - Cons
    - Can be timing consuming and costly, even if some the review process can be automated
    - Sensitive the size and distribution of selected sample set

# THE MATCHING QUALITY PROBLEM

- Approach #3 Run against a known testbed
  - Feed test records to the matcher
  - Compare matching decisions against expected (known) matching decisions for the testbed
  - Track true matches (TP), false matches (FP), true non-matches (TN), and missed matches (FN)
  - Compute sensitivity, specificity, precision, and accuracy
  - Pros
    - Can provides a good indicator of matching quality, if the testbed is representative the real records in the data sources
  - Cons
    - Very costly to setup a testbed that is truly representative of the records in the real data sources
    - Can be hard to wire the testbed into the matcher

### AN ALTERNATIVE: APPROACH #4

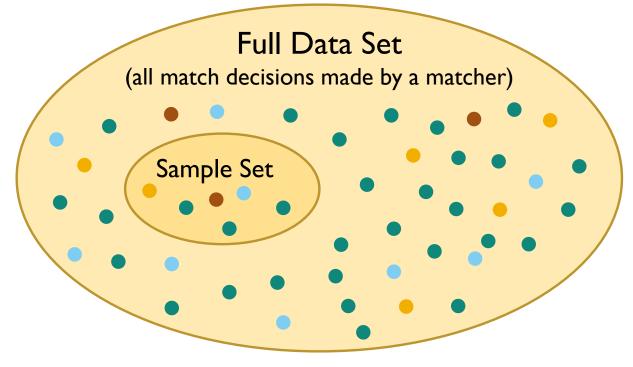
 Compare the decisions made by two independent matchers and then sample conflicting match decisions

Pros

- Can provide excellent indicators of matcher quality
- Doesn't require extensive sampling, like Approach #2
- Doesn't require creating a testbed that is representative of records from each data source and doing manually matching for all those records, like #3
- Cons
  - Requires two independent matchers
- CHARM and DOHMPI both match records from the EHDI database and from a birth registry, referred to here as Vital Statistics (VS)

# BACKGROUND

Classification Analysis via Sampling

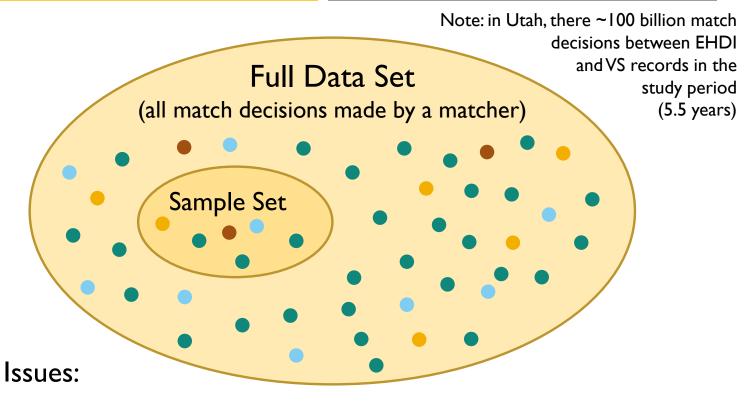


General Process

- I. Select a sample set
- 2. Evaluate each match decision, i.e., determine whether it is a TP, FP, FN, or TN
- 3. Generalize to entire data set

# BACKGROUND

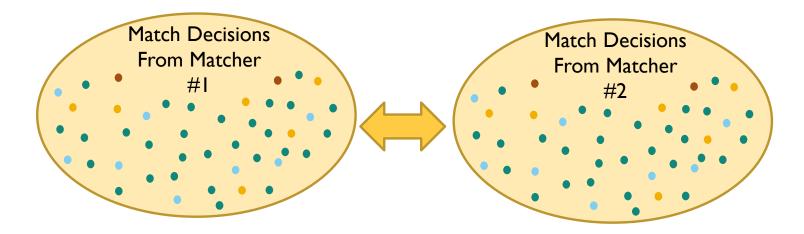
Classification Analysis via Sampling



- The Sample Set needs to be BIG
  - The classification of the matches is not a normal distribution
  - FP + FN is expected to be very small compare to the number TP + TN
- The bigger the sample set, the more costly it is to do the manual analysis of the match determination

# APPROACH #4: THE METHOD

Use two independent matchers to classify "most" of the match decisions automatically



### **General Process**

- For each record from each data source, compare the match decision(s) made by each matcher (#1 and #2) for that record
  - If the match decisions are the same, then classify them as TP and TN
  - If the match decisions are different, mark match decisions as "potential problems"

# APPROACH #4

Use two independent matchers to classify "most" of the match decisions automatically

### General Process (continued)

- 2. Categorize the potential problems as
  - Matched by #1 but not #2
  - Matched by #2 but not #1
  - #I's matches are a subset of #2's
  - #2's matches are a subset of #1's
  - #I's and 2's matches intersect
  - #1's and 2's matches are completely different
- 3. Randomly select samples from each potentialproblem category
- 4. Review the match decisions in each sample set and classify them as TP, FP, FN, and TN; also, record observations about the data
- 5. Generalize results to all matching decisions for both matchers

### APPROACH #4

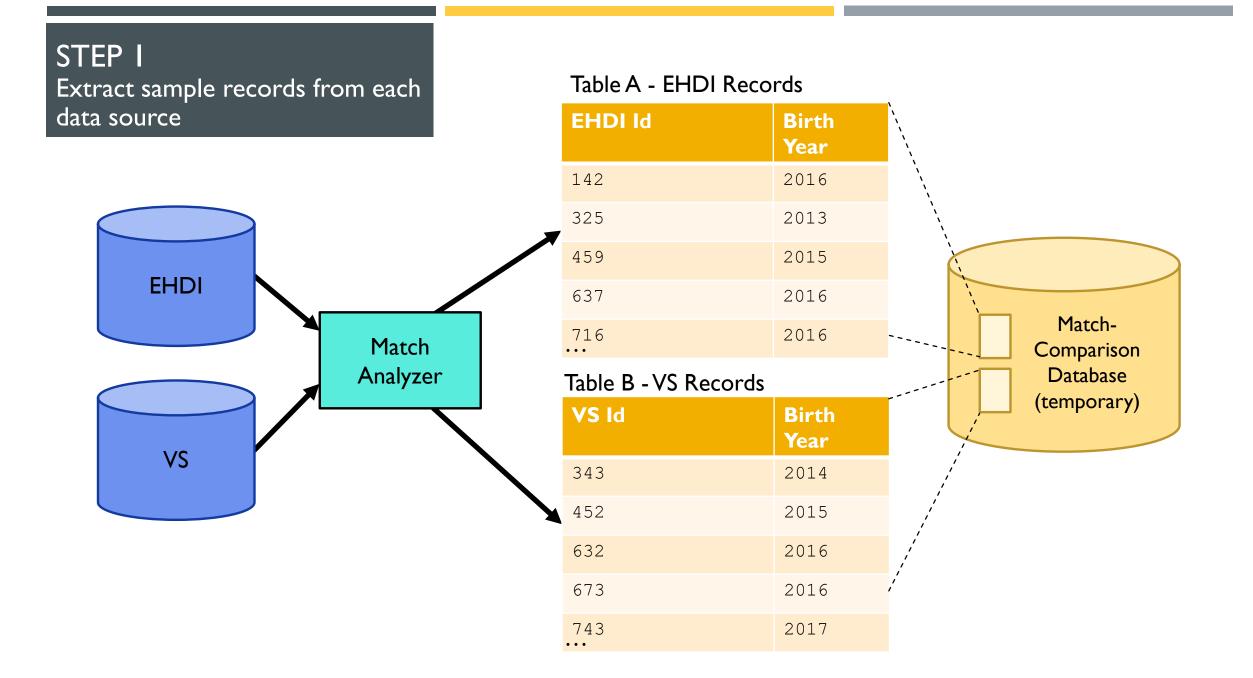
Specific steps from a technical perspective

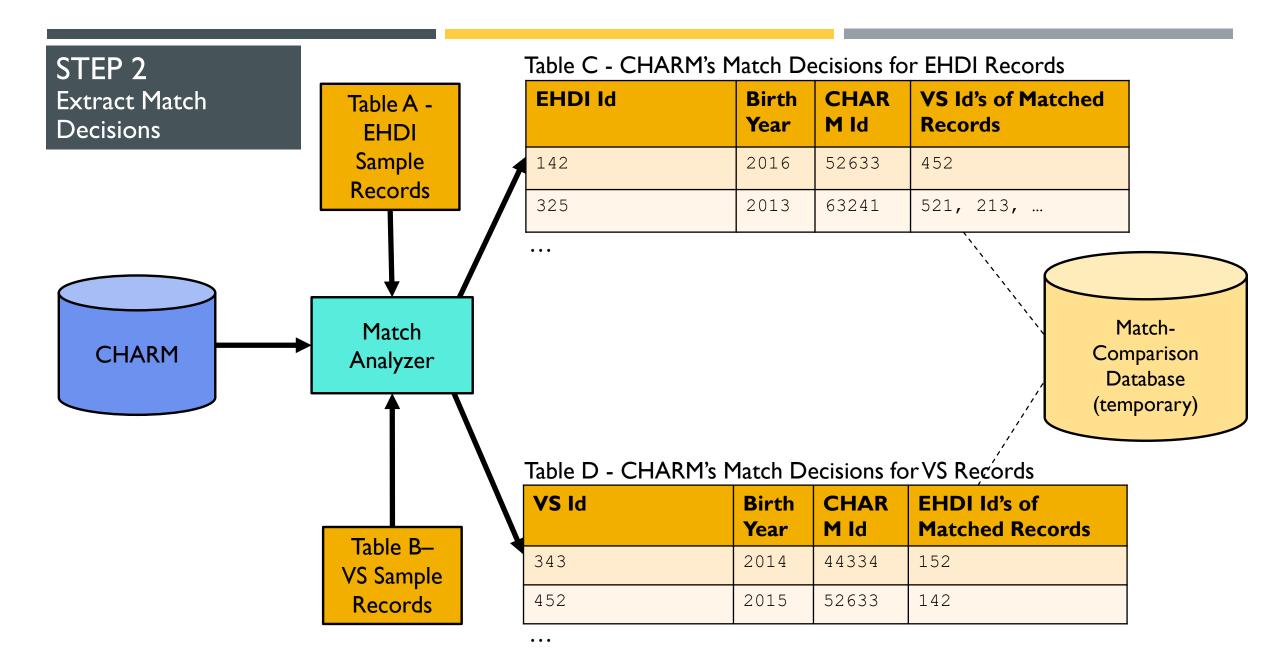
- I. Extract sample records from each data source
- 2. Extract match decisions
- 3. Categorize match decisions
- 4. Select sample sets for each category that represents potential problems
- 5. Extract detailed data for each record in each sample set
- 6. Manual review the potential problems and classify each associated match decision as TP, FP, FN, or TN
- 7. Analyze and generalize the results
- 8. Formulate recommendations for improvement

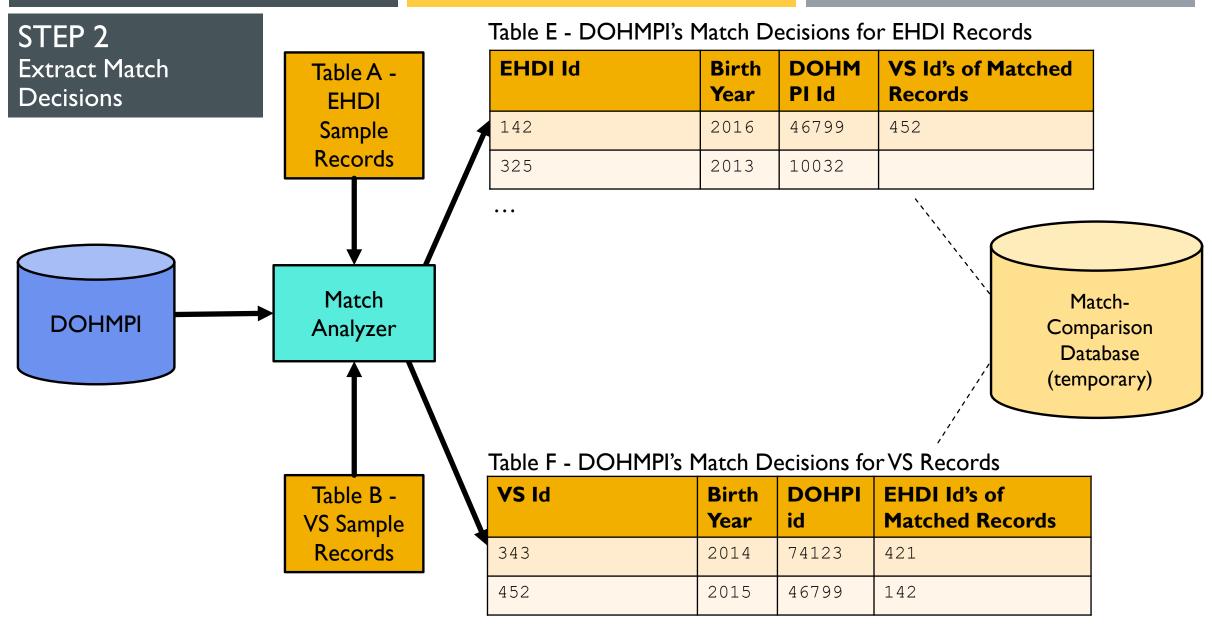
### APPROACH #4

Automated steps

- Extract sample records from each data source
- 2. Extract match decisions
- 3. Categorize match decisions
- Select sample sets for each category that represents potential problems
- 5. Extract detailed data for each record in each sample set
- 6. Manual review the potential problems and classify each associated match decision as TP, FP, FN, or TN
- 7. Analyze and generalize the results
- 8. Formulate recommendations for improvement







Categorize match decisions

- The Match Analyzer compares the match decisions in Table C with Table E and those in Table D with Table F – record by record
  - Because a record from one data source can match zero or more record from the other, these are set comparisons
- The Match Analyzer places each record in one of the following categories:
  - MCC<sub>1</sub> Same Matches in Both Systems
  - MCC<sub>2</sub> Neither System found a Match
  - MCC<sub>3</sub> Matched by CHARM but Not DOHMPI
  - MCC<sub>4</sub> Matched by DOHMPI but Not CHARM
  - MCC<sub>5</sub> CHARM Matches Subset of DOHMPI Matches
  - MCC<sub>6</sub> DOHMPI Matches Subset of CHARM Matches
  - MCC<sub>7</sub> Matches Intersect
  - MCC<sub>8</sub> Matches Differ
- For MCC<sub>1</sub> and MCC<sub>2</sub>, the Match Analyzer automatically classifies associated match decisions as TP's and TN's

Table C - CHARM's Match Decisions for EHDI Records

EHDI Id	Birth Year	CHAR M Id	VS Id's of Matched Records
142	2016	52633	452
325	2013	63241	521, 213,

#### Table E - DOHMPI's Match Decisions for EHDI Records

EHDI Id	Birth Year	DOHM Pld	VS Id's of Matched Records
142	2016	46799	452
325	2013	10032	

- Since both matchers linked EHDI record 142 to VS record 452, EDHI record 142 is categorized as MCC<sub>1</sub> and
  - The (EHDI 142,VS 152) pairing are classified as TP match decisions for both matchers.
  - Also, all other (EHDI 142,VS x) pairings, where x is one of the 316,847 other records in VS for the study period, are automatically considered TN match decisions for both matchers.

### STEP 3

Examples

More Examples

### Table C - CHARM's Match Decisions for EHDI Records

EHDI Id	Birth Year	CHAR M Id	VS Id's of Matched Records
142	2016	52633	452
325	2013	63241	521, 213

#### Table E - DOHMPI's Match Decisions for EHDI Records

EHDI Id	Birth Year	DOHM PI Id	VS Id's of Matched Records
142	2016	46799	452
325	2013	10032	

- Since the CHARM matcher linked EHDI record 325 to VS records 521 and 213 and DOHMPI did not link 325 at all, this EDHI record is categorized as MCC<sub>3</sub> and a subsequent manual review will determine
  - if the (EHDI 325,VS 521) and (EHDI 325, 213) pairings are TP for CHARM and FN for DOHMPI, or
  - if they are FP for CHARM and TN for DOHMPI

Results of matching categorization

### Population Counts by Year

Year	# of EHDI Records	# of VS Records
2013	52840	51907
2014	53576	52211
2015	52577	51769
2016	52088	51550
2017	50295	49667
2018	48642	48221
2019*	11644	11523
Totals	321662	316848

\*2019 was only for the months of Jan - May

# Categorizations matchings for EHDI Records

Year	MCC	MCC <sub>2</sub>	MCC <sub>3</sub>	MCC <sub>4</sub>	MCC <sub>5</sub>	MCC6	MCC <sub>7</sub>	MCC <sub>8</sub>
2013	39790	3200	3242	6216	357	4	0	31
2014	35970	4012	4121	9174	257	2	0	40
2015	38266	787	73	13362	74	4	0	11
2016	39855	482	76	11598	56	4	0	17
2017	39460	469	69	10213	66	Ι	0	17
2018	39831	249	81	8423	44	0	0	14
2019	9472	130	101	1916	20	I	0	4
Totals	242644	9329	7763	60902	874	16	0	134

MCC<sub>1</sub> Same Matches in Both Systems

MCC<sub>2</sub> - Neither System found a Match

- MCC<sub>3</sub> Matched by CHARM but Not DOHMPI
- MCC<sub>4</sub> Matched by DOHMPI but Not CHARM

MCC<sub>5</sub> - CHARM Matches Subset of DOHMPI Matches

MCC<sub>6</sub> - DOHMPI Matches Subset of CHARM Matches

 $MCC_7$  - Matches Intersect

MCC<sub>8</sub> - Matches Differ

### STEP 3

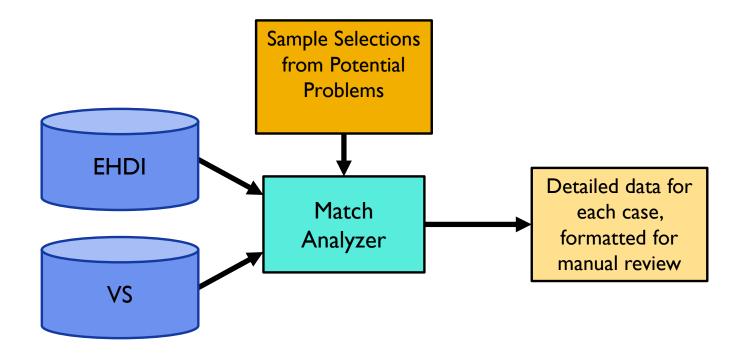
# Results of matching categorization

Select sample sets for each category that represents potential problems  The Match Analyzer randomly selects a percentage of the match comparisons from each potential problem category {MCC<sub>3</sub>, ..., MCC<sub>8</sub>}

	Comparison with EHDI as Basis									
Year	MCC <sub>3</sub> MCC <sub>4</sub> MCC <sub>5</sub> MCC <sub>6</sub> MCC <sub>7</sub>									
2013	3242	6216	357	4	0	31				
2014	4121	9174	257	2	0	40				
2015	73	13362	74	4	0	11				
2016	76	11598	56	4	0	17				
2017	69	10213	66	I	0	17				
2018	81	8423	44	0	0	14				
2019	101	1916	20	I	0	4				
Totals	7763	60902	874	16	0	134				

Extract detailed data for each potential problem in the sample sets

- For each selected match comparison, the Match Analyzer extracts detailed data for all involved child records
- These detailed data are (were) stored that in a temporary file on a secure server within the UDOH intranet



Manual review those potential problems and classify each associated match decisions as TP, FP, FN, or TN

- In this step, we systematically studied all the randomly selected match comparisons from each potential-problem MCC and identify the following for each match or missed match, for each matcher:
  - Whether a match made by each matcher is a TP or FP
  - Whether a match made by the CHARM matcher but not the DOHMPI matcher is a TN or FN for DOHMPI
  - Whether a match made by the DOHMPI matcher but not the CHARM matcher is a TN or FN negative for DOHMPI
  - The characteristics of the data may have led to a bad decision, i.e., a FP or FN

### Matches Found by CHARM but Not DOHMPI (MCC<sub>3</sub>)

CHARM: Manual Matching of Sample Pairings From EHDI's Perspective							
Year	# Case for manual review		ТР	FP	TN	FN	
2013	34		34	0	0	0	
2014	61		61	0	0	0	
2015	2		2	0	0	0	
2016	0		0	0	0	0	
2017	2		2	0	0	0	
2018	0		0	0	0	0	
2019	1		1	0	0	0	
Total	100		100	0	0	0	

#### DOHMPI: Manual Matching of Sample Pairing

ТР	FP	TN	FN
0	0	0	34
0	0	0	61
0	0	0	2
0	0	0	0
0	0	0	2
0	0	0	0
0	0	0	1
0	0	0	100

#### From VS's Perspective

Year	# Case for manual review	
2013	50	
2014	59	
2015	0	
2016	1	
2017	0	
2018	1	
2019	2	
Total	113	

тр	50	TN	EN
TP	FP	TN	FN
50	0	0	0
61	0	0	0
0	0	0	0
1	0	0	0
0	0	0	0
1	0	0	0
2	0	0	0
115	0	0	0

ТР	FP	TN	FN
0	0	0	50
0	0	0	61
0	0	0	0
0	0	0	1
0	0	0	0
0	0	0	1
0	0	0	2
0	0	0	115

Matches Found by DOHMPI but Not CHARM  $(MCC_4)$ 

From	CHARM: Manual Matching of Sample Pairings From EHDI's Perspective						
Year	# Case for manual review		ТР	FP	TN	FN	
2013	8		2	0	2	6	
2014	17		0	0	0	17	
2015	24		0	0	2	22	
2016	18		0	0	0	18	
2017	16		0	0	0	16	
2018	14		0	0	1	13	
2019	3		0	0	0	3	
Total	100		2	0	5	95	

#### DOHMPI: Manual Matching of Sample Pairing

ТР	FP	TN	FN
IF	FF		FIN
6	4	0	0
17	0	0	0
22	2	0	0
18	0	0	0
16	0	0	0
13	1	0	0
3	0	0	0
95	7	0	0

#### From VS's Perspective

11011	10 3 1 613	pee
Year	# Case for manual review	
2013	12	
2014	8	
2015	30	
2016	24	
2017	15	
2018	16	
2019	3	
Total	108	

ТР	FP	TN	FN
0	0	1	11
0	0	4	5
0	0	1	29
0	0	2	22
0	0	1	14
0	0	0	16
0	0	0	3
0	0	9	100

ТР	FP	TN	FN
11	1	0	0
5	4	0	0
29	1	0	0
22	2	0	0
14	1	0	0
16	0	0	0
3	0	0	0
100	9	0	0

CHARM's Matches are Subset DOHMPI's Matches (MCC<sub>5</sub>)

From	EHDI's Pe	rsnective	CHARM: Manual Matching of Sample Pairings			
Year	# Case for manual review	ispective	ТР	FP	TN	FN
2013	16		16	0	22	0
2014	14		14	0	25	0
2015	3		3	0	5	0
2016	2		2	0	3	0
2017	3		3	0	3	0
2018	2		2	0	2	0
2019	2		2	0	2	0
Total	42		42	0	62	0

#### DOHMPI: Manual Matching of Sample Pairing

ТР	FP	TN	FN
16	22	0	0
14	25	0	0
3	5	0	0
2	3	0	0
3	3	0	0
2	2	0	0
2	2	0	0
42	62	0	0

#### From VS's Perspective

11011	1031013	puu
Year	# Case for manual review	
2013	21	
2014	20	
2015	9	
2016	5	
2017	7	
2018	5	
2019	1	
Total	68	

ТР	FP	TN	FN
21	0	21	3
20	0	20	2
14	0	8	4
5	0	3	2
7	0	5	3
5	0	5	2
1	0	2	0
73	0	64	16

ŀ	TP	FP	TN	FN
	23	22	0	0
	22	20	0	0
	18	8	0	0
	7	3	0	0
	11	4	0	0
	7	5	0	0
	1	2	0	0
	89	64	0	0

DOHMPI's Matches are Subset CHARM's Matches  $(MCC_6)$ 

From	EHDI's Pe	rspective	CHARM: Manual Matching of Sample Pairings spective				
Year	# Case for manual review		ТР	FP	TN	FN	
2013	1		2	0	0	0	
2014	1		1	1	0	0	
2015	0		0	0	0	0	
2016	0		0	0	0	0	
2017	0		0	0	0	0	
2018	0		0	0	0	0	
2019	0		0	0	0	0	
Total	2		3	1	0	0	

### DOHMPI: Manual Matching of Sample Pairing

ТР	FP	TN	FN
1	0	0	1
1	0	1	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
2	0	1	1

#### From VS's Perspective

Total

11011	1031013	pee
Year	# Case for manual review	
2013	4	
2014	7	
2015	9	
2016	7	
2017	9	
2018	1	
2019	1	
Total	38	

ТР	FP	TN	FN
8	0	0	0
17	0	0	0
19	4	0	0
13	4	0	0
17	1	0	0
2	0	0	0
1	1	0	0
77	10	0	0

ТР	FP	TN	FN
4	0	0	4
8	0	0	9
9	0	4	10
7	0	4	6
9	0	1	8
1	0	0	1
1	0	1	0
39	0	10	38

CHARM's Matches intersect DOHMPI's Matches (MCC<sub>7</sub>)

#### From VS's Perspective # Case for manual Year review Total

CHARM: Manual Matching of Sample Pairings

#### TP FP ΤN FN

DOHMPI: Manual Matching of Sample Pairing

ТР	FP	TN	FN
4	0	0	4
8	0	0	9
9	0	4	10
7	0	4	6
9	0	1	8
1	0	0	1
1	0	1	0
39	0	10	38

CHARM's Matches are completely different from DOHMPI's Matches  $(MCC_8)$ 

From	CHARM: Manual Matching of Sampl Pairings From EHDI's Perspective					
Year	# Case for manual review		ТР	FP	TN	FN
2013	4		2	2	0	0
2014	9		8	1	0	0
2015	2		1	1	0	0
2016	3		0	3	0	0
2017	0		0	0	0	0
2018	3		3	0	1	0
2019	1		1	0	1	0
Total	22	]	15	7	2	0

#### DOHMPI: Manual Matching of Sample Pairing

TP	FP	TN	FN
0	4	0	0
1	8	0	0
1	1	0	0
2	1	0	0
0	0	0	0
0	4	0	0
0	2	0	0
4	20	0	0

#### From VS's Perspective

11011	1031613	peer
	# Case for manual	
Year	review	
2013	1	
2014	4	
2015	5	
2016	2	
2017	5	
2018	1	
2019	0	
Total	18	

ТР	FP	TN	FN
1	0	0	1
4	0	0	4
4	1	0	3
2	0	0	1
2	3	0	2
1	0	0	1
0	0	0	0
14	4	0	12

ТР	FP	TN	FN
1	0	0	1
4	0	0	4
3	2	1	2
1	1	0	1
3	2	1	1
1	0	0	1
0	0	0	0
13	5	2	10

Analyze and generalize the results

- Analyze the data from multiple perspectives and looking for patterns.
- Estimate the sensitivity, specificity, precision, and accuracy for each matcher
- Two approaches:
  - A. Generalize the results of the manual review to predicate the classification of all match decisions in the potential problem categorizes
  - B. Generalize the sampling of potential problems to create corresponding samplings of the MCC<sub>1</sub> and MCC<sub>2</sub> categories, for each the classifications are automatically computed

### **Base Numbers for Generalization Method A**

# GENERALIZATION

Method A - Generalize of classifications to all match decisions

	Total Number of Potential Problem Records	Number of Match Pair Among Potential Problems	Total Number of Records	Total Number of Possible Match Pairs
From EHDI's Perspective	69,689	87,504	321,662	103,466,120,582
From VS' Perspective	68,949	102,147	316,848	100,392,338,256

# GENERALIZATION

Method A - Generalize of classifications to all match decisions

# Match-Decision Classifications for Generalization Method A

		<b>Overall Estimated Match-Decision Classifications</b>			
		ТР	FP	TN	FN
From EHDI's Perspective	CHARM	285,086	2,096	103,465,808,511	24,889
	DOHMPI	278,385	23,317	103,465,792,419	26,461
From VS's Perspective	CHARM	300,003	2,750	100,392,007,805	27,698
	DOHMPI	292,191	15,322	100,391,997,545	33,198
Average	CHARM	292,545	2,423	101,928,908,158	26,294
	DOHMPI	285,288	19,320	101,928,894,982	29,830

# GENERALIZATION

Method A - Generalize of classifications to all match decisions

# Estimated Matching Quality Using Generalization Method A

		<b>Overall Estimated Match-Decision Classifications</b>				
		Sensitivit	Specificity	Precision	Accuracy	
		У				
From EHDI's Perspective	CHARM	91.970643%	99.999998%	99.270149%	99.999974%	
	DOHMPI	91.319880%	99.999977%	92.271513%	99.999952%	
From VS's Perspective	CHARM	91.547783%	99.999997%	99.091669%	99.999970%	
	DOHMPI	89.797442%	99.999985%	95.017446%	99.999952%	
Average	CHARM	91.753336%	99.999998%	99.178554%	99.999972%	
	DOHMPI	90.533848%	99.999981%	93.657576%	99.999952%	

### **Base Numbers for Generalization Method B**

# Method B - Generalize of potential-problem sampling to the good categories

GENERALIZATION

	Total Records	Total Potential Problems	Samples from the Potential Problems	% of Potential Problems Samples
From EHDI's Perspective	321662	69689	266	0.38170%
From VS' Perspective	316848	68949	351	0.50907%

# GENERALIZATION

Method B - Generalize of potential-problem sampling to the good categories

# Match-Decision Classifications for Generalization Method B

		<b>Overall Estimated Match-Decision Classifications</b>				
		ТР	FP	TN	FN	
From EHDI's Perspective	CHARM	I,088	8	105	95	
	DOHMPI	١,069	89	37	101	
From VS's Perspective	CHARM	1,518	14	113	4	
	DOHMPI	I,487	78	52	169	
Average	CHARM	1,303	11	109	118	
	DOHMPI	1,278	84	45	135	

# GENERALIZATIONS

Method B - Generalize of potential-problem sampling to the good categories

# Estimated Matching Quality Using Generalization Method B

		<b>Overall Estimated Match-Decision Classifications</b>				
		Sensitivit	Specificity	Precision	Accuracy	
From EHDI's Perspective	CHARM	<b>9</b> 1.969569%	92.920354%	99.270073%	92.052469%	
	DOHMPI	91.367521%	29.365079%	92.314335%	85.339506%	
From VS's Perspective	CHARM	91.500904%	88.976378%	99.086162%	91.321389%	
	DOHMPI	89.794686%	40.000000%	95.015974%	86.170213%	
Average	CHARM	91.695989%	90.833333%	99.162861%	91.628812%	
	DOHMPI	90.445860%	34.765625%	93.867058%	85.820896%	

Formulate recommendations for improvement  This step involves identifying patterns in the results and making some meaning recommendations for each matcher and for improving the quality of the source data

### RECOMMENDATIONS

For CHARM

### Data Cleaning Improvements

- Ensure that bad Newborn Screening Numbers (ones that don't match the expected formats) are converted to null
- Reformat all Newborn Screening Numbers to a standard format for easy comparison
- Convert a birth order to null, if it is 0 or if the multiple-birth flag is false
- Convert a bad birth weight to null
- Tweak Matching Rules
  - Ensure that there are no positive and less negative match influences for missing birth orders and birth weights
  - Have more negative match influence for mismatched birth orders
  - Have more positive match influence for matched birth weights
- Enhance CHARM so it can do re-matching

### RECOMMENDATIONS

For DOHMPI

- Data Cleaning Improvements
  - Standardize the format of newborn screening numbers
- Tweak Matching Rules
  - Raise the "join" threshold for all data sources (i.e. the match threshold for a record to link to a different data source record).
  - Require a minimum of 3 non-gender data elements to link with another identity record.
  - Add more restrictive matching rules related to different last names where other fields match
- Re-match updated records
- Implement an explicitly unlink and re-match feature

### RECOMMENDATIONS

For EHDI Data

- EHDI's data appears to have improved over time
- Continue efforts to improve the quality of
  - First and middle names
  - Birth weight
  - Birth orders for multiple births
  - Newborn screening numbers for multiple births
- Consider changing the sequencing of newborn screening kits to make it less likely for newborn screening numbers to be mixed up for multiple births

### SUMMARY

- Accurate matching of person records is critical to the success of any federated or integrated data system
- Traditional approaches to measuring matching quality are either very time consuming, expensive, or limited
- If there are two independent matchers, then there is a costeffective alternative, where
  - A significant portion of the work can be automated
  - The amount manual reviewing of matching decisions need is relatively small
  - There are two viable approaches to generalizing the results of the manual reviews to estimated overall match quality

# QUESTIONS?

