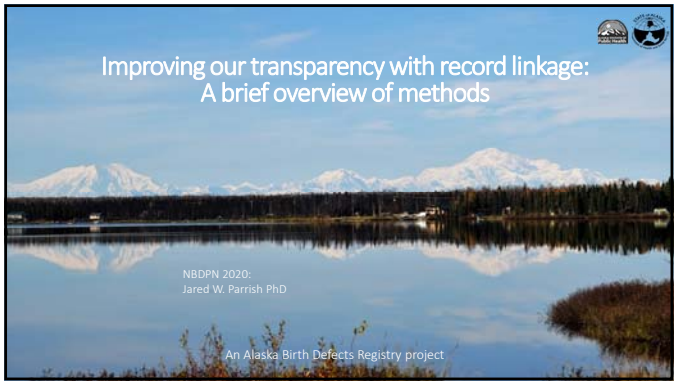
Improving our transparency with record linkage:
A brief overview of methods
NBDPN 2020:
Jared W. Parrish PhD
An Alaska Birth Defects Registry project

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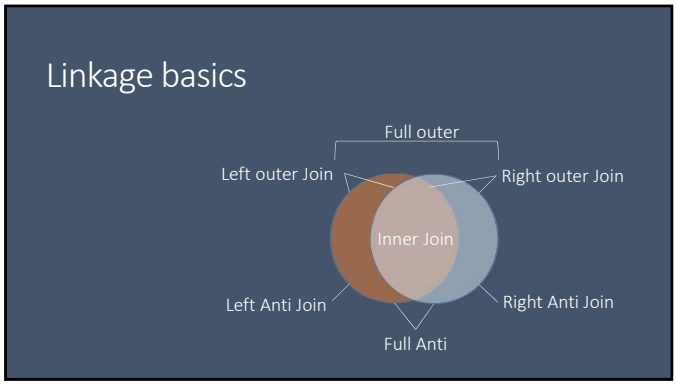
Linkage basics
Full outer
Left outer Join
Right outer Join
Inner Join
Left Anti Join
Right Anti Join
Full Anti

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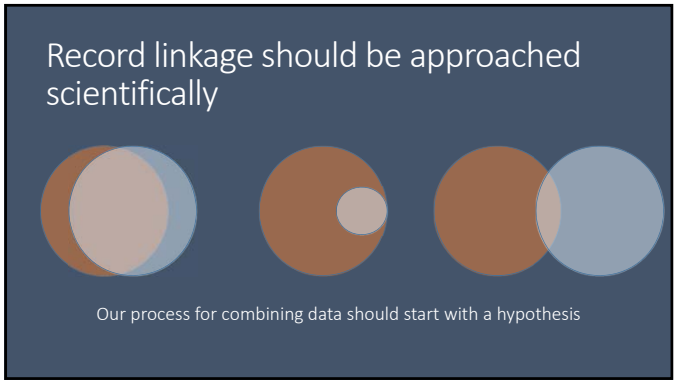
Record linkage should be approached scientifically
Our process for combining data should start with a hypothesis

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Image source: unbiasedresearch.blogspot.com

Statistics are based on probabilities.

Statistical conclusions are subject to error!

		True Match Status		
		Matches	Non-matches	
Link status (assigned by computer)	Links	True Links (True Positives)	False Links (False Positives / Type I error)	Total links
	Non-Links	Missed Links (False Negatives / Type II error)	True Non-Links (True Negatives)	Total Non-links
		Total Matches	Total Non-matches	Total record pairs

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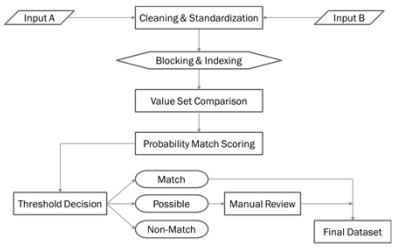

Both Systematic and Random error must be considered

In General

- Systematic error occurs at decision points
- Random error occurs during scoring and matching

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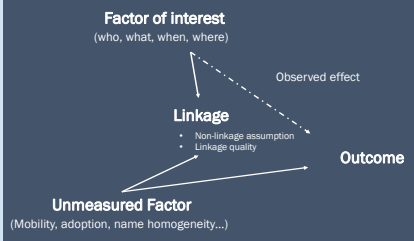
Poor linkages can result in bias

Bias can occur when linkage quality is differential by any unmeasured factor "U".



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Quick example of distance algorithms

Modified Levenshtein algorithm
Q-grams algorithm
Jaro-Winkler Algorithm

Compare “Chlid” and “Child”
Compare “Cihld” and “Child”
Compare “John-Adams” and “Adams-John”

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Modified Levenshtein Algorithm

Test how many operations needed for string “A” to = string “B”

$$ED_{w\,(s1,s2)} = \begin{cases} if\ e(s1,s2) > d * \max(L(s1),L(s2))\ then\ 0 \\ if\ e(s1,s2) < a * \max(L(s1),L(s2))\ then\ 1 \\ \left(\dfrac{[d * \max(L(s1),L(s2))] - e(s1,s2)}{(d-a) * \max(L(s1),L(s2))}\right) \end{cases}, otherwise$$

$e(s1,s2)$ = edit distance score a = approve level
$(s1,s2)$ = Strings 1 and 2 L = String length
d = Disapprove level

$$\begin{bmatrix} 0 & C & h & l & i & d \\ C & 0 & & & & \\ h & & 0 & & & \\ i & & & 1 & & \\ l & & & & 1 & \\ d & & & & & 1 \end{bmatrix} \begin{bmatrix} 0 & C & i & l & h & d \\ C & 0 & & & & \\ h & & 1 & & & \\ i & & & 1 & & \\ l & & & & 2 & \\ d & & & & & 2 \end{bmatrix}$$

$$ED_{w\,(Child,Child)} = \begin{cases} if\ 1 > 0.4 * 5\ then\ 0, False \\ if\ 1 < 0.1 * 5\ then\ 1, False \\ \left(\dfrac{[0.4 * 5] - 1}{(0.4 - 0.1) * 5}\right) \end{cases} = \frac{1}{1.5} = 0.67.$$

$$ED_{w\,(Cihld,Child)} = \begin{cases} if\ 2 > 0.4 * 5\ then\ 0, True \\ if\ 2 < 0.1 * 5\ then\ 1, False \\ \left(\dfrac{[0.4 * 5] - 2}{(0.4 - 0.1) * 5}\right) \end{cases} = \frac{0}{1.5} = 0$$

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Q-Grams Algorithm

Substrings string “A” and “B” into sets of length “q”

$$Q_{Bw\,(S1,S2)} = \begin{cases} if\ D[Gs(s1),Gs(s2)] > R[a * (|Gs(s1)| + |Gs(s2)|)]\ then\ 0 \\ if\ D[Gs(s1),Gs(s2)] < R[a * (|Gs(s1)| + |Gs(s2)|)]\ then\ 1 \\ \left(1 - \dfrac{D[Gs(s1),Gs(s2)] - R[a * (|Gs(s1)| + |Gs(s2)|)]}{R[d * (|Gs(s1)| + |Gs(s2)|)] - R[a * (|Gs(s1)| + |Gs(s2)|)]}\right) \end{cases}, otherwise$$

D = Disjoint grams a = approve level
Gs = grams of length ‘q’ d = Disapprove level
$(s1,s2)$ = Strings 1 and 2 R = Round

$$Q_{Bw\,(S1,S2)} = \begin{cases} if\ 6 > R[0.4 * (|10| + |10|)]\ then\ 0 \\ if\ 6 < R[0.1 * (|G10| + |10|)]\ then\ 1 \\ \left(1 - \left(\dfrac{6 - R[0.1 * (|10| + |10|)]}{R[0.4 * (|10| + |10|)] - R[0.1 * (|10| + |10|)]}\right)\right) \end{cases}, otherwise$$

$$= \begin{cases} if\ 6 > 2\ then\ 0, False \\ if\ 6 < 8\ then\ 1, False \\ \left(1 - \left(\dfrac{6-2}{8-2}\right)\right) = 1 - \dfrac{4}{6} = 0.33 \end{cases}$$

For example, setting q=2 the strings “John-Adams” and “Adams-John”:
- have the following 2-gram vectors {Jo, oh, hn, n-, -A, Ad, da, am, ms, s} and {Ad, da, am, ms, s-, -J, Jo, oh, hn, n}.
- The two vectors share the 2-grams of {Jo, oh, hn, Ad, da, am, ms}, with the disjointed 2-grams of {n-, -A, s, s-, -J, n}.

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Jaro-Winkler Algorithm

Scores the number of elements in common

$$d_{jw} = \left(\frac{1}{3}\left(\frac{m}{|s1|} + \frac{m}{|s2|} + \frac{m-t}{m}\right)\right) + l * f(1 - \left(\frac{1}{3}\left(\frac{m}{|s2|} + \frac{m}{|s2|} + \frac{m-t}{m}\right)\right))$$

$m = matchin\ characters$ $l = length\ of\ common\ characters\ (n < 5)$
$(s1, s2) = Strings\ 1\ and\ 2$ $f = scaling\ factor\ for\ common\ characters$
$t = \#of\ transpositions/2$

Using the same example Edit Distance example above we can calculate the *JW* distance for the two string comparison of "CHILD" and "CHLID" which experiences a single letter transposition between strings.

$S_i = \left\lfloor \frac{MAX(|S1|,|S2|)}{2} \right\rfloor - 1 = 1.5,$

m = 5, and $t = \frac{2}{2} = 1$ based on the characters I/L and L/I which are less than 1.5 characters apart

Thus,

$$d_{jw} = \left(\frac{1}{3}\left(\frac{5}{|5|} + \frac{5}{|5|} + \frac{5-1}{5}\right)\right) + 2 * 0.1\left(1 - \left(\frac{1}{3}\left(\frac{5}{|5|} + \frac{5}{|5|} + \frac{5-4}{5}\right)\right)\right) = 0.95$$

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Comparing these algorithms

	Levenshtein	Q-grams (g=2)	Jaro-Wikler
Child Chlid	0.67	0.00	0.95
Child Clhd	0.00	0.00	0.88
John-Adams Adams-John	0.00	0.33	0.30

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Setting manual review thresholds

Setting a threshold for manual review depends on the value of missing or making an erroneous match

- Trying to replicate a longitudinal prospective cohort missing a linkage (loss to follow-up) may be paramount
- Conducting population level surveillance in a large population balancing erroneous linkages and missed linkages while mitigating differential matching between subpopulations may be paramount

- Some helpful guidelines:
  - *Use machine learning tools on a subset of data with manually reviewed known parameters to develop a starting point*
  - *Training datasets from your input sources can help establish sensitivity of specificity of decision rules and comparison algorithms*
  - *The generalized Petro Distribution can be leveraged to establish minimum thresholds*

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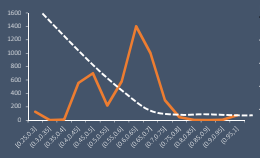
Threshold example

Two Fictitious data sets with 100 records each-
-Strings: DOB, Last Name, First Name,
-Block: Sex
-Method Jaro-Winkler



Threshold		Classification			Identified	Truth
Upper	Lower	N	P	L		
0.99	0.8	4944	33	55	70	71
0.95	0.8	4944	14	74	75	71
0.9	0.8	4944	7	81	81	71
0.99	0.75	4898	79	55	71	71
0.99	0.7	4598	379	55	71	71

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Linkage projects in process

Child Protective Services

- Are children reported for birth defects over-represented in Child Welfare
- Are children reported for NAS over-represented in Child Welfare

Permanent Fund Dividend – In process

- Map birth defects to identify clusters and overlay environmental exposures
- Map location of pregnancy and population movement

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Child Protection linkage example

Linkage Approach

1. Base population all births in Alaska during 2015
2. Left outer join (All birth records and matching CPS records)
3. Elements: First & Last name, Date of birth, Sex (manual review on middle name, residence, maternal name)
4. First subset to multiple births, Second non multiple births
   a. Linkage: Deterministic (reconcile duplicates)
   b. Linkage: Probabilistic (Jaro-Winkler, auto at 1.0, manual 0.89 – 0.99, block on year of birth)
5. Manual review: middle name match priority with DOB, minor typos, First name priority (name probability <=1%)
6. Duplication reconciliation

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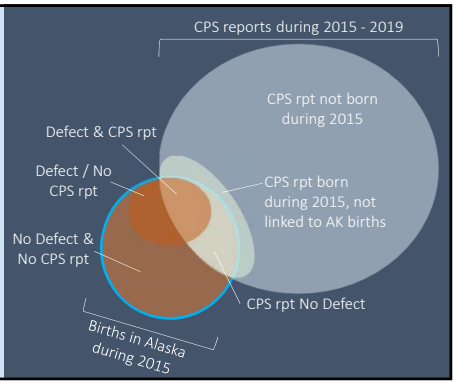
Linkage to 2015 birth cohort

- 11, 356 Live births in Alaska
- 58,455 Reports to AK CPS between 2015 – 2019
- 2,942 Reports to AK CPS born during 2015
  - 2,780 AK births linked to AK CPS reports born during 2015
  - 194 CPS reports not linked to AK births



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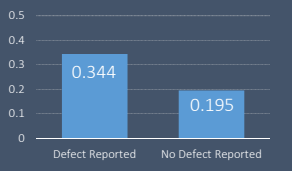
Proportion reported to CPS by 2019

Finding:

Relative to children born without a birth defect in Alaska during 2015, children born with a defect, are 76% more likely to be reported to CPS by 2019.

	CPS rpt	No CPS rpt	
Defect Reported	1301	2480	3781
No Defect Reported	1479	6096	7575
	2780	8576	11356



Prevalence Ratio: 1.76 (1.65, 1.87)

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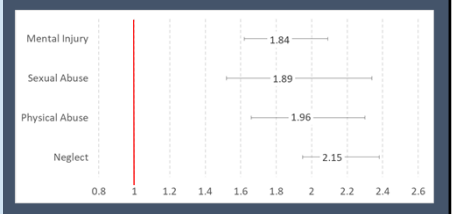
Relative proportion reported to CPS by maltreatment type



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Wrap up

In general in a manuscript describe:

Methods:
- The base population
- Type of join
- Linkage methodology and assumptions
- Identifiers used for linkages
- General data cleaning rules
- Manual review methods and thresholds

Results:
- Base population, proportion linked, non-linked, final study population
- If doing something fancy, provide validation results

Discussion:
- Limitations and potential / quantified bias
- Strengths of approach

Appendix/online only:
- Expand upon methods
- Algorithms used and how you determined
- Any ad-hoc analysis demonstrating linkage validity
- Full linkage specification and results

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Questions?

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ABDR website:
http://www.dhss.alaska.gov/dph/wcfh/Pages/mchepi/abdr/default.aspx

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