Data Cleaning Pipeline

Rebecca C. Steorts

August 30, 2024

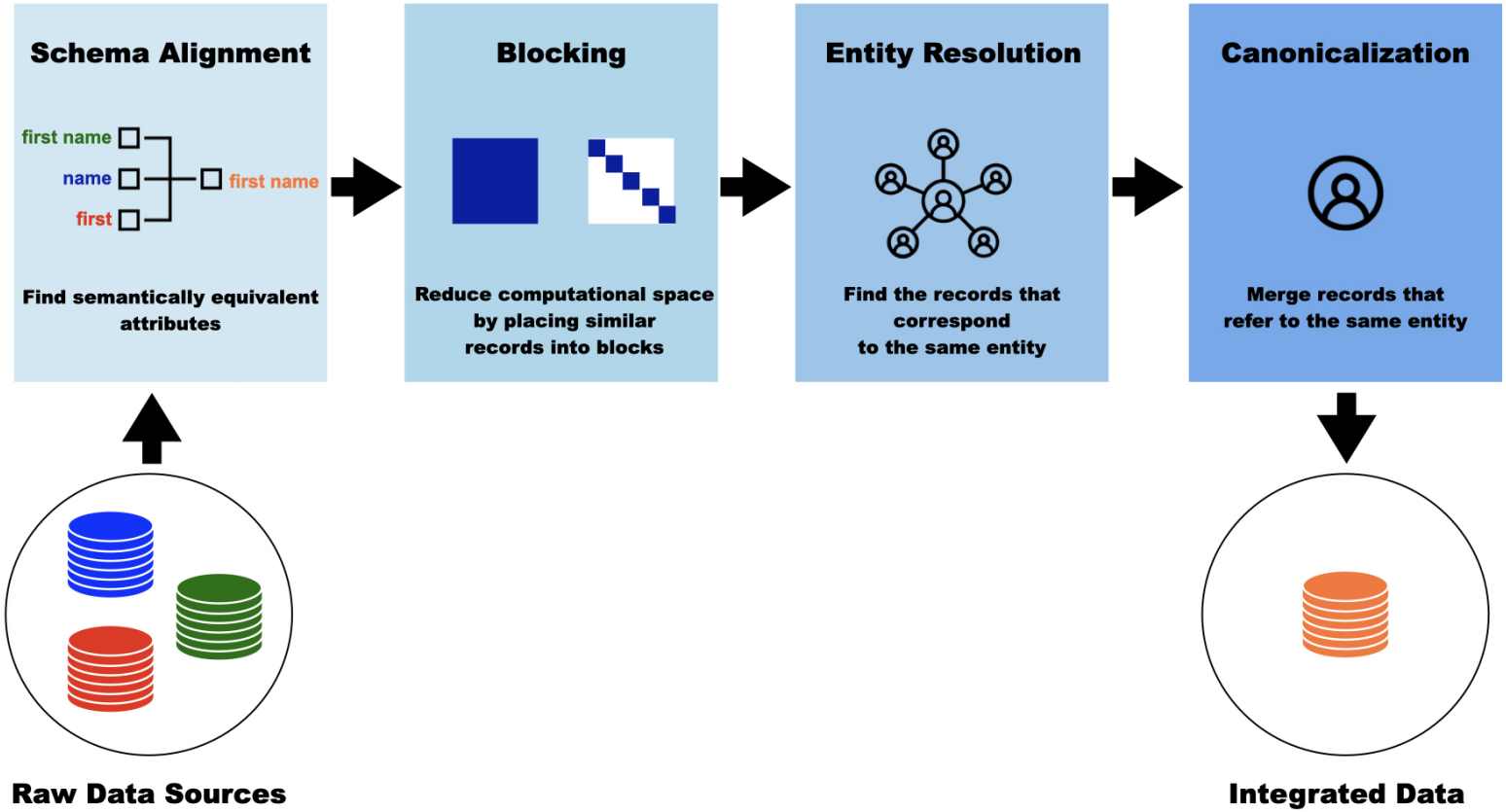
Objectives

- Cover some basic pipeline approaches from the database literature.
- Understanding how they integrate with one another.
- Understand pros and cons about the approaches.
- These methods are a basic starting point for moving forward with more complex methods.
- Due to their simplicity, they are used in many production or industrial pipelines. Let's try and understand why that would be the case by the end of the lecture.

Goals

1. Enumerating a census.
2. Enumerating those that have died in a conflict (such as Syria).
3. Predicting those in poverty in small regions from survey data.
4. Predicting results of elections from voter registration data.
5. Predicting housing/rental prices from Zillow data.

Each task may contain duplicated information, which is problematic for the underlying task at hand.


Schema Alignment
first name
name
first
first name
Find semantically equivalent attributes
Blocking
Reduce computational space by placing similar records into blocks
Entity Resolution
Find the records that correspond to the same entity
Canonicalization
Merge records that refer to the same entity
Raw Data Sources
Integrated Data

1. The most important information in the pipeline is known as the profile or the record.

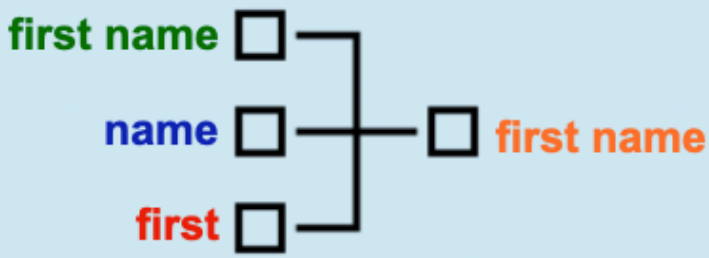
2. Each profile or record is a collection of attributes/fields about a person, organization, or object.

3. Commonly collected attributes about people are name, address, phone number, gender, among other types of information.

profile	name	address	gender	state
d1	Alan Smith	123 Main Street	M	NC
d2	Alan Smith	123 Main Street	M	NC
d3	Ann Waters	155 Green Way	F	NC
d4	Anne Waters	155 Green Way	F	NC
d5	Sally Glines	18 Court Road	F	NC
d6	Matt Box	1871 Red Drive	M	NC
d7	Joe Smith	2971 Orchard Court	M	NC
d8	Joe Smith	2971 Orchard Court	M	NC
d9	Joe Smith	2971 Orchard Court	M	NC
d10	Joe Smith	2971 Orchard Court	M	NC

Entity 1	Entity 2	Entity 3	Entity 4	Entity 5
d1 d2	d3 d4	d5	d6	d7 d8 d9 d10

Schema Alignment



Find semantically equivalent attributes

1. It is important that we align attributes when our schemata are disparate.
2. The goal is to create alignments of attributes based upon the following:
    1. Similarity
    2. Structure
    3. Attributes Present

Formally, this is known as identifying "semantically equivalent attributes", such as first name, first, and name.

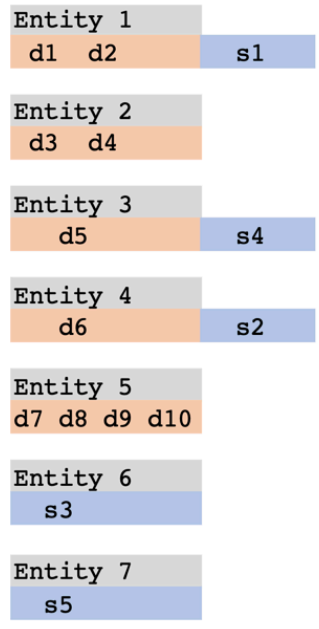
[Bernstein et al., 2011, Madhavan et al., 2001].

1. This stage leverages the attribute values from the records/profiles.
2. Schema knowledge is used (if available).
3. The goal is to learn attribute mappings between the data sources.
4. The goal is to also find "transformations, correspondences, or rules between the attributes." [Tejada et al., 2002, Yan et al., 2001].
5. Common transformations are used, such as: "Dr." to "Drive" or "3rd" to "third" [Active Atlas, Tejada et al., 2002].

profile	name	address	gender	state
d1	Alan Smith	123 Main Street	M	NC
d2	Alan Smith	123 Main Street	M	NC
d3	Ann Waters	155 Green Way	F	NC
d4	Anne Waters	155 Green Way	F	NC
d5	Sally Glines	18 Court Road	F	NC
d6	Matt Box	1871 Red Drive	M	NC
d7	Joe Smith	2971 Orchard Court	M	NC
d8	Joe Smith	2971 Orchard Court	M	NC
d9	Joe Smith	2971 Orchard Court	M	NC
d10	Joe Smith	2971 Orchard Court	M	NC

profile	first	last	sex	state	age
s1	Alan T.	Smith	M	NC	50
s2	Matt	Box	M	NC	
s3	Sammy	Smith	M	NC	23
s4	Sally	Glines	F	NC	
s5	Joe	Green	M	NC	34

(a)



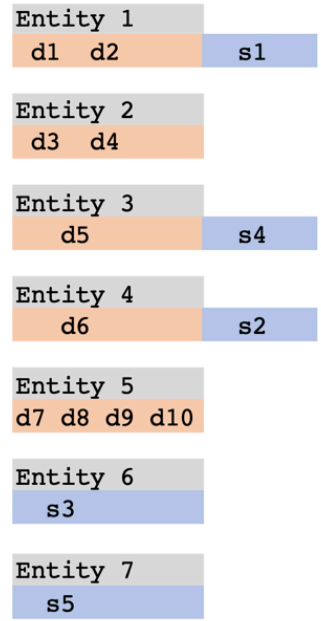
(b)

Figure: An example two databases: (a) the input databases and (b) the corresponding entities.

profile	name	address	gender	state
d1	Alan Smith	123 Main Street	M	NC
d2	Alan Smith	123 Main Street	M	NC
d3	Ann Waters	155 Green Way	F	NC
d4	Anne Waters	155 Green Way	F	NC
d5	Sally Glines	18 Court Road	F	NC
d6	Matt Box	1871 Red Drive	M	NC
d7	Joe Smith	2971 Orchard Court	M	NC
d8	Joe Smith	2971 Orchard Court	M	NC
d9	Joe Smith	2971 Orchard Court	M	NC
d10	Joe Smith	2971 Orchard Court	M	NC

profile	first	last	sex	state	age
s1	Alan T.	Smith	M	NC	50
s2	Matt	Box	M	NC	
s3	Sammy	Smith	M	NC	23
s4	Sally	Glines	F	NC	
s5	Joe	Green	M	NC	34

(a)



(b)

Figure: An example two databases: (a) the input databases and (b) the corresponding entities.

Alignment rules: first and last/name; sex and gender.

1. It is important that the schema are coded for all databases in the same way.
2. The naming structured should be well organized and documented in a relational database.
3. More information can be found in Papadakis et. al (2021) for more information and other illustrations.

Blocking

Reduce computational space by placing similar records into blocks

1. Blocking operates in a schema-aware fashion, assuming that the input data adheres to a known schema or to aligned schemata.
2. Based on this assumption and respective domain knowledge, the most suitable attributes are used for extracting one or more representative signatures from each profile.
3. These signatures are called blocking keys and are composed of (combinations of) parts of values from the most informative attributes.
4. Assuming that these keys reflect the overall similarity of profile pairs, profiles with identical or similar keys are placed into the same block to be compared in the entity resolution stage.

1. Standard Blocking (SB) [Fellegi and Sunter, 1969] requires an expert to manually define a part or a transformation of one or more attribute values as the single blocking key of each profile.
2. Every profile is then placed in the block corresponding to its blocking key.
3. To increase its robustness, a multi-pass functionality is applied in practice, i.e., SB is combined with several different definitions of blocking keys.

1. One common type of blocking is using q-grams (or shingling) [Christen, 2012b, Papadakis et al., 2015].
2. This converts SB keys into sub-sequences of q characters (q-grams) and defines a block for every distinct q-gram.

There are multiple extensions to these in the computer science and database management literature.

1. A record can be thought of as a string of characters.
2. A q-gram (or shingle) is a substring (or word) of length q found within the record.
3. We are interested in a set of k-grams that appear one or more times in the record.

Observe that in the manner of this approach, one finds the standard blocking (SB) key and then proceeds with another blocking approach or pass.

In summary, the blocking stage is made into many blocking passes, iteratively.

How might we define a blocking criteria for these data sources?

Define the blocking key the concatenation of the following three pieces of information:

1. (i) {"Name," Last2Characters},
2. (ii) {"Address," Last2Characters},
3. and (iii) {"Gender," FirstCharacter}.

profile	name	address	gender	state
d1	Alan Smith	123 Main Street	M	NC
d2	Alan Smith	123 Main Street	M	NC
d3	Ann Waters	155 Green Way	F	NC
d4	Anne Waters	155 Green Way	F	NC
d5	Sally Glines	18 Court Road	F	NC
d6	Matt Box	1871 Red Drive	M	NC
d7	Joe Smith	2971 Orchard Court	M	NC
d8	Joe Smith	2971 Orchard Court	M	NC
d9	Joe Smith	2971 Orchard Court	M	NC
d10	Joe Smith	2971 Orchard Court	M	NC

(a)

id	key
d1	thetM
d2	thetM
d3	rsayF
d4	rsayF
d5	esadF
d6	oxveM
d7	thrtM
d8	thrtM
d9	thrtM
d10	thrtM

(b)

id	key
d1	thet, hetM
d2	thet, hetM
d3	rsay, sayF
d4	rsay, sayF
d5	esad, sadF
d6	oxve, xveM
d7	thrt, hrtM
d8	thrt, hrtM
d9	thrt, hrtM
d10	thrt, hrtM

(c)

thet, hetM
d1 d2
rsay, sayF
d3 d4
thrt, hrtM
d7 d8 d9 d10

(d)

Figure: (a) the input data source with bolded information used in blocking keys, (b) the blocking keys via SB, (c) the blocking keys of 4-grams blocking, and (d) the blocks of 4-grams blocking.

id	Name	Affiliation	Areas of Interest	#Articles	#Citations
G1	Robert Smith	University of California	Artificial Intelligence, Text Mining	25	1602
G2	Joan Clarke	University of Buenos Aires	Entomology	12	441
G3	Anthony H. Kane	City, University of London	Database	9	41
G4	Joe Green	PSL University, Paris	Computer Science, Algorithms	149	6221
G5	Joanne Clark	University of Buenos Aires	Entomology	12	429
G6	Annabelles Greenwood	University of Toronto	Algorithms	2	1
G7	Robert Smith	University of California	Database, Text Mining	26	1610
G8	Antony Kane	Unknown	Biological Databases	9	39
G9	Serge Lenglet	New York University	Entomology	22	2291
G10	Antony Kane	City, University of London	Bioinformatics	5	26

(a)

id	Key
G1	thArt1
G2	keEnt4
G3	neDat4
G4	enCom6
G5	rkEnt4
G6	odAlg1
G7	thDat1
G8	neBio3
G9	etEnt2
G10	neBio2

(b)

id	Key
G1	thAr, hArt, Art1
G2	keEn, eEnt, **Ent4**
G3	neDa, eDat, Dat4
G4	enCo, nCom, Com6
G5	rkEn, kEnt, **Ent4**
G6	odAl, dAlg, Alg1
G7	thDa, hDat, Dat1
G8	**neBi, eBio**, Bio3
G9	etEn, tEnt, Ent2
G10	**neBi, eBio**, Bio2

(c)

Ent4
G2
G5

neBi
G8
G10

eBio
G8
G10

(d)

Figure 3.3: Applying Standard and 4-grams Blocking to the Dirty DS of Figure 2.2: (a) the input DS with highlighted the information used in blocking keys, (b) the blocking keys of Standard Blocking per profile, (c) the blocking keys of 4-grams Blocking per profile, and (d) the blocks of 4-grams Blocking—Standard Blocking yields no blocks.

Figure: Blocking from Pap. et. al (2022), page 20. Observe that no blocks result from the full pass.

There are many other ways that blocking criteria can be defined and many options are reviewed in Papadakis et. al (2021).

We have just gone through an iterative approach that is simple to code up. What might be limitations of this approach in practice?

Entity Resolution

Find the records that correspond to the same entity

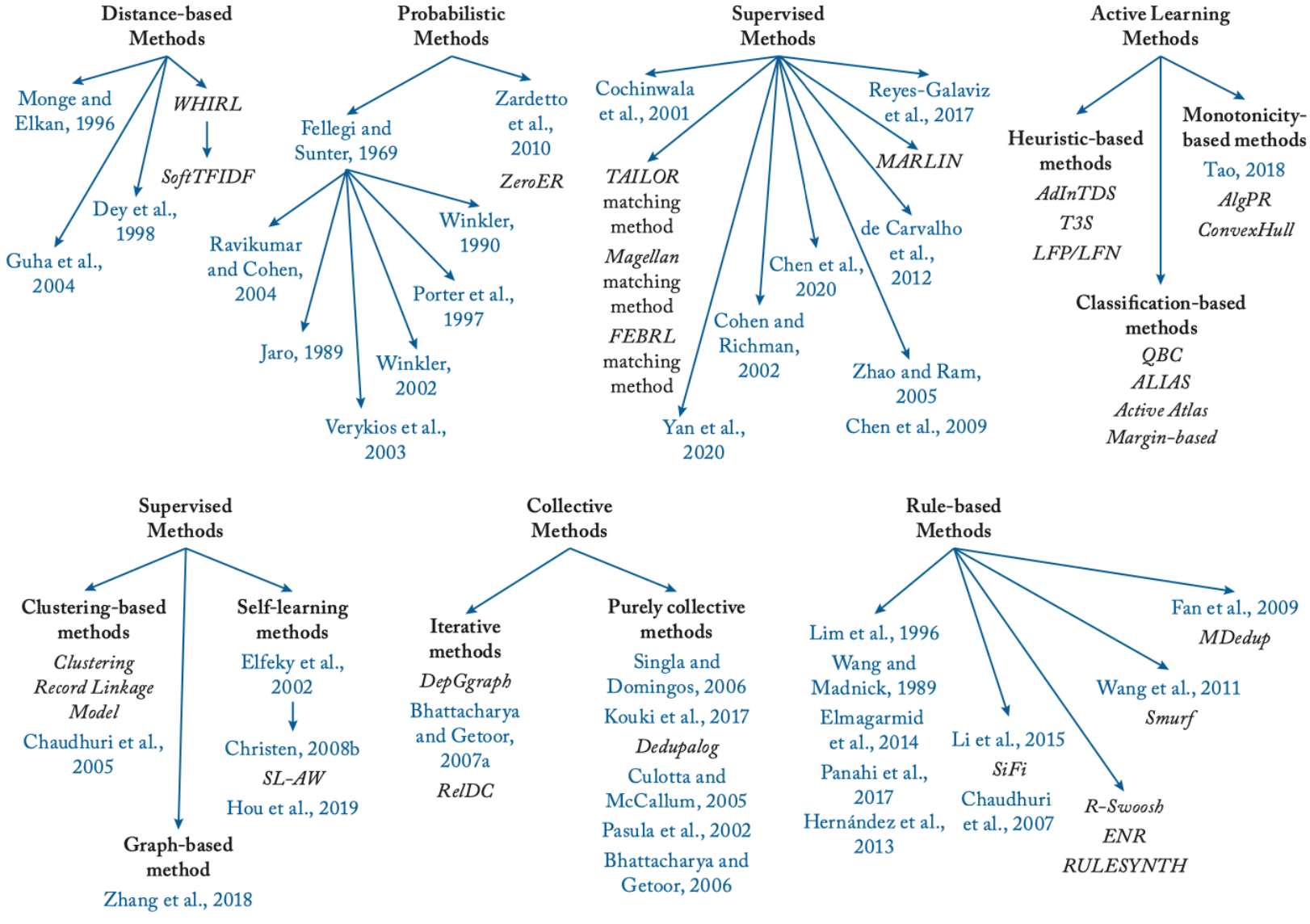


Figure: Citation: Papadakis et. al (2021).

Canonicalization

Merge records that refer to the same entity

In summary, after all the stages the output is an integrated data set with unique identifiers that can be used in statistical analyses.

Thank you!
Questions?
Contact: beka@stat.duke.edu

`https://github.com/resteorts/record-linkage-tutorial`

`https://www.science.org/doi/10.1126/sciadv.abi8021`

`https://github.com/cleanzr`

Thank you to Anup Mathur, Krista Park, Kristen Olsen, and Jenny Thompson for conversations or feedback that led to this presentation.