Paper Review - Auto-FuzzyJoin: Auto-Program Fuzzy Similarity Joins Without Labelled Examples

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Fuzzy-join (or similarity join)

Left Table

id	Isem
l1	Peppi Azzopardi
l2	Annetto Depasquale
l3	Karmenu Vassallo

Right Table

id	Isem
r1	Karmnu Vassallo
r2	Ġużeppi Azzopardi
r3	Annetto De Pasquale

Left Table

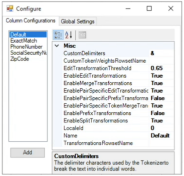
L-id	L-name	L-director	L-description
l1	Carrie	Brian De Palma	Carrie White is shy and outcast ...
l2	Vibes	Ken Kwapis	Psychics hired to find lost temple...

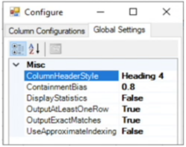
Right Table

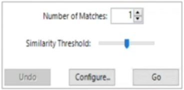
R-id	R-name	R-director	R-description
r1	Carrie	Brian DePalma	This classic horror movie based ...
r2	Vibes	Ken Kwapis	Two hapless psychics unwittingly...

- Fuzzy join takes two tables as inputs and identify record pairs that refer to the same entity
- As an example, l1 and r2 refer to the same person
- The concept can be extended to rows consisting of multiple columns

Fuzzy-join configuration







- Fuzzy-join has been integrated many commercial applications
- These systems are normally not easy to use as they have a big number of configuration parameters
- The extension in Microsoft Excel has 19 options that span across 3 dialog boxes
  - 11 are binary, thus resulting in 2048 possible configuration scenarios
  - 8 continuous, such as thresholds and biases
- In order to execute quality Fuzzy-joins, these configurations must be set up properly by the user

Theoretical foundation: fuzzy join

Given a **reference table** L and a table R containing records that may be **imprecise** or noisy, a **fuzzy join** J establishes approximate matches between them.

- J connects elements of R to similar elements in L based on a chosen **similarity measure** (e.g., Levenshtein distance, cosine similarity, Jaccard similarity).
- Each record $r \in R$ is mapped to at most one record $l \in L$, or **no match at all** (denoted by $\perp$).
- The join is **many-to-one** because multiple records in R can be associated with the **same** record in L, but each $r \in R$ has only **one** possible match.

Formally:

$$J : R \to L \cup \perp$$

Theoretical foundation: fuzzy join configuration space

A **fuzzy join** f compares two strings, r and l, by computing a distance score that reflects their similarity. The computation of this score is governed by a variety of parameters, forming a **parameter space**.

Definition: Each unique combination of these parameters defines a specific **join function** $f \in \mathcal{F}$, where $\mathcal{F}$ is the space of all possible join functions.

Example: Fuzzy Join Distance Score Computation

Join Function: $f = (L, SP, EW, JD)$

- **L**: Lower-casing (Preprocessing)
- **SP**: Space Tokenization
- **EW**: Equal Weights
- **JD**: Jaccard Distance

Inputs:

- $l =$ `"2012 tigers lsu baseball team"`
- $r =$ `"2012 lsu baseball team"`

Tokenization (SP):

- $l \rightarrow \{2012, \textit{tigers}, \textit{lsu}, \textit{baseball}, \textit{team}\}$
- $r \rightarrow \{2012, \textit{lsu}, \textit{baseball}, \textit{team}\}$

Jaccard Distance:

- $A \cap B = \{2012, \textit{lsu}, \textit{baseball}, \textit{team}\} \rightarrow |A \cap B| = 4$
- $A \cup B = \{2012, \textit{tigers}, \textit{lsu}, \textit{baseball}, \textit{team}\} \rightarrow |A \cup B| = 5$
- Jaccard Similarity $= \frac{4}{5} = 0.8$
- Jaccard Distance $= 1 - 0.8 = 0.2$

Result: $f(l, r) = 0.2$

Theoretical foundation: threshold and join configuration

- Once the distance $f(l, r)$ is computed:
  - It is compared to a threshold**compared to a threshold** θ to decide whether to join the string pair l and r.
  - If $f(l, r) \leq \theta$, the pair is considered **a match**.
- Together, the function f and the threshold θ define what the authors call a **join configuration**:

$$C = (f, \theta)$$

- This configuration encapsulates both:
  - How distance is computed.
  - When two strings are considered similar enough to be joined.

Definition: A join configuration C is a 2-tuple $C = \langle f, \theta \rangle$, where $f \in \mathcal{F}$ is a join function, and θ is a threshold.
We use $\mathcal{S} = \{\langle f, \theta \rangle \mid f \in \mathcal{F}, \theta \in \mathbb{R}\}$ to denote the space of join configurations.

Theoretical foundation: fuzzy join mapping

Given two tables L and R , a join configuration $C \in \mathcal{S}$ induces a **fuzzy join mapping** J_C , defined as:

$$J_C(r) = \underset{l \in L,\ f(l,r) \leq \theta}{\arg\min} f(l, r),\ \forall r \in R$$

That is

- For each record $r \in R$, find $l \in L$ that minimizes the distance $f(l, r)$, **only if** that distance is less than or equal to the threshold θ.
- If no such $l \in L$ exists such that $f(l, r) \leq \theta$, then $J_C(r)$ is **empty** — i.e., no match for that record.

Theoretical foundation: the problem with single join configurations

Real-world data can exhibit **multiple types of variations simultaneously**, such as:

- **Typos**
- **Missing tokens**
- **Extraneous information**

As a result, relying on a **single join configuration** often fails to capture all valid matches, particularly when high **recall** is required.

To handle this diversity, the algorithm uses a **set of join configurations**:

$$U = \{C_1, C_2, \ldots, C_K\}$$

Instead of relying on a single configuration, the system computes join results from each one. This approach allows the system to:

- Accommodate diverse types of variations.
- Improve overall recall by **combining multiple perspectives** on similarity.

L-id	L-Table (Reference Table)		R-id	R-Table (Input Table)
l_1	2008 LSU Tigers baseball team	✓	r_1	2008 LSU baseball team
l_2	2008 LSU Tigers football team	✓	r_2	2008 LSU football team
l_3	2008 Mississippi State Bulldogs baseball team	✓	r_3	2008 Missisippi State Bulldog baseball team
l_4	2008 Mississippi State Bulldogs football team	✓	r_4	2008 Mississippi State Bulldog football team
l_5	...		r_5	...
l_6	2007 LSU Tigers football team	✗	r_6	2007 LSU Tigers baseball team
l_7	2007 Wisconsin Badgers football team	✗	r_7	2008 Wisconsin Badgers football team
l_8	2011 LSU Tigers football team	✗	r_8	2010 LSU Tigers football team
l_9	2007 LSU Tigers baseball team	✗	r_9	2007 LSU Tigers football team

- A **Jaccard distance** with threshold 0.2 works well for pairs like (l_1, r_1), which differ by only one or two tokens.
- However, for pairs like (l_3, r_3) with **spelling variations**, Jaccard similarity is not enough:
  - Jaccard distance $\approx 0.5 \rightarrow$ too high to match under the 0.2 threshold
  - A more suitable metric is **Edit Distance**, which can better align such pairs.

Theoretical foundation: fuzzy join via multiple configurations

- To handle this diversity, the algorithm uses a **set of join configurations**:

$$U = \{C_1, C_2, \ldots, C_K\}$$

- Instead of relying on a single configuration, the system computes join results from each.
- This approach allows the system to:
  - Accommodate diverse types of variations.
  - Improve overall recall by **combining multiple perspectives** on similarity.

Given L and R, a set of join configurations $U = \{C_1, C_2, \ldots, C_K\}$ induces a **fuzzy join mapping** J_U, defined as:

$$J_U(r) = \bigcup_{C_i \in U} J_{C_i}(r), \ \forall r \in R$$

This means that the overall result of the fuzzy join using configuration set U is the **union** of results from all individual configurations $C_i \in U$.

Each configuration $C_i \in U$ is designed to capture a **specific type of string variation** (e.g., typos, missing tokens, extra tokens).
Two records are considered **joined by the set** U **if and only if** they are joined by **at least one** configuration $C_i \in U$.

- Each configuration contributes **high-quality joins** targeted at particular data challenges.
- The overall join is more **robust and comprehensive**.

Evaluating Join Quality: Precision

Given two tables R and L, and a **space of join configurations** $\mathcal{S}$, the objective is to find a subset $U \subseteq \mathcal{S}$ that produces **good fuzzy join results**.
Let:

- J_U be the fuzzy join mapping induced by configuration set U
- J_G be the **ground truth** join mapping — the ideal join result

Precision measures how many of the predicted joins are correct:

$$\text{precision}(U) = \frac{\underbrace{|\{r \in R \mid J_U(r) \neq \emptyset,\ J_U(r) = J_G(r)\}|}_{\text{True Positives (TP)}}}{\underbrace{|\{r \in R \mid J_U(r) \neq \emptyset\}|}_{\text{TP + FP (all predicted joins)}}}$$

- **Numerator (TP)**: Records where a join was predicted and it matched the ground truth.
- **Denominator (TP + FP)**: All records where a join was predicted (correct or not).

Evaluating Join Quality: Recall

Recall measures how many of the correct (ground truth) joins were successfully predicted:

$$\text{recall}(U) = \underbrace{|\{r \in R \mid J_U(r) \neq \emptyset,\ J_U(r) = J_G(r)\}|}_{\text{True Positives (TP)}}$$

- This is the **absolute count of True Positives**, i.e., records for which:
  - A join was predicted ($J_U(r) \neq \emptyset$), and
  - It matches the ground truth ($J_U(r) = J_G(r)$)

False Negatives (FN) — cases where a correct join was missed — are defined as:

$$\text{FN} = |\{r \in R \mid J_G(r) \neq \emptyset,\ J_U(r) = \emptyset\}|$$

Note: The denominator $TP + FN$ is constant across all U for a fixed dataset, so it is omitted in comparisons.

Estimating Precision/Recall for a Single Join Configuration

Given:

- A **single join configuration** $C = \langle f, \theta \rangle$
- Two tables:
  - L: reference table
  - R: query table

Assumption: Complete Reference Table L

- L is assumed to contain **all possible true matches** for records in R.
- Ensures that for each $r \in R$, there exists a correct match $l \in L$.
- Simplifies analysis by reducing the chance of missing true positives due to an incomplete reference.

Geometric View of the Distance Function f

- Join function f embeds records into a **metric space**.
- Records are modeled as points on a **unit grid**.
- Each $l \in L$ is surrounded by **close variants** (differing by a token, character, etc.).

Analogy: Stars and Planets

- Reference records $l \in L$ are like **stars** on a grid.
- Query records $r \in R$ are like **planets** that orbit these stars.
- Identifying the best join $J_C(r)$ is like determining **which star a planet orbits**.

Safe Joins and the Geometry of Fuzzy Matching

Safe Joins with a Complete L

- Define the **grid width** w: typical distance between a record l and its closest neighbors in L.
- A join is considered **safe** if the distance $d = f(l, r)$ satisfies:

$$d < \frac{w}{2}$$

- This guarantees that r lies **closer to its true match** l than to any other reference point.

Why This Matters:

- Ensures high **precision** — avoiding false positives caused by ambiguous joins.
- Avoids joining r to an incorrect l' that lies at a similar distance.

Analogy: Stars and Planets

- A planet that lies **equidistant** between two stars (at $\frac{w}{2}$ each) **cannot be confidently claimed by either**.
- In fuzzy joining, such cases are inherently **ambiguous** and risky to resolve.

Estimating Join Precision (Local Heuristic)

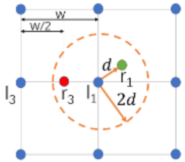
Given a query record $r \in R$ and its closest match $l \in L$, with distance $d = f(l, r)$, we can estimate how **precise** this join is — i.e., how likely it is that (l, r) is a **correct match**.

- The **more candidate records** in L that are close to r, the **less confident** we are about any one being the true match.
- So we count how many other records $l' \in L$ fall within the **2d-ball** centered at l:

$$\text{precision}(l, r) = \frac{1}{\underbrace{|\{l' \in L \mid f(l, l') \leq 2f(l, r)\}|}_{\text{TP + FP (local competitors)}}}$$

- A small $2d$-ball $\rightarrow$ high precision (few competitors)
- A large $2d$-ball $\rightarrow$ low precision (many competitors)

This provides a **data-driven estimate** of join quality **without needing ground truth**.



- To join r_1, we find the closest $l \in L$, say l_1
- Compute the distance: $d = f(l_1, r_1)$
- Draw a ball of radius $2d$ centered at l_1
  - If no other L records fall in the ball $\rightarrow$ high confidence
- In this case, the $2d$-ball contains only l_1:

$$\text{precision}(l_1, r_1) = \frac{1}{1} = 1$$

- **High confidence join**

When L is Incomplete

Problem: When L is incomplete (i.e., some records are missing):

- Missing records in L result in **missing stars** in the grid.
- A record r may join to the wrong l, causing **false positives** and reducing **precision**.
- Example: If r_2 should match with l_2 (but l_2 is missing), it might instead match l_1 using $d = f(r_2, l_1)$.

Note:

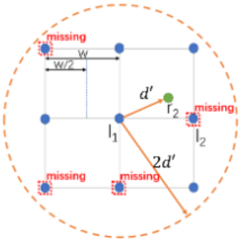
- Even if some records in L are missing, **safe decisions** can still be made.
- In 2D figure, can tolerate up to **7 out of 11** missing.

Precision estimation:

- r_2 should match l_2 (missing), so l_1 becomes the fallback.
- The $2d'$-ball around l_1 contains **5 records**.
- Precision:

$$\text{precision}(l_1, r_2) = \frac{1}{5}$$

- $\Rightarrow$ **Low confidence join**



(b) l_1 is the closest left record to r_2, since l_2 is missing from L. We can infer that (l_1, r_2) is not a "safe" join, because we find many L records in the ball of $2d'$.

- r_2 should join with l_2, but l_2 is **missing**
- l_1 becomes the closest available record
- Compute distance $d' = f(l_1, r_2)$
- Draw a $2d'$-ball around l_1
  - If the ball includes many other L records $\Rightarrow$ d' is too **lax**
  - Join becomes unreliable

Estimating Precision and Recall for a Configuration

A configuration $C = \langle f, \theta \rangle$ includes:

- A join function f
- A threshold θ

1. Local Precision for a Join

$$\text{precision}(r, C) = \frac{1}{|\{l' \in L \mid f(l, l') \leq 2f(l, r)\}|}$$

- $J_C(r) = l$: join match for $r \in R$
- Denominator = number of plausible alternatives

2. Expected True Positives

$$TP(C) = \sum_{r \in R, J_C(r) \neq \emptyset} \text{precision}(r, C)$$

3. Expected False Positives

$$FP(C) = \sum_{r \in R, J_C(r) \neq \emptyset} (1 - \text{precision}(r, C))$$

4. Overall Precision and Recall

$$\text{precision}(C) = \frac{TP(C)}{TP(C) + FP(C)} \qquad \text{recall}(C) = TP(C)$$

Note: Recall is estimated absolutely since ground truth is unavailable.

Precision and Recall Estimation: Example

Setup: Assume 3 records in R, joined to L using configuration $C = \langle f, \theta \rangle$.
Join Results:

- $J_C(r_1) = l_1$, $f(l_1, r_1) = 0.1$, 5 plausible matches $\Rightarrow$ precision$(r_1, C) = \frac{1}{5} = 0.20$
- $J_C(r_2) = l_2$, $f(l_2, r_2) = 0.05$, 2 plausible matches $\Rightarrow$ precision$(r_2, C) = \frac{1}{2} = 0.50$
- $J_C(r_3) = l_3$, $f(l_3, r_3) = 0.2$, 4 plausible matches $\Rightarrow$ precision$(r_3, C) = \frac{1}{4} = 0.25$

Estimated TP and FP:

$$TP(C) = 0.20 + 0.50 + 0.25 = 0.95$$
$$FP(C) = (1 - 0.20) + (1 - 0.50) + (1 - 0.25) = 2.05$$

Estimated Precision and Recall:

$$\text{precision}(C) = \frac{0.95}{0.95 + 2.05} = \frac{0.95}{3.00} \approx 0.317$$
$$\text{recall}(C) = TP(C) = 0.95$$

Note: This example assumes no ground truth; hence recall is based on expected TP count.

Precision and Recall for a Set of Configurations

Let $U = \{C_1, C_2, \ldots, C_K\}$ be a set of configurations.

Case 1: No Conflicts in U

- Each record $r \in R$ is matched by at most one configuration:

$$\forall r \in R, \quad |J_U(r)| \leq 1$$

- Then:

$$TP(U) = \sum_{C \in U} TP(C), \quad FP(U) = \sum_{C \in U} FP(C)$$

Case 2: Conflicting Assignments in U

- Multiple configurations suggest different joins for the same r
- Resolve conflicts by:
  1. Compare precision scores: precision(r, C_i) vs. precision(r, C_j)
  2. Choose the match with higher precision
  3. Assign that join to $J_U(r)$
  4. Recompute $TP(U)$ and $FP(U)$

Final Estimates:

$$\text{precision}(U) = \frac{TP(U)}{TP(U) + FP(U)} \qquad \text{recall}(U) = TP(U)$$

Example: Resolving Conflicting Joins from Multiple Configurations

Context: Two configurations propose different joins for the same record $r \in R$ using different string similarity methods.

Configurations:

- $C_1 = \langle f_1, \theta_1 \rangle$, where f_1 uses Jaccard distance over space-tokenized lowercase strings with equal weights.
- $C_2 = \langle f_2, \theta_2 \rangle$, where f_2 uses Cosine similarity over character trigrams with TF-IDF weighting.

Join Proposals for r:

- C_1: $J_{C_1}(r) = l_1$ with $\text{precision}(r, C_1) = \frac{1}{4} = 0.25$
- C_2: $J_{C_2}(r) = l_2$ with $\text{precision}(r, C_2) = \frac{1}{2} = 0.50$

Conflict Resolution Strategy:

1. Compare estimated precision:

$$\text{precision}(r, C_1) = 0.25 < \text{precision}(r, C_2) = 0.50$$

2. Assign $J_U(r) = l_2$ (higher-confidence match from C_2)

Effect:

- $TP(U)$ and $FP(U)$ incorporate only the winning match.
- Competing matches are discarded.

Auto-FuzzyJoin Algorithm: Single Column Case

Problem: Recall-Maximizing Fuzzy Join (RM-FJ) is **NP-hard**.

Solution: Use a **greedy approximation algorithm** called `AutoFJ`.

Objective:

- Maximize recall: $TP(U)$
- Subject to: maintain precision$(U) \geq \tau$

Greedy Strategy:

- Select configurations that:
  - Increase true positives (recall)
  - Minimize false positives (preserve precision)
- Guided by the **Profit Metric**:

$$\text{profit}(U) = \frac{TP(U)}{FP(U)}$$

Blocking Heuristic:

- Apply 3-gram-based blocking:

$$LL, LR \leftarrow \text{apply blocking on } L{-}L, L{-}R$$

Algorithm 1 AutoFJ for single column

Require: Tables L and R, precision target τ, search space S

```
LL, LR ← apply blocking with L − L and L − R
LR ← Learn negative-rules from LL and apply rules on LR (Alg. 2)
Compute distance with different join functions f ∈ S
Pre-compute precision estimation for each configuration C ∈ S
U ← ∅
while S \ U ≠ ∅ do
    max_profit ← 0
    for all C ∈ S \ U do
        if profit(U ∪ {C}) > max_profit then
            C* ← C, max_profit ← profit(U ∪ {C})
    if precision(U ∪ {C*}) > τ then
        U ← U ∪ {C*}
    else
        break
return U
```

Blocking Example: 3-Grams and TF-IDF

Reference Table L:

	l_1	`"john smith"`
	l_2	`"jane smythe"`
	l_3	`"alice johnson"`

Query Record r_1: `"jon smyth"`

Step 1: Preprocessing (P)

- Lowercasing (already lowercase)
- Add padding for 3-grams: e.g., `"jon"` $\rightarrow$ `"##jon#"`

Step 2: Tokenization (T)

- r_1: `##j, #jo, jon, on , n s, sm, smy, myt, yth, th#`
- l_1, l_2: similar 3-gram sequences

Step 3: Token Weighting (W)

- Use TF-IDF to emphasize rare, meaningful trigrams (e.g., `smy`, `yth`)
- r_1–l_2: **High score**, r_1–l_1: Medium, r_1–l_3: Zero

Blocking Result:

- Only compare r_1 with l_1, l_2 $\rightarrow$ prune l_3

Optimization: Filtering with Negative Rules

Assumption: Although 3-gram blocking may have pruned l_3, we assume here it was retained due to weak overlap, allowing us to illustrate negative-rule filtering.

Goal: Use **obvious non-matches** in L–L to learn rules that help **filter unlikely** L–R **pairs** before costly distance computations.

Step 1: Generate LL — Self-Join on L using 3-gram blocking

Pair	Shared 3-grams	Interpretation
l_1 vs l_2	`sm, smy, th`	Possibly similar
l_1 vs l_3	`jo, on`	Clearly different
l_2 vs l_3	Weak overlap	Probably different

Learn Negative Rule:
"If 3-gram overlap ≤ 2, treat as a non-match."

Step 2: Apply Rule on LR Candidate Pairs

Pair	Overlap	Apply Rule?	Keep?
r_1, l_1	~ 4	No	Yes
r_1, l_2	~ 5	No	Yes
r_1, l_3	~ 1	Yes	No

Effect: *Filter out clearly irrelevant pairs early — no need to compute Jaccard or Edit Distance!*

Compute Distances: Apply Join Functions

Once candidate pairs are identified (via blocking and optional negative rules), we compute the actual similarity using multiple join functions $f \in \mathcal{S}$.

Each join function is defined by:

- Preprocessing (e.g., lowercasing, punctuation removal)
- Tokenization (e.g., char 3-grams, word tokens)
- Token weights (e.g., TF-IDF)
- Distance function (e.g., Jaccard, Cosine, Edit)

Example Candidate Pairs (after blocking):

r (query)	l (reference)
`"jon smyth"`	`"john smith"`
`"jon smyth"`	`"jane smythe"`

Join Functions in $\mathcal{S}$:

Function f	**Tokenizer**	**Distance**	**Description**
f_1	char 3-grams	Jaccard	Overlap in token sets
f_2	char 3-grams	Cosine (TF-IDF)	Weighted similarity
f_3	raw string	Levenshtein	Edit distance

Computed Scores:

Pair	f_1	f_2	f_3
`jon vs john`	0.4	0.5	2
`jon vs jane`	0.6	0.7	3

Note: Distances may follow different scales — lower often means more similar.

Start of Greedy Algorithm

`Initialize:` $U \leftarrow \emptyset$

U will hold the **selected join configurations**:

$$C = \langle f, \theta \rangle$$

Each configuration includes:

- A join function $f \in \mathcal{F}$ (defined by P, T, W, D)
- A distance threshold θ (max allowed distance for a match)

Goal:

- Select a subset $U \subseteq \mathcal{S}$ from all candidate configurations
- Maximize recall: $TP(U)$
- Maintain precision: precision$(U) \geq \tau$

Example: Precomputed Configuration Set S

Config C	Description
$C_1 = \langle f_1, 0.37 \rangle$	Jaccard distance with $\theta = 0.37$
$C_2 = \langle f_2, 0.42 \rangle$	Cosine distance with $\theta = 0.42$
$C_3 = \langle f_3, 2 \rangle$	Edit distance with $\theta = 2$

These θ values were selected based on prior precision–recall evaluation for each f.

Main Greedy Loop

`Main Loop: while` $S \setminus U \neq \emptyset$ `do`

We continue as long as there are still unused configurations to consider.

Notation:

- S: full set of candidate configurations, each $C = \langle f, \theta \rangle$
- U: set of selected configurations
- $S \setminus U$: unused configurations

At each iteration:

1. Evaluate each $C \in S \setminus U$
2. Compute profit: how many true positives vs. false positives it contributes
3. Select the best configuration C^*
4. If precision$(U \cup \{C^*\}) \geq \tau$:

   $U \leftarrow U \cup \{C^*\}$

Example State:

- $S = \{\langle f_1, 0.37 \rangle, \langle f_2, 0.42 \rangle, \langle f_3, 2 \rangle\}$
- $U = \emptyset$

Loop continues while there are remaining candidates and precision can be preserved.