INTERNATIONAL JOURNAL OF LATEST TECHNOLOGY IN ENGINEERING, MANAGEMENT & APPLIED SCIENCE (IJLTEMAS)

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue I, January 2026

The Probability of Coincidence in Citation and Alphabetical Ordering an Exhaustive Analysis of the Rencontres Problem

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DOI : https://doi.org/10.51583/IJLTEMAS.2026.150100010

Received: 31 December 2025; Accepted: 09 January 2026; Published: 23 January 2026

ABSTRACT

This analysis explores the likelihood that a reference's original citation number, based on its initial position in the text, matches its final number after sorting the bibliography alphabetically. It models this as counting the fixed points in a random permutation—a classic problem in combinatorial probability known as the Rencontres or Hat-Check problem—assuming a uniform random order. Using the Principle of Inclusion-Exclusion, an exact probability mass function for the number of references (n) with exactly k matches is derived, based on derangements. The study reveals a key asymptotic result: as n grows, the distribution of matches quickly and strongly approaches a Poisson distribution with a mean of $\lambda=1$. This means that for typical bibliography sizes ($n \geq 10$), the chance of any given number of matches becomes nearly independent of total references. Thus, the expected number of matches remains 1, regardless of the bibliography's length. The study also provides specific probabilities for at least k matches, computed via the Poisson approximation and involving the Incomplete Gamma Function. Notably, there is a 63.2% chance of at least one match, 26.4% for two or more, and 8.0% for three or more, indicating that multiple coincidences are rare. By distinguishing this from phenomena like the Birthday Paradox and highlighting its use in assessing shuffling algorithms and cryptographic security, the report presents a clear framework for understanding fixed-point matches in permutations. It concludes that despite the apparent randomness of reordering references, the number of matches follows a strict, predictable probabilistic law governed by the constant e.

Keywords: Rencontres problem, Fixed points in permutations, Derangements, Poisson distribution, Citation ordering

INTRODUCTION:

The Intersection of Bibliographic Structure and Combinatorial Probability

The organisation of academic literature relies heavily on structured referencing systems. When a researcher drafts a manuscript, references are typically accumulated in a chronological or "order of appearance" sequence. This initial listing represents the temporal flow of the author's engagement with existing literature. However, the final presentation of these references often adheres to style guides—such as those of the American Psychological Association (APA) or the Modern Language Association (MLA)—that mandate an alphabetical arrangement by the primary author's surname. This transformation from a chronological input to an alphabetical output constitutes a permutation of the original set of reference indices.

The query addressed in this report poses a fundamental probabilistic question arising from this editorial process: given a manuscript with n references, what is the likelihood that the original citation number (based on order of appearance) and the final reference number (based on alphabetical sorting) are identical in at least k instances? This problem, while rooted in the mundane mechanics of academic formatting, maps directly onto one of the most celebrated and rigorously studied problems in combinatorial probability: the **Rencontres problem** (or the Problem of Encounters), also widely known as Montmort's matching problem or the Hat-Check problem.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue I, January 2026

This report provides a comprehensive, expert-level analysis of this phenomenon. We will explore the mathematical formalisation of the problem as a search for fixed points in random permutations. We will derive the exact probability distributions for finite bibliographies, investigate the asymptotic behaviour as the number of references grows large, and demonstrate the remarkable convergence to the Poisson distribution. Furthermore, we will delve into the deep connections between this problem and the Incomplete Gamma function, providing both theoretical proofs and computational algorithms for assessing these probabilities. By synthesising historical context, rigorous derivation, and modern computational statistical methods, we aim to offer a definitive answer regarding the probability of at least *k* ordinal matches.

Formalising the Bibliographic Permutation

To rigorously analyse the probability of reference numbers remaining unchanged, we must first establish a mathematical model of the "listing" and "sorting" processes.

Let $R = \{r_1, r_2, \dots, r_n\}$ be the set of *n* distinct references cited in the paper.

The listing process assigns a unique integer index $i \in \{1, \dots, n\}$ to each reference based on its first appearance in the text. This defines a bijection $L: \{1, \dots, n\} \to R$, where $L(i)$ is the reference cited at position i.

The sorting process rearranges the elements of R into a sequence defined by the lexicographical order of the author names (and titles/years for same-author works). This defines a second bijection $S: \{1, \dots, n\} \to R$, where $S(j)$ is the reference that appears at the j-th position in the sorted bibliography.

A "match" occurs for a specific reference if its position in the citation list is identical to its position in the sorted bibliography. Mathematically, we are comparing the two orderings. We can define a permutation σ of the set $\{1, \dots, n\}$ that maps the citation index to the sorted index. Alternatively, and more intuitively for this problem, we can consider the "alphabetical rank" of the reference cited at position i. Let π be the alphabetical rank of the reference that appeared i-th in the text.

- If the first reference cited (i=1) happens to be the one that comes first alphabetically, then $\pi(1) = 1$.
- If the first reference cited (i=1) is the one that comes last alphabetically, then $\pi(1) = n$.

The condition that the "original reference number and the reference number after sorting will be the same" is mathematically equivalent to the condition $\pi(i) = i$. In the theory of permutations, such an index i is called a **fixed point** of the permutation π.

The Assumption of Randomness

A critical assumption in this analysis is the distribution of the permutation π. In the absence of specific information regarding the author's citation habits (e.g., a propensity to cite authors with surnames beginning with 'A' earlier in the text), we model π as a **uniform random permutation**. This means that any of the n! possible orderings of the n alphabetical ranks are equally likely to occur as the citation order.

While real-world citation behaviours might exhibit slight biases—perhaps foundational texts (often older and potentially distributed differently alphabetically) are cited first—the uniform random permutation model is the standard "null hypothesis" for such problems and provides the baseline probabilistic truth. Under this assumption, the problem transforms into finding the probability that a permutation chosen uniformly at random from the symmetric group S_n has at least k fixed points. [15]

Historical and Theoretical Context: The Legacy of Montmort

The mathematical lineage of the fixed-point problem dates back to the early 18th century, embedding the question in a rich history of gaming and probability. Understanding this history clarifies why certain mathematical tools (like the subfactorial) were developed and how they apply to the sorting of references.

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The Problem of Rencontres

The specific framing of "matches" is classically referred to as the **Rencontres problem**. Pierre Rémond de Montmort first formulated it in his seminal work *Essay d'analyse sur les jeux de hazard* (1708). Montmort was investigating a card game called *Treize* (Thirteen), where a dealer turns over cards while counting "one, two, three..." up to thirteen. A "rencontre" (encounter or meeting) occurred if the card revealed matched the number spoken.

The scenario is an isomorphism of this game:

- **The Counter:** The citation numbers 1, 2, …, n correspond to the dealer calling out numbers.
- **The Card/Object:** The reference's actual alphabetical rank corresponds to the value of the card revealed.
- **The Win Condition:** A reference number matching the sorted number corresponds to a *rencontre*.

Montmort, along with correspondents Nicholas Bernoulli and later Leonhard Euler, sought to calculate the probability of having *no* encounters (a derangement) and, by extension, the probability of exactly k encounters.

The Hat Check Problem Analogy

In modern combinatorial literature, this problem is frequently illustrated as the **Hat Check Problem**. [2]

n men check their hats at a cloakroom. The attendant, having lost the claim tickets, returns the hats entirely at random. What is the probability that exactly k men receive their own hats?

This analogy perfectly mirrors the bibliography sorting problem:

- The "men" are the positions in the original citation list.
- The "hats" are the alphabetical ranks associated with the references.
- A man receiving his own hat is equivalent to a reference where the citation index i equals the sorted index $\pi(i)$.

The widespread use of this analogy underscores the counterintuitive nature of the result: as we will see, the probability of a specific number of matches stabilises very quickly. Whether there are 10 men (references) or 10,000, the probability that exactly one man gets his hat back remains almost constant. This property, known as **asymptotic stability**, is a central theme of our analysis and provides a robust answer to the query regardless of the exact length of their bibliography (assuming n is reasonably large). [15]

Mathematical Significance

The study of fixed points in permutations serves as a gateway to broader topics in group theory and statistics.

Cycle Structure: A fixed point is simply a cycle of length 1. John Baez and other mathematicians have highlighted that the expected number of cycles of length k in a random permutation is 1/k. For k=1, this yields the elegant result that the expected number of fixed points is 1. [1]

Derangements: The case where k=0 (no matches) defines the **derangement numbers** or **subfactorials**, denoted !n or D_n. The calculation of D_n is fundamental to solving the general case for k matches. [12]

Combinatorial Derivation of Exact Probabilities

To answer the question regarding the probability of *at least* k matches, we must first construct the probability mass function for *exactly* k matches. [4] This derivation relies on the Principle of Inclusion-Exclusion.

The Number of Derangements (D_n)

We begin by calculating the number of permutations of n elements that have zero fixed points. Let S_n denote the set of all permutations of {1, …, n}, so $|S_n| = n!$. Let P_i be the property that a permutation π fixes the element i (i.e., π(i) = i). We seek the number of permutations that satisfy none of the properties $P_1, P_2, \ldots, P_n$.

According to the Principle of Inclusion-Exclusion, the number of permutations with none of these properties is: [13]

$$D_n = \sum_{T \subseteq \{1,\ldots,n\}} (-1)^{|T|} \, (N(T)$$

where N(T) is the number of permutations that fix at least the elements in the set T.

If we fix a set of elements T with |T| = j, the remaining n-j elements can be permuted in any order. Thus:

$$N(T) = (n-j)!$$

There are $\binom{n}{j}$ distinct subsets T of size j. Therefore, the term corresponding to size j in the inclusion-exclusion sum is: $\binom{n}{j}$ (n-j)!

Expanding the binomial coefficient:

$$\binom{n}{j} (n-j)! = \frac{n!}{j!(n-j)!} (n-j)! = \frac{n!}{j!}$$

Substituting this back into the sum:

$$D_n = \sum_{T \subseteq \{1,\ldots,n\}} (-1)^{|T|} \, (N(T) = \sum_{j=0}^{n} (-1)^j \frac{n!}{j!} = n! \sum_{j=0}^{n} \frac{(-1)^j}{j!}$$

$$D_n = n! \left(\frac{1}{0!} - \frac{1}{1!} + \frac{1}{2!} - \frac{1}{3!} + \ldots + \frac{(-1)^n}{n!}\right)$$

This formula for D_n (often written as !n) is the exact count of bibliographies where *no* reference retains its original number after sorting. [14]

Generalising to Exactly k Matches

Let X be the random variable representing the number of fixed points (matches) in a random permutation of n elements. We wish to find the probability P(X=k).

To form a permutation with exactly k fixed points, we perform a two-step constructive process: [9]

Selection of Matches: We must choose exactly k indices out of the n available positions to be the fixed points. The binomial coefficient gives the number of ways to choose these k indices $\binom{n}{k}$.

Derangement of the Remainder: The remaining n-k elements must be permuted such that *none* of them map to their own locations (otherwise, we would have more than k fixed points). The number of ways to arrange these n-k elements as a derangement is D_{n-k}.

Combining these steps, the total number of permutations with exactly k fixed points, denoted $N_n(k)$, is:

$$N_n(k) = \binom{n}{k} D_{n-k}$$

The probability P(X=k) is the ratio of favourable permutations to the total number of permutations (n!):

$$P(X = k) = \frac{\binom{n}{k} D_{n-k}}{n!}$$

We can simplify this expression by expanding the binomial coefficient and the derangement term:

$$P(X = k) = \frac{n!}{k!(n-k)!}\frac{D_{n-k}}{n!} = \frac{D_{n-k}}{k!(n-k)!}$$

Now, substitute the inclusion-exclusion formula for D_{n-k}:

$$P(X = k) = \frac{1}{k!(n-k)!}(n-k)!\sum_{j=0}^{n-k}\frac{(-1)^j}{j!} = \frac{1}{k!}\sum_{j=0}^{n-k}\frac{(-1)^j}{j!}$$

This equation provides the **exact probability** that the reference number matches the sorted number in exactly k cases for a bibliography of size n. [7]

The "At Least k" Formulation

We need to find the probability of the numbers being the same in at least k cases. This corresponds to the cumulative probability of the upper tail of the distribution:

$$P(X \geq k) = \sum_{m=k}^{n} P(X = m)$$

Substituting the derived formula for P(X=m):

$$P(X \geq k) = \sum_{m=k}^{n}\left(\frac{1}{m!}\sum_{j=0}^{n-m}\frac{(-1)^j}{j!}\right)$$

While this double summation provides the precise answer for any finite n, calculating it manually is tedious. However, the structure of the inner sum (the partial series for 1/e) hints strongly at a convergent limit, which we will explore in the next section. This limit allows for a much simpler "closed form" approximation that is highly accurate for typical bibliography sizes (n > 10).

Asymptotic Analysis: Convergence to the Poisson Distribution

One of the most powerful results in combinatorial probability is the convergence of the fixed-point distribution to the Poisson distribution. This fact implies that the length of the bibliography (n) effectively "drops out" of the equation once it becomes sufficiently large, simplifying the problem to a universal probability calculation.

The Limit of the Derangement Sum

Consider the inner summation derived earlier:

$$S_{n-k} = \sum_{j=0}^{n-k}\frac{(-1)^j}{j!}$$

We recognise this immediately as the partial sum of the Maclaurin series expansion for the exponential function e^x, evaluated at x = -1:

$$e^x = \sum_{j=0}^{\infty}\frac{x^j}{j!} \Rightarrow e^{-1} = \sum_{j=0}^{\infty}\frac{(-1)^j}{j!}$$

As n → ∞ (assuming k is fixed), the upper limit of the sum n-k also approaches infinity. Therefore:

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ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue I, January 2026

$$\lim_{n\to\infty} \sum_{j=0}^{n-k} \frac{(-1)^j}{j!} = e^{-1} = \frac{1}{e}$$

The Poisson Probability Mass Function

Applying this limit to the probability formula for exactly k matches:

$$\lim_{n\to\infty} P(X = k) = \frac{1}{k!} \lim_{n\to\infty} \sum_{j=0}^{n-k} \frac{(-1)^j}{j!} = \frac{1}{k!}\frac{1}{e}$$

$$P(X = k) \approx \frac{e^{-1}1^k}{k!}$$

This expression, $\frac{e^{-\lambda}\lambda^k}{k!}$ with λ = 1, is the probability mass function (PMF) of a Poisson distribution with mean parameter λ = 1.

Thus, we formally state:

The number of fixed points in a uniform random permutation of n elements converges in distribution to a Poisson(1) random variable as n → ∞.

This result is robust and well-documented in the research literature. [11] It implies that for a reasonably long bibliography (e.g., n=50), the probability of having exactly k matching reference numbers is independent of n.

Error Analysis and Rate of Convergence

You might wonder: "How large does n need to be for this approximation to be valid?"

The speed of convergence of the alternating series determines the error in the approximation $\sum \frac{(-1)^j}{j!}$. The absolute value of the first neglected term bounds the error of an alternating series truncation.

The approximation replaces $\sum_{j=0}^{n-k} \frac{(-1)^j}{j!}$ with $\sum_{j=0}^{\infty} \frac{(-1)^j}{j!}$.

The difference is the tail of the series starting from j = n-k+1:

$$|\text{Error}| = |\frac{(-1)^{(n-k+1}}{(n-k+1)!}| = \frac{1}{(n-k+1)!}$$

For a bibliography of n=20 references and checking for k=2 matches:

$$|\text{Error}| = \frac{1}{(20-2+1)!} = \frac{1}{19!}$$

This error is infinitesimally small ($< 10^{-17}$).

Even for very small n (like n=5), the approximation is remarkably good.

- **Exact P(X=0) for n=5:** 0.36666...
- **Poisson Approximation (1/e):** 0.36787...
- **Difference:** ≈0.0012 (0.12%)

Unless the paper has fewer than five references, the Poisson model is functionally exact. We can ignore this, as most journals require a minimum of 15 references.

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Implications of λ = 1

The fact that the parameter λ = 1 is profoundly significant.

Expected Value: The mean of a Poisson(1) distribution is λ = 1. This confirms the result derived via linearity of expectation: on average, exactly **one** reference number will remain unchanged after sorting. [5]

Variance: The variance of Poisson(1) is also 1. The spread of the distribution is moderate; extremely high numbers of matches are exponentially rare. [3]

Calculating the "At Least k" Probability

Having established the Poisson(1) model, we can now provide the specific computational solution for our requirement: determining the probability of *at least* k matches.

The Complementary Approach

Directly summing the Poisson probabilities for k, k+1, k+2, … to infinity (or n) is valid, but it is often computationally easier to use the complement. The probability of at least k matches is 1 minus the probability of fewer than k matches.

$$P(X \geq k) = 1 - P(X < k) = 1 - \sum_{j=0}^{k-1} P(X = j)$$

Using the Poisson approximation:

$$P(X \geq k) \approx 1 - \sum_{j=0}^{k-1} \frac{e^{-1}}{j!} = 1 - \frac{1}{e} \sum_{j=0}^{k-1} \frac{1}{j!}$$

This formula is the most efficient way to calculate the probability manually or with a simple calculator. One sums the inverse factorials up to 1/(k-1)!, divides by e, and subtracts from 1.

Connection to the Incomplete Gamma Function

For more advanced analysis or software implementation, this probability is often expressed using the **Incomplete Gamma Function**. This connection is explicitly highlighted in the research snippets. [11]

The cumulative distribution function (CDF) of a Poisson random variable with mean λ is related to the Regularised Upper Incomplete Gamma Function, denoted Q(s, x) or $\Gamma_{reg}(s, x)$. [8]

The identity states:

$$P(Y < k) = \frac{\Gamma(k,\lambda)}{\Gamma(k)} = Q(k, \lambda)$$

where Y ~ Poisson(λ).

Note the slight nuance in definitions. The probability of at most k-1 events (which corresponds to X < k) is often given as:

$$\sum_{j=0}^{k-1} \frac{e^{-\lambda}\lambda^j}{j!} = \frac{\Gamma(k,\lambda)}{(k-1)!} = Q(k, \lambda)$$

Therefore, the probability we seek, P(X ≥ k), is the complement of this CDF:

P(X ≥ k) = 1 - P(X < k) = 1 - Q(k, λ).

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Since P(s, x) + Q(s, x) = 1 (where P is the Regularised Lower Gamma function), we have:

$$P(X \geq k) = P(k, \lambda) = \frac{\gamma(k,\lambda)}{\Gamma(k)}$$

For our specific case where λ = 1:

$$P(X \geq k) \approx \frac{\gamma(k,1)}{(k-1)!}$$

where $\gamma(k, 1) = \int_0^1 t^{k-1}e^{-t}\,dt$.

This "closed form" is extremely useful because many statistical software packages (like Python's scipy.stats or MATLAB) implement optimised routines for Incomplete Gamma functions, allowing for high-precision calculation of these tail probabilities. [11]

Tabulated Probabilities

To provide immediate value, we calculate the probabilities for typical values of k using the Poisson(1) model.

Minimum Matches (k)	Formula $(1-\frac{1}{e}\sum_{j=0}^{k-1}\frac{1}{j!})$	Probability	Percentage	Interpretation
At least 1	$1 - \frac{1}{e}(1)$	1 - 0.3679 = 0.6321	**63.21%**	More likely than not to have ≥ 1 match.
At least 2	$1 - \frac{1}{e}(1 + 1)$	1 - 0.7358 = 0.2642	**26.42%**	About a 1 in 4 chance.
At least 3	$1 - \frac{1}{e}(1 + 1 + 0.5)$	1 - 0.9197 = 0.0803	**8.03%**	Fairly rare (less than 1 in 10).
At least 4	$1 - \frac{1}{e}(1 + 1 + 0.5 + 0.1667)$	1 - 0.9810 = 0.0190	**1.90%**	Very rare (~2%).
At least 5	$1 - \frac{1}{e}(1 + 1 + 0.5 + 0.1667 + 0.04166667)$	0.00365	**0.37%**	Extremely unlikely.
At least 6	$1 - \frac{1}{e}(1 + 1 + 0.5 + 0.1667 + 0.04166667 + 0.00833333)$	0.00058	**0.06%**	Less than 1 in 1000.

Table 1: Probability of Reference Coincidences.

Insight: The table reveals a rapid decay. While a single match is expected and common (63%), finding three or more references that keep their original numbers is a statistically significant anomaly (only 8%).

Computational Algorithms and Implementation

For researchers wishing to verify these results or compute exact probabilities for small N where the Poisson approximation might have a theoretically distinct (though numerically negligible) error, specific algorithms are preferred over the summation formula.

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Recursive Calculation of Derangements

Computing factorials for large N leads to overflow errors in standard integer arithmetic. A more stable approach for finding the probability relies on the recurrence relation for derangements.

Recall $D_n = (n-1)(D_{n-1} + D_{n-2})$.

Dividing by n!, we can derive a recurrence for the probability $p_n = D_n/n!$ (the probability of 0 matches in a list of size n):

$$p_n = \frac{(n-1)(D_{n-1} + D_{n-2})}{n!} = \frac{n-1}{n} p_{n-1} + \frac{1}{n} p_{n-2}$$

Wait, the simpler recurrence is $D_n = n D_{n-1} + (-1)^n$.

Dividing this by n!:

$$\frac{D_n}{n!} = \frac{n\, D_{n-1}}{n!} + \frac{(-1)^n}{n!}$$

Or, $p_n = p_{n-1} + \frac{(-1)^n}{n!}$

This confirms the partial sum series directly: $p_n = \sum_{j=0}^{n} \frac{(-1)^j}{j!}$.

Dynamic Programming for Exact "At Least k"

To find the exact probability of *at least* k matches for a fixed n without approximation:

Construct D array: Generate $D_0, D_1, \ldots, D_n$ using $D_i = i\, D_{i-1} + (-1)^i$.

Sum Favourable Outcomes: Count = $\sum_{m=k}^{n} \binom{n}{m} D_{n-m}$

Calculate Probability: P = $\frac{Count}{n!}$

This approach avoids floating-point precision issues inherent in summing alternating series by keeping all calculations in integers until the final division. It is the preferred method for computer algebra systems. [6]

Code Logic

A Python code for the exact calculation:

```python
import math

# Precompute Derangements using D_n = n * D_{n-1} + (-1)^n
from functools import lru_cache
@lru_cache(maxsize=None)
def derangements(n):
  if n < 0:
    raise ValueError("Derangements are not defined for negative numbers.")
  if n == 0:
    return 1
  result = n * derangements(n - 1) + (-1) ** n
  return result

def probability_at_least_k_matches(n, k) -> float:
```

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```
  if n < 0:
    raise ValueError("'Number of references' (n) should not be negative.")

  if k < 0:
    raise ValueError("'Number of matches' (k) should not be negative.")

  if k > n:
    return 0.0

  # Sum favourable permutations
  favourable_permutations = 0
  fact_n = math.factorial(n)
  for m in range(k, n + 1):
    # n choose m
    n_choose_m = fact_n // (math.factorial(m) * math.factorial(n - m))
    # Add to total: (ways to choose fixed) * (ways to derange rest)
    favourable_permutations += n_choose_m * derangements(n - m)

  return favourable_permutations / fact_n

probability_at_least_k_matches(25, 2)

0.26424111765711533

probability_at_least_k_matches(50, 2)

0.26424111765711533

probability_at_least_k_matches(30, 4)

0.018988156876153815

probability_at_least_k_matches(35, 1)

0.6321205588285577
```

This algorithm provides the **exact** probability $P(X \geq k)$, valid for any n and k.

Broader Context and Applications

While the query arises from a specific academic task, the underlying probabilistic mechanics have far-reaching implications in fields ranging from cryptography to statistical testing.

The "Birthday Paradox" Distinction

A common misconception is equating "matches" or "collisions" in this problem with the famous **Birthday Paradox**. [10] It is crucial to distinguish them:

Birthday Problem (Sampling With Replacement): We ask if *any two* items share a value. The mappings are independent. The sample space is n^n. Probabilities scale with $\sqrt{n}$.

Rencontres Problem (Sampling Without Replacement): We ask if an item maps to *its own specific location*. The mappings are dependent (a permutation). The sample space is n!. The probability is constant (1/e).

In the birthday problem, the probability of a match approaches 1 rapidly as n grows (for fixed days). In the

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bibliography problem, the probability of a match *stabilises* at ≈63.2% and never reaches 1. This highlights a fundamental difference between "collisions between arbitrary elements" and "collisions with a fixed index."

Applications in Random Number Testing

The distribution of fixed points is a standard metric in evaluating the quality of Random Number Generators (RNGs) and shuffling algorithms (like the Fisher-Yates shuffle).

If a software library claims to shuffle a list "randomly," one can test this by shuffling a list of n items millions of times and counting the fixed points.

- The mean number of fixed points should be close to 1.
- The variance should be close to 1.
- The distribution should match Poisson(1). Significant deviation from these expected values (e.g., if the average number of matches is 1.5 or 0.5) indicates a flaw in the shuffling algorithm, known as bias. The sorting process can effectively be seen as a "physical" test of randomness. If they consistently find 5 or 6 matches in every paper, it suggests their citation process is not random but correlated with alphabetical order (e.g., they systematically cite 'A' authors earlier).

Cryptography and Hashing

In cryptography, the "birthday attack" relies on finding collisions. However, the Rencontres model applies to **fixed-point attacks** on permutation-based cyphers. If a block cypher (which is a permutation of the message space) has significantly more fixed points than a random permutation, it is considered a weakness. The probability analysis derived here (1/e for no fixed points) is the baseline against which cryptographic security is measured.

CONCLUSION

The problem of determining the likelihood that a reference's original citation number matches its sorted number is a classical application of the **Rencontres problem**. By modelling the citation and sorting process as a uniform random permutation, we have derived the following exhaustive conclusions:

Exact Probability: For a paper with n references, the probability of exactly k matches is given by $\frac{1}{k!} \sum_{j=0}^{n-k} \frac{(-1)^j}{j!}$.

Universal Approximation: For any typical bibliography size (n ≥ 10), the distribution of matches is effectively independent of n. It follows a **Poisson distribution with parameter λ = 1**.

The Answer to "At Least k": The probability that the reference numbers match in at least k cases is approximately:

$$P(\text{Matches} \geq k) \approx 1 - \frac{1}{e}\sum_{i=0}^{k-1}\frac{1}{i!}$$

Alternatively, this can be calculated using the Regularised Lower Incomplete Gamma Function: $P \approx \frac{\gamma(k,1)}{(k-1)!}$.

Key Probabilities:

- There is a **63.2%** chance of at least one match.
- There is a **26.4%** chance of at least two matches.
- There is an **8.0%** chance of at least three matches.

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Expectation: Regardless of the length of the bibliography, the expected number of references that retain their original number is exactly **1**.

These findings illustrate a fascinating interplay between order and chaos: while the shuffling of references appears random, the number of coincidences adheres to a strict and predictable probabilistic law governed by the constant e. Whether analysing bibliographic data, shuffling cards, or securing data, the principles of the Rencontres problem provide the definitive mathematical framework for understanding fixed points in permutations.

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ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue I, January 2026

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