The Linkage of the 2021 National Ambulatory Medical Care Survey (NAMCS) Health Center (HC) Component to 2020-2022 U.S. Department of Housing and Urban Development Administrative Data: Linkage Methodology and Analytic Considerations

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Contents

List of Acronyms

DOB, date of birth

EHR, electronic health record

E-M, expectation-maximization

ERB, Ethics Review Board

FQHC, Federally Qualified Health Centers

HC, Health Center

HCV, Housing Choice Voucher program

HUD, U.S. Department of Housing and Urban Development

JW, Jaro-Winkler

MF, Multi-family housing programs

MTW, Moving to Work demonstration program

NAMCS, National Ambulatory Medical Care Survey

DHCS, Division of Health Care Statistics

NCHS, National Center for Health Statistics

NDI, National Death Index

PBS8, project-based Section 8

PIC, Public & Indian Housing Information Center

PH, Public Housing program

PHA, Public Housing Agency

PII, personally identifiable information

PW, pair weight

RDC, Research Data Center

SSN, Social Security number

TRACS, Tenant Rental Assistance Certification System

1 Introduction

As the nation's principal health statistics agency, the mission of the National Center for Health Statistics (NCHS) is to provide statistical information that can be used to guide actions and policy to improve the health of the American people. In addition to collecting and disseminating the Nation's official vital statistics, NCHS conducts several population-based surveys and healthcare establishment surveys, including the National Ambulatory Medical Care Survey (NAMCS) (accessed August 2024). In 2021 the National Ambulatory Medical Care Survey (NAMCS) began collecting electronic health records (EHRs) for ambulatory care visits that took place in health centers, known as the NAMCS Health Center (HC) Component. Even though the NAMCS HC Component is a provider survey (i.e., health centers are the sampling unit) it collects patient level personally identifiable information (PII), which enable data linkages.

Through its Data Linkage Program, NCHS has been able to expand the analytic utility of the NAMCS HC Component data by linking the patient level data with housing assistance program data collected by the U.S. Department of Housing and Urban Development (HUD). This report will describe the linkage of the 2021 NAMCS HC Component to 2020-2022 HUD administrative data. The linkage of the NAMCS HC Component patient data with HUD administrative housing assistance program participation data creates a new data resource that can support a wide array of public health surveillance and policy evaluation studies focused on the role of housing assistance program participation as a key social determinant of health.

This report includes a brief overview of the linked data sources, a description of the methods used for linkage, and analytic guidance to assist researchers when using the files. Detailed information on the linkage methodology is provided in Appendix I: Detailed Description of Linkage Methodology.

The linkage of the 2021 NAMCS HC Component and the 2020-2022 HUD administrative data was performed at NCHS through contract #HHS75D30123A17667 by NORC at the University of Chicago with funding from the Department of Health and Human Services' Office of the Secretary Patient-Centered Outcomes Research Trust Fund (OS-PCORTF) under a project titled "Enhancing Surveillance of Maternal Health Clinical Practices and Outcomes with Federally Qualified Health Centers' (FQHCs) Electronic Health Records Visit Data."

2 Background on Linked Files

2.1 National Ambulatory Medical Care Survey (NAMCS) Health Care (HC) Component

The National Ambulatory Medical Care Survey (NAMCS), administered by NCHS, is a national survey designed to meet the need for objective, reliable information about the provision and use of ambulatory medical care services in the United States. First fielded in 1973, NAMCS is one of the NCHS National Healthcare Surveys, a family of provider-based surveys, covering a broad spectrum of health care settings (https://www.cdc.gov/nchs/dhcs/index.htm) (accessed August 2024). In 2012, NCHS added a separate national sample of community health centers to NAMCS in order to produce nationally representative estimates on health center provided ambulatory care services. Beginning in 2021, NCHS developed a more targeted NAMCS Health Center (HC) Component sampling frame to focus on the collection of Electronic Health Records (EHR) for all patient visits within a sampled HC. Sampled health centers include both

Federally Qualified Health Centers (FQHCs)[1] and FQHC look-alikes[2] in the 50 U.S. states and the District of Columbia, which provide ambulatory (or direct outpatient) care to the public and use an EHR system in one or more of their delivery sites.[3]

Participating health centers were asked to submit electronic health record (EHR) data for all patient encounters in calendar year 2021. These data included patient identifiers such as name, address, and social security number when it is available; date of visit; diagnoses and services provided or ordered during the visit; reason for visit; and clinical notes. In calendar year 2021, 29 of the 111 sampled health centers submitted data on 3,543,927 patient visits from January 1, 2021 to December 31, 2021, for an unweighted response rate of 26.1% and a weighted response rate of 26.8%. The 2021 NAMCS HC Component data are weighted and can be used to produce nationally representative estimates for visits at FQHCs.[4] However, due to the low response rate in 2021, NCHS did not release a public use file for the 2021 NAMCS HC Component, but rather made the data available for research via the NCHS Research Data Center Network. More information about the research data files available for the 2021 NAMCS HC Component can be found here: 2021 National Ambulatory Medical Care Survey Health Center Component RDC Data Dictionary (cdc.gov) (accessed August 2024).

2.2 U.S. Department of Housing and Urban Development (HUD) Public and Assisted Housing Programs and Data

2.2.1 HUD Public and Assisted Housing Programs

The U.S. Department of Housing and Urban Development (HUD) is the federal agency responsible for overseeing domestic housing programs and policies. While HUD is responsible for administrating various housing and community development programs, the linkage with the 2021 NAMCS HC Component focuses on HUD's three largest housing assistance programs: Housing Choice Vouchers, Public Housing, and assisted Multifamily programs. Persons and households participating in these program types are referred to as "HUD-assisted" in this document.

People living in HUD-assisted households are represented in HUD's administrative data because they receive a rental subsidy or pay a below-market rent. HUD uses data about household characteristics (for example, household size and citizenship status, income, and expenses) to determine the amount of the rental subsidy under federal law. Generally, rental subsidies seek to reduce gross housing costs for the tenant to approximately 30% of household income, although program rules may allow for variations in that ratio. A HUD subsidy pays the remaining amount up to a specified limit that varies by program.

The HUD Housing Choice Voucher (HCV) program is the federal government's largest housing assistance program, allowing families with lower incomes, older adults (persons 62 or older), and persons with disabilities to choose and lease safe and affordable housing. In the HCV program, housing assistance is tenant-based, meaning participants find their own housing in the private market. Participants are free to

[1] Federally Qualified Health Centers (FQHCs) are health centers that receive funding from the Department of Health and Human Services' Health Resources and Services Administration (HRSA) to deliver comprehensive and affordable primary healthcare services to the nation's most vulnerable populations, including people experiencing homelessness, agricultural workers, residents of public housing, and veterans.

[2] FQHC look-alikes are health centers that meet the HRSA Health Center Program requirements but do not receive HRSA funding.

[3] More detailed information about the 2021 NAMCS sampling procedures are available at: Williams SN, Ukaigwe J, Ward BW, Okeyode T, Shimizu IM. Sampling procedures for the collection of electronic health record data from federally qualified health centers, 2021–2022 National Ambulatory Medical Care Survey. National Center for Health Statistics. Vital Health Stat Series 2(203). 2023.

[4] More detailed information on producing weighted analyses based on the 2021 NAMCS HC Component data is available at: https://www.cdc.gov/rdc/data/b1/2021-NAMCS-HCC-RDC-Data-Dictionary-508.pdf. (accessed August 2024).

choose any housing unit that meets program requirements. In the NAMCS HC Component-HUD linked data, the HCV program also includes several smaller programs including: Homeownership Vouchers, Project-Based Vouchers, Section 8 Moderate Rehabilitation, and the Section 8 Rental Certificate programs. Among the 2021 NAMCS HC Component patients that linked to HUD administrative data, approximately 39% were participating in an HCV program.

The public housing (PH) program was established to provide safe rental housing for eligible low-income families, the elderly, and persons with disabilities. HUD provides capital subsidies and operating subsidies to local Public Housing Agencies (PHAs) that manage public housing for eligible low-income residents. Unlike the HCV program, PH is project-based meaning tenants do not choose their housing but are instead assigned housing in a specific unit, building, or development. Approximately 14% of the 2021 NAMCS HC Component patients that linked to HUD were participating in a PH program.

HCV and PH HUD program participants may also be participants in the Moving to Work (MTW) demonstration program. MTW provides PHAs the opportunity to design and test innovative, locally designed strategies that use Federal dollars more efficiently, help residents find employment, and increase housing choices for low-income families. Tenants participating in programs at MTW PHAs may need to verify their income and family composition less frequently than tenants in non-MTW HUD programs. These difference in program re-certification requirements were incorporated in the development of the linked NAMCS HC Component- HUD administrative data files. (See Section 2.2.2 for more information on HUD administrative data).

The assisted multi-family housing (MF) program category in the linked NAMCS HC Component – HUD data encompasses a number of separate, distinct HUD programs, including: Project-Based Section 8 (PBS8) the largest MF program, Section 221(d)(3) Below Market Interest Rate, Section 236 Multi-family Housing, Rental Assistance, Section 202 Supportive Housing for the Elderly Program, Section 202/162—Project Assistance Contract, Section 811 Supportive Housing for Persons with Disabilities, and Rent Supplement. Because each of the remaining MF programs lacked sufficient sample size on an individual basis in the linked file, they were combined into a single MF program category. In all MF programs, subsidies are paid directly to private property owners who provide a certain percentage of their housing units at affordable rates for low-income persons who qualify. MF program assistance is tied to the property, unlike tenant-based rental assistance programs (e.g., HCVs), and tenants cannot take their rental housing assistance subsidy elsewhere. Approximately 54% of the 2021 NAMCS HC Component patients that linked to HUD were participating in any MF program.

2.2.2 HUD Administrative Data

HUD administrative data systems contain program participation data for recipients of HCV, PH, and MF programs for all states, the District of Columbia, and some territories (for example, Puerto Rico and the U.S. Virgin Islands). The data collected through the administration of HUD’s housing assistance programs are stored in two information management systems, the Public & Indian Housing Information Center (PIC) and the Tenant Rental Assistance Certification System (TRACS).

PIC contains household-level and person-level administrative records pertaining to persons and households participating in HUD’s HCV and PH program types. The underlying forms used to capture information for these programs are the HUD-50058 and the HUD-50058MTW. The PIC data extract created for the 2021 NAMCS HC Component-HUD data linkage was based on HUD’s PIC point-in-time quarterly files, which capture a household’s most recent transaction with HUD during the prior 18 months (with the exception of Moving to Work (MTW) demonstration program participants, where 36 months is used as the threshold). A transaction refers to any activity for which a HUD form was completed (e.g., new admission to a HUD program, annual recertification, end of participation, etc.). These files are released four times a year (March, June, September, and December).

TRACS is a system developed to collect and maintain certified tenant data from owners and management agents of MF housing programs. The underlying form used to capture information for MF programs is HUD – 50059. The TRACS data extract created for the 2021 NAMCS HC Component-HUD data linkage was based on TRACS point-in-time quarterly extracts from the TRACS production system. Similar to the PIC data, these data capture transactions occurring within the 18 months immediately prior to the date of extract. Transactions with the same SSN, effective date, and transaction code were considered duplicates and removed.

To determine program overlap, HUD transactions collected from PIC and TRACS were used to create participation episodes and monthly HUD program participation variables for the final NAMCS HC-HUD linked data files. For more detailed information on the specific HUD data available on the NAMCS HC-HUD linked data files, see Section 4.2.1.

For more information on HUD programs, their administration, and the PIC and TRACS data systems, please refer to "A Primer on HUD Programs and Associated Administrative Data" (accessed August 2024).

3 Linkage Methodology

3.1 Linkage Eligibility Determination

The linkage of NAMCS HC Component patient records to HUD data was conducted through a designated agent agreement between NCHS and HUD. Approval for the linkage was provided by NCHS's Research Ethics Review Board (ERB).[5]

Linkage was attempted only for NAMCS HC Component patient records that had at least two of the following three identifiers present:

- valid SSN[6]
- valid date of birth (month, day, and year)[7]
- valid name (first, middle initial, and last)[8]

For example, if the PII on the NAMCS HC Component patient record had no SSN, a full name, and only the year of birth, the record would be considered ineligible for linkage, as only one of the criteria (i.e., that for name) was met.

[5] The NCHS ERB is an appointed ethics review committee that is established to protect the rights and welfare of human research subjects.

[6] Nine-digit SSN is considered valid if: 9-digits in length, containing only numbers, does not begin with 000, 666, or any values after 899, all 9-digits cannot be the same (i.e., 111111111, etc.), middle two and last 4-digits cannot be 0's (i.e., xxx-00-xxxx or xxx-xx-0000), and digits are not consecutive (ex. 012345678). Additionally, special SSN values (i.e., 123-123-1234, 111-22-3333, 010-010-0101, 001-01-0001, etc.) were changed to missing. Four-digit SSN is considered valid if: 4-digits in length, containing only numbers, and is between 0001 and 9999.

[7] A date of birth is considered valid if at least two of the three date parts are valid date values.

[8] A name is considered valid if: either first or last name has two or more characters, and two of the three name parts (first, middle initial, and last) are non-missing.

The variable ELIGSTAT, included on the linked NAMCS HC Component -HUD match file, provides the linkage eligibility status for each NAMCS HC Component patient record. ELIGSTAT values include 0 (ineligible) or 1 (eligible). The 2021 NAMCS HC Component included 726,384 (99.9%) patients who were determined to be eligible for linkage with HUD administrative data. Note that linkage eligibility is distinct from program eligibility, which defines whether a person meets the eligibility criteria for a specific government-administered or funded program.

3.2 Overview of Linkage

This section outlines steps used to link the NAMCS HC Component data to the 2020-2022 HUD enrollment data. The linkage was conducted at a patient level using patient identifiers collected from health center submitted patient visit records. The patient identifiers collected from the visit records were used to link HUD program participation records covering the calendar years 2020 through 2022. For more detailed information on linkage methodology see Appendix I: Detailed Description of Linkage Methodology.

Linkage-eligible NAMCS HC Component patient records were linked to the HUD enrollment database using the following identifiers: SSN, first name, last name, middle initial, month of birth, day of birth, year of birth, 5-digit ZIP code of residence, state of residence, and sex.

The NAMCS HC Component patient records and the HUD enrollment database were linked using both deterministic and probabilistic approaches. For the probabilistic approach, scoring was conducted according to the Fellegi-Sunter method.[9] Following this, a selection process was implemented with the goal of selecting pairs that represented the same individual between the two data sources. It is important to note that both deterministic and probabilistic linkages were conducted separately for each sex category (males and females). That is, records on the NAMCS HC Component and HUD linkage submission files were first separated using the recorded sex value and then each set of files were separately linked.[10] The Fellegi-Sunter method assumes independence between the agreement status of variables used to score the records. Because first names are commonly associated with sex, running the linkage by sex ensures independence and enables more appropriate weighting of name comparisons when using the methods described by Fellegi-Sunter.[11] The following steps were implemented:

1. Separate NAMCS HC Component and HUD submission files using sex. HUD submission records were further restricted to the linkage period (i.e., 2020-2022).
2. Deterministic linkage joined records on exact SSN and validated links by comparing other identifying fields (i.e., first name, last name, day of birth, etc.)
3. Probabilistic linkage identified likely matches, or links, between all records. All records were probabilistically linked and scored as follows:
    a. Formed pairs via blocking
    b. Scored pairs
    c. Modeled probability - assigned estimated probability that pairs are links

[9] Fellegi, I. P., and Sunter, A B. (1969), "A Theory for Record Linkage," JASA 40 1183-1210.

[10] Before the submission records were separated, alternate submission records (see Appendix I, section 1) with an imputed sex value of male and female were created for records with missing sex.

[11] First names are often sex specific (i.e., first name Robert is usually associated with males and Mary is usually associated with females). Additionally, multiple part first and last names are more likely to be associated with females, which are handled differently when creating the linkage submission file. See Table 2 in Appendix I, Section 1 for additional information on the alternate record generation process for multiple part names.

4. Pairs were selected that were believed to represent the same individual between data sources (i.e., they are a match).
    a. Deterministic matches (from step 2) were assigned a match probability of 1
    b. Record pairs selected from the probabilistic match (step 3) were assigned the model match probability. Record pairs with a match probability above the established probability cut-off value were determined to be matches.

For each NAMCS HC Component patient record that was deemed a match, HUD extracted information from the PICS and TRACS systems and sent them to NCHS through a secure data transfer system.

Table 1 presents the total number of 2021 NAMCS HC Component patients by age group and sex, the number who were eligible for linkage, the number who were linked to HUD administrative data, and the percentage of all patients and those eligible for linkage who were linked to HUD administrative program data.

Table 1. Linked 2021 NAMCS HC Component – 2020-2022 HUD Administrative Records: Sample Sizes and Percent Linked, by Age and Sex

	Sample Size			Percent Linked	
	Total Sample	**Eligible for Linkage[2]**	**Linked to 2020-2022 HUD Administrative Data[3]**	**Total Sample[4]**	**Eligible Sample[5]**
2021 NAMCS HC Component					
Age[1]					
0-17	185,969	185,968	8,253	4.44	4.44
18-44	271,315	271,312	8,169	3.01	3.01
45-64	184,080	184,080	5,712	3.10	3.10
65 and over	85,020	85,019	3,994	4.70	4.70
Not Calculated	848	5	0	0.00	0.00
Total	727,232	726,384	26,128	3.60	3.60
Sex					
Male	309,817	309,815	8,951	2.89	2.89
Female	414,112	414,109	17,128	4.14	4.14
Missing	3,303	2,460	49	1.48	1.99
Total	727,232	726,384	26,128	3.60	3.60

[1] Age is as of final health center visit (date of last known contact). Age is calculated by subtracting patient date of birth (DOB) from the final visit date. When more than one DOB was present, the minimum of the non-missing DOB was selected.

[2] Eligibility for linkage is based upon having sufficient PII in at least two of three data element groups: SSN, name, and date of birth.

[3] This group includes linkage-eligible patients who linked to HUD enrollment database at any time during the linkage interval (2020-2022).

[4] This percentage is calculated by dividing the number of linked patients by the number of patients in the total sample.

[5] This percentage is calculated by dividing the number of linked patients by the total number of linkage-eligible patients.

4 Analytic Considerations

This section summarizes some key analytic issues for users of the linked NAMCS HC Component data and HUD administrative records. It is not an exhaustive list of the analytic issues that researchers may encounter while using the linked NAMCS HC Component-HUD data. This document will be updated as additional analytic issues are identified and brought to the attention of the NCHS Data Linkage Team (datalinkage@cdc.gov). Users of the NAMCS HC Component-HUD linked data files are encouraged to read "A Primer on HUD Programs and Associated Administrative Data" (accessed August 2024) for additional information on HUD program and corresponding administrative data, including important analytic considerations.

4.1 Analytic Considerations for NAMCS HC Component Data

4.1.1 2021 NAMCS HC Component Restricted-Use Files (RUF)

The 2021 NAMCS HC Component restricted-use survey data are made available for research use through the NCHS RDC network. For more information about obtaining access to NAMCS HC Component RUFs see Section 5.0. The NAMCS HC Component RUFs are organized as relational data tables organized by Visits, Patients, Conditions, Procedures and Weights. For more information about the specific variables and the observational unit for each data table please see the NAMCS HC Component data documentation available at: https://www.cdc.gov/rdc/data/b1/2021-NAMCS-HCC-RDC-Data-Dictionary-508.pdf (accessed August 2024).

During the 2021 NAMCS data collection period some health centers did not provide certain data elements for any of their reported visits. NCHS has provided detailed analytic guidance on how users should adjust their analysis of NAMCS HC Component data to account for complete missing data. More detailed information on methods to adjust for data missingness in the NAMCS HC Component survey data are available at: https://www.cdc.gov/rdc/data/b1/2021-NAMCS-HCC-RDC-Data-Dictionary-508.pdf (accessed August 2024).

4.1.2 Using 2021 NAMCS HC Component Visit Weights

The Division of Health Care Statistics (DHCS), NCHS, has produced visit weights that can be used to produce nationally representative estimates of ambulatory care visits occurring in Federally Qualified Health Centers.[12] For more detailed information regarding producing weighted estimates with NAMCS HC Component data please see: https://www.cdc.gov/rdc/data/b1/2021-NAMCS-HCC-RDC-Data-Dictionary-508.pdf

The linkage between the 2021 NAMCS HC Component data and HUD housing assistance program data was conducted at a patient level using patient identifiers collected from health center submitted patient visit records. The patient identifiers collected from the visit records were used to link HUD program participation records covering the calendar years 2020 through 2022. For patients with linked HUD program participation data, it will be possible for analysts to align the month of the patient visit with the month of HUD program participation for all months in 2021 and apply the NAMCS HC Component visit weights. For more information on producing weighted estimates with NAMCS Component data please see https://www.cdc.gov/rdc/data/b1/2021-NAMCS-HCC-RDC-Data-Dictionary-508.pdf. Because the linked HUD program participation record cover the time period from 2020-2022, NAMCS HC Component patients

[12] Sampled NAMCS health centers include both Federally Qualified Health Centers (FQHCs) and FQHC look-alikes. FQHC look-alikes are health centers that meet the HRSA Health Center Program requirements but do not receive HRSA funding.

may also have additional information available about their HUD program participation in the calendar year prior to the 2021 NAMCS data collection period and the calendar year after._For more information on the temporal alignment of HUD program participation data and NAMCS HC Component visit data please see Section 4.2.2.2 and Section 4.2.2.3. Although DHCS has developed visit level weights for use with the 2021 NAMCS HC Component visit data, NAMCS patient level weights have not been created. Analysts wishing to analyze linked HUD data at the patient level will not be able to perform weighted analyses.

4.2 Analytic Considerations for Linked HUD Data Files

4.2.1 Description of Linked NAMCS HC Component - HUD Data Files

4.2.1.1 HUD Match File

The linked HUD Match file can be used to identify which of the NAMCS HC Component patients were eligible for linkage and linked to a HUD record. This file contains one record for each unique NAMCS HC Component patient ID and contains the variables ELIGSTAT, PROBVALID, and HUD_MATCH_STATUS.

The variable ELIGSTAT should be used to determine linkage eligibility (Section 3.1). NAMCS HC Component patient IDs with an ELIGSTAT value of 1 were considered eligible for linkage to the HUD enrollment records.

Data linkages include some uncertainty over which pairs represent true matches. An estimated probability of match validity (PROBVALID) was computed for each candidate pair and compared against a probability cut-off value to determine which pairs were links (an inferred match). For additional discussion on how PROBVALID was estimated, see Appendix I, Sections 3.3 and 3.4. NCHS used a probability cut-off value which minimized the total estimated counts of Type I error (false positive links – identified as participating in a HUD program but actually are not) and Type II error (false negative links – identified as not participating in a HUD program but actually are).

In the HUD Match file, NCHS used a probability cut-off value of 0.8925 to determine final match status. Candidate pairs with a PROBVALID that exceeded the probability cut-off value (i.e., PROBVALID>0.8925) were deemed a link. For additional discussion on probability cut-off value determination and record selection, please see Appendix I, Section 4. For some analyses, it may be desirable to reduce the Type I error. To do this, researchers should increase the probability cut-off value to a value closer to 1.0. Researchers wishing to increase the probability cut-off value should request PROBVALID in their RDC proposal. Note, the probability cut-off value cannot be decreased from 0.8925 as pairs estimated with lower match probability are not made available to researchers.

The HUD_MATCH_STATUS variable can be used to identify which of the NAMCS HC Component patients were participating in any HUD program during the HUD linkage period. When equal to one, HUD_MATCH_STATUS indicates that a NAMCS HC Component patient was matched to at least one HUD housing assistance program administrative transaction record during the 2020-2022 linkage period.

4.2.1.2 Linked HUD Program Participation Files

The NAMCS HC Component data have been linked to multiple years of HUD data. HUD program participation data may be available for patients during the 2021 NAMCS HC Component data collection year as well as the calendar year prior to or after the 2021 survey period.

The linked HUD program specific participation files contain monthly indicator variables to indicate whether a linked 2021 NAMCS HC Component patient received HUD housing assistance benefits within a given month during the 3-year linkage period. There are four HUD program participation files, including a summary program participation file (any HUD program participation) and then three program specific participation files for each of the three main HUD housing assistance programs (HCV, PH, and MF).

Each of the HUD program-specific participation files contains one record for each linked NAMCS HC Component patient ID and 36 monthly HUD participation indicators (one for each month during the linked data time span). The monthly indicators are created from program participation episodes that were derived using the transaction dates from the HUD transaction file. For each month in which at least one day of HUD participation is identified, the monthly indicator is set to 1, indicating program participation for that month. Monthly indicator variables for months with no HUD program participation are set to 0. For example, a HUD program participation episode that began in June 2021 and ended in December 2022 would have monthly indicator variables set to 1 for all months from June 2021 through December 2022. All other monthly program participation variables from January 2020 to May 2021 would be set to 0. It is not possible for analysts using the HUD program-specific participation files to determine whether a HUD program participation period began prior to or ended after the NAMCS HC Component - HUD linkage period (January 2020 – December 2022).

For more detailed information on the types of housing-assistance programs administered by HUD and how HUD administrative data are collected, please refer to "A Primer on HUD Programs and Associated Administrative Data" (accessed August 2024).

4.2.2 Identification of Ever and Concurrent HUD-Assisted Patients

4.2.2.1 Ever Received HUD-assisted Housing

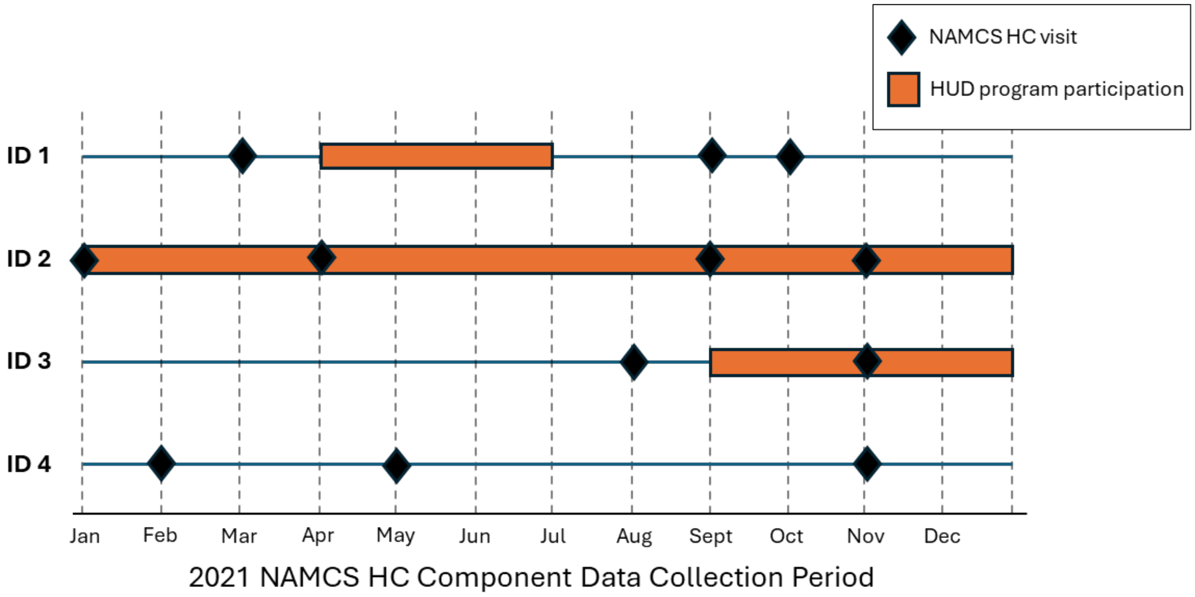
To identify NAMCS HC Component patients who were participating in a HUD-assisted housing program at any time during the linkage period, researchers should use HUD_MATCH_STATUS in the linked HUD Match file. A HUD_MATCH_STATUS value of 1 indicates that an NAMCS HC Component patient ID was linked with a HUD record at least once during the HUD linkage period (calendar years 2020-2022). To determine which months the NAMCS HC Component patient was ever enrolled in a HUD assistance program, researchers should use the monthly program participation variables found in the Any HUD Program Participation File. To determine which of the specific HUD programs the patient was participating in, researchers should use the program specific participation files (HCV, MF and PH).

4.2.2.2 Temporal Alignment of HUD Assistance with NAMCS HC Component Patient Visit Data

To identify whether the NAMCS HC Component patient was enrolled in a HUD program during, before, or after a specific health center visit, researchers can compare the month and year of the NAMCS HC Component patient visit with the monthly indicators included the linked HUD program participation data files (Any, HCV, MF, and PH).

Figure 1 below depicts potential temporal alignment scenarios for 2021 NAMCS HC Component patient visit data and monthly 2021 HUD program participation data for four hypothetical patients noted as patient ID1 through patient ID4. In each timeline, the diamond represents the month during which the NAMCS HC Component patient visit occurred, and the orange bar represents the month(s) during which the patient received HUD assistance. For example, Patient ID1 was participating in a HUD program during the months of April, May, and June but did not participate in July. The orange bar of Patient ID 1 spans only the months April through June and stops at July.

Figure 1. Temporal Alignment of 2021 NAMCS HC Component Patient Visit Data Linked to 2021 HUD Program Participation Data.



Notes: HUD is the U.S. Department of Housing and Urban Development
Sources: 2021 NAMCS HC Component patient data linked to 2020-2022 HUD administrative data.

The examples shown in Figure 1 are as follows,

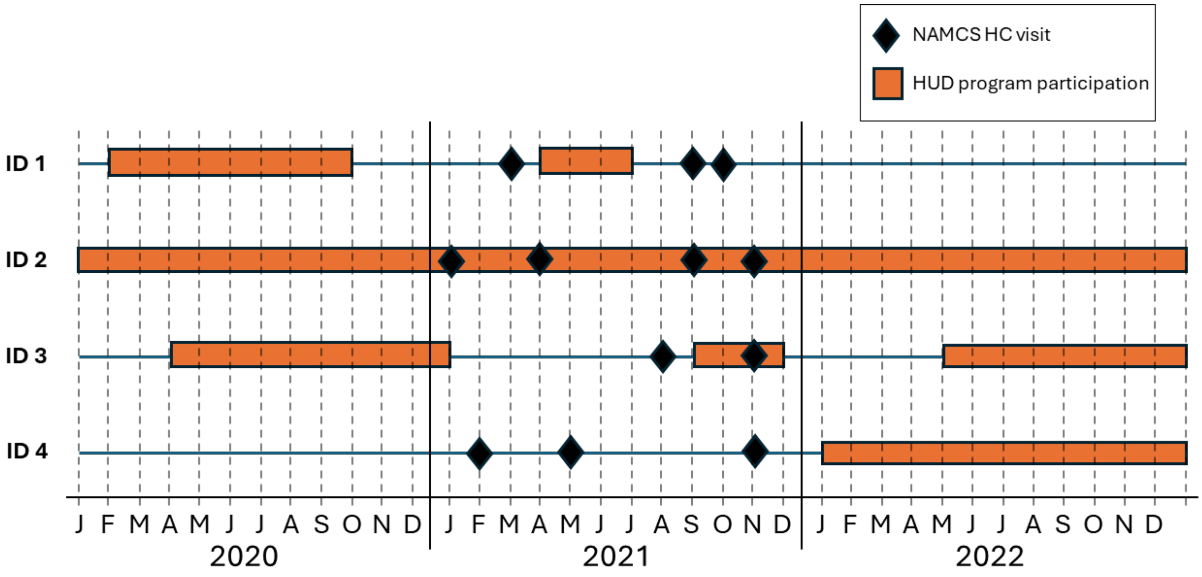
- Patient ID1 did receive HUD assistance during the 2021 NAMCS HC Component data collection period but their HUD program participation period was not concurrent with any of the months in which Patient ID1 had a NAMCS HC Component reported health center visit.
- Patient ID2 was receiving HUD assistance for all months in calendar year 2021 and had four health center visits during this period.
- Patient ID3 was receiving HUD assistance during the month of their November 2021 health center visit but was not receiving HUD assistance during their August 2021 health center visit.
- Patient ID4 had three health center visits but was not receiving HUD assistance at the time of any of their NAMCS HC Component reported health center visits.

To determine which HUD program the patient was participating in at the time of their 2021 health center visit, the researcher would utilize the monthly indicator variables for 2021 found in each of the specific HUD program participation files (HCV, MF, and PH). If a monthly indicator variable is equal to 1, this indicates that the patient was participating in that specific HUD program at the time of their health center visit. Note that it is possible for a patient to be participating in more than one HUD program in any given month. For more information on how to incorporate the NAMCS HC Component Visit Weights with monthly 2021 HUD program participation variables see Section 4.1.2.

4.2.2.3 Temporal Alignment of HUD Assistance with NAMCS HC Component Patient Data

The linked data files include monthly HUD program participation variables for calendar years 2020 through 2022. Therefore, HUD monthly program participation status may be available for NAMCS HC Component patients during the calendar year prior to, the year of, or the year after the NAMCS HC Component 2021 data collection period. Expanding on Figure 1, which shows four hypothetical patient visit and HUD program participation scenarios for 2021, Figure 2 provides examples of how the 2020-2022 HUD program participation periods may align with NAMCS HC Component patient data for the entire HUD linkage period.

Figure 2. Temporal Alignment of 2021 NAMCS HC Component Patient Visit Data Linked to 2020-2022 HUD Program Participation Data.



Notes: HUD is the U.S. Department of Housing and Urban Development
Sources: 2021 NAMCS HC Component patient data linked to 2020-2022 HUD administrative data.

The examples shown in Figure 2 are as follows,

- Patient ID1 was receiving HUD assistance from February through September 2020, during the calendar year prior to the 2021 NAMCS HC Component data collection period, as well as during the 2021 NAMCS HC Component data collection period (April 2021 - June 2021); but was not receiving HUD assistance during any month of the calendar year following the 2021 NAMCS HC Component data collection period.
- Patient ID2 was receiving HUD assistance throughout the entire NAMCS HC Component - HUD linked data period (January 2020 - December 2022) including at the time of each their 2021 NAMCS HC Component patient visits.
- Patient ID3 was intermittently receiving HUD assistance with periods of HUD participation prior to (April 2020 - December 2020), during (September 2021 - November 2021), and after (May 2022-December 2022) the 2021 NAMCS HC Component data collection period.
- Patient ID4 was not receiving HUD assistance at the time of any of their 2021 NAMCS HC Component reported patient visits but was receiving HUD assistance for all months of the calendar year following the 2021 NAMCS HC Component data collection period.

5 Access to Data Files

5.0 Access to the Restricted-Use Linked NAMCS HC Component – HUD Administrative Data Files

To ensure confidentiality, NCHS provides safeguards including the removal of all personal identifiers from analytic linked files. Additionally, the linked data files are only accessible through the NCHS Research Data Center (RDC) network for approved research projects. Researchers who wish to access the restricted-use 2021 NAMCS HC Component survey files and the linked 2021 NAMCS HC Component-HUD administrative data files must submit a research proposal application to the NCHS RDC. The RDC staff will review all submitted proposals to determine if the proposed project is feasible and to identify any potential disclosure risks. More information regarding the NCHS RDC network and the RDC proposal application process are available from: https://www.cdc.gov/rdc/ (accessed August 2024).

5.1 Merging NAMCS HC Component Survey Data to the Linked NAMCS HC Component-HUD Administrative Data Files

The linkage between the 2021 NAMCS HC Component data and HUD program data was conducted at a patient level using patient level identifiers. The shared variable, PATIENT_ID, will be used by the RDC to merge the 2021 NAMCS HC Component-HUD linked data files with the restricted-use 2021 NAMCS HC Component data. Analysts should request all variables of interest from the 2021 NAMCS HC Component restricted-use data files and the 2021 NAMCS HC Component-HUD linked data files in their RDC proposal.

5.2 Additional Related Data Sources

The linkage of the 2021 NAMCS HC Component patient data with HUD housing assistance program data was conducted with funding support from the Department of Health and Human Services' Office of the Secretary Patient-Centered Outcomes Research Trust Fund (OS-PCORTF). OS-PCORTF is also supporting the linkage of the 2021 NAMCS HC Component data with mortality information obtained through linkage with the NCHS National Death Index (NDI) and Medicaid and Children's Health Insurance Program Data obtained through linkage with the Transformed Medicaid Statistical Information System (T-MSIS) from the Centers for Medicare & Medicaid Services (CMS). More information about these linked data files will be published at https://www.cdc.gov/nchs/data-linkage/index.htm (accessed August 2024).

Appendix I: Detailed Description of Linkage Methodology

1 2021 NAMCS HC Component and HUD Linkage Submission Files

A linkage submission file is a dataset created for conducting linkages between two sources of data. Linkage submission files, which contained the cleaned and validated PII fields, were created separately for NAMCS HC Component patient records and for HUD administrative records.[13] The following PII fields were individually processed and output to separate files (i.e., there were separate files for SSN, DOB, name, etc., each record showing a possible value for that field for each NAMCS HC Component patient or HUD enrollee:

- SSN (validated)[14]
- DOB (month, day, and year)
- Sex
- 5-Digit ZIP code and state of residence
- First, middle initial, and last name

Identifier values deemed invalid by the cleaning and standardization routine were changed to a null value. A few examples where this occurred include:

- Date values: when invalid or outside of expected range
- Sex values: when multiple sex values are recorded for the same person
- Name values: multiple edits are applied:
    - Removal of special characters such as [“-.,<>/?, etc.]
    - Removal of descriptive words such as twin, brother, daughter, etc.
    - Nulling of baby names—name parts that contain specific keywords such as baby, infant, girl or boy are set to null
    - Names listed as Jane/John Doe
    - Removal of titles such as Mister, Miss, etc.
    - Removal of suffixes such as Junior, II, etc.
    - Removal of special text such as first name listed as “Void”

To increase the likelihood of finding a link, multiple or alternate submission records could be generated for each linkage eligible record in the NAMCS HC Component patient and HUD submission files based on variation of the linkage variables. Similar to the cleaning process, a more elaborate routine was used to

[13] NCHS conducted an assessment of the 2021 NAMCS HC Component Patient PII. The results of the assessment are published in Appendix II of ‘The Linkage of the 2021 National Ambulatory Medicare Care Survey (NAMCS) Health Center (HC) Component to 2021-2022 National Death Index: Linkage Methodology and Analytic Considerations’ report (Accessed XXX 2024).

[14] Nine-digit SSN is considered valid if: 9-digits in length, containing only numbers, does not begin with 000, 666, or any values after 899, all 9-digits cannot be the same (i.e., 111111111, etc.), middle two and last 4-digits cannot be 0’s (i.e., xxx-00-xxxx or xxx-xx-0000), and digits are not consecutive (ex. 012345678). Additionally, special SSN values (i.e., 123-123-1234, 111-22-3333, 010-010-0101, 001-01-0001, etc.) were changed to missing. Four-digit SSN is considered valid if: 4-digits in length, containing only numbers, and is between 0001 and 9999.

generate alternate records involving the name fields. Alternate records were generated for patients according to the following rules.

- Sex was missing. Two alternate records (one with male sex and the other with female) were created (note that this would result in having generated records run through both male and female specific linkage passes, and resulting duplicated links would be subsequently resolved.
- SSN with less than nine digits. A single alternate record was created where leading zeros were added to SSN values of length 7 or 8 to make a 9-digit SSN. Note, no alternate record was created if an invalid SSN would be created by adding 0's.
- Improbable date of birth. Age at time of survey was computed by subtracting the year of the survey and the year of birth. Records with age greater than 114 had a single alternate record created,
    - If month and day were suspected of being imputed (ex. Jan 1st or June 15th), entire DOB was changed to missing[15]
    - Otherwise, only year was changed to missing
- State of residence outside of U.S. and not in rest of world (RW) list. Alternate record was created with ZIP and state codes changed to missing
- ZIP code represents a different state. Using the ZIPSTATE() SAS function, state was imputed using the non-missing ZIP code. If the imputed state was different from the recorded state of residence, an alternate record using imputed state was created
- Multiple name parts and common nicknames (see below)

NCHS created a common nickname lookup file which was used to generate a second record replacing the nickname with the associated formal name. Similarly, multiple part names (first or last) are addressed by creating alternate name records. Table 2 below provides three examples of how alternate records were generated for nick names (Patient ID 1) and multiple part names (Patient ID 2 & 3), using hypothetical data. For patient 2, the first name was used to generate multiple records, and for patient 3, the last name was used.

Table 2. Example of Alternate Record Generation using Name Fields

Patient ID	First Name	Middle Initial	Last Name	Alternate Record
1	Beth	A	Roberts	0
1	Elizabeth	A	Roberts	1
2	Mary Ann		Davis	0
2	Mary	A	Davis	1
2	Ann		Davis	1
2	Mary		Davis	1
3	Patricia	R	Drew Hamilton	0
3	Patricia	R	Drew	1
3	Patricia	R	Hamilton	1

NOTES: The information presented in the table was fabricated to illustrate the applied approach.

Submission files, which combined the cleaned and validated PII fields, were created separately for NAMCS HC Component patient records and for HUD enrollment records. During this process, multiple submission

[15] Note, the date values are often recorded when the actual value is unknown.

records were created for each patient/enrollee to show all combinations of the recorded values for these fields. That is, if a patient/enrollee had two states–of-residence recorded and three dates-of-birth recorded and each of the remaining fields had only one variant, then a total of six submission records would have been created for the patient/enrollee (see Table 3 for example). Submission records that did not meet the eligibility requirements (see Section 3.1 Linkage Eligibility Determination) were removed from the submission file.

Table 3. Example of Alternate Records Caused by Different PII Values

Patient ID	Day of Birth	Month of Birth	Year of Birth	State of Residence
1	31	12	1999	PA
1	30	12	1999	PA
1	15	12	1999	PA
1	31	12	1999	NY
1	30	12	1999	NY
1	15	12	1999	NY

NOTES: Data have been fabricated for this example. Other PII fields not shown as they are the same across all records.
PII – Personally Identifiable Information.

Additional post processing steps were taken after the initial 2021 NAMCS HC Component and HUD linkage submission files were created. First, records from both the NAMCS HC Component and HUD submission files were separated according to the sex value (male or female). As mentioned in section 3.2, the probabilistic linkage method assumes independence between the PII variables used to score the potential links. Records in the submission files were separated by sex to avoid violating this assumption, especially when first and/or last name and sex would be used as blocking and/or scoring variables. Additionally, the HUD submission file is limited to records with an effective date between one year before and after the survey year (2021). This step was taken to reduce the computational burden of linking records that will ultimately be rejected because they occur outside of the 2020-2022 linkage period.

2 Deterministic Linkage Using Unique Identifiers

The deterministic linkage, which was the next step in the linkage process, used only the NAMCS HC Component and HUD submission records that included a valid SSN. The algorithm performed two passes on the data, the first pass joining records when all 9-digits of the SSN matched and then for records where the last four digits of the SSN matched. Further, records in the 2nd pass had to have a non-missing first or last name **AND** a non-missing date of birth part (month, day, or year) to be eligible for deterministic matching using the last 4 of SSN. After records had been linked using SSN, the algorithm validated the deterministic links by comparing first name, middle initial, last name, month of birth, day of birth, year of birth, ZIP code of residence, and state of residence. If the ratio of agreeing identifiers to non-missing identifiers was greater than 50% (1st pass using SSN-9) or greater than 2/3 (2nd pass using last 4 of SSN), the linked pair was retained as a deterministic match. In addition to the 2/3's agreement ratio, linked pairs in the 2nd pass were required to have at least first or last name in agreement to be deemed a deterministic match. Of note, NAMCS HC Component patients were excluded from the second pass (i.e., using the last 4-digits of SSN) if they were deterministically linked in the first pass. The collection of records resulting from the deterministic match is referred to as the 'truth source.'

3 Probabilistic Linkage

The second step in the linkage process was to perform the probabilistic linkage for all records. To infer which pairs are links, the linkage algorithm first identified potential links and then evaluated their probable validity (i.e., that they represent the same individual). The following sections describe these steps in detail.

The weighting procedure of this linkage process closely followed the Fellegi-Sunter paradigm, the foundational methodology used for record linkage. Based on Fellegi-Sunter, each pair was assigned an estimated probability representing the likelihood that it is a match – using pair weights computed (according to formula) for each identifier in the pair – before selecting the most probable match between two records.

3.1 Blocking

Blocking is a key step in the probabilistic record linkage process. It identifies a smaller set of potential candidate pairs, eliminating the need to compare every single pair in the full comparison space (i.e., the Cartesian product). According to Christen, blocking or indexing, "splits each database into smaller blocks according to some blocking criteria (generally known as a blocking key)."[16] Intuitively developed rules can be used to define the blocking criteria, however, for this linkage, variable values in the data being linked were used to inform the development of a set of blocking passes that efficiently join the datasets together (i.e., multiple, overlapping blocking passes are run, each using a different blocking key). By using these data to create an efficient blocking scheme (or set of blocking passes), a high percentage of true positive links were retained while the number of false positive links were significantly reduced. A supervised machine learning algorithm used the 'truth source' (see Appendix I section 2) as the validation dataset and the NAMCS HC Component and HUD submission records as training data. For more detailed information on the supervised machine learning algorithm used, please refer to "Learning Blocking Schemes for Record Linkage" and "Using supervised machine learning to identify efficient blocking schemes for record linkage".[17] [18]

The machine learning algorithm produced 14 blocking passes to be used in the blocking scheme. Table 4 provides the PII variables that were assigned to each of the blocking passes and the PII variables that were used to score the potential links in each of the blocking passes. Note, the variables listed in the scoring key are all PII variables not used as a blocking variable. Further, if only the ZIP code of residence was used as a blocking variable, then state of residence was excluded from the list of scoring variables as it is implied to agree on all records.

[16] Christen, Peter. Data Matching: Concepts and Techniques for Record Linkage, Entity Resolution, and Duplicate Detection. Data-Centric Systems and Applications. Berlin Heidelberg: Springer-Verlag, 2012. http://www.springer.com/us/book/9783642311635 (accessed August 2024).

[17] Michelson, Matthew, and Craig A. Knoblock. "Learning Blocking Schemes for Record Linkage." In Proceedings of the 21st National Conference on Artificial Intelligence - Volume 1, 440–445. AAAI'06. Boston, Massachusetts: AAAI Press, 2006. https://pdfs.semanticscholar.org/18ee/d721845dd876c769c1fd2d967c04f3a6eeaa.pdf (accessed August 2024)).

[18] Campbell, S. R., Resnick, D. M., Cox, C. S., & Mirel, L. B. (2021). Using supervised machine learning to identify efficient blocking schemes for record linkage. Statistical Journal of the IAOS, 37(2), 673–680. https://doi.org/10.3233/SJI-200779 (accessed August 2024).

Table 4. Blocking and Scoring Scheme Used to Identify and Score Potential Links

Key Number	Blocking Key	Scoring Key
1	Last name, month of birth, day of birth, year of birth	First name, middle initial, state of residence, ZIP code of residence
2	Month of birth, day of birth, year of birth, state of residence	First name, middle initial, last name, ZIP code of residence
3	Last name, first name, state of residence	Middle initial, month of birth, day of birth, year of birth, ZIP code of residence
4	Last name, month of birth, year of birth, state of residence	First name, middle initial, day of birth, ZIP code of residence
5	First name, month of birth, year of birth, state of residence	Middle initial, last name, day of birth, ZIP code of residence
6	Last name, month of birth, day of birth, state of residence	First name, middle initial, year of birth, ZIP code of residence
7	First name, month of birth, day of birth, state of residence	Middle initial, last name, year of birth, ZIP code of residence
8	Last name, first name, month of birth, year of birth	Middle initial, day of birth, state of residence, ZIP code of residence
9	Day of birth, year of birth, state of residence, ZIP code of residence	First name, middle initial, last name, month of birth
10	Last name, first name, day of birth	Middle initial, month of birth, year of birth, state of residence, ZIP code of residence
11	First name, month of birth, day of birth, year of birth	Middle initial, last name, state of residence, ZIP code of residence
12	Last name, year of birth, state of residence, ZIP code of residence	First name, middle initial, month of birth, day of birth
13	Last name, day of birth, year of birth, state of residence	First name, middle initial, month of birth, ZIP code of residence
14	Month of birth, year of birth, state of residence, ZIP code of residence	First name, middle initial, last name, day of birth

3.2 Score Pairs

Next, each pair within a given block was scored using an approach based on the Fellegi-Sunter paradigm. The Fellegi-Sunter paradigm specifies the functional relationship between agreement probabilities and agreement/non-agreement weights for each identifier used in the linkage process. The scores – pair weights – calculated in this step were used in a probability model (explained in Section 3.3), which allowed the linkage algorithm to select final links to include in the linked file. The scoring process followed the order below:

1. Calculate M- and U- probabilities (defined in Section 3.2.1)
2. Calculate agreement and non-agreement weights
3. Calculate pair weight scores

The pair scores were calculated on the agreement statuses of the following identifiers (excluding specifically the variables used to define each block—e.g., if blocking is by first name and last name, then neither were used to evaluate the pairs generated by the block):

- First Name or First Initial (when applicable)
- Middle Initial
- Last Name or Last Initial (when applicable)
- Year of Birth
- Month of Birth
- Day of Birth
- State of Residence
- ZIP Code (conditional on state agreement)

3.2.1 M and U Probabilities

The M-probability is the probability that the identifiers on a pair of records agree, given that records represent the same person (i.e., the records are a match). M-probabilities were estimated separately within each individual blocking pass and were calculated for each of the identifiers used for scoring (Table 4). Within the blocking pass, pairs with agreeing SSN were used to calculate the M-probabilities, as these are assumed to represent the same individual. SSN agreement was defined as having 8 or more digits being the same for pairs with a full 9-digit SSN or the last 4-digits being the same for pairs with only a 4-digit SSN (ex. XXXXX9999). Further, to account for the alternate submission records generated during the creation of the submission files, the “best” agreement was taken for each of the scoring variables among the blocked records for each NAMCS HC Component patient ID and HUD ID (see Tables 5 and 6 for example of alternate record summarization). Table 5 is an example of how the agreement flags for each of the scoring variables in Blocking pass 10 are created. A value of 1 means the information in the variable is exactly matching, while a 0 means they are not. Table 6 then represents how the multiple submission records in Table 5 are summarized into one record for each NAMCS HC Component patient and HUD administrative ID. If any of the identifiers agree across multiple records, they are flagged as agree (i.e., set to 1). The summarized records in Table 6 are then used to estimate the M-probabilities for each of the specific scoring variables.

Table 5. Example of Agreement Flags Using Blocking Pass 10

Person Identifiers		PII Agreement flags[1]				
Patient ID	**HUD ID**	**Middle Initial**	**Month of birth**	**Year of birth**	**ZIP Code**	**State of residence**
1	1	1	0	1	0	.
1	1	.	1	1	0	0
1	1	1	0	1	0	0
2	2	1	0	1	0	0
3	789	1	1	.	0	1
3	789	0	1	0	1	1
3	789	.	1	0	1	.
3	789	0	0	1	1	1
3	322	1	0	1	1	1

NOTES: Data have been fabricated for the purposes of this example. PII – Personally Identifiable Information.

[1] Agreement status of 1 = match, 0 = non-match, and . = missing values

Table 6. Example Showing Summarization of Blocked Record Pairs for M-Probability Estimation, based on Table 5 example

Person Identifiers		PII Agreement flags[1]				
Patient ID	HUD ID	Middle Initial	Month of birth	Year of birth	ZIP Code	State of residence
1	1	1	1	1	0	0
2	2	1	0	1	0	0
3	789	1	1	1	1	1
3	322	1	0	1	1	1

NOTES: Data have been fabricated for the purposes of this example. PII – Personally Identifiable Information.

[1] Agreement status of 1 = match, 0 = non-match, and . = missing values

Several additional comparison measures were created for first and last name identifiers and ZIP code in the calculation of M-probabilities:

- First/last initial agreement – used in the scoring process when only an initial was present in one or more of values (i.e., one from each of the two records being compared for a specific name variable)
- Jaro-Winkler Similarity Levels – this process is explained in greater detail in Section 3.2.2
- ZIP Code of residence – because ZIP codes are dependent on the state in which they are located, only the records where state of residence agreed were used in the computation of the ZIP code M-probability (i.e., if state was not in agreement, then it would be assumed that ZIP code would also not agree)

The U-probability is the probability that the two values for an identifier from paired records agreed given that they were NOT a match. Similar to the M-probabilities, U-probabilities were calculated only for the PII variables not included in the blocking keys and with the exception of first and last names, were computed within the blocking pass. The U-probabilities were computed using records where non-missing SSNs were not in agreement (defined as having less than 5 matching digits when records had a full 9-digit SSN and less than 4 matching digits for records with a 4-digit SSN). In order to avoid skewing U-probabilities in blocking passes that contained a high percentage of deterministic matches, assumed matches (i.e., records where SSN was not in agreement and had majority of the non-missing PII among scoring variables in agreement) were excluded prior to calculating the U-probabilities. For example, when computing the U-probability for day of birth in blocking pass 12, record pairs that did not agree on SSN that had a majority (i.e., greater than 50%) of the PII among first name, middle initial, and month of birth in agreement were excluded from the assumed non-matches. Even though SSN did not agree, these records were assumed to be probable links given that a majority of the PII between the NAMCS HC Component and HUD submission records agreed.

Unlike the M-probabilities, individual U-probabilities were calculated for each value of an identifier if the value was sufficiently represented in the blocking pass. Sufficient representation was defined as satisfying the following criteria:

1. Appeared in more than 2,500 record pairings (i.e., n>2,500).
2. More than 5 record pairings agreed on the value (i.e., number agree>5).
3. Agreement rate (i.e., Number or pairing that agree on value/total records pairings for that value) exceed the 5th percentile of the agreement rate across all values that met the first two conditions.

For example, if for blocking pass 1, the state of residence code for FL appeared in 30,000 record pairings, agreed on 1,560 of those pairs, and the agreement rate for state of residence exceeded the 5th percentile, then the U-probability for Florida would have been computed as 1,560/30,000=0.052 or 5.2%. A 'catch-all' category was created for all identifier values that did not meet the above criteria. The U-probability of the 'catch-all' category was computed by dividing the total number of record pairs that agreed by the total number of record pairs being used to estimate the 'catch-all' category. Further, if there was no agreement in the 'catch-all' category, the U-probability would have been set to 0. To avoid a U-probability of 0, the 'catch-all' U-probability was computed by halving the minimum (i.e., lowest) U-probability among the individual value's U-probabilities. Further, if no individual value received a U-probability (i.e., all values assigned to 'catch-all') and there was no agreement, then the U-probability was set to 0.0001. For example, if the minimum U-probability among state of residence codes was 0.052 and there was no agreement among the catch-all records, the catch-all U-probability for state of residence would be 0.026 (0.052/2). If no state of residence code received a U-probability and there was no agreement, the U-probability for state of residence code would be 0.0001. The process for calculating U-probabilities for first and last name differs from these methods and is described in Section 3.2.2.

Lastly, an adjustment was made to the final U-probabilities to account for alternate records in the submission file. With the addition of each alternate record, the chance of agreement between the NAMCS HC Component and HUD submission records increases. For example, a NAMCS HC Component patient with different months of birth reported on two different patient visit records, has twice the chance of linking to a HUD submission record. Therefore, the U-probability for that patient's month of birth should represent the combined chance of agreement across both month values. Section 3.2.3 provides a detailed description of the methods used to adjust the U-probabilities to account for the additional alternate submission records.

3.2.2 M and U Probabilities for First and Last Names

For first and last name M and U-probabilities, corresponding Jaro-Winkler levels (0.85, 0.90, 0.95, and 1.00) were calculated. Because agreement levels fall over a range, first and last name U-probabilities were computed for each Jaro-Winkler score level. The Jaro-Winkler algorithm assigns a string similarity score, between 0 and 1 (both inclusive), depending on the likeness between two strings. For example, if the first name on the NAMCS HC Component record was "Albert" and on the HUD record it was "Abert", this comparison would receive a Jaro-Winkler score of 0.96. M-probabilities are computed as the rate of agreement for all first/last names within a specific Jaro-Winkler level. For example, the M-probability for first name at the Jaro-Winkler 0.90 level is the rate of agreement for all first names with a Jaro-Winkler score of 0.90 and above.

Because of the large number of unique name values, it was impractical to compute U-probabilities specific name for each blocking pass (i.e., there would not be enough records available for it to be done accurately). Instead, U-probabilities were estimated using pairs generated by the Cartesian product of all records in the 2021 NAMCS HC Component linkage submission file and a simple random sample of 10% of records with non-missing name information from the HUD submission file. See Table 7 for the number of sampled HUD submission records.

Table 7. Count of Records from a 10% Simple Random Sample of HUD Submission Records used to Estimate U-Probabilities for First and Last Names by Sex

	Count of Sampled Records by Name	
Sex	**First Name**	**Last Name**
Female	3,412,344	3,427,331
Male	2,231,647	2,243,904

Complete name tallies (separately, for first and last names) were then produced for the 2021 NAMCS HC Component linkage submission file. For each level of name on the file, 100,000 names were randomly selected from the HUD submission file 10% sample for comparison. Comparisons were made based on the Jaro-Winkler distance metric at four different levels: 1.00 (Exact Agreement), 0.95, 0.90, and 0.85. For each Jaro-Winkler level, the number of names in agreement of the 100,000 randomly selected HUD file names were then tallied.[19] [20] [21]

3.2.3 Adjustment of U-Probabilities for Alternate Submission Records

As previously mentioned in section 3.2.1, an adjustment was made to the U-probabilities to account for alternate submission records. The addition of unique values for an identifier increases the likelihood of a spurious linkage between records from the files being linked. Thus, the U-probabilities were adjusted to account for the increased probability of variable agreement (i.e., if records for the same person had multiple values for a variable, the chance of agreement with any compared record from the other file increases). Therefore, patients received an adjusted U-probability if they had identifier values that were different across their set of submission records. The adjusted U-probabilities were then applied to each record in the set of submission records that paired with a HUD administrative record. Lastly, the U-probability that is used to compute the agreement and disagreement weights (see Section 3.2.4) is the maximum between the original and adjusted U-probability (i.e., U_{Max}=Max($U_{Original}$, U_{Adjust})).

Excluding first and last name and ZIP code of residence, the adjustment process began by identifying the unique set of values, and their U-probabilities, for each of the identifiers appearing in the scoring key (Table 4), for each patient. Because each value is assumed to be independent of the others, the adjusted U-probabilities were computed using the additive rule for probability as the summation of the individual value U-probabilities for each patient. That is, if a patient had three different month of birth values, the adjusted U-probability for month of birth was simply the summation of the three individual U-probabilities. Table 8 provides an example of the process used to compute the adjusted and maximum U-probabilities for month of birth.

Table 8. Example Showing Computation of the Adjusted and Maximum U-probability for Month of Birth

Patient ID	Month of Birth	U-Probability	Adjusted U-Probability[1]	Maximum U-Probability[2]
1	6	0.091	0.253	0.253
1	5	0.083		0.253
1	7	0.079		0.253
2	1	0.110	0.191	0.191
2	10	0.081		0.191
3	6	0.091	0.091	0.091

NOTES: Data have been fabricated for the purposes of this example

[1] The adjusted U-probability is computed by summing the individual month of birth U-probabilities by patient ID.

[2] The maximum U-probability is the max U-probability value between the original and adjusted U-probabilities.

[19] Jaro M. Advances in Record-Linkage Methodology as Applied to Matching the 1985 Census of Tampa, Florida. J Am Stat Assoc. 1987 Jan 01;406:414-420.

[20] Winkler W. String Comparator Metrics and Enhanced Decision Rules in the Fellegi-Sunter Model of Record Linkage. Proceedings of the Section on Survey Research Methods. American Statistical Association. 1990. 354-9.

[21] Resnick, D., Mirel, L., Roemer, M., & Campbell, S. (2020). Adjusting Record Linkage Match Weights to Partial Levels of String Agreement. *Everyone Counts: Data for the Public Good*. Joint Statistical Meetings (JSM). https://ww2.amstat.org/meetings/jsm/2020/onlineprogram/AbstractDetails.cfm?abstractid=312203 (accessed August 2024).

The first three columns of Table 8 show the unique values of month of birth and their corresponding U-probabilities (see Section 3.2.1) for patients 1, 2, and 3. The column titled “Adjusted U-Probability” is computed by totaling the individual probabilities in the third column for each patient. Finally, the maximum U-probability (last column), which was used to compute the agreement and disagreement weights (see Section 3.2.4), is the maximum value between the original and adjusted U-probability values.

Because ZIP codes are nested within the state of residence codes, a slightly different process was used to compute the adjusted U-probability for ZIP code. The process began by identifying the unique set of state and ZIP of residence codes, along with the U-probability for each ZIP code, for each patient. Next, each of the U-probabilities for ZIP code of residence were summed to the patient and state of residence level. Finally, the patients adjusted U-probability for ZIP code was computed as the average of the summed U-probabilities for ZIP codes across the reported state of residence codes. The computation of the adjusted U-probability for ZIP code of residence can be represented by the following equation,

$$U_{Adjust\ \ ZIP} = \frac{\sum_{i=1}^{n}(\sum_{j=1}^{m} U_j)}{n}$$

where n is the number of unique state codes, m is the number of unique ZIP codes, and U_j is the U-probability for the j^th ZIP code. Table 9 provides an example of the process used to compute the adjusted U-probability for ZIP code of residence.

Table 9. Example Showing Computation of the Adjusted and Maximum U-probability for ZIP Code of Residence

Patient ID	State of Residence	ZIP Code of Residence	U-Probability	Adjusted U-Probability[1]	Maximum U-Probability[2]
8	CA	90002	0.001	0.0047	0.0047
8	CA	90313	0.003		0.0047
8	FL	32011	0.01		0.01
25	GA	31013	0.001	0.0015	0.0015
25	GA	39845	0.002		0.002
78	CT	06752	0.001	0.001	0.001

NOTES: Data have been fabricated for the purposes of this example

[1] The adjusted U-probability is computed by summing the individual ZIP code U-probabilities within each state code and then taking the average of the summed U-probabilities across the states for each patient ID.

[2] The maximum U-probability is the max U-probability value between the original and adjusted U-probabilities. Recall, the maximum U-probability is the maximum U-probability value between the original (column 4) and adjusted (column 5) U-probabilities.

The first four columns of Table 9 provide the Patient ID, state of residence, ZIP code of residence codes, and the corresponding U-probability for each ZIP code of residence for three NAMCS HC Component patients. The adjusted U-probability (i.e., 5th column) is computed first by summing each individual U-probability within each state code and then taking the average of the summed values. The maximum U-probability (i.e., last column) is the max U-probability value between the original and adjusted ZIP-code of residence U-probabilities. Notice, for patients 8 and 25, the maximum U-probability value that was used for ZIP code 32011 and 39845, respectively, was the original U-probability. This was because the average U-probability across all state codes (column 5) did not exceed the original U-probability (column 4).

For first and last names, only the 85% Jaro-Winkler level U-probability was adjusted. The higher levels (i.e., 90, 95, and 100) were not adjusted because of the hierarchical method being used to compute each of the U-probabilities at those levels (i.e., 90 is dependent on 85, 95 is dependent on 90, and 100 is dependent on

95). Before the 85% level was adjusted, names that were similar to one another were combined into a single name field. This step is necessary to avoid 'double counting' names that are highly likely to match to the same name on the HUD administrative data file. Similarity in names was defined as having a Jaro-Winkler score between 0.95 and 1 (not inclusive at the upper bound) or if one name is fully contained within another (ex. Elizabeth and Eliza). If for example, a patient had two different names, Elizabeth and Elizabith (JW_{Score}=0.967), only one would be used to adjust the 85% Jaro-Winkler U-probability. The name that is selected was determined by whichever had the highest 100% Jaro-Winkler U-probability. Using the list of 'unduplicated' names, the adjusted U-probability for the 85% Jaro-Winkler level was computed as the summation of each of the individual U-probabilities for the patient. Table 10 provides an example of the methods used to compute the adjusted U-probabilities for the 85% Jaro-Winkler level, using first name as an example.

Table 10. Example Showing Computation of the Adjusted and Maximum U-probability for First Name

Patient ID	First Name	U-Probability at 85% JW	U-Probability at 100% JW	Collapsed U-Probability[1]	Adjusted U-Probability[2]	Maximum U-Probability[3]
8	Margaret	0.008	0.99	0.008	0.009	0.009
8	Peggy	0.001	0.97	0.001		0.009
8	Marg	0.001	0.85	Collapsed		0.009
25	Elizabeth	0.09	0.99	0.09	0.09	0.09
25	Beth	0.01	0.95	Collapsed		0.09
78	Cathy	0.05	0.99	0.05	0.05	0.05

NOTES: Data have been fabricated for the purposes of this example. JW is the Jaro-Winkler string comparator function.

[1] The collapsed U-probability includes only the U-probabilities after similar names have been collapsed into a single name.

[2] The adjusted U-probability is computed by summing each of the collapsed 85% JW U-probabilities within each patient ID.

[3] The Maximum U-probability is the max U-probability value between the original and adjusted 85% U-probabilities.

The first four columns of Table 10 provide example Patient IDs, first names, and their U-Probabilities at the Jaro-Winkler 85 and 100 level for three NAMCS HC Component patients. The collapsed U-probability column (i.e., 5th column) shows that two names were collapsed into another, i.e., for patient 8, Marg was collapsed into Margaret (full-containment) and Beth was collapsed into Elizabeth (full-containment) for patient 25. Further, the collapsed U-probability is equal to the 85% JW U-probability for the name with the highest 100% JW U-probability among the names being collapsed. The adjusted U-probability (i.e., column 6) is the summation of each collapsed U-probability for each patient ID. Finally, the maximum U-probability (i.e., last column) is the max value between the adjusted U-probability and original U-probability at the 85% JW level.

3.2.4 Calculate Agreement and Non-Agreement Weights

The agreement and non-agreement weights for each record's indicators were computed using their respective M- and U-probabilities:

$$\text{Agreement Weight (Identifier)} = \log_2\left(\frac{\text{M}}{U_{Max}}\right)$$

$$\text{Non-Agreement Weight (Identifier)} = \log_2\left(\frac{(1\text{- M})}{(1 - U_{Max})}\right)$$

Agreement weights were only assigned to identifiers that had agreeing values. Similarly, non-agreement weights were only assigned to identifiers that had non-agreeing values. A non-agreement weight was always a negative value and reduced the pair weight score. It is important to note that if the M-probability was smaller than the U-probability (i.e., M<U), the pair score (see Section 3.2.5) was not adjusted according to the agreement/non-agreement weight. Because of the logarithmic function, having a M-probability that is smaller than the U-probability would have an inverse effect on the identifier agreement weights. That is, an agreement weight computed using a M-probability that was smaller than the U-probability would produce a negative weight, while the non-agreement weight would be positive. For example, if the M-probability for month of birth was 0.989 and the U-probability was 0.9999 then the agreement and non-agreement weights would be as follows,

$$\text{Agreement Weight (Identifier)} = \log_2\left(\frac{\text{M}}{\text{U}}\right) = \log_2\left(\frac{0.989}{0.9999}\right) = -0.0158$$

$$\text{Non-Agreement Weight (Identifier)} = \log_2\left(\frac{(1\text{- M})}{(1\text{ - U})}\right) = \log_2\left(\frac{0.011}{0.0001}\right) = 6.781$$

3.2.5 Calculate Pair Weight Scores

In the next step, pair weights were calculated for each record in the blocking pass, which were then used in the probability model. The pair weights were calculated differently for each blocking pass (due to different PII variables contributing to the pair weight), but followed the same general process:

1. Start with a pair weight of 0.
2. Identifier agrees: add identifier-specific agreement weight into pair weight
3. Identifier disagrees: add identifier-specific non-agreement weight (which has a negative value) into pair weight
4. Identifiers cannot be compared because one or both identifiers from the respective records compared were missing, or M-probability was less than the U-probability: no adjustment made to the pair weight

First name and last name weights were assigned using Jaro-Winkler similarity scores described in Section 3.2.2. These scores ranged from 0 to 1, with 0 representing no similarity and 1 representing exact agreement. The weighting algorithm assigned all similarity scores 0.85 and below 0.85 a disagreement weight. The algorithm assigned all similarity scores above 0.85 an agreement weight associated with the 0.85 level. If there was an agreement at the 0.85 level, the algorithm assessed the pair at the 0.90 level given that it agreed at the 0.85 level. If the names disagreed at this level, the algorithm assigned them a disagreement weight (specific to the 0.90 level given agreement at the 0.85 level). If the names agreed, the algorithm assigned them an additional agreement weight (specific to the 0.90 level). This process continued two more times: for the 0.95 and 1.00 thresholds.

3.3 Probability Modeling

A probability model, developed from a partial expectation-maximization (E-M) analysis, was applied individually to each of the blocks in the blocking scheme. Each model estimated a link probability, $P_{EM}(Match)$, for the potential matches in each blocking pass. The match probability represents the approximate likelihood that a given link is a match. These probabilities in turn allowed the linkage algorithm to:

- Combine pairs across blocking passes (Pair-weights are specific to each blocking pass and are not comparable)
- Select a “best” record among 2021 NAMCS HC Component patient IDs that have linked to multiple administrative records.
- Select final matches based on a probability cut-off value (discussed in the following Section 4)

The partial E-M model was an iterative process that can be described in 4 steps:

1. A pair-weight adjustment was computed (Adj_B) specific to blocking pass, B, by taking the log base 2 of the estimated number of matches (within blocking pass B) divided by the estimated number of non-matches in the blocking pass. For convenience, the estimated number of matches, $\widehat{N_{matches,B}}$, used in the first iteration was set to half of the pairs in the blocking pass (i.e., all pairs generated by the blocking pass specification). The number of non-matches was computed by subtracting the estimated number of matches from the number of pairs (regardless of how likely they are to be matches) in the blocking pass.

   $$Adj_B = log_2\left(\frac{\widehat{N_{matches,B}}}{\widehat{N_{non-matches,B}}}\right) = log_2\left(\frac{\widehat{N_{matches,B}}}{N_{Pairs,B} - \widehat{N_{matches,B}}}\right)$$

   Note that in the first iteration, it was assumed that $\widehat{N_{matches,B}}$ = $\widehat{N_{non-matches,B}}$, resulting in $Adj_B = 0$. If, however, in a later iteration, the number of matches was estimated to be, $\widehat{N_{matches,B}}$ = 20,000 (for example), out of the number of pairs, $N_{Pairs,B}$ = 1,000,000, then

   $$Adj_B \ = log_2\left(\frac{20{,}000}{1{,}000{,}000 - 20{,}000}\right) \approx -5.61$$

2. The odds of a given pair, *P*, being a match were computed in blocking pass, *B*, by taking 2 to the power of the adjusted pair-weight (sum of pair-weight (*PW*) and Adj_B, the blocking pass pair weight adjustment).

   $$Odds_{P,B} = 2^{PW_{P,B}+Ad}$$

   Continuing with the example from Step 1…
   if for Pair 1 of blocking pass B, the pair-weight is 8.4, then $Odds_{1,B} =$ $2^{(8.4+\ -5.61)}$ ≈6.9
   if for Pair 2 of blocking pass B, the pair-weight is -2.5, then $Odds_{2,B} =$ $2^{(-2.5+\ -5.61)}$ ≈0.0036
   …and this continues for the remaining $N_{Pairs,B}$ pairs of the blocking pass

3. Each record pair had a match probability estimated using the odds. This was accomplished by taking the odds for pair, P, in blocking pass, B, and dividing by the (Odds+1).

   $$P_{EM,P,B}(Match) = \left(\frac{Odds_{P,B}}{Odds_{P,B} + 1}\right)$$

   Continuing with the example…
   For Pair 1 in blocking pass B, $P_{EM,P,B}(Match) = \left(\frac{6.9}{6.9 + 1}\right) \approx 0.87$

For Pair 2 in blocking pass $P_{EM,P,B}(Match) = (\frac{0.0036}{0.0036+1}) \approx 0.0036$

…and this continues for the remaining $N_{Pairs,B}$ pairs of the blocking pass.

4. The new number of matches in blocking pass were estimated. This was done by summing each of the estimated probabilities in the block.

$$N_{\widehat{matches},B} = \sum P_{EM,P,B}\widehat{(Match)}$$

Continuing with the example, add the probabilities for every pair in the blocking pass:

$$N_{\widehat{matches},B} = 0.87 + .0036 + P_{\widehat{EM,3},B} + \ldots + P_{\widehat{EM,N_{Pairs,B}},B}$$

This process was repeated until convergence was reached in the number of matches being estimated. Once convergence was achieved, the final probabilities were estimated based on the last value of $N_{\widehat{matches},B}$ to be estimated. These estimated probabilities were then used to select the final matches, as described below in Section 4.

3.4 Adjustment for SSN Agreement

Up to this point, every pair generated through the probabilistic routine was assigned a value that estimates its probability of being a match. However, this estimate did not take SSN agreement into account. This was conducted as a separate step because for the other comparison variables, M- and U- probabilities were estimated based on probable matches or non-matches that were determined based on SSN agreement, and clearly this was infeasible for SSN itself.[22]

To remedy this, before the algorithm adjudicated the matches against the probability cut-off value, one final adjustment was made to the match probabilities (for probabilistic pairs). For pairs that had an SSN on both the 2021 NAMCS HC Component and HUD submission record, the estimated probability was adjusted based on the last four digits of the SSN.

When the last four digits of SSN agreed (i.e., are exactly the same):

$$Probvalid_{SSN_{Adj}} = \frac{\left(\frac{P_{EM}(Match)}{1-P_{EM}(Match)} \cdot \frac{M_{SSN-SSN4}}{U_{SSN-SSN4}}\right)}{\left(\left(\frac{P_{EM}(Match)}{1-P_{FM}(Match)} \cdot \frac{M_{SSN-SSN4}}{U_{SSN-SSN4}}\right)+1\right)}$$

When the last four digits of SSN did not agree:

…………………….

$$Probvalid_{SSN_{Adj}} = \frac{\left(\frac{P_{EM}(Match)}{1-P_{EM}(Match)} \cdot \frac{(1-M_{SSN-SSN4})}{(1-U_{SSN-SSN4})}\right)}{\left(\left(\frac{P_{EM}(Match)}{1-P_{EM}(Match)} \cdot \frac{(1-M_{SSN-SSN4})}{(1-U_{SSN-SSN4})}\right)+1\right)}$$

[22] The M and U probabilities in the formulas refer specifically to the M and U of the last four digits of the SSN.

No adjustment was made for pairs that did not have an SSN on either the 2021 NAMCS HC Component patient or HUD submission record. So, for these pairs:

$$Probvalid_{SSN_{Adj}} = P_{EM}(Match)$$

4 Estimate Linkage Error, Set Probability Cut-off Value, and Select Matches

The scored (probabilistic) and deterministic linkage files for males and females were combined prior to estimating the linkage error and selecting matches. Recall the purpose for separating the records by sex was to avoid violating the independence assumption for name identifiers mentioned by Fellegi-Sunter. Now that records from each sex have been separately scored, there is no need to keep them separate.

4.1 Estimating Linkage Error to Determine Probability Cut-off Value

Subsequent to performing the record linkage analysis an error analysis was performed. There are two type of errors that were estimated:

- Type I Error: Among pairs that are linked, what percentage of them were not true matches.
- Type II Error: Among true matches, how many were not linked.

Because all records were included in the probabilistic linkage (i.e., even deterministic links), SSN agreement status (defined as seven or more matching digits for nine-digit SSN's and for SSN's that had only the last four digits, all four digits must match) was used to measure Type I error. Type I error for probabilistic links was measured as the total number of probabilistic links with non-agreeing SSN divided by the total number of probabilistic links with a valid SSN available on both the NAMCS HC Component and HUD submission record. Also, deterministically established links were considered to have 0% Type I error rates. While it was believed that the error for these links was quite small and near 0, it is expected that some error does exist even with the deterministically established links and so the estimate was likely biased low. For example, if 40% of links were derived from the deterministic method, this would reduce the estimated Type I error by the proportion of probabilistically determined linkages among all linkages. To further illustrate, if the Type I error rate for probabilistic links was estimated as 1.2%, then the estimated Type I error rate for the combined linkage process would be (0.40*0.012) = 0.0048 or 0.48%.

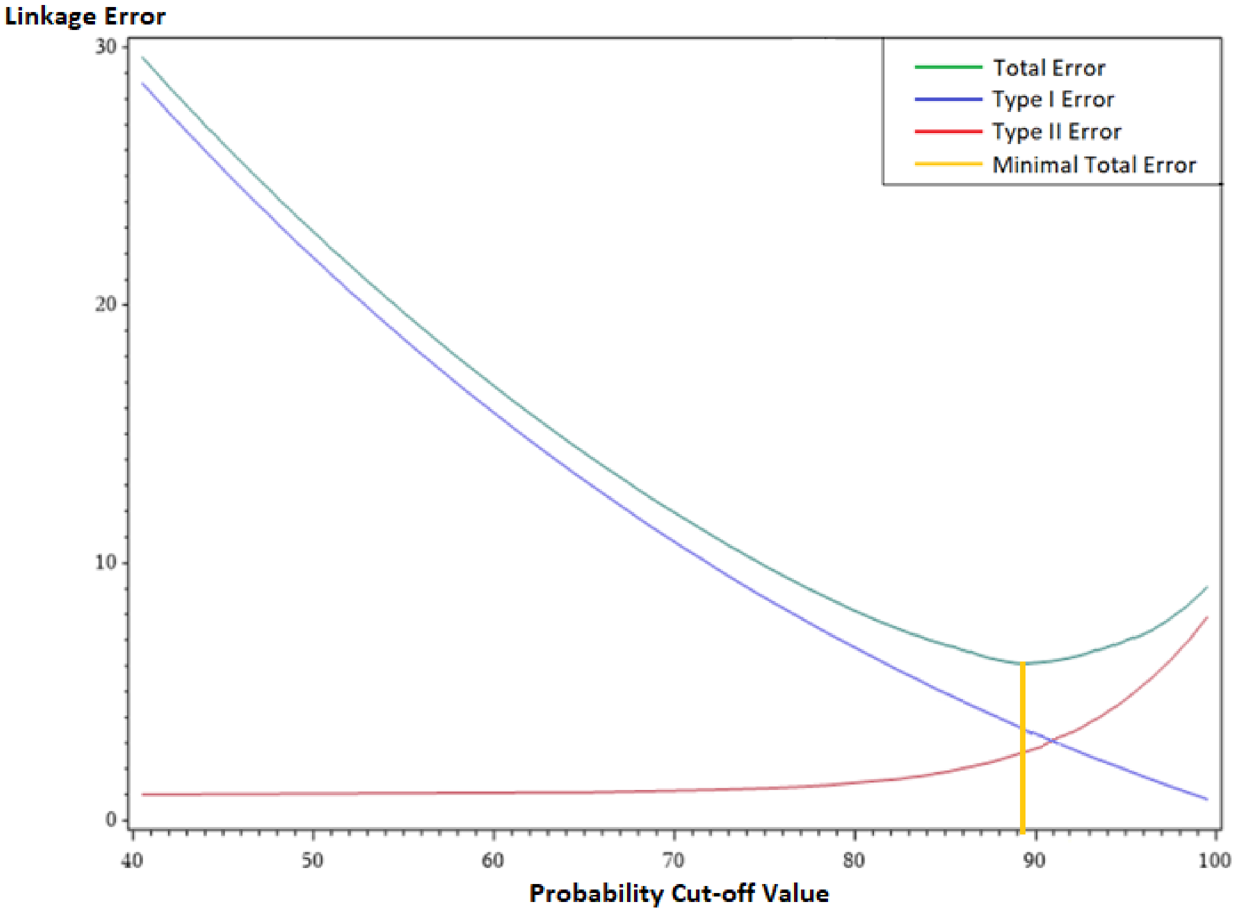
To measure Type II error, the truth source comprised of all matches identified in the deterministic linkage was used. Recall, the truth source contains records with full nine-digit SSN agreement (step 1) or with the last four digits of SSN in agreement (step 2). Potential deterministic matches were then validated using the available PII (see, Appendix I section 2). It was expected that this truth source had only a few exceptional pairs that were not true matches. For the probabilistic records, Type II error was estimated as the percentage of the truth source records that were not returned as links by the probabilistic method. Similarly to the computation of Type I error, an adjustment was made to the Type II error since some links having agreeing SSNs were being linked deterministically even if they were not returned by the probabilistic approach. For example, say that the probabilistic approach was able to return 97% of true matches as links. If only a probabilistic linkage was conducted, the Type II error would then be 3%. However, among the 3% not linked probabilistically, some pairs could be linked deterministically. If the deterministic linkage rate is 50% (and if we assume the same rate among the non-linked pairs), then the Type II error rate can be estimated as 0.5*(1 – 0.97) = 0.015 or 1.5%.

4.2 Set Probability Cut-off Value

One goal of record linkage is to have the lowest errors possible. However, as more pairs are accepted, pairs that are less certain to be matches but accepted as links increase the Type I error and decrease Type II error. And as less pairs are accepted, pairs that are more certain to be matches but not accepted as links decrease the Type I error and increase Type II error. The optimal trade-off between Type I error and Type II error is not known, but it can be assumed to be optimal when the sum of Type I and Type II error is at a minimum. For this reason, Type I and Type II error are estimated at various probability cut-off values and the one that showed the lowest estimate of total error is selected (see Figure 3). For the linkage of the 2021 NAMCS and 2020-2022 HUD, the optimal probability cut-off value was set to 0.8925.

Figure 3. Illustrating linkage error by probability cut-off value

(Illustrative schematic not based on actual values)



4.3 Select Links Using Probability Cut-off Value

The final step in the linkage algorithm was to determine links, which were record pairs inferred to be matches. Links were pairs where the $Probvalid_{SSN_{Adj}}$ exceeded the probability cut-off value (from Section 4.2). All record pairs with an adjusted probability value that fell below the probability cut-off value were not linked.

4.4 Resolving NAMCS HC Component Patient IDs that Linked to Multiple HUD Records

Due to the nature of the administrative program data, it is possible that PII information may vary, due to PII changes over time or recording errors, among HUD enrollment records that represent the same person. In the 2021 NAMCS HC Component data, 58.2% of patients were linked to more than one HUD enrollment record with the same HUD ID. In situations where a NAMCS HC Component patient ID linked to more than one HUD enrollment record with different HUD IDs, and the PROBVALID score calculated for each unique linked enrollment record exceeded the 0.8925 probability cut-off value, all HUD ID matches were assumed to represent the same individual. In the 2021 NAMCS HC Component data, about 1% of linked patients were linked to more than one HUD ID. For more information on how to use PROBVALID values to reduce potential Type 1 errors see Section 4.2.1.1.

4.5 Computed Error Rates of Selected Links

Final error rates were computed for selected links (described in Section 4.3). Table 11 provides the total number of selected links, the number of total links identified through deterministic and probabilistic methods, and the Type I and Type II error rates for the 2021 NAMCS HC Component HUD linkage. Because the links were selected using the SSN adjusted probability (described in Section 4.1), the overall Type I error rate was computed using the estimated match probabilities rather than using SSN agreement. For the probabilistic links, the estimated match probabilities represented the probability that the NAMCS HC Component record was a match to the HUD administrative record. In other words, if a link had an estimated probability of 0.98, then it was understood that there was a 98% chance this was a match. To estimate the Type I error rate for the probabilistic links, the chance that a link is not a match was summed (i.e., $\sum 1 - Probvalid_{SSN_{Adj}}$) and then divided by the total number of probabilistic records. The method to measure the overall Type II error remained unchanged (see Section 4.1).

Table 11. Algorithm Results for Total Selected Links

	Probability Cut-off Value	Total Selected Links	Deterministic Matches	Probabilistic Links	Est Incorrect (Type I)	Est Not Found (Type II)
2021 NAMCS HC Component	0.8925	26,781	16,536	10,245	0.04%	0.52%