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Research and Applications

Harmonizing units and values of quantitative data elements in a very large nationally pooled electronic health record (EHR) dataset

Katie R. Bradwell ¹, Jacob T. Wooldridge², Benjamin Amor¹, Tellen D. Bennett ³, Adit Anand², Carolyn Bremer², Yun Jae Yoo², Zhenglong Qian², Steven G. Johnson⁴, Emily R. Pfaff ⁵, Andrew T. Girvin¹, Amin Manna¹, Emily A. Niehaus¹, Stephanie S. Hong⁶, Xiaohan Tanner Zhang⁷, Richard L. Zhu ⁷, Mark Bissell¹, Nabeel Qureshi¹, Joel Saltz², Melissa A. Haendel ⁸, Christopher G. Chute ⁹, Harold P. Lehmann⁷, and Richard A. Moffitt ²; on behalf of the N3C Consortium

¹Palantir Technologies, Denver, Colorado, USA, ²Department of Biomedical Informatics, Stony Brook University, Stony Brook, New York, USA, ³Section of Informatics and Data Science, Department of Pediatrics, University of Colorado School of Medicine, University of Colorado, Aurora, Colorado, USA, ⁴Institute for Health Informatics, University of Minnesota, Minneapolis, Minnesota, USA, ⁵Department of Medicine, North Carolina Translational and Clinical Sciences Institute, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA, ⁶School of Medicine, Section of Biomedical Informatics and Data Science, Johns Hopkins University School of Medicine, Baltimore, Maryland, USA, ⁷Department of Medicine, Johns Hopkins, Baltimore, Mary-Iand, USA, ⁸Center for Health AI, University of Colorado, Aurora, Colorado, USA, and ⁹Schools of Medicine, Public Health, and Nursing, Johns Hopkins University, Baltimore, Maryland, USA

Corresponding Author: Richard A. Moffitt, PhD, Department of Biomedical Informatics, Stony Brook University, MART L7 0810, Stony Brook, NY 11794, USA; richard.moffitt@stonybrookmedicine.edu

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ABSTRACT

Objective: The goals of this study were to harmonize data from electronic health records (EHRs) into common units, and impute units that were missing.

Materials and Methods: The National COVID Cohort Collaborative (N3C) table of laboratory measurement data—over 3.1 billion patient records and over 19 000 unique measurement concepts in the Observational Medical Outcomes Partnership (OMOP) common-data-model format from 55 data partners. We grouped ontologically similar OMOP concepts together for 52 variables relevant to COVID-19 research, and developed a unitharmonization pipeline comprised of (1) selecting a canonical unit for each measurement variable, (2) arriving at a formula for conversion, (3) obtaining clinical review of each formula, (4) applying the formula to convert data values in each unit into the target canonical unit, and (5) removing any harmonized value that fell outside of accepted value ranges for the variable. For data with missing units for all the results within a lab test for a data partner, we compared values with pooled values of all data partners, using the Kolmogorov-Smirnov test. **Results**: Of the concepts without missing values, we harmonized 88.1% of the values, and imputed units for

78.2% of records where units were absent (41% of contributors' records lacked units). **Discussion**: The harmonization and inference methods developed herein can serve as a resource for initiatives aiming to extract insight from heterogeneous EHR collections. Unique properties of centralized data are harnessed to enable unit inference.

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Conclusion: The pipeline we developed for the pooled N3C data enables use of measurements that would otherwise be unavailable for analysis.

Key words: reference standards, SARS-CoV-2, electronic health records, data accuracy, data collection

OBJECTIVE

Quantitative data in the National COVID Cohort Collaborative (N3C) originate from data partners who submit electronic health record (EHR) data via different Common Data Models (CDMs), which are then harmonized into the Observational Medical Outcomes Partnership (OMOP) CDM. Our objective was to harmonize measurement units and to reclaim usable data via unit inference for values missing units.

BACKGROUND AND SIGNIFICANCE

N3C has built a repository of EHR data from a growing number of data partners across the United States to facilitate research on coronavirus disease of 2019 (COVID-19).¹ Our data partners submit clinical and laboratory data, using one of several CDMs used for distributed EHR-based research, which are then mapped to the OMOP CDM.^{2,3} While the CDMs specify the structure for storing data, not all fields are required, and what data can be entered in these fields is not tightly controlled.²

One of the key resources of N3C is laboratory measurement data, central to almost all research on COVID-19. Sites submit these data in a variety of units even within the same measurement concept. Most sites map their local lab data to the Logical Observation Identifiers Names and Codes (LOINC) system.⁴ As part of the LOINC standard, properties being measured, such as mass concentration (mass/volume), number concentration (count/volume), or rate (count/time), is specified as part of the code but the units to be used are not specified. Instead, for many codes, example units are provided, often including units in the Unified Code for Units of Measure (UCUM) format.⁵ UCUM formatting is designed to remove ambiguity (g vs gm for example) and to integrate with electronic messaging standards. However, UCUM does not dictate which unit is preferred for any particular analyte. Because of this lack of uniformity in reporting, it is almost always necessary to convert units before comparing measurement results from different sites. As an example of OMOP unit concept name diversity in the N3C measurement table, units for body weight can include kilogram, gram, ounce (avoirdupois), oz and pound (US).

Additionally, units of measure are often missing. Dropping these entries from analyses would result in significant data loss and even bias, especially if the units were consistently missing for a given result or from a given data partner. Another option would be to solicit each data partner for their missing units, which would be feasible if working on a small number of data elements and with a small number of data partners, but is not a sustainable solution as the number of data contributors grows over time (55, at as of June 10, 2021). A third option would be to assume a unit based on what is commonly used in clinical practice; while this may work for simple measurements such as heart rate, it is highly error prone for most cases.

In order to preserve as much data as possible without placing an undue burden on the data partners or individual researchers, we determined that an automated method is needed to automatically convert units in a systematic fashion as well as determine, on a site-bysite basis, what the most likely unit is for a given OMOP measurement concept where units are absent. To address this problem of missing units, we propose a method comparing the value distribution of measurements⁶ which are missing units to those from the same concept set with known units. In general, if the distributions are not found to be significantly different we infer that they use the same unit.

LOINC unit conversion has been addressed by other research groups in a variety of contexts including analysis of aggregated datasets,^{7–9} Hauser describes creation of a standard set of conversions between compatible LOINC laboratory codes expressed in different units^{10,11} along with publicly accessible conversions to support conversion of common LOINC codes. We contribute and extend the state of the art by making available reproducible computational pipelines to impute units in cases where units were missing.

In summary, we aimed to develop approaches that incidentally have a broad impact beyond the COVID-19 research of N3C, addressing the need to harmonize units by grouping similar laboratory tests and by converting all data points for each measurement to a single predetermined canonical unit. In addition, we aimed to reclaim as much data as possible missing units of measure to maximize their use. The resulting methods are broadly applicable to contexts of pooled EHR data.

MATERIALS AND METHODS

The design of the N3C data set and a comprehensive characterization of the data available prior to December 2020 have been previously described.^{1,12} In the current study, we included data ingested as of June 10, 2021. Our analysis did not put any restrictions on the patient population, and included all available measurements. The N3C ingestion pipeline includes comprehensive mapping of measurement concepts and unit concepts to standard concepts in the OMOP CDM. While we had access to information from source vocabularies, all work discussed in this manuscript began with the data after conversion to OMOP.

Working with a community of physicians and informatics experts, we created an initial list of measurements that were of high priority for harmonization, driven primarily by the needs to describe the N3C cohort.¹² We gained subject matter expert (SME) consensus on broad sets of semantically similar analytes (and, where relevant, of specimen type) expected by the SMEs to have interoperoberable and convertible measurement units, even though the particulars may differ. For example, differences between venous and arterial measurements are meaningfully different, but their analytes are measured with the same units. Measurement concepts with relative results (eg, ratio or percent) were grouped into different concept sets than absolute measures. All concept sets were reviewed by a clinical SME to ensure that only concepts which would be interpreted similarly in a clinical setting, despite potential differences in sampling time and sample specimen, were included. We also required that the concepts be unique to a single concept set, so that values did not get harmonized in multiple ways. The full list of concepts per concept set can be found in Supplementary Table S1. Notably, the concept sets were used only for unit harmonization

optimization and implementation purposes and are not intended to represent clinically synonymous collections of concepts for downstream analysis. In fact, the grouping of concepts for research and clinical use is often necessarily different from the broader grouping that suits unit harmonization and inference purposes. As an extra validation of concept set membership we analyzed measurement concept cumulative distribution functions (CDFs) for each concept set (Supplementary Figure S1), and the few concept sets that appeared to contain an outlier were examined in depth. These outlier concepts in reviewed concept sets included Leukocytes [#/volume] in Blood by Manual count, whose CDF differed from others', because a manual count is performed under circumstances where automated counts fail due to low or unusual blood cell counts. This distribution was not, however, considered sufficiently different to deserve its own concept set, at least for the purposes of unit harmonization and inference due to (A) being synonymous in terms of the range of plausible units and (B) for reasons detailed in Results.

Working with our SMEs, we then chose a single "canonical" unit for each measurement concept set; in most cases the unit where the values are in the most easily interpretable scale, or units where derived variables can subsequently be calculated, for example kilogram for weight was selected due to familiarity, and since it is the most commonly used unit by the clinicians within N3C to calculate the derived variable BMI. Additionally, we identified acceptable value ranges, beyond which a measurement would be discarded, for example percents below 0% or above 100%, and values that are not clinically possible in any patient as determined by our SMEs. These ranges were made as liberal as possible to avoid losing extreme cases yet conservative enough to allow us to filter out poor-quality data that could affect downstream analyses. A list of the measurements and values for the required fields are shown for selected examples in Table 1, and in full, within Supplementary Table S2. Lastly, we manually curated conversion formulae suitable for converting from other units to this canonical unit (Supplementary Table S3).

Unit harmonization

Using the concept sets, canonical units, acceptable ranges and formulae from Supplementary Tables S2 and S3, we assessed the diversity of units present in the data (Figure 1) and implemented a pipeline (Figure 2) that converted value data (ie, *value_as_number*) to harmonized value data. In our implementation, we created 2 new

lable 1. Example canonical units t

fields in our measurement table, *harmonized_unit_concept_id* and *harmonized_value_as_number*, to preserve the original value data for maximum transparency and flexibility. Conversions were performed using a mapping function, composed of the units to convert and the measurement concept as a lookup for the corresponding conversion equation (Figure 2). After conversion, if the value was outside of the accepted value range, the *harmonized_unit_concept_id* and *harmonized_value_as_number* fields were set to null.

Unit inference

We applied unit inference to measurement records that were missing units in the source data or, missing a valid mapping from the source unit to the OMOP standard unit. The basis of unit inference derives from a previous study⁶ that developed a method for determining if lab results from 2 different labs represented the same type of measurement, in part, by comparing distributions of the results between the 2 tests using the Kolmogorov-Smirnov test (KS test).¹³ We adapted this approach, and compared value distributions within each OMOP measurement concept for laboratory tests per data partner, converted to the canonical unit for every plausible unit for that measurement concept (termed "test" value), to a selection of values with known units converted into the canonical unit (termed "reference" value). For each test unit, following the conversion to the canonical unit using the appropriate conversion formula, we assessed whether the distribution of values closely matched the canonical unit reference distribution of values, using the KS test P value, above a threshold, to define "close." When the match passed our empirically derived threshold and other quality control criteria (described below), the test unit was then assigned as the accepted inferred unit. Figure 3 and Supplementary Figure S2 outline the unitinference process.

Unit-inference threshold and sample-size validation

To determine the correct KS-test threshold, we created a workflow (Figure 3A and Supplementary Figure S2A) that masks known units for each 4-element tuple of measurement variable, data partner, measurement concept, and unit, which were then compared to the reference values (the collection of values of known units where all the appropriate conversions have taken place into the canonical unit). Because of the combinatorial explosion in the number of comparisons, the work was done with samples from each tuple.

Measured variable	Enclave codeset ID	Canonical unit concept ID	Canonical unit concept name	Maximum plausible value	Minimum plausible value	Measurement table row count
Respiratory rate	286601963	8483	Counts per minute	200	0	201 976 073
Sodium, mmol/L	887473517	8753	Millimole per liter	250	50	147 177 271
SpO2	780678652	8554	Percent	100	0	145 403 614
Systolic blood pressure	186465804	8876	Millimeter mer- cury column	400	0	136 188 546
Temperature	656562966	586323	Degree celsius	45	25	123 986 764
Glucose, mg/dL	59698832	8840	Milligram per deci- liter	1000	0	104 743 184
Heart rate	596956209	8483	Counts per minute	500	0	67 530 040
Height	754731201	9546	Meter	3	0	53 998 207
Body weight	776390058	9529	Kilogram	500	0.1	42 113 217
Diastolic blood pressure	573275931	8876	Millimeter mer- cury column	200	0	42 024 537

Note: Chosen canonical units and plausible value range for the top 10 most frequent measured variables in the data out of those selected for unit harmonization and inference.



Figure 1. Diversity of equivalent and nonequivalent units across measured variables: Units present per measurement variable and their equivalency to the selected canonical unit. Equivalent units to the canonical unit are described as "identity" and those with nonequivalent units are referred to as "non-identity."



Figure 2. Unit conversion workflow summary. Overview of the process for harmonizing unit in the OMOP measurement table. SME: subject matter expert.



Figure 3. Unit inference and harmonization workflows. (A) Unit-inference threshold validation workflow. Masking of known units was used as a guide to assess the range of KS test *P* values that pertain to values in equivalent units across populations. The final threshold selected after plotting all *P* values together was 1e–5, which was then used for identifying units when they are missing. (B) Unit inference workflow. Process for sampling and performing KS tests on values across data partner and measurement concept combinations, checking for *P* values above the 1e–5 threshold, and applying thresholds to omit unit inference in cases where units cannot be confidently assigned. (C) Unit harmonization workflow. Conversion of values for each record into the canonical unit. KS test: Kolmogorov-Smirnov test.

Within each sample, all possible conversions to the canonical unit take place, each becoming a list of "test" values, simulating the variety of potential originating units and their converted values. The KS test was then performed on each test value list, and the resulting P value (Figure 4) and KS-test statistic (Supplementary Figure S3) were compared for equivalent units (test unit is equivalent to the masked "known" unit) versus nonequivalent units (test unit is not equivalent to the masked "known" unit). This calibration of P values stands instead of the Bonferroni correction.¹⁴ The range of KS-test P values or test statistics that uniquely pertain to equivalent

unit value distribution comparisons is the potential range to set a threshold in order to avoid false unit assignments; the base of the peak within the left tail of the distribution of P values was chosen as the threshold for inferring units across all variables. The size of the value lists used for value distribution comparisons in the KS test was found empirically to perform similarly at 50 and 100 elements and thus was determined to be robust at those population sizes, and 100 elements was chosen due to being sufficient for stable performance while sufficiently small to avoid long processing times and memory usage. Value-list sizes were held constant as the



Figure 4. KS test *P*-value threshold validation. KS *P* values for equivalent versus nonequivalent units per data partner ID/measurement concept name. CRP was omitted due to having various completely overlapping value distributions in nonequivalent units after visual inspection. CRP: c-reactive protein; KS test: Kolmogorov-Smirnov test.

KS test otherwise has to be corrected for population size to give results that can be compared.

Unit inference and criteria for unit inference omission

Figure 3B and Supplementary Figure S2B summarize the work done on these sets of 100 values to determine potential units, which included inspection of the test values exceeding the threshold for presence of distinct (multiple) units, in which case unit inference was skipped. Additionally, entire measurement variables for unit inference omission were derived from 2 main filters: (1) We compared relative dispersion of values to the relative unit conversion fold change and excluded measured variables that had a large amount of uncertainty (Supplementary Figure S2B). (2) We used a combination of the number of distinct units over the P value threshold (Supplementary Figure S4), the proportion of fold change differences between the reference and test value lists within a fold change range 1.5-15× indicating nonequivalent units (as supported by Supplementary Figure S5), and the spread of the data, assessed by median absolute deviation from the median within test value lists. The combination of these thresholds is displayed in Supplementary Figure S6.

Incorporating inferred units and implementing the final unit harmonization workflow

Following these quality-control checks, the inferred units were consolidated with the original units, where present, to create a new column in the Measurement OMOP table for unit harmonization (Figure 3C and Supplementary Figure S2C). We retained any variables that were unitless or where only 1 unit was possible and therefore not entered by the sites, for example, BUN/Cr ratio; these variables received a 1:1 mapping from *value_as_number* to *harmonized_value_as_number*.

All codes for unit inference and harmonization were optimized within the N3C pipeline using PySpark v3.0.0 and Spark 3 on the Palantir Foundry platform,¹ and deposited to GitHub along with a full package version list (https://github.com/kbradwell/N3C-units).

RESULTS

The June 10, 2021 release set comprised data from 55 data partners, with 2.716 billion rows of quantitative measurement lab data, composed of 12 390 distinct measurement concepts and 361 distinct OMOP unit concepts.

Diversity of measurement units

Unique OMOP units per measurement variable, stratified by equivalency to the selected canonical unit, are shown in Figure 1 (across the 52 concept sets there were 40 canonical, 27 equivalent to canonical, and 23 nonequivalent to canonical units). Height and body weight display the greatest number of nonequivalent units, whereas variables such as diastolic blood pressure and AST had just 2 units, 1 equivalent to the canonical unit and the canonical unit itself. Diversity of units within populations (values from individual data partner and measurement concept combinations) was minimal (Supplementary Figure S7), indicating that generally just 1 unique unit was used per laboratory test at data partner sites.

Unit conversion workflow

A total of 52 measurement variables important to COVID-19 research, including respiratory rate, body weight, and temperature, were selected for unit harmonization (Figure 2), corresponding to a total of 1.608 billion rows of data and 297 measurement concepts. A total of 299 mapping functions (Supplementary Table S3) were manually curated by clinicians and informaticians for use in unit harmonization.

KS test P-value threshold determination

The distributions of validation-step KS test P values were plotted to identify the best threshold (Figure 4). At P values above 0.00001 (1e-5) we saw almost exclusive presence of KS-test results for comparisons between equivalent inferred units versus known units. Supplementary Figure S8A and B highlight the example of body weight, where the only exception to this pattern occurred due to an incorrect unit assignment by the data partner site. Based on this body weight example, Figure 4 distribution profile, and Supplementary Figure S4 that demonstrates lack of false positive outlier variables (aside from CRP, described below), we judged the threshold of .00001 sufficient to accurately distinguish the "true" from "false" units. We additionally checked Leukocytes [#/volume] in Blood by Manual count. As described above, this measurement concept appeared to be an outlier within its concept set, but on inspection of P values for "equivalent" versus "nonequivalent" inferred units versus the masked known units, we obtained good distinction above and below the threshold, thus supporting our decision to avoid separating out these concepts into their own concept set.

Unit inference omission criteria and measurement variables omitted from unit inference

Further analysis of CDFs indicated that, compared to variables such as body weight (Supplementary Figure S9A), c-reactive protein (CRP) has highly overlapping and even interleaved value distributions across its 2 nonequivalent units of milligram per deciliter and milligram per liter, that is distributions for milligram per deciliter can either be found with higher values or lower values than milligram per liter (Supplementary Figure S9B). This overlap indicated that CRP would not be amenable to unit inference. We systematically identified all measurement variables that were refractory to unit inference (Materials and Methods, Figure 3B and Supplementary Figure S2B), including a comparison of transformed measures of dispersion and minimum conversion factor fold change (Figure 5). CRP was the only variable to fall above a threshold of 0.25, indicating substantial overlap across distinct units.



Figure 5. Omitting variables where units cannot be uniquely assigned; Unit inference omission criteria. The standard deviation of the log median harmonized values (above the KS test *P*-value threshold) was used as a measure of closeness of different populations of values, and was compared to the log of the minimum conversion factor to determine the level of overlap expected between different units. Ratios: 0.125–0.25 (right-most shaded segment), 0.25–0.5 (middle shaded segment), and >0.5 (left-most shaded segment). KS test: Kolmogorov-Smirnov test.

Proportions of data partner contributions to measured variable reference distributions

The proportion each data partner contributed to the "known units" used for unit inference reference distributions for measured variables is summarized in Supplementary Figure S10, which shows proportion sizes along with their counts. Due to the large number of data partners and general homogeneity in contribution size from each of the data partners, in no case is there a single site that is in the majority for the generation of a reference distribution within 1 unit inference pipeline. The highest proportion found is 0.39, and only 4 concept sets contain any data partner that claims greater than a quarter of the data, 2 being vitals measurements that have only 1:1 or canonical units. The median data partner proportion over all concept sets was 0.017, and mean (SD) of 0.028 ± 0.036 , and the vast majority of data partner proportions are of similar size.

Harmonized and inferred units across measurement variables

An overview of the total counts and percentages of harmonized and inferred units can be found in Table 2. There were 1.61 billion input records with values for the harmonization pipeline from the 52 measurement variables of research priority, of which 933 million had valid units. The 675 million that were missing units were processed through the unit inference pipeline, of which 527 million were successfully in-

Table 2. Counts and percentages of harmonized and inferred units

Metric	Count	Percentage
Total measurements with values present	1 607 758 125	N/A
Total measurements with valid units	933 030 577	58.0
Total measurements without units	674 727 548	42.0
Total nonequivalent units harmonized	725 051 924	45.1
Total harmonized	1 416 354 459	88.1
Total units inferred	527 400 086	78.2 ^a , 32.8 ^b

Note: Harmonized and inferred unit counts and percentages were calculated across all measured variables out of a total of 1 607 758 125 measurements with values, of which 674 727 548 (42%) had missing units.

^aOut of total records that were missing units.

^bOut of total measurements with values.

ferred (78%). In total, 32.8% of the records with values had an inferred unit successfully ascribed. Harmonized values were present for 88% of the data, with 45% coming from nonequivalent units. Figure 6A shows the proportion of inference and harmonization per measurement variable, and identifies large data quality disparities from the source, with temperature particularly problematic for unit missingness.

Sources of unit missingness

Supplementary Figure S11 illustrates the proportion of missing units from the source CDMs, proportion of records with source units that



Figure 6. Overview and examples of successful harmonized and inferred units. (A) Percentage of values with harmonized and inferred units by measurement variable. Roughly half of the data had correct units and did not require conversion (light green), while half of the data had their units inferred (blue). A minority of values had units that needed conversion (dark green), and the smallest group of data had nonsensical or mislabeled units (black). (B) Original units and their values for body weight and harmonized data for body weight. (C) Inferred versus observed harmonized value distributions.

are mapped to standard OMOP units, and proportions of final inferred and noninferred units, showing the high level of data salvage via our unit inference pipeline in cases where units were missing.

Harmonized value distributions indicate successful unit harmonization and inference

An example of successful unit harmonization is shown for body weight in Figure 6B, where grams, kilograms, ounces, and pounds are harmonized to kilograms with similar distributions across the distinct units. Harmonized values for inferred versus reference (known) units across measured variables displayed highly similar distributions (Figure 6C), indicating significant bias or error was not introduced during the unit inference process.

DISCUSSION

We were successful in harmonizing lab data across a very large set of pooled EHR data, and were able to reclaim data that would otherwise have been lost to analysis. With SME consensus, we grouped together sets of semantically similar analytes (and, where relevant, of specimen type) expected by the SMEs to have interoperoberable and convertible measurement units into concept sets for 52 variables important to the understanding of COVID-19. We found, on average (SD), 2.9 ± 1.4 different units used per concept set. Using our pipeline, we harmonized 88.1% of the measurement data that had values present, and inferred units for 78.2% of measurements where units were absent. Missing units pertained to 41.9% of the measurements with values, and our pipeline for inferring missing units shows a false positive rate of 2.7% and a false negative rate of 14.0% (true rates are likely lower due to apparent unit misassignments by sites). We found CRP refractory to unit inference, as previously shown.⁶ Our approach has several attractions. First, the unitharmonization pipeline can be integrated with other data-quality review pipelines. The burden of improving lab-data quality is not placed on the sites, except for specific areas of data quality that our harmonization and inference cannot address (eg, Figures 5 and 6A). Misassigned units can be easily identified and shown to sites for correction, which in turn is an example of the potential of this pipeline to improve data partner sites' own data integrity.

Second, our process reduces or eliminates the need for individual researchers to perform unit conversions.

Third, our work enables consistent research within N3C: all analyses using the harmonized variables can share programming code and the resulting numerical results will be harmonized. For example, calculation of derived variables, such as BMI, was enabled due to the unit harmonization of height and weight.

Fourth, our pipeline enables use of measurements that would otherwise be unavailable for analysis. Reclaiming 78% of data associated with missing data raises the precision of our results (through increased amount of data) and reduces potential bias, due to important factors that may have been associated with the data that were missing units.

Fifth, some of the concept sets we used for unit harmonization are broader than one would use for clinical purposes or analyses and so the distributions are, of necessity, broad. In the case where further distinctions within concept sets may be important (eg, in measurements of venous vs arterial blood), our approach can be applied to assess whether the distinctions matter: If the CDFs of contributing sites lead to nonsignificant KS *P* values when units are converted then compared to reference values, then no further work on unit harmonization is needed. Researchers should still distinguish the arterial and venous measurements, for example, in their analyses. Our approach has implications for other researchers beyond N3C. The canonical units, concept sets, conversion formulae, and accepted-value ranges for each measurement variable that we developed can serve as a harmonization resource for the growing number of initiatives aiming to extract insight from patient medical lab records, particularly if present in the widely used OMOP format. The comprehensive and easily interpretable table of unit conversions for labs provided in Supplementary Table S3 can serve as a resource in the context of CDM unit harmonization and any other application that requires unit conversions. The canonical units defined herein have been included as example units for measurement concepts on the LOINC by Regenstrief website.¹⁵

Finally, while unit conversions could be applied in a distributeddata environment, our reclaiming of data with missing units relies on the availability of data from all sites. Thus, the ability to reclaim these data is an advantage of a pooled-data architecture. For example, 51.2% of the data partner sites contained body weight records without units (with 7 sites missing units entirely), and 82.4% of data partner sites had only 1 valid source unit to act as a reference. The approach taken of determining *P* value differences and value distribution differences across units in order to more confidently assign inferred units was thus uniquely enabled by pooling data from all contributing sites, and would be impossible to replicate on a siteby-site basis for the majority of data partner sites. Additionally, even in the case that a site's unit diversity mirrors centralized unit diversity for a lab measurement, ground truth of the expected value distribution for each unit cannot be accurately obtained on a siteby-site basis due to the potential for misassigned units.

There is further work to determine whether our method for selecting values for the reference distributions per measurement variable for unit inference can be improved. For example, an alternative to random selection over all data partners would be to ensure, where possible, that the same numbers of data points are sampled per data partner, per measured variable, to avoid data partner oversampling and potentially reduce the impact of any one site on the reference distributions. However, the current sampling regime shows good performance for identifying canonical units, rescuing missing data, and identifying outlier sites.

Future work will also involve maintenance of the pipeline over time. As new source units emerge from sites this will result in further standard OMOP unit concepts entering the lab measurement data that require mapping to conversions. Additionally, some sites have included varying amounts of custom units that differ from those expected from the source CDM, and thus are missing from our source to standard OMOP mapping. There is therefore continuous work in N3C to improve the comprehensiveness of source unit mapping.

In cases where a centralized approach is not feasible, or to distribute the resources collected at the centralized level, we also envisage that our centralized approach could be adapted to enable federated use of aggregated resources such as reference distributions to allow for unit inference at the data partner site-level, or the unit harmonization conversions could be shared to the federated sites.

There are some limitations in our approach. The range of units found for each lab measurement may not constitute the full universe of potential units, and thus unit comparisons can only be made for the units we see in the N3C Enclave. In imputing missing units, there is the risk of false positive imputation. Measured variables such as body weight were found to contain nonequivalent reference and inferred units above the assigned KS-test *P* value threshold (1e-5) during unit inference validation (Supplementary Figure S8A). CDF

analysis (Supplementary Figures S8B and S9A) suggested that these were from incorrectly assigned units from the data-contributing sites; for example, one of the CDFs from pounds matched the typical distribution for ounces. Aside from examining false positives at the upper end of the KS-test P value distribution, we also looked for false negatives (units with low P values containing equivalent reference and inferred units), which would lead to data not included in analyses that should be. CDFs of measured variables with P values <1e-5 were plotted (as in Supplementary Figure S8B), and for some variables, such as SpO2, the distributions for certain measurement concepts, for example, oxygen saturation [Pure mass fraction] in Blood, appeared to be different from the average distribution that focuses on arterial blood. While our concept sets largely capture equivalent concepts, this difference in CDFs exemplifies the challenges to inferring units for concepts that may be differentially employed. The same is also true for variables such as body weight in subpopulations such as children, where the correct units are assigned but the overall distribution of values does not match the typical distribution of the general population. These examples highlight the urgent need for more sophisticated unit-inference techniques that take into account specific patient subgroups and samples. Since our unit-inference method assumed just 1 unique unit per measured variable-data partner-measurement concept triple (as supported by Supplementary Figure S7), there also may be poor unit inference in the few cases where there are instead multiple distinct unknown units, although we did not rigorously test how mixtures of units affect unit inference via the KS test. Bayesian inference or machine learning using values from other measurement variables within each patient or patient subgroup as a cross check to infer likely units would be a possible next step for our workflow, for example values from height and BMI could help infer a missing weight measurement within an individual patient.

Although more sophisticated machine learning approaches to the problem of unit inference can potentially be developed, and maintenance of the pipeline over time will be necessary, our pipeline is easily interpretable, and runs in <2.5 h on the billions of rows of measurement data processed weekly within the N3C Enclave.

CONCLUSION

As collaborative research projects continue to grow and to incorporate larger and more diverse sources of data, we need to minimize time spent preparing data and to maximize its usability. In this work we have developed and implemented a pipeline to harmonize measurements to a canonical unit and to infer missing units of measurement. This pipeline allowed our team to salvage otherwise unusable data and to remove the need for duplicative work converting units for each N3C project. While this work was driven by the specific needs of the N3C, such a pipeline could be incorporated into the analysis of any large dataset of pooled EHR data.

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AUTHOR CONTRIBUTIONS

KRB, BA, AM, EN, ATG, and RAM prepared code utilized in the pipeline. KRB, JW, and HL created the conversion formulas. KRB, RAM, CB, and JY prepared tables and figures. KRB, JTW, HL, and RAM prepared the manuscript. All authors reviewed the manuscript and provided feedback.

SUPPLEMENTARY MATERIAL

Supplementary material is available at *Journal of the American Medical Informatics Association* online.

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CONFLICT OF INTEREST STATEMENT

KRB, BA, AM, EN, MB, and ATG are employees of Palantir Technologies. MH is a founder of Pryzm Health.

DATA AVAILABILITY

The N3C data transfer to NCATS is performed under a Johns Hopkins University Reliance Protocol # IRB00249128 or individual site agreements with

NIH. The N3C Data Enclave is managed under the authority of the NIH; information can be found at ncats.nih.gov/n3c/resources. Enclave data are protected, and can be accessed for COVID-related research with an NIHapproved approved (1) IRB protocol and (2) institutional Data Use Request (DUR). A detailed accounting of data protections and access tiers is found at https://ncats.nih.gov/n3c/resources/data-access. Enclave and data access instructions can be found at https://covid.cd2h.org/for-researchers; all code used to produce the analyses in this manuscript is available within the N3C Enclave to users with valid login credentials to support reproducibility.

REFERENCES

- Haendel MA, Chute CG, Bennett TD, et al.; N3C Consortium. The National COVID Cohort Collaborative (N3C): rationale, design, infrastructure, and deployment. J Am Med Inform Assoc 2021; 28 (3): 427–43.
- Observational Health Data Sciences and Informatics (OHDSI). Definition and DDLs for the OMOP Common Data Model (CDM) l Version 5.3. Github; 2018. https://github.com/OHDSI/CommonDataModel Accessed April 13, 2020.
- Hripcsak G, Duke JD, Shah NH, *et al.* Observational Health Data Sciences and Informatics (OHDSI): opportunities for observational researchers. *Stud Health Technol Inform* 2015; 216: 574–8.
- Huff SM, Rocha RA, McDonald CJ, et al. Development of the Logical Observation Identifier Names and Codes (LOINC) vocabulary. J Am Med Inform Assoc 1998; 5 (3): 276–92.
- Schadow G, McDonald CJ. *The Unified Code for Units of Measure* [Internet]. Indianapolis, IN: Regenstrief Institute, Inc.; c1999–2013 [cited 2021 Sept 01]. http://unitsofmeasure.org/trac/. Jointly published with the UCUM Organization.
- Ficheur G, Chazard E, Schaffar A, Genty M, Beuscart R. Interoperability of medical databases: construction of mapping between hospitals laboratory results assisted by automated comparison of their distributions. *AMIA Annu Symp Proc* 2011; 2011: 392–401.
- Rajput AM, Ballout S, Drenkhahn C. Standardizing the unit of measurements in LOINC-coded laboratory tests can significantly improve semantic interoperability. *Stud Health Technol Inform* 2020; 275: 234–5.
- Drenkhahn C, Ingenerf J. The LOINC content model and its limitations of usage in the laboratory domain. *Stud Health Technol Inform* 2020; 270: 437–42.
- Drenkhahn C, Duhm-Harbeck P, Ingenerf J. Aggregation and visualization of laboratory data by using ontological tools based on LOINC and SNOMED CT. *Stud Health Technol Inform* 2019; 264: 108–12.
- Hauser RG, Quine DB, Ryder A, Campbell S. Unit conversions between LOINC codes. J Am Med Inform Assoc 2018; 25 (2): 192–6.
- Vreeman DJ, Abhyankar S, McDonald CJ. Response to unit conversions between LOINC codes. J Am Med Inform Assoc 2018; 25 (5): 614–5.
- Bennett TD, Moffitt RA, Hajagos JG, et al., National COVID Cohort Collaborative (N3C) Consortium. Clinical characterization and prediction of clinical severity of SARS-CoV-2 infection among US adults using data from the US National COVID Cohort Collaborative. JAMA Netw Open 2021; 4 (7): e2116901.
- Chakravarti IM, Laha RG, Roy J. Handbook of Methods of Applied Statistics. Vol. 1. New York, NY: Wiley; 1967.
- Schuemie MJ, Ryan PB, Hripcsak G, Madigan D, Suchard MA. Improving reproducibility by using high-throughput observational studies with empirical calibration. *Philos Trans A Math Phys Eng Sci* 2018; 376 (2128): 20170356.
- LOINC release notes. LOINC by Regenstrief; 2021. https://loinc.org/kb/ loinc-release-notes/. Accessed February 15, 2021.