Critical Care Project Report

Research Software Development Group

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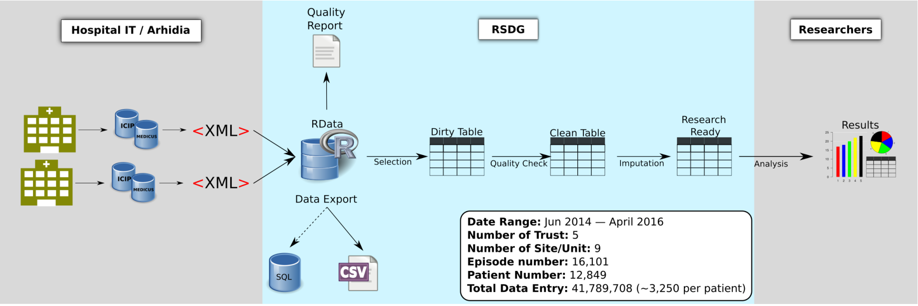
1 Introduction

The critical care patient data will be the cornerstone of many future medical and health services research. However, the raw data need to be converted into a research-ready structure to enable and ease its scientific analysis. Thus, to cover that gap the data have to be transformed into a queryable form and its properties and quality to be understood. The UCL Research Software Development Group's mission is to provide an open source software solution to bridge this gap and deliver the ready-to-use data alongside with the data manipulation tools for the researchers.

We have built a pipeline which converts the `XML` raw data to the queryable RData format. Additionally enabling to export the resultant data into `CSV` format to be used outside R (*e.g.*, with Excel). A business readable data quality check dictionary is used in the pipeline to clean the data. The non-validated data are either modified or removed according to the such criteria. Subsequently, an auto-generated data quality report is produced to report the key fields missingness and data sanity by each site and unit. By the end of the pipeline the researchers obtain a R table which is queryable and validated. We also have demonstrated the ability of deriving data products, such as SOFA score from physiology data and identification of sepsis. A publication about this process is in due course.

We believe a robust, understandable and accessible software is the first step of solid research. Therefore, beyond the functionalities, we focus in the usability and sustainability of the software produced. All of our development is constantly updated in the GitHub platform which is accessible to all the allowed users. The installation process of our software aims to simplicity. The code is self-explanatory and well documented providing accessibility to the (empowering?) users and future developers. Testings are conducted after any modification of code automatically on the Travis CI system. Overall this ensures the software to be a gateway to the data which plays a critical role in the future success of the community.

2 The Data Process Pipeline



Date Range: Jun 2014 — April 2016
Number of Trust: 5
Number of Site/Unit: 9
Episode number: 16,101
Patient Number: 12,849
Total Data Entry: 41,789,708 (~3,250 per patient)

Figure 1: Data Process Pipeline with summary report of the data processed

2.1 The XML data and the Data Safe Haven

Data associated with more than 12,000 patients from five NHS trusts are available in XML format. The data were drawn from the ICIP and Medicuse databases which contains demographic, drugs, laboratory, nursing and physiology data. The de-identifiable and identifiable data are processed locally and on the UCL Data Safe haven (IDHS) respectively. In order to create the pipeline on IDHS, we requested and configured a Linux virtual environment. Due to the limited capacity of IDHS, it is still useful to keep a local de-identifiable copy for development purposes. The pipeline is designed to be portable on multiple platforms. It can be executed on both local environments and IDHS with de-identifiable and identifiable data.

2.2 XML parser

The XML parser in R combines and restructures the XML files into a newly defined R data structure `ccRecord`, which significantly improves the clarity of the data by organising it under tables and removing the redundancy of the XML files. `ccRecord` is designed as a flexible, simplified, and queryable data structure for critical care measurements. Data in `ccRecord` format is eventually stored in a RData file which is about 500 times smaller than the original XML files. In addition the data provenance is recorded by each episode, henceforth we are able to tell from which file each episode comes and when it has been parsed. The selected data fields can be exported into a CSV file for Excel users or to be used with any other analysis tool or programming language.

It is worth mentioning that a C++ equivalent XML parser, which has a much better performance comparing to the currently used in R, has been developed but not deployed yet due to the time constraints of the project. The incorporation of the C++ parser into the pipeline will boost the speed in which all the files are converted.

2.3 Auto-generated quality report

Data may have imperfections in various ways. Therefore a synthetic quality assessment that allows us to report back to the data source is extremely useful. An automatic generated data quality report which reflects the quality issues have been developed and deployed. Based on the report, we are able to inform the major missingness issues and some data sanity problems together with basic information such as the duration, sites, number of episodes, and number of patients.

2.4 Data validation and cleaning

Data validation and cleaning functions in included in the `ccdata` package. Data sanity check is conducted in many aspects regarding to the intrinsic property of the individual fields. There are three major validations: the numeric range, the text category, and the missingness. The users are required to fill a `yaml` form to guide the validation check. Consequently, the data is flagged accordingly to the the level of the data sanity excluding the data that do not make sense. After this stage, we are able to deliver a “cleaned” and queryable R table to the researchers. Next section discusses in more detail the `yaml` dictionary.

3 The R package: ccdata

The ccdata R package is the centralised toolset developed for piping and data manipulation. The package bundles not only all the R/C++ code but also its documentation and tests making easier code sharing. The ccdata package is portable to almost all platforms where a R environment is available. It can be installed effortlessly on Windows or UNIX based systems. Although it is necessary to provide further tidy-ups in the subsequent development cycle, the main part of the R code in the current stage is well documented and properly tested.

In order to prepare the first scientific publication, many data manipulation processes were needed. Instead of making one-off scripts, we incorporated the data manipulation processes as re-usable functions in the ccdata package. The frequently used functions such as detecting unique patient and spell and data imputation can be called from the package reducing therefor the duplication of work in the future. The package is still growing as the research goes on.

3.1 Data Selection and cleaning in the yaml configuration

Notwithstanding the fact that to be able to use and program with ccdata package offers a great flexibility in data analysis, the pipeline can be performed without any programming knowledge. The users can run the pipeline by only filling a yaml configuration file. The yaml form is straight forward and self-explanatory for non-programmers. The user selects data fields for the cleaning process obtaining a single CSV file at the end of the pipeline which can be open in MS Excel.

Below is an example of the yaml data cleaning configuration of heart rate, in which three filters nodata, range, missingness are presented in the following data selection and cleaning configuration.

```yaml
NIHR_HIC_ICU_0108:
  shortName: hrate
  dataItem: Heart rate
  distribution: normal
  decimal_places: 0

  # filter1: do not use the episode where hrate cannot be found.
  nodata:
     apply: drop_episode

  # filter2: mark all the values based on reference range (traffic
    colour) remove entries where the range check is not fullfilled.
  range:
      labels:
          red: (0, 300)
          amber: (0, 170)
          green: (50, 150)
      apply: drop_entry

  # filter3: compute the item missing rate on given cadences; in
    this case, we compute the daily (red) and hourly (amber)
    missing rate, and only accpet episodes of which hourly missing
    rate (amber) is lower than 30%.
  missingness:
      labels:
          red: 24
          amber: 1
      accept_2d:
          amber: 70
  apply: drop_episode
```

4 Summary

RSDG got involved in the critical care data project since January 2016. In the last six months we contributed to the paper preparation with the critical care team while developing the re-usable and sustainable software tools for the data pipeline and data manipulation. In the next phase of this project, we are focusing on the linkage of the data of other HIC groups and external sources. We continue supporting researchers by providing sustainable software tools.