SOFTWARE METAPAPER

Transplant2Mongo: Python Scripts that Insert Organ Procurement and Transplantation Network (OPTN) Data in MongoDB

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transplant2mongo allows users to transform Standard Transplant Analysis and Research (STAR) ASCII data files from the Organ Procurement and Transplantation Network (OPTN) into a MongoDB database [1, 2]. The STAR data are a complex collection of tab-separated files with inter-related records that are not amenable to complex queries. A researcher planning to use OPTN STAR data can use transplant2mongo to convert the data into a MongoDB database and then use open-source tool software for analysis. The source code for transplant2mongo is available on GitHub at https://github.com/ceharvs/transplant2mongo and includes sample data files for initial testing and queries.

Keywords: Python; OPTN; UNOS; organ transplant; organ donation; health care; analysis; MongoDB

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(1) Overview

Introduction

The OPTN keeps a record of all organ donations, transplants, and waiting list registrations since 1987 in the United States [1]. This complex data set can be used to review, query, and analyze the US organ donation system over time and across various facets. The total database size is ~9 GB and contains records on hundreds of thousands of donors and over a million patients [2]. OPTN provides STAR data as tab-separated variable (TSV) files, SPSS [3] files, or SAS [4] files. SPSS and SAS are proprietary software and the TSV files are not suitable for non-trivial queries. The transplant2mongo Python scripts insert the TSV data into a MongoDB database. transplant2mongo was developed to allow researchers to use open-source software to explore, manage, and analyze the data without the need for proprietary software. There is no similar open-source software available for transferring STAR data into a database that does not require proprietary software for use.

Due to the sensitive nature of STAR data, the development of transplant2mongo was completed in a secure lab environment at The MITRE Corporation and the code repository does not include any STAR files. Special consideration was made to process the data and remove erroneous symbols and characters that are not compatible with MongoDB. The resulting MongoDB database has been used to perform an analysis of the OPTN dataset and the results of the analysis will be presented in a future publication.

Users are able to test the code using sample synthetic TSV data. In order for users to run the code on actual UNOS STAR data, they must update the Makefile to specify the file types they have and the data location using instructions detailed fully in the README file. Once they have updated the Makefile to their specifications, the make all command will populate the database with all referenced STAR files.

Implementation and architecture

This software was developed on a machine running CentOS with Python 3.6 and MongoDB 3.6 and was tested using all available OPTN STAR TSV files obtained from the OPTN in June 2014 and then in March 2015. The general file configuration of OPTN STAR files and directories is shown in Figure 1. (Users of transplant2mongo may
As shown in Figure 1, the TSV files are all stored in subdirectories of the Delimited Text Files directory. This directory contains a sub-directory for each of the data types: Deceased Donor, Intestine, Kidney_Pancreas_Kidney-Pancreas, Liver, Living Donor, and Thoracic. The Kidney_Pancreas_Kidney-Pancreas sub-directory contains information on all patients and transplant recipients for kidney and pancreas, and combined kidney/pancreas transplants. The Thoracic sub-directory includes data on both heart and lung transplant patients. The Deceased Donor and Living Donor sub-directories contain details on all organ donors, while the other subdirectories provide data on all patients registered to the waiting list and those who received a transplant. Each of these major groups is represented as collections in the generated MongoDB database with the patient or donor information as documents and the sub-folders as sub-documents.

MongoDB was chosen as the database due its NoSQL format, allowing multiple patient fields to be combined into a single document with multiple sub-documents. Many of the STAR file fields have changed over the years, and many of the patient fields are missing information, making this data suitable for NoSQL storage. Alternatively, a SQL database system could be used. However, with such a structured database implementation, the number of columns would be very large and there would be many NULL fields in the database.

**Figure 1:** Structure of the OPTN STAR files. The top-level directory is Delimited Text Files and the subdirectories are shown to the right.

not have the complete set of UNOS STAR files, and may only have certain subsets of this information. In this case, the Makefile can be edited so that only a subset of the STAR files are processed.)
A Makefile is used to execute the scripts that build the database from the contents of the Delimited Text Files folder. The Makefile has targets for cleaning, processing, and inserting the data into a MongoDB database. Users need to specify their database server and port in the Makefile before execution. The default server and port is localhost:27017 and the default database name is organ_data. Users also need to define the components to process, which corresponds to the STAR files that the researcher has obtained from the OPTN (corresponding to the subdirectories of Deceased Donor shown in Figure 1). These values are selected from the following list: deceased, living, intestine, kidney, liver, and thoracic. Data are first copied from the original location and file structures are flattened to establish a simple structure for parsing.

Once the flattened data files have been generated, another Python script is run to generate JSON and add the documents into the MongoDB database. For the base files, corresponding to the main donor and organ data files, the add_patients.py script is run to generate major documents in the appropriate tables. For files that contain sub-document information such as follow-up visits or medications, the supplemental_data.py script adds this information as a sub-document to the main patient or donor document. This script uses a unique identifier, such as DONOR_ID, TRR_ID_CODE, or WL_ID_CODE, to match the supplemental data file entry with a unique record for the donor or organ type. Once a match is found, the supplemental data is added to the document in the database. The TSV files, having the extension .DAT, only contain data and do not include column names; columns are determined by the .htm files corresponding to each .DAT file.

Data are cleaned before insertion into the database. The cleaning process is handled in the Python scripts add_patients.py and supplemental_data.py, which use the clean_string function. These scripts remove extraneous values such as extra commas, quotations, and newlines. The scripts do not assume a particular data type for any column. The database contains many different columns and the typing is automatically determined by Python and MongoDB. All data are by default imported as a string. The Python scripts check if the data is a date or an integer, and if not, the data are kept as strings.

Following the execution of each of the import scripts, follow-up scripts are run to add age bins to all age fields of the data to allow fast and simple aggregation queries.

Quality control
The scripts have been tested on two distinct UNOS STAR file data sets from 2014 and 2015. Each script prints out the number of lines in the file being processed and then the number of patient documents successfully imported into the database. With the two data sets, the line count results match the imported entry counts in all scenarios with the exception of a particular data file where a newline was hidden with quotation marks and the reported file length is one more than the imported record count. The data were manually confirmed in this situation and additional manual spot checks were performed.

The GitHub repository includes sample data that can be used for testing the installation. These data contain no real patient information and were generated by the developers of the software. The Makefile is set up by default to run on this sample data set with the localhost MongoDB database by following the directions provided in the README. A test target in the Makefile can be used to verify that the sample data was imported correctly and a query can be performed.

A MongoDB viewer, such as Robo 3T, is recommended for browsing and spot checking the data after the sample data or STAR data has been inserted into the database. A Python script is included, query.py, that performs database queries and prints the output to a comma-separated values (CSV) file. A Jupyter Notebook, query-examples.ipynb, is also included that can be used as a starting point for analysis and demonstrates querying the database, performing statistical analysis, and graphics.

(2) Availability

Operating system
All operating systems should be compatible.

Programming languages
Python 2.7 or 3.6+ (Tested with Python 2.7, 3.6, and 3.7)

Additional system requirements
None.

 Dependencies
MongoDB 2.6+ (Tested with 2.6 and 3.4)
- Python packages: pymongo, pandas, tqdm, and seaborn
- Users need to obtain UNOS STAR files directly from the OPTN. This data contains private health data and can only be obtained directly from the OPTN.

List of contributors
Christine Harvey was the lead developer on this project and R.S. Weigel provided contributions.

Software location

Archive
Name: Transplant2Mongo Version 1.0
Persistent identifier: 10.5281/zenodo.2528840
License: GNU GENERAL PUBLIC LICENSE Version 3, 29 June 2007
Publisher: Christine Harvey
Version published: 1.0
Date published: 29/12/2018

Code repository
Name: GitHub
Persistent identifier: https://github.com/ceharvs/transplant2mongo
License: GNU GENERAL PUBLIC LICENSE Version 3, 29 June 2007
Date published: 15/02/17

Language
English
(3) Reuse potential

This tool is available for re-use by anyone working with UNOS STAR files seeking to do research on the organ transplant system. This tool generates a database that can be used with open-source software.

The software has a high potential for extension. This database creation scripts are written in Python 3 and they could be modified to allow the insertion of the data into alternative databases such as SQL. A GUI could be developed that allows visualization and query of the contents of the database that is customized for the type of analysis done by organ transplant researchers.

There is no official support for this software, but those with questions or interested in collaboration can contact Christine Harvey at ceharvey@mitre.org or via GitHub.

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Competing Interests

The authors have no competing interests to declare.

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