Utilizing Document Digitization and Recognition Technology for Genetic Testing Results in an Oncology Practice - a pilot study

Barinaepkee Banuna¹, Jeffrey Lombardo PharmD¹,²,³, Gene D. Morse PharmD¹,²,³

¹University at Buffalo; ²Translational Pharmacology Research Core, ³New York State Center of Excellence in Bioinformatics and Life Sciences

ABSTRACT

The Medication Management Research Network (MMRN) conducts innovative research using health information technology. MMRN’s focus is to integrate pharmacogenomics reports with clinical data and medications from electronic health records (EHR) systems into Patient Safety Organization work products for an oncology practice. The purpose of this study is to establish an algorithm for the digitalization of genetic testing results using genetic testing companies that provide results in varying formats so that they can be incorporated into an EHR system with a larger database. Genetic testing results stored in PDF formats from different EHRs are de-identified and converted into a standardized template. A digitalization test is conducted for 100% accuracy then the results are integrated into the EHR. Once a health record is established it will be used to optimize medication management and patient safety.

PURPOSE & SIGNIFICANCE

The PSO works with practices seeking to establish a patient safety evaluation system and reduce the occurrence of adverse events.

Practices utilizing electronic health records (EHRs) de-identify data for submission to the PSO for aggregate review and feedback.

The PSO generates reports for each site highlighting any patient safety medication review concerns.

- While working with an oncology practice, the PSO identified an area of patient safety concern utilizing HIT.
- Genetic testing results were not fully incorporated into a patient’s EHR, but kept as static scanned documents in an attachment section of the patient’s profile.
- This study investigates the use of document digitization technologies for converting scanned genetic testing results into a smart document for integration with the EHR.
- Goals:
  - Develop an algorithm and lexicon to accurately decipher and extract information from the genetic tests.
  - Measure the accuracy of the recognition and digitization technology.
  - Genomic tests are used to identify patient-specific disease susceptibility and clinical decision strategies
  - The ability to extract and integrate these information "real time" in a useable format within a patient’s record allows for a comprehensive and cohesive data set to be made available to clinicians when determining therapeutic options.

RESULTS

This is an ongoing project that began in April 1, 2014. Results are still in progress.

On Line Access to Genoptix.lab - This year 102 reports
- ALK Rearrangement by FISH – 6
- BRAF Mutation Analysis – 1
- CALR – 1
- Cobas BRAF - 1
- COMPASS - 14
- Cytogenetics – 14
- EGFR Mutational Analysis – 5
- FISH - 8
- Flow Cytometry – 17
- Hematopathology – 20
- HER2 by FISH Technology -1
- IgVH Hypermutation Analysis - 2
- JAK2 PCR – 3
- KRAS Mutation Analysis - 4
- MET by Fish - 1
- MPL W515 – 2
- NEXOURESE NSCLC - 5
- ROS1 by FISH – 1

Figure 1: This shows the number of each type of report MMRN received from one genetic company alone for 2014

Sample Template from One Genetic Testing Company

METHOD

- Genetic testing results stored in PDF formats from different EHR systems of the oncology practice are de-identified
- A lexicon of all possible terms is developed and programmed into the document digitization and recognition program
- Standardized template is identified from each reporting agency and stored in the lexicon
- Each genetic test document is run through the program
- Review detection accuracy. Once 100% accuracy is reached, the results are integrated into the EHR in a more usable format

CONCLUSION: NEXT STEPS

Quality EHR system
- Optimize medication management
- Expand patient safety by reducing errors
- Savings for the patients, their providers and health payment systems

SELECTED REFERENCES


ACKNOWLEDGMENTS

- Jeffrey Lombardo, PharmD, BCOP, Gene D. Morse, PharmD, BCPS, FCCP, Farzia Kaufman, Tyler Muller, Jesse Hanschet from Translational Pharmacology Research Core
- University at Buffalo Ronald E. McNair Post-Baccalaureate Achievement Program
- CCS Oncology
- UB Center for Unified Biometrics and Sensors
- UB School of Pharmacy and Pharmaceutical Sciences

Figure 2: Example of one company’s report. Red letters represent elements preprogrammed into the lexicon/dictionary to filter out noise and increase accuracy of the technology. Black letters are specific to each report.