PLATFORM Short Abstract Presentations

Tuesday, May 23, 2017

Wednesday, May 24, 2017

Location:

Wyndham Grand Pittsburgh Hotel

Kings Garden 1

Tuesday, May 23, 2017
9:00am – 9:35am

Towards Computable Cancer Synoptic Reports

W. Scott Campbell, PhD[1] (wcampbel@unmc.edu); Geoff Talmon, MD[1]; Audrey Lazenby, MD[1]; Alexis Carter, MD[2]; Rajesh Dash, MD[3]; James R. Campbell, MD[1]

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Content
The synoptic report contains the summative pathology assessment of malignant tissue to communicate diagnostic and prognostic information to clinicians. To realize the full potential of synoptic data for use in patient care, decision support, analytics and population health, the synoptic report elements must be computable, that is the data elements must be machine readable and support computational analysis. To date, this objective has not been achieved. A collaborative terminology development effort to expand SNOMED CT content in support of computable cancer synoptic reports is presented.

Technology
In conjunction with the LOINC-SNOMED International collaborative agreement, the SNOMED CT concept model was expanded to support robust definitions for Observable entity concepts and was employed to encode the College of American Pathologists (CAP) cancer protocol worksheets.

Design
Investigators at University of Nebraska Medical Center in conjunction with pathologists from the CAP and trained SNOMED CT terminologists analyzed the CAP protocols for colorectal and breast cancers. SNOMED CT definitional content was authored using the expanded SNOMED CT concept model and incorporated into the pathology information system at the Nebraska Medical Center. HL7 messages were used to transmit encoded synoptic data to an institutional tissue biobank. Biobank queries were performed to support clinical and research use cases.

Results
A total of 194 concepts were developed for colorectal cancer and invasive breast cancer CAP worksheets including biomarker worksheets. Between October 2016 and March 2017, 81 breast and 45 colorectal tumors were encoded as part of routine rendering of anatomic pathology diagnoses and successfully transmitted to the biobank registry. Queries of the biobank database supported the use cases submitted by clinicians and researchers and demonstrated the ability to use synoptic data independently of the context of the original synoptic worksheet. Data query use cases will be presented, as well as, SNOMED CT concepts definitions created.

Conclusions
The properties of SNOMED CT provided the necessary computable underpinnings to support a standards-based approach to capture, transmit and computationally assess syntopic data. Additional work is ongoing to encode all CAP cancer worksheets. Authored content is available from the NLM UMLS knowledge server.

9:45am – 10:20am

Next Generation Decision Support Tool for Variant Reporting

Michael G Zomnir (mzomnir@andrew.cmu.edu); Jochen K. Lennerz, M.D., Ph.D.; Maciej Pacula; Nishchal Nadhamuni; Lev Lipkin; Sekhar Duraisamy; Enrique Dominguez Meneses; Allison MacLeay; Saeed H. Al Turki; Zongli Zheng; Miguel N. Rivera, M.D.; Valentina Nardi, M.D.; Dora Dias-Santagata, Ph.D.; Long P. Le, M.D., Ph.D.; A. John Iafrate, M.D., Ph.D.

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Content
Bioinformatics pipelines have markedly improved next- generation sequencing data analysis and genotyping; however, the decision to include a variant in the final report remains challenging. We aim to address this challenge by creating a next-generation decision support tool for variant reporting, using next generation sequencing data and metadata as our inputs.

Technology
Here we employed a machine learning approach, leveraging the scikit-learn machine learning library of the Python programming language, to capture the collective clinical sign-out experience of six board-certified molecular pathologists and build a decision support tool for variant reporting.

Design
We extracted all clinically reviewed and reported variants from our laboratory database and tested several classification models. We used ten-fold cross validation for our final variant call prediction model that derives a contiguous score from 0-1 (no-yes) for reporting. Through cross validation, we tested several different supervised machine learning approaches, including Naïve Bayes, Logistic Regression, Decision Trees, Random Forests, and Support Vector Machines. We also performed feature selection to identify our most predictive independent variables.

Results
For each of the 19,594 variants, our pipeline generates 507 features resulting in a matrix of roughly 9.9 million data points. From a comparison of Naïve Bayes, decision trees, random forests, and logistic regression models we selected the latter because logistic regression assigns individual coefficients for each feature, which increases interpretability. The model results in 1% false negatives and 2% false-positives. The final model's Youden indices are 0.87 and 0.80 for screening and confirmatory cut-offs, respectively. Re-training the model on a different assay confirmed the transferability of the approach. We additionally derived individual pathologist-centric models ('virtual consensus conference function") and a drill-down functionality allows review of the underlying features contributing to a particular score for clinical implementation.

Conclusion
Our decision support tool for variant reporting is one approach to capture the clinical genomics sign-out experience.

11:20am – 12:00pm

Web-Based Facilitation of Communication and Coordination of Clinical Laboratory Services

Aaron West[1], Michael Dowlin[1] and **Gregory Buffone[1,2]** (gbuffone@bcm.edu)

Department of Pathology, Texas Children's Hospital[1] and Baylor College of Medicine[2]

Content

Clinical Laboratories, particularly those serving geographically distributed health care systems, demand an efficient and effect means of communication, coordination and documentation of various aspects of their services. Specifically, four key areas, including staffing, instrument readiness, patient and specimen handling and sharing, and shift-to-shift transitions all contribute to the level, efficiency and quality of service delivered by any given clinical laboratory. The ability to manage these dimensions of service in real-time requires a means of creating and sharing content relevant to each that can be proactively addressed at one or more operational and professional levels.

Technology

A web-based application, Electronic Quality for Laboratories (EQL), has been created to address the aforementioned needs of the Pathology Laboratories serving the Texas Children's health system in Houston, Texas. EQL links workbenches, sections, shifts, laboratories and campuses across the system in near real-time (screen refresh rate 1 min) for the purposes of communication and coordination along the dimensions of service highlighted above. The facility to share information in this manner not only improves immediate outcomes but also provides documentation for ongoing quality assurance and regulatory review. Checklist for shift-to-shift hand-off and for task management is supported and can be customized to address different functions.

Design

Real-time communication and coordination is organized along several interrelated hierarchies: operational structure, technical and administrative roles and professional roles are logically linked in the workflow and information sharing functionality. EQL also accommodates campus and discipline-specific (e.g., General Laboratory, Histology, Blood Bank) operational integration. The use of EQL reduces 15 different means of logging and communicating operation issues or potential issues to five for a 66% overall decrease.

Results

Additionally, much of the data captured in EQL is now available in a structured form for analysis and reporting to affect operational and or quality improvement. For example, issues logged in EQL can be designated as a potential causal event. Those events can be programmatically associated with performance outcomes defined in an interfaced Quality Dashboard. Ongoing systematic association of events and outcomes provides a means of not only simplifying the quality review process for laboratories but also enables efficient and effective analysis and improvement of systems failure.

Conclusion

EQL linked to a dash board monitoring operations/quality provides the facility to move beyond simple discovery of poor outcomes to concurrent understanding of potential causes.

Wednesday, May 24 2017
9:00am – 9:35am

Development of A Novel Quality Assessment Tool for Digital Microscopy

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Content
Image fidelity is of utmost importance when using digital pathology for routine diagnostic work. Digital radiology has developed many Quality Assurance (QA) measures to help ensure that the display is suitable for diagnosis, but little work has been conducted within the corresponding area of digital pathology. An international, cross-site audit was conducted to evaluate the performance of displays and viewing environments within two tertiary histopathology departments using a unique QA tool.

Technology
We designed a QA tool based on the RGB values of haematoxylin and eosin obtained from analysing the spectral data of stained biopolymer. The tool was developed using MATLAB, and involved a 5x5cm haematoxylin and eosin coloured patch with a superimposed random letter of progressively varying RGB values from the background colour. The test environment was created using the previously published web-based experiment platform, Prospector, and involved 180 test images shown individually and in random order.

Design
Two pathology departments were involved in the audit; one where most primary diagnoses are made digitally using medical grade displays, and one that uses light microscopes only.
The audit was divided into three phases across the two institutions. Participants were enrolled on an opportunistic basis. A total percentage correct for each test was obtained for each participant.

Results
Eleven participants completed 11 tests in Phase 1. Phase 2 was carried out by 6 participants who completed 16 tests in total. Phase 3 included 26 tests conducted by 6 participants. The results will be presented, including comparison of performance between the two institutions, comparison between different displays, comparisons between participants, and variation in performance with changes in the environmental conditions.

Conclusions
The use of the QA tool provides a standardised method of comparing displays and viewing environments. Our findings are in accordance with existing International Colour Consortium recommendations regarding the importance of ambient light consistency when using digital pathology for primary diagnosis. Further development of the QA tool will be conducted.

9:45am – 10:20am

A Machine-Learning Model for Personalized Trial Data Exploration

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Content
Benefits and risks for individual patients cannot be easily extrapolated from aggregated clinical trial data. We construct and validate a tool that uses artificial intelligence to predict the individualized risks and benefits of changing blood-pressure medication from a standard to an intensive regimen using the SPRINT trial data. We then use the model to identify two clinically relevant populations with drastically different risk-benefit profiles. Finally, we make the tool available as a mobile/web application: http://mpacula.com/sc_app.

Technology
We used machine learning to derive a weighted k-nearest neighbor model which can identify similar patients and use those patients to estimate the hazard ratios for 'benefits' and 'risks' as originally defined in the SPRINT trial.

Design
The data matrix of the SPRINT trial contains >1,000,000 data points distributed over >28 variables. We used a randomly selected 80% subset (N=7488) of the SPRINT data as a training set, then validated the predictions on a held-out set of 20% (N=1873) patients.

Results
The model demonstrated a statistically significant separation on the held-out set. Briefly, within the standard treatment, the high-risk group had a 2.04x higher event rates for the primary events ($p<0.01$) and 1.47x higher rates of adverse events ($p<0.001$); in the intensive group the numbers were comparable with 2.05x ($p<0.001$) and 1.41x ($p<0.001$), respectively. These unbiased validation data confirm that our model can accurately predict unseen data. We further used the model to discover that the risk ratio for adverse events from intensive therapy differs in women with/or without hypercholesterolemia whereas male patients with a history of clinical cardiovascular disease and risk factors have the greatest benefit with relatively few adverse events.

See Figure 1 next page

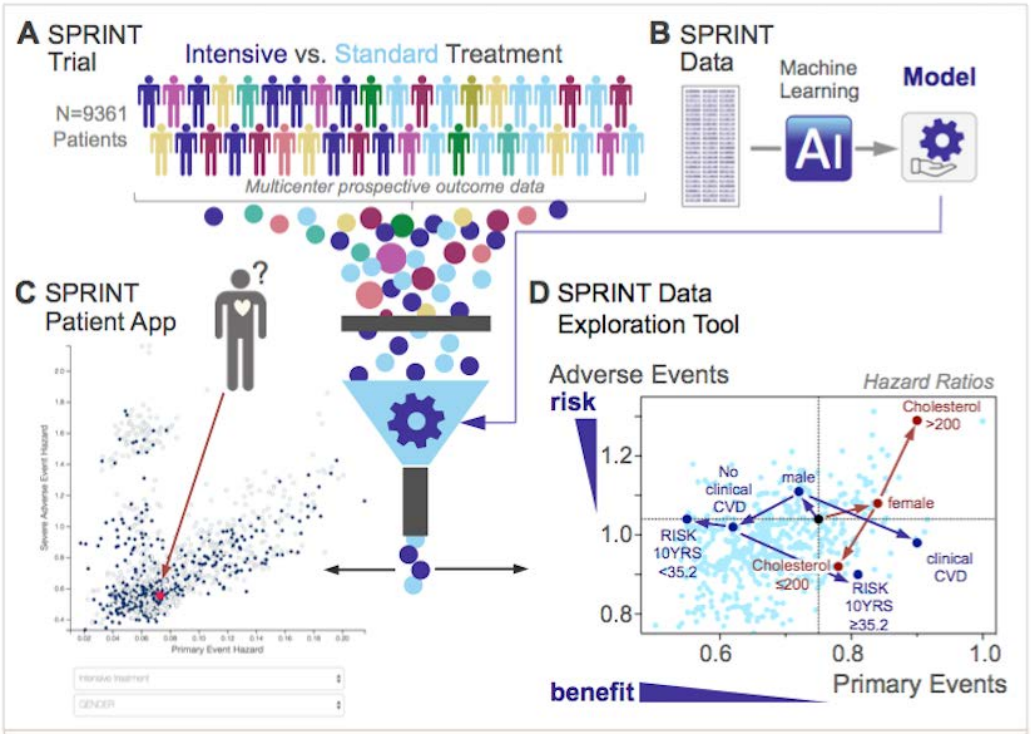

Figure 1: The SPRINT trial (A) compared two regiments (standard vs. intensive) for lowering blood pressure. Using the published trial data (B) we developed and validated a patient tool (C) and a data exploration app (D) that calculates risk and benefits for individual patients.

Conclusion

In conclusion we report an artificial intelligence approach to employ shared trial data for personalized data exploration. We envision that similar tools will become a powerful approach to explore shared trial data to improve patient care.

11:20am – 12:00pm

Bringing the Blood Bank to the Bedside: Multi-Institutional Evaluation of Gaps in Positive Patient ID Systems for Blood Administration

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Content
Positive patient identification for blood administration (PPID-BA) systems have improved safety by preventing wrong blood products from being transfused. However, poor technology and/or implementation strategy may fail to improve or worsen safety and can jeopardize compliance with regulations. Guidance is needed for information technology, transfusion, and nursing staff to improve utilization and for software developers to reduce existing functionality gaps.

Technology
Various PPID-BA systems, blood bank information systems and electronic health records served as sources of the guidance. All PPID-BA systems were 510(k) approved by the FDA.

Design
A multi-institutional group of pathology informaticists convened to create guidance on selecting and implementing PPID-BA systems. Recommendations were categorized into groups and sequenced according to typical workflow. Only those elements which were determined to be system-agnostic by consensus were selected for inclusion.

Results
The categories of guidance were as follows: Design, Implementation, Validation and Training. Design was broken into subcategories of why, who, what, where, when and how in which the "how" was workflow design. Workflow design was the largest subcategory of design with the following phases: pre-transfusion specimen collection, patient armbands, blood product barcode usage, PPID-BA software algorithm, transfusion documentation, post-transfusion auditing and downtime preparation.

Conclusions
PPID-BA systems are considered by some to be primarily a nursing tool, but transfusion services feed these systems with data and have the most responsibility for ensuring regulatory compliance. Each PPID-BA system should have a set of standard basic functions including pre-built quality assurance reports, audits and safety monitors. The group unanimously felt that both the ISBT 128 donor identification number and ISBT 128 product code should be required to match between the scanned barcodes on the blood product label and the data present in the PPID-BA system that is acquired from the blood bank information system. This is critical to patient safety because a single blood product may be split into modified (e.g., washed, irradiated) and non-modified components. Third party safety reports for PPID-BA systems are warranted to help institutions pick the right software. Future work may include surveying users of PPID-BA systems to determine what other guidance may be necessary.