Prognostic model

- Development of a Radiomic-clinical Nomogram for Prediction of Survival in Patients with Nasal Extranodal Natural Killer/T-cell Lymphoma
- Predicting podoplanin expression and prognostic significance in high-grade glioma based on TCGA TCIA radiomics
- Ectopic expression of GDF15 in cancer-associated fibroblasts enhances melanoma immunosuppression via the GFRAL/RET cascade
- Machine learning-driven SLC prognostic signature for glioma: predicting survival and immunotherapy response
- Interrogation of macrophage-related prognostic signatures reveals a potential immune-mediated therapy strategy by histone deacetylase inhibition in glioma
- MicroRNA- 103 as a novel potential biomarker of poor prognosis and durg resistance in solid tumours
- Clinical outcomes following stereotactic radiosurgery for brain metastases from sarcoma primaries: An international multicenter analysis
- MitCOM-based prognostic model identifies GLUD1 as a key suppressor of glioblastoma growth and invasion through regulation of mitochondrial structure and metabolism

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A **predictive model** and a **prognostic model** are related but not the same. Their distinctions lie in their purpose and application:

1. **Predictive Model**:

1. Aims to **predict** the **outcome of an intervention** or treatment.
2. Typically used to estimate the response to a therapy or procedure.
3. Example: A model predicting how well a patient will respond to chemotherapy based on genetic markers.

2. **Prognostic Model**:

1. Aims to **predict the natural course** of a disease or a patient's outcome **independent of treatment**.
2. Used to estimate disease progression or survival rates.
3. Example: A model estimating the survival probability of a glioblastoma patient based on age, tumor grade, and other clinical factors.

Key Difference: - A **prognostic model** gives insight into what will likely happen **without intervention**. - A **predictive model** helps guide treatment decisions by estimating the **effect of a specific intervention**.

Many clinical models integrate both aspects, but they serve different decision-making purposes in medicine.

Medical Prognostic Models: These predict the future health outcomes of patients based on various factors like medical history, clinical parameters, and demographic information. For example:

Cancer Prognostic Models: These might predict survival rates or recurrence based on factors like tumor type, stage, and patient demographics. Cardiovascular Risk Models: These estimate the likelihood of heart disease or stroke based on risk factors such as blood pressure, cholesterol levels, and lifestyle.

Clinical outcome prediction

A prognostic model is a formal combination of multiple predictors from which risks of a specific endpoint can be calculated for individual patients. Other names for a prognostic model include the prognostic (or prediction) index or rule, risk (or clinical) prediction model, and predictive model.

Prognostic models are used in medicine for investigating patient outcome in relation to patient and disease characteristics. Such models do not always work well in practice, so it is widely recommended that they need to be validated. The idea of validating a prognostic model is generally taken to mean establishing that it works satisfactorily for patients other than those from whose data it was derived.

In a paper Altman and Royston, examine what is meant by validation and review why it is necessary. They consider how to validate a model and suggest that it is desirable to consider two rather different aspects - statistical and clinical validity - and examine some general approaches to validation. They illustrate the issues using several case studies [1)].

Example

IMPACT prognostic calculator.

There are two main prognostic models: International Mission for Prognosis and Clinical Trials in Traumatic Brain Injury (IMPACT) prognosis calculator and the Corticosteroid Randomization after Significant Head Injury (CRASH) prognosis calculator. The prognosis model has three or four levels: (1) model A included age, motor GCS, and pupil reactivity; (2) model B included predictors from model A with CT characteristics; and (3) model C included predictors from model B with laboratory parameters. In consideration of the fact that interventions after admission, such as ICP management also have prognostic value for outcome predictions and may improve the models' performance, Yuan F et al developed another prediction model (model D) which includes ICP. With the development of molecular biology, a handful of brain injury biomarkers were reported that may improve the predictive power of prognostic models, including neuron-specific enolase (NSE), glial fibrillary acid protein (GFAP), S-100β protein, tumour necrosis factor-alpha (TNF-α), interleukin-6 (IL-6), myelin basic protein (MBP), cleaved tau protein (C-tau), spectrin breakdown products (SBDPs), and ubiquitin C-terminal hydrolase-L1 (UCH-L1), and sex hormones. A total of 40 manuscripts reporting 11 biomarkers were identified in the literature. Many substances have been implicated as potential biomarkers for TBI; however, no single biomarker has shown the necessary sensitivity and specificity for predicting outcome. The limited number of publications in this field underscores the need for further investigation. Through fluid biomarker analysis, the advent of multi-analyte profiling technology has enabled substantial advances in the diagnosis and treatment of a variety of conditions. Application of this technology to create a

bio-signature for TBI using multiple biomarkers in combination will hopefully facilitate much-needed advances. We believe that further investigations about brain injury biomarkers may improve the predictive power of the contemporary outcome calculators and prognostic models, and eventually improve the care of patients with TBI [2]. Predictive modelling uses statistics to predict outcomes.

Most often the event one wants to predict is in the future, but predictive modelling can be applied to any type of unknown event, regardless of when it occurred. For example, predictive models are often used to detect crimes and identify suspects, after the crime has taken place.

In many cases the model is chosen on the basis of detection theory to try to guess the probability of an outcome given a set amount of input data, for example given an email determining how likely that it is spam.

Models can use one or more classifiers in trying to determine the probability of a set of data belonging to another set, say spam or 'ham'.

Depending on definitional boundaries, predictive modelling is synonymous with, or largely overlapping with, the field of machine learning, as it is more commonly referred to in academic or research and development contexts. When deployed commercially, predictive modelling is often referred to as predictive analytics.

Clinical outcome prediction, as strong implications for health service delivery of clinical treatment processes (CTPs), is important for both patients and healthcare providers. Prior studies typically use a priori knowledge, such as demographics or patient physical factors, to estimate clinical outcomes at early stages of CTPs (e.g., admission). They lack the ability to deal with temporal evolution of CTPs. In addition, most of the existing studies employ data mining or machine learning methods to generate a prediction model for a specific type of clinical outcome, however, a mathematical model that predicts multiple clinical outcomes simultaneously, has not yet been established. In this study, a hybrid approach is proposed to provide a continuous predictive monitoring service on multiple clinical outcomes. More specifically, a probabilistic topic model is applied to discover underlying treatment patterns of CTPs from electronic medical records. Then, the learned treatment patterns, as low-dimensional features of CTPs, are exploited for clinical outcome prediction across various stages of CTPs based on multi-label classification. The proposal is evaluated to predict three typical classes of clinical outcomes, i.e., length of stay, readmission time, and the type of discharge, using 3492 pieces of patients' medical records of the unstable angina CTP, extracted from a Chinese hospital. The stable model was characterized by 84.9% accuracy and 6.4% hamming-loss with 3 latent treatment patterns discovered from data, which outperforms the benchmark multi-label classification algorithms for clinical outcome prediction. The study indicates the proposed approach can potentially improve the quality of clinical outcome prediction, and assist physicians to understand the patient conditions, treatment inventions, and clinical outcomes in an integrated view [3].

Accurate prediction of outcomes among patients in intensive care units (ICUs) is important for clinical research and monitoring care quality. Most existing prediction models do not take full advantage of the electronic health record, using only the single worst value of laboratory tests and vital signs and largely ignoring information present in free-text notes. Whether capturing more of the available data and applying machine learning and natural language processing (NLP) can improve and automate the prediction of outcomes among patients in the ICU remains unknown.

To evaluate the change in power for a mortality prediction model among patients in the ICU achieved by incorporating measures of clinical trajectory together with NLP of clinical text and to assess the generalizability of this approach.

This retrospective cohort study included 101 196 patients with a first-time admission to the ICU and a length of stay of at least 4 hours. Twenty ICUs at 2 academic medical centers (University of California, San Francisco [UCSF], and Beth Israel Deaconess Medical Center [BIDMC], Boston, Massachusetts) and 1 community hospital (Mills-Peninsula Medical Center [MPMC], Burlingame, California) contributed data from January 1, 2001, through June 1, 2017. Data were analyzed from July 1, 2017, through August 1, 2018. : In-Hospital mortality and model discrimination as assessed by the area under the receiver operating characteristic curve (AUC) and model calibration as assessed by the modified Hosmer-Lemeshow statistic.

Among 101 196 patients included in the analysis, 51.3% (n = 51 899) were male, with a mean (SD) age of 61.3 (17.1) years; their in-Hospital mortality rate was 10.4% (n = 10 505). A baseline model using only the highest and lowest observed values for each laboratory test result or vital sign achieved a cross-validated AUC of 0.831 (95% CI, 0.830-0.832). In contrast, that model augmented with measures of clinical trajectory achieved an AUC of 0.899 (95% CI, 0.896-0.902; P < .001 for AUC difference). Further augmenting this model with NLP-derived terms associated with mortality further increased the AUC to 0.922 (95% CI, 0.916-0.924; P < .001). These NLP-derived terms were associated with improved model performance even when applied across sites (AUC difference for UCSF: 0.077 to 0.021; AUC difference for MPMC: 0.071 to 0.051; AUC difference for BIDMC: 0.035 to 0.043; P < .001) when augmenting with NLP at each site.

Intensive care unit mortality prediction models incorporating measures of clinical trajectory and NLP-derived terms yielded excellent predictive performance and generalized well in this sample of hospitals. The role of these automated algorithms, particularly those using unstructured data from notes and other sources, in clinical research and quality improvement seems to merit additional investigation [4].

Clinical prediction and decision rules use evidence based medicine to assist clinicians in diagnosing and treating illness. Although widespread in modern medical practice, there are relatively few clinical rules for neurosurgical conditions. Stein et al. reviews the background of how clinical prediction and decision rules are derived, validated, evaluated, and used in practice. It also summarizes a list of clinical rules published for neurosurgical illnesses and analyzes each rule for how it was derived and whether it was validated and/or evaluated compared with similar rules. It reports on whether the implementation of each rule was studied and grades the overall quality of each report [5].

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clinical outcomes, i.e., length of stay, readmission time, and the type of discharge, using 3492 pieces of patients' medical records of the unstable angina CTP, extracted from a Chinese hospital. The stable model was characterized by 84.9% accuracy and 6.4% hamming-loss with 3 latent treatment patterns discovered from data, which outperforms the benchmark multi-label classification algorithms for clinical outcome prediction. Our study indicates the proposed approach can potentially improve the quality of clinical outcome prediction, and assist physicians to understand the patient conditions, treatment inventions, and clinical outcomes in an integrated view.

Current outcomes prediction tools are largely based on and limited by regression methods.

Outcome prediction studies have become the avante garde in many areas of Healthcare research

Especially in critical care and trauma. However acceptable models for outcome prediction have been difficult to develop [6].

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