to prevention colitis in adulthood. **Methods.** p40-containing hydrogels was administered to BalB/c pups at 0.5, 1.0, and 1.5 mg/day for the first, second, and third postnatal week, respectively. Hydrogels without p40 were used as control. 8-week old mice were treated with TNBS in 50% ethanol intrarectally for inducing colitis or 50% ethanol as control. Mice were also co-treated with a neutralizing anti-TGFβ antibody or IgG isotype control antibody via intraperitoneal cavity injection once in every other day starting one day before TNBS treatment. Mice were euthanized 4 days after TNBS treatment. Inflammation scores and proinflammatory cytokine levels in the colonic tissues were assessed. TGFb gene expression in colonic mucosa was examined by RT-PCR, and differentiation of Tregs in intestinal laminar propria by flow cytometry analysis of $Foxp3^{+}CD25^{+}$ $CD4^{+}$ T cell populations. **Results.** As compared to TNBS-induced colitis in mice without neonatal p40 treatment (inflammation score: 4.0±0.3), colitis in mice with neonatal p40 supplementation was significantly decreased (score: 1.9±0.5, $p<0.05$). This effect was abolished by anti-TGFβ antibody, but not control IgG treatment. TNBS up-regulated expression levels of TNF (2.5±0.3 fold, $p<0.05$) and IFN-g (2.7±0.4 fold, $p<0.05$) in the colonic mucosa in mice without p40 treatment, and in mice with co-treatment of p40 and anti-TGFβ antibody (TNF: 2.5±0.3 fold, $p<0.05$, IFN: 2.8±0.3 fold, $p<0.05$), but not in mice with neonatal p40 supplementation and with p40 and IgG co-treatment. Adult mice with neonatal p40 treatment exhibited increase in TGFb gene expression in colonic mucosa (1.9±0.3 fold, $p<0.05$) and upregulated induction of Tregs (2.2 fold, $p<0.05$). The increase in Tregs was blocked by treatment with anti-TGFβ antibody, but not IgG control. **Conclusions**. These findings reveal a novel mechanism underlying long-lasting effects of the symbiotic relationship between the gut microbiome and the host in the early stage on maintaining intestinal health in adulthood, and support neonatal p40 supplementation as a preventative strategy for individuals at high risk of developing IBD.

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PREDICTING GASTROINTESTINAL (GI) HEMORRHAGE USING A MACHINE LEARNING APPROACH: RISK FACTORS AND PREDICTIVE ANALYSIS IN CLINICAL STUDIES

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Background: Currently, it is difficult to estimate and predict the risk of adverse events for clinical trial studies. GI hemorrhage is one of the serious adverse events which could harm patients in clinical trial studies. ***Aim:*** The aim of this study is to build machine-learning models to predict and analyze the risks of GI hemorrhage using large clinical studies data. Multiple factors could contribute to GI bleeding, such as patient demographics, targeted medical conditions of clinical trials, trial interventions, and other related adverse events. ***Methods:*** We extracted data from 28,340 clinical trials that reported the outcomes. The risks of different types of GI events were analyzed. Factors contributing to the GI events were extracted through association analysis. Leveraging the extracted clinical factors, we built a machine learning-based algorithm (i.e., Random Forest) to predict the occurrence of the GI hemorrhage events in clinical trials. ***Results***: Our method allowed us to extract GI hemorrhage-associated risk factors. For example, GI hemorrhage events are associated with trial interventions (e.g., Sunitinib, Apixaban). The events were also associated with complications from other severe conditions (e.g., severe diarrhea, pyrexia, deep vein thrombosis, sepsis). The developed machine learning model was able to predict whether the GI hemorrhage would likely to occur in the testing trials, with an 86.5% accuracy. This study provides clinical investigators with an evidence-based method to assess the risk of GI hemorrhage and has the potential to improve the safety of clinical studies. Figure 1 shows the ROC curves of different types of GI hemorrhage reported in the 28,340 trials. ***Conclusion***: With most ROC area values > 0.85, the results show strong predictive power toward GI hemorrhage prediction using the big data and developed machine learning model. This study also indicates the potential use of data-driven evidence-based risk estimation for clinical trials. ***Limitation:*** The adverse event terminologies across different trials are not normalized at this point. In the future, we will normalize the adverse event terms, such as synonyms (e.g., rectal hemorrhage & hematochezia), to enhance the study.

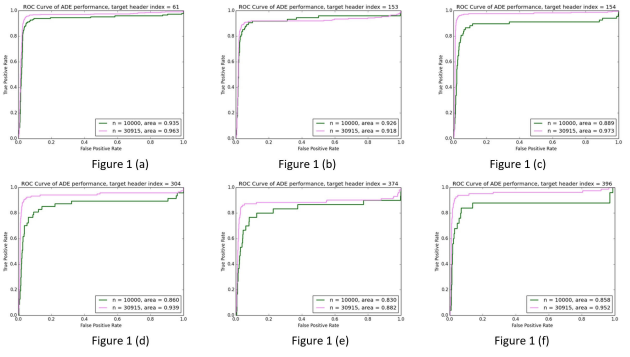

Figure 1: The ROC curve to assess the predicting accuracy in six related events: (a) gastrointestinal hemorrhage; (b) rectal hemorrhage; (c) upper gastrointestinal-hemorrhage; (d) lower gastrointestinal hemorrhage; (e) hematochezia; (f) gastric hemorrhage

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BUILDING AN AI SYSTEM ON HIGH-RESOLUTION MANOMETRY USING THIRTY-TWO THOUSAND LABELED SWALLOW DATA

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Introduction: High-resolution Esophageal Manometry (HRM) is the gold standard in the diagnosis of esophageal motility disorders and its interpretation and classification is developed based on the Chicago Classification (CC). However, due to reliance on only several predefined outcomes, the current Chicago Classification is too rigid and limited leading to misclassification. Moreover, outcome calculation that involves manual landmark identification often leads to inter-rater disagreement. We hypothesize that an AI-based system built with a clearly labeled and large HRM dataset could learn relevant features/patterns that separate phenotypes with a high accuracy, and automate the interpretation of HRM data. Hence, we aim to first develop such a large dataset and then build a multi-stage AI system for HRM data. **Methods:** Using the manometries obtained at Northwestern Memorial Hospital from Feb 2018 to July 2019, we selected HRM studies from patients with no history of esophageal surgery, and exported pressure and impedance data per swallow using customized data tools. In the following data-clean step, we further processed the exported data and restricted our dataset to contain HRM studies that satisfied the following criteria: 1) clearly labeled with the CC type; 2) having 10 supine and 5 upright swallows, all of which have labels of both swallow type and pressurization type. The swallow types included Normal, Weak, Failed, Fragmented, Premature and Hypercontraction, and the pressurization types included Normal (N), Compartmental pressurization (CP) and Panesophageal pressurization (PEP). With the raw pressure data and labels, we developed a swallow-level AI system as the first stage to classify swallow type (6 classes) and swallow pressurization (3 classes). We then designed a study-level manometry AI system that builds upon the learned swallow-level information. The models, including a novel data generator to pre-process/augment data, were implemented using python and tuned to run efficiently on both multiple-core workstation and Northwestern Cluster (Northwestern Quest). **Results**: 2,161 HRM studies, consisting of 32,415 labeled swallows, were retrieved and cleaned after the data-export step and the data-clean step. A 70-15-15 split was used to get statistically consistent train-validation-test dataset. Through parameter tuning, we arrived at two CNN classifiers, one for swallow pressurization with test accuracy as 0.90, the other for swallow type with test accuracy as 0.88. **Conclusions:** A clean and large dataset of HRM is essential in developing AI systems focused on diagnosis. This dataset allowed for the development of a swallow-level AI system that achieved high accuracy in understanding swallow type and pressurization. Further refinements will be achieved through additional data and training.

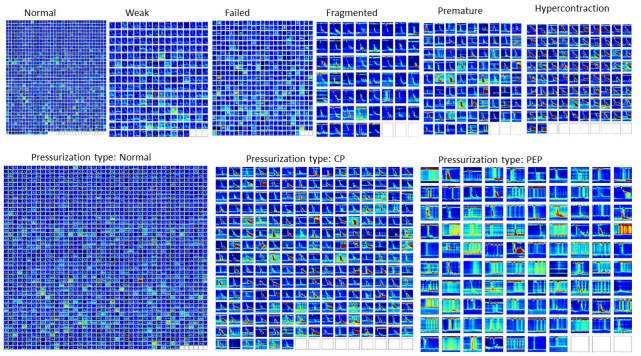

Figure 1: Samples of exported pressure data in each category of swallow type (Upper) and swallow pressurization (Lower) highlighting the uneven data distribution and visual patterns (CP: compartmentalized pressurization, PEP: Panesophageal pressurization)