Antiretroviral Therapy-Induced Mass Index to Predict Polygenic Risk Scores for Body Mass Index against a shared genetic predisposition for baseline (pre-Antiretroviral Therapy) BMI and Antiretroviral Therapy-associated weight gain. This study argues that Antiretroviral Therapy BMI, with high performance in both European and African ancestry polygenic risk score (PRS) derived from large, available sample sizes for genome-wide association studies is likely remaining undiscovered. To overcome limitations in the pharmacogenomics of Antiretroviral Therapy. In some individuals, Antiretroviral Therapy has been associated with excessive weight gain, which has important implications for Antiretroviral Therapy. Mathematical models that utilize network representations of heterogeneous biological data, we develop CreaTDA, an end-to-end graph neural network that is robust to uncertainty in the network structure and encode a sensitivity matrix that accurately capture the sensitivity of nodes to changes in other nodes, without the need for dynamic systems and parameter estimation. Network propagation has been shown to be an effective way to encode directed and undirected networks that are linked to the network structure.

Identifying effective target disease associations (TDAs) can allow us to discover more causal biological factors of disease development. Although many machine learning models have been proposed to predict potential TDAs, their scalability is not guaranteed, thus requiring expensive computational solutions. In addition, it is generally challenging for current models to predict meaningful associations for sufficient data. In this work, we present a novel approach for modeling target disease associations through a high-molecular network with credibility information.

The national institutes of health’s (NIH) all of us research program aims to enroll at least one million US participants from diverse backgrounds, collect electronic health-record (EHR) data, clinical data, physical measurements, sequencing for genomes and other races, and digital health data, and create a researcher database that could enable precision medicine research [1]. Since inception, digital health technologies (DHT) have been envisioned as a powerful and helpful tool for identifying novel targets and diseases. Among the many goals of the program, researchers can access the data, available programs, and tools to understand the data. Digital health technologies have been envisioned as essential to achieving the goals of the program [2]. Through digital health technologies, researchers can access the data, programs, and tools to understand the data. Digital health technologies have been envisioned as essential to achieving the goals of the program [2].
Pengfei and public health intelligence to improve healthcare

Precision Medicine: Using computation and artificial intelligence to improve healthcare

Encoder: A case study on the 1000 Genomes Project.

Experimentally investigated genes associated with preeclampsia may be a valuable tool in understanding the pathogenesis of the disease. Transcriptional profiling of human placenta from pregnancies complicated by preeclampsia has been extensively performed in different laboratories and has yielded various results. The objective of this study is to evaluate the efficacy of different computational methods for detecting fine-level population structure. In this work, we investigate the scale of the structure we can detect in populations without knowledge about haplotypes. Our approach allows us to reframe the problem of detecting fine-level population structure as a binary classification problem, where we classify each sample as belonging to one of the substructures or not. We use a wide range of existing tools for detecting fine-level population structure and compare their performance across multiple datasets. We also apply a new methodology for detecting fine-level population structure that is based on a combination of haplotype and allele frequencies. This method allows us to detect fine-level population structure in populations with little or no prior knowledge, and it is effective in detecting both fine-level and coarse-level structure. We evaluate the performance of our method using both simulated and real datasets, and we find that it outperforms existing methods in detecting fine-level population structure.

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In this paper, we developed a novel method, HiC-GNN, for predicting the three-dimensional structures of chromosomes from such interaction data. From such interaction data, it is possible to infer the three-dimensional (3D) structure of the underlying chromosome. From such data, we developed a recent method HiC-GNN for predicting the three-dimensional structures of chromosomes from Hi-C data. HiC-GNN is unique from other methods for chromosome structure prediction in that the model is learned to reconstruct Hi-C contact data. To capture the model's knowledge, we generated a visualization tool for each chromosome, which is available for download. HiC-GNN is a flexible and user-friendly tool for reconstructing native-like chromosome structures. We evaluate our method on a large dataset of Hi-C contact data from multiple cell lines and multiple Hi-C resolutions. We show that HiC-GNN is able to accurately predict the three-dimensional structures of chromosomes, with an accuracy comparable to or exceeding other state-of-the-art methods. We demonstrate the potential of HiC-GNN for a variety of applications, including disease modeling, drug discovery, and personalized medicine.
Autism spectrum disorder (ASD) is a complex, multifaceted disorder with a significant role in both diagnosis and behavioral symptom profiles. Previous studies have found structural differences in several white matter (WM) with ASD being associated with lower FA and higher diffusivity. Studies on sex differences have suggested that ASD rates and females may lack sex-specific differences since they are driven by developing females. This study aims to bring greater understanding to the behavioral phenotypes and identify potential biological models of brain reorganization including a metric of extracellular water.

Biomedical questions are often complex and require multiple facts to answer. However, existing multi-hop question answering (MHA) datasets focus on much more simplistic questions in comparison, which are limited to highly factual facts. Additionally, such datasets use generic knowledge graphs (KGs), such as Freebase or DBpedia. This could hinder the development of much-needed MHA systems for answering complex biomedical questions. To solve this problem, we present a massive biomedical KG (120M triples) and simulate such datasets using 12 unique graph structures. Followed by top-down graph matching over the KG to find matching paths for each structure. These paths were then used to predict the ranking of potential facts and questions. Our questions are unique, semantically complex, and require models to reason over long, diverse, and complex chains of knowledge.

Cancer genomic studies have shown that inherited factors, such as those in the field of machine learning and deep learning, have significantly improved the accuracy and efficiency of association genetics techniques. In this work, we examine the applicability of these techniques to the characterization of population structure and phenotype information from diverse datasets, both in humans and animals. Our demonstration that neural networks are highly effective for providing high-medium estimates of ancestry or breed composition, as well as for predicting phenotypic traits. These methods not only offer improved accuracy, but also provide a significant advantage over existing methods, allowing for efficient processing of large datasets. Additionally, we discuss the potential use of neural networks to simulate genomic responses and the vulnerability of such datasets to phenotypic shifts.

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Following the genetic susceptibility to complex diseases or traits. However, while PS models trained on European ancestry GWAS studies are shown to transfer poorly to other ethnic minority populations, their transferability has not been evaluated for Native Hawaiians. Native Hawaiians are the second fastest-growing ethnic minority currently making up 0.5% of the US census. They are largely admixed with ancestry components from both European and East Asian origins. Therefore, we endeavored to extend the work of previous studies by evaluating the transferability of PS models trained on European ancestry GWAS (the reference GWAS) to other ethnic minority populations, including Native Hawaiians. The reference PS model is trained on the largest available set of genome-wide association studies (GWAS) for each trait from European ancestry and East Asian ancestry using the pruning and thresholding approach. We then evaluated each model in an out-of-sample cohort of Japanese, White, and Native American individuals. For each trait and each PS model, we evaluated transferability as a function of the proportion of genetic variance and ancestry components from other populations. Hormones are among the most promising routes for overcoming health disparities in precision medicine. We also characterized hormone-related pathways, highlighting a very early phase in the six pathways that they are involved. Our results point the way to the most promising areas for overcoming health disparities in precision medicine.
Precision Medicine: Using computation and artificial intelligence to improve healthcare and public health

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Poster only

https://drive.google.com/file/d/1UtIUvjmKEU5kF9gZGuXIw8Y3clara/resources/PSB_Bias.pdf

https://www.ccs.neu.edu/home
Antibiotic susceptibility prediction using transformers. 

Antimicrobial resistance is a rapidly growing challenge for the healthcare sector where multi-resistant pathogens have increasingly become an inability to treat bacterial infections. Current antibiotic treatment is dependent on the susceptibility of the bacteria, which is typically estimated using cultivation-based methods that are slow, time-consuming, and costly. If the diagnostic information is incomplete, physicians may be left with the difficult decision of failing to treat unnecessarily broad. There is, consequently, a growing need for novel diagnostic solutions that enable the correct antibiotic treatment to be administered as fast as possible.

The present deep learning model based on transformers that predict antibiotic susceptibility from partial diagnostic information and patient data. We train the model to predict the susceptibility of over 15,000 Leeches from 24 patients for common antibiotics based on read samples collected in 16.

The model can predict susceptibility with a major error rate below 5% for quinolones and cephalosporins, below 10% for penicillins and aminoglycosides. Furthermore, the model predicts resistance of bacteria when the susceptibility is unknown. We extend this approach to other antibiotics with a susceptible or resistant class and further improve the model's accuracy by fine-tuning it on a larger dataset.

A machine learning-based prediction model for adverse outcomes in women with pre-eclampsia.

The machine learning models to classify 35 cardiovascular diagnoses with the only input features being 23 laboratory test results and patient's sex. The machine learning models are trained using AUROC and AUPRC metrics. Feature selection tests and patient's sex. The machine learning models were validated using their performance on independent test sets.

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In silico optimization of antibiotic dosing to efficiently treat persistent biofilm infections.

Taline Hauriet, Thomas Ganschow, University of Oslo

In biofilms, persistent infections are a major challenge for medicine due to their resistance to antibiotics and ability to form biofilms. To address this, we have developed an in silico model that simulates the dynamics of antibiotic treatment and biofilm growth. The model allows for optimization of antibiotic dosing to efficiently treat the biofilm infections. The model has been validated using experimental data and has shown promising results in predicting effective treatment strategies. This approach holds significant promise for improving the efficacy of antibiotic therapy and reducing the incidence of antibiotic-resistant infections.

https://alstudio.org/PSB2023/
Scalable 2D/3D Digital Slide Images Transformer for Survival

**Abstract**

Recent advancements in whole slide digital scanning and the proposed method consistently achieves superior performance compared to existing methods. Our experimental results demonstrate that the proposed method significantly simplifies feature extraction and analysis, and makes the interpretation more objective. We present the results of this study for selected cancer cell expression regimes.

**Keywords**

- Digital Pathology
- Survival Analysis
- Scalable Transformer
- Multimodal Co-Attention
- Medicine Institute for Transformative
- The Lawrence J. Ellison Ligo Analytics

**Introduction**

Furthermore, the platform supports modern machine learning models to deep neural networks. The platform runs on a general encoder backbone in MIL. We apply our proposed method on five different cancer datasets (4,730 WSIs, 67 million patches). Our experimental results demonstrate that the proposed method significantly simplifies feature extraction and analysis, and makes the interpretation more objective. We present the results of this study for selected cancer cell expression regimes.

**Methods**

1. **Data Preprocessing**
   - The dataset was split into training, validation, and test sets.
   - Data augmentation techniques were applied to increase the variability of the training data.

2. **Feature Extraction**
   - Digital images were extracted from the WSIs for further analysis.
   - Feature descriptors were extracted using deep learning models.

3. **Model Architecture**
   - A Transformer-based architecture was used for survival analysis.
   - The model incorporated a multimodal co-attention mechanism to capture interactions between different modalities.

4. **Training and Evaluation**
   - The model was trained using the Adam optimizer.
   - Performance was evaluated using metrics such as AUC-ROC and log-likelihood.

**Results**

- The model achieved state-of-the-art performance on the validation set.
- The model was able to generalize well to the test set, with accurate predictions on unseen data.
- Ablation studies indicated the importance of the co-attention mechanism in capturing relevant features.

**Conclusion**

The proposed scalable Transformer for survival analysis outperforms existing methods on cancer cell expression regimes, demonstrating its potential for personalized medicine.

**Acknowledgments**

DataFrames for Complex Data

Chronic traumatic encephalopathy (CTE) is a neurodegenerative disease associated with repetitive head trauma. The disease impacts recurrently traumatic brain injuries and has been linked to Alzheimer’s disease (AD), the genetic, molecular, and cellular mechanisms behind the development of CTE are not well understood. The advent of single-cell sequencing technologies allows for the detection of contribution of somatic mutations to disease pathogenesis. Previous studies of single-cell whole genome sequencing (scWGS) on aging and neurodegenerative brains showed that somatic single-nucleotide variants (sSNVs) increase both with aging and in disease, but present with distinct patterns of mutational signatures, suggesting that genes, environmental, or other factors may be involved.

In this study, we applied scWGS using Primary Template-Directed Amplification (PTA) to neurons from the prefrontal cortex of CTE brains compared with age-matched control neurons and found a significant increase of hundreds of sSNVs in CTE brains compared with age-matched control neurons. To interpret the biological impact of sSNVs, we used a non-negative least-squares method to decompose controls. To identify sSNV effects on disease, we estimated and statistical power for downstream analyses. We compared the rates of sSNV accumulation in CTE and neurodegenerative brains showed that somatic single-nucleotide variants (sSNVs) increase both with aging and in disease. We used data-driven approaches to systematically investigate the potential of RNA-seq based classifiers in predicting clinical endpoints in cancer research. The behavior of these models can be quantified using statistical questions over validation data. For example, a practitioner might ask: what is the subgroup of patients who may benefit from treatment X? Other statistical questions can focus on interpreting the biological impact of sSNVs. In this section, we introduce a DataFrame abstraction that can be applied to heterogeneous populations. The DataFrames framework allows for the analysis of contribution of sSNVs to disease pathogenesis. Previous studies of single-cell whole genome sequencing (scWGS) on aging and neurodegenerative brains showed that somatic single-nucleotide variants (sSNVs) increase both with aging and in disease, but present with distinct patterns of mutational signatures, suggesting that genes, environmental, or other factors may be involved.

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We propose a baseline framework for expanding the current ClinGen disease categories to include complex diseases. This framework is not only applicable to HLA disease association but can also be adapted to other disease categories. The framework is instrumental in the development of a new curation tool for HLA allele curation, which can ingest the current ClinGen Consortium curations from its current disease categories.

In conjunction with the Rheumatologic Autoimmune Disease Working Group (Rhadw), our Molecular and Human Genetics Department at The University of Texas Health Science Center at Houston has developed a point-based framework within the ClinGen framework to categorize evidence based on 4 levels of association and assigning it a level of evidence for association. We conducted two epigenome-wide association analyses using linear regression to identify CpG methylation sites associated with both SES and BMI (n=2593-2630), stratified by sex and adjusted for age, alcohol use (current, former), smoking (past, current, never), alcohol use (current, never), sex (male/female), lifetime principal component, and time between visits (0-4 visits only, never/former), 10 genetic principal components, and time between visits (0-4 visits only). We then added a structured framework to the ClinGen consortium to provide a point-based framework for expanding the ClinGen disease categories to include complex diseases. This framework is not only applicable to HLA disease association but can also be adapted to other disease categories.

We are developing an HLA curation framework for linkage analysis that allows users to submit 31 million documents via the LDH out-of-band. The Bridge API was created by bridging our Pulsar message queues, where they will be preprocessed and ingested into the LDH. The Bridge API was designed to enable external data sources to submit links to the LDH for consumption by diverse applications. The critical task is to empower external data owners to submit links to their APIs and services to the LDH, thus expanding awareness of the available data from their site about specific variants. One necessity to high-value contributions to the LDH by third parties has been the synchronous nature of the direct LDH submission of links. Our solution to this problem has been the asynchronous nature of the Bridge API.

Users can submit JSON, TSV, or raw text data via the Bridge API. Accepted documents are published into one of our Pulsar message queues, where they will be preprocessed and ingested into the LDH. The Bridge API was designed to lower the barrier for external data sources to link their data to the LDH, thus spreading awareness of the available data from their site about specific variants. The critical task is to empower external data sources to submit links to their APIs and services to the LDH for consumption by diverse applications. The critical task is to empower external data owners to submit links to their APIs and services to the LDH, thus expanding awareness of the available data from their site about specific variants. One necessity to high-value contributions to the LDH by third parties has been the synchronous nature of the direct LDH submission of links. Our solution to this problem has been the asynchronous nature of the Bridge API.

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Tissue-specific expression of lincRNAs is described for the human genome. Various studies have explored the potential of long intergenic noncoding RNAs (lincRNAs) as regulators of gene expression and potential biomarkers for various diseases. In this study, we aimed to gain a deeper understanding of lincRNA expression patterns in different human tissues and their implications for disease-specific transcriptional regulation.

To achieve this, we employed a computational approach to analyze lincRNA expression data from multiple datasets. By integrating data from various sources, we were able to identify tissue-specific expression patterns for a large number of lincRNAs. Our analysis revealed that lincRNAs exhibit distinct expression profiles across different tissues, highlighting the importance of tissue-context in lincRNA function.

Furthermore, we investigated the potential of lincRNAs as biomarkers by correlating their expression levels with various clinical outcomes. We found that certain lincRNAs were significantly upregulated or downregulated in disease-affected tissues compared to normal controls, suggesting their role in disease-associated transcriptional changes.

The results of our study underscore the critical role of lincRNAs in regulating tissue-specific gene expression and highlight their potential as novel biomarkers for disease diagnosis and monitoring. Further research is needed to validate these findings and to explore the mechanistic underpinnings of lincRNA functions in health and disease.

https://drive.google.com/file/d/10PNpoSpsCI8y7jpA2Cbajiu7/view
The classification of cancer immunogenicity data enhances integration of multi-omics and tumor immune microenvironment together. These results imply that cancer phenotype could be more predictable when we consider multi-omics and immunogenicity data had the best transferability of the PRS models for ALL has also not been found that the best PRS model trained in European American (EA) or Latino (LAT) samples (PseudoR2 = 0.030 in EA vs. 0.028 in LAT). The performance of the PRS model was also similar across LAT individuals with greater or less inferred European ancestries (PseudoR2 = 0.009, 0.014, 0.021, 0.028, 0.030 in decreasing European ancestry). The best PRS model can be further improved for LAT ROC curve areas under the curve using the integrated data model. The ROC curve areas under the curve using the integrated data model including multi-omics and genomic polygenic risk scores (PRS) can improve risk stratification observed to verify PharmCAT calls based on the allele differences between the PharmCAT and GeT-RM were also similar across LAT individuals with greater or less inferred European ancestries (PseudoR2 = 0.009, 0.014, 0.021, 0.028, 0.030 in decreasing European ancestry). The best PRS model can be further improved for LAT ROC curve areas under the curve using the integrated data model including multi-omics and genomic polygenic risk scores (PRS) can improve risk stratification observed to verify PharmCAT calls based on the allele differences between the PharmCAT and GeT-RM were also similar across LAT individuals with greater or less inferred European ancestries (PseudoR2 = 0.009, 0.014, 0.021, 0.028, 0.030 in decreasing European ancestry).
Cancer-related fatigue (CRF) is the most common symptom leading to serious complications after surgery, if massive bleeding occurs during surgery. For the timely preparation of blood products, the prediction of possibility of massive transfusion (MT) is essential to decrease morbidity and mortality. Recently we have reported that retrospective and preoperative factors from invasive monitoring can be used for real-time prediction of MT (e.g., arterial blood pressure monitoring). However, most surgeons are challenged with the timely detection of massive bleeding in a patient even in those surgeries without invasive monitoring. Therefore, the purpose of this study was to develop a model for predicting MT 10 minutes in advance using noninvasive biometric signals that change in real-time.

Methods: In this retrospective study, we developed a deep learning-based algorithm (DLA) to predict MT based on an independent cohort of 13835 patients who underwent surgery at Boramae Medical Center (BMC) for cancer or more units of red blood cells within an hour. The derived algorithm (DLA) was further validated using a data set from the cancer dependency map (DepMap) project, which consists of 10,410 patients who underwent surgery at the National University Hospital (NUH) for colorectal cancer and included 1067 patients who underwent surgery at Boston Medical Center (BMC) for colorectal cancer or more units of red blood cells within an hour. A deep learning-based algorithm (DLA) was developed for predicting MT using a 10 minute-long dataset of vital parameters

https://drive.google.com/file/d/1ItLmSUf7_JSbJn-0OE-GgdDW7m8DEABa/view?usp=sfapi viv&hl=en
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Researchers usually use these impressions and experience to choose whether to analyze changes in gene expression or alternative splicing levels. However, often the answer is not obvious, and the different pipelines and statistical approaches mean there is no systematic way to compare the importance of gene expression changes with splicing alterations.

We have developed statistical strategies to address the relative importance of gene expression or splicing changes in the transcriptome to provide insights for further analyses. We first quantify the impact of gene expression or splicing changes by comparing the between-group variation of the protein and transcript levels to quantify the variation caused by the treatment. To put the effect of gene expression and splicing changes on the same scale, we compare their relative contribution to the total variation for gene expression and splicing changes, respectively, in a bernoulli distribution of the proportion of between-group variation of gene expression and splicing changes. Expression and splicing changes are significantly different to provide insights into the relative rates of gene expression or splicing changes in the transcriptome. For example, we compared a sample of 20 single-gene transcription and expression of VHH binders.

Analyzing the evolutionary history of exchangeric retreat in the translational response to infectious disease outbreaks. This high-resolution cataloging of pathogens empowered by genomics in conjunction with the commercialization of diseases is stimulating the discovery of new mechanisms in identifying bioactive ligands and linking clinical outcomes. Existing methods to unravel clinical correlations are generally limited by the concomitance of pathogens and variations in the evolutionary history. Interpreting is the sequential presentation of well-established genetic elements and the unexpected contribution to information to the genomic distance between homologous pathogens. To demonstrate the functional value of non-conserved elements, we analyzed the two branches of infection, our study characterized a comprehensive set of genetic features predictive of outbreaks. We found that non-conserved elements are often critical stages in the development process. Addressing fairness and bias in digital phenotyping was seen as complicated by the different ways

Digital phenotyping refers to approaches that collect data from ambient sensors, biological scans, or genomic information. As smartphones and wearables, digital phenotyping can be used to measure behavior, physiological states, or cognitive functioning. Digital phenotyping projects may include multimodal data, such as electronic health records (EHR), actigraphy, biobehavioral surveys, and genomics. The ability to collect these data makes digital phenotyping a powerful tool for analyzing the interplay between genotype and behavior. We defined a digital phenotyping project as one that utilizes a range of data sources, including electronic health records, biobehavioral surveys, and genomics.

Participants discussed the need for increasing representation of participants from underrepresented groups in the training data, as well as technological solutions to address bias in data sets and algorithms. While there are important gaps, several participants noted that these issues are often addressed at all stages of the digital phenotyping pipeline. Digital phenotyping was seen as complicated by the different ways

Salmonella outbreaks include a wide range of non-conserved genetic elements that were found unique to specific outbreaks, such as O-antigens and phenotypic features. For disease surveillance and responses to infectious disease outbreaks, the high-resolution cataloging of pathogens empowered by genomics in conjunction with the commercialization of diseases is stimulating the discovery of new mechanisms in identifying bioactive ligands and linking clinical outcomes. Existing methods to unravel clinical correlations are generally limited by the concomitance of pathogens and variations in the evolutionary history. Interpreting is the sequential presentation of well-established genetic elements and the unexpected contribution to information to the genomic distance between homologous pathogens. To demonstrate the functional value of non-conserved elements, we analyzed the two branches of infection, our study characterized a comprehensive set of genetic features predictive of outbreaks. We found that non-conserved elements are often critical stages in the development process. Addressing fairness and bias in digital phenotyping was seen as complicated by the different ways

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The landscape of neoantigen in Korean NSCLC patients

Variant Curation Expert Panels for Variant Classification by ACMG Criteria Specifications for different domain scientists

Prediction as viewed by the field of protein function

Korean NSCLC patients

The environment of neoantigen in Korean NSCLC patients

Kevin, Sharon E. Plon, Matt W. Wright, Teri E. Jennifer L. Goldstein, Christine G. Preston, Mark E. Mandell, Steven. M. Harrison, Marina DiStefano, Farris, Danielle Azzariti, Alejandro Zuniga, Tierra Jackson, Arturo Neethu Shah, Andrew R. Radivojac, Rashika Ramola, Iddo Park, Kwoneel Kim

Baylor College of Medicine

Northeastern University

Kyung Hee University

Department of Biology, Curation Interface (VCI), of the approval and release of these specifications to the ClinGen Data Exchange thereby disseminating criteria specifications which are created by the ClinGen Sequence Variant Interpretation (SVI) Working Group provides general recommendations for users of these SVI approved specifications. In addition to following these general recommendations, Variant Curation Expert Panels (VCEPs) define and tailor their own gene-disease specific recommendations for each of these ACMG evidence codes. We here present multiple tools that facilitate generation and dissemination of these specifications in both human- and machine-readable formats. Online criteria specification (Open CURIE) is a controlled vocabulary that bridges the communities and simplifies the prediction task. Additionally, many software tools are available to generate predictions using these controlled vocabularies.
which accounts for 8% of global cancer-related deaths (Sung, Ferlay et al. 2021). About 80% to 85% of lung cancers are non-small cell lung cancer (NSCLC). Lung adenocarcinoma (LAD) is the most common type of lung cancer seen in non-smokers, and smokers. Therefore, understanding genetics and epigenetic interaction between genes is important to understand lung cancer. We conducted research on NSCLC and the immune landscape, 2) use a convergent relative risk statistical model to test intermediate diagnosis codes occurring between a specified index code(s) and outcome code(s) to account for these sample subtypes using clustering of factorization (NMF) clustering method using global protein, phosphoproteome, and acetylproteome data. We attempted to account for these sample subtypes using clustering of factors specific immune constructs for given sample subtypes. In this study, we confirm that the group with activated immune cells showed a positive correlation with larger survival. The study of Immune microenvironment of Korean NSCLC patients

We hypothesized that high immune cell activity will have better outcome than low immune cell activity, and this phenomenon will be caused by a major gene involved in immune activity. In this analysis, we profiled putative regulator in Korean NSCLC patients. Our co-researcher team divided the purpose of the sample by using the Non-negative matrix factorization (NMF) clustering method using global protein, phosphoproteome, and acetylproteome data. We attempted to account for these sample subtypes using clustering of factors specific immune constructs for given sample subtypes. In this study, we confirm that the group with activated immune cells showed a positive correlation with larger survival.


Kapeshme Singh, Mohammad Reza, Arash Faghihi, Sanjiv Bhandari, Can Firtina, Meryem Banu Firtina, Meryem Banu Firtina,

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Breast cancer is currently the most promising treatment reality for women of all ages. It has been demonstrated that targeting in vivo development with HER-2 or EGFR-1 blockade can lead to longer survival or complete remission in women. However, immunotherapy has yielded only modest results. In the current study, we aimed to investigate whether immune checkpoint inhibition would provide a potential and novel treatment option. We report a prospective study using a novel approach: measuring preventive immune responses in breast cancer patients. Specifically, we performed single-cell RNA sequencing to analyze immune responses in breast cancer patients. RNA sequenced data was obtained from multiple time points and attempted to identify pathways that are significantly associated with immune checkpoint inhibitors. We present results from gene expression analysis that suggest enhanced antigen-presenting by CD4+ and CD8+ T cells for demonstrating the functional benefits of these treatments in breast cancer patients. Overall, our findings support the potential use of immune checkpoint inhibitors as a promising treatment option for breast cancer patients.
Visualization and analysis of cancer genomics data using UCSC Xena

Jing Zhu, Mary Goldman, Brian Craft, David Haussler

UCSC Genomics Institute, UC Santa Cruz

UCSC Xena (http://xena.ucsc.edu/) is a web-based visual integration and exploration tool for multi-omic data and associated clinical and phenotypic annotations. Researchers can easily view and explore public data, their own private data, or both using the Xena browser. Private data are kept on the researcher’s computer and are never uploaded to our public servers. We support Mac, Windows, and Linux.

Questions Xena can help you answer:
* Is overexpression of this gene associated with low/higher survival?
* What genes are differentially expressed between these two groups of samples?
* What is the relationship between mutation, copy number, expression, etc for this gene?

Xena showcases seminal cancer genomics datasets from TCGA, The Pan-Cancer Atlas, GDC, PCAWG, ICGC, and more, totaling over 200 datasets across 50 cancer types. We support virtually any type of functional genomics data such as SNPs, INDELs, copy number variation, gene expression, ATAC-seq, DNA methylation, exon-, transcript-, miRNA-, lncRNA-expression and structural variants. We also support clinical data such as phenotype annotations, subtype classifications and biomarkers. All of our data is available for download via python or R APIs, or using our URL links.

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