and age composition of participants versus non-participants. Patients ≥5 years old with known race and gender and at least one healthcare encounter between 2021 and 2024 were included. Interventional trial enrollment was identified by a "research flag" indicating current or past participation in an interventional study within an Epic system contributing data to Cosmos. Race was categorized as American Indian, Asian, Black, Native Hawaiian, or White. Age-adjusted relative representation (RR) ratios were used to compare participation, with RR >1 indicating over-representation and RR RESULTS/ANTICIPATED RESULTS: Of 130,455,189 patients meeting eligibility criteria, 0.52% (673,425) of patients were active or inactive in an interventional clinical trial. Results are shown in the figure below. The poorest representation was from Asian and NH/PI persons. Representation was most similar to the patient population for whites and AI/AN persons. Black males participated less and women, more than predicted by patient composition. Older patients participated more frequently than younger (age, mean (SD), y, 53 (22) vs. 46 (23); p DISCUSSION/SIGNIFICANCE OF IMPACT: This is the first study we know of describing interventional trial participation in the USA across millions and millions of patients. Further research is needed to clarify whether these differences are due to the nature of the studies themselves (e.g., OB/GYN trials including only women, etc.) versus disparities in recruitment or otherwise.

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Host-bacterial immune responses to ventilator-associated pneumonia in COVID-19 patients

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OBJECTIVES/GOALS: Ventilator-associated pneumonia (VAP) is an infection caused by bacteria, viruses, or fungi during mechanical ventilation. We analyzed a cohort of COVID-19 patients admitted to the intensive care unit with respiratory failure with different VAP outcomes. We hypothesize that the multiomics data can help predict VAP development within this cohort. METHODS/STUDY POPULATION: We recruited participants from a cohort on a NYU IRB protocol (i22–00616), who had COVID19 respiratory failure, admitted to ICU, and required invasive mechanical ventilation (n = 245). We collected and analyzed research specimens (bronchoalveolar lavage [BAL, n = 213], tracheal aspirates [n = 246], background [n = 18]) and clinical cultures (sputum and BAL) for 245 participants. A panel of experts adjudicated VAP within the cohort, resulting in 92 VAP diagnoses. We annotated metatranscriptome (Illumina NovaSeq) using a Kraken/Bracken database, and KEGG for functional annotation of transcriptome data (Illumina HiSeq). We used edgeR (v.4.0.16) to analyze differential expression of metatranscriptome and transcriptome data. RESULTS/ANTICIPATED RESULTS: We diagnosed VAP in n = 92 (38%) participants. We found significant differences in days of overall hospital stay (p DISCUSSION/SIGNIFICANCE OF IMPACT: VAP is a serious complication of mechanical ventilation, and oral commensals alter the lung microbiome and host immunity. We identified a transcriptome-metatranscriptome signature that identifies those at VAP risk. VAP was associate with both pro- and anti-inflammatory gene expression resulting in increased risk for lower airway infection.

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Online graphical interface for bulk to single-cell transcriptomics

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OBJECTIVES/GOALS: We aim to develop an intuitive interface to understand the possible relationships between data from different RNA-Seq technologies. It can help novice users and educators to understand, analyze, explain, and visualize such datasets from diverse platforms, all without the need for additional software installations or strong programming expertise. METHODS/STUDY POPULATION: An online interactive interface is developed, integrating robust algorithms for three distinct types of analyses: DESeq2 for bulk RNA-seq, CIBERSORTx for deconvolution, and Seurat for single-cell analysis, with plans to include more algorithms. It allows a demo mode for training using the sample datasets and option for tailored analysis using user's partially processed data. The interface provides capability to process bulk RNA-seq data from raw counts or a differential gene list. Further, deconvolution analysis for bulk RNA-seq data can be done using raw counts and single-cell data analysis can be performed using processed sequence reads, organized into three key files: barcodes, matrix, and features. Users also have an option to download the results as a zipped file, for samples from human and mouse studies. RESULTS/ANTICIPATED RESULTS: Users with an active internet connection can access the interface from any major web browser. They can adjust parameters – such as genome type, cutoff thresholds, and batch effect correction – according to their specific needs. Bulk RNA-seq results are presented in the form of volcano plots, heatmaps, clusters, gene expression across samples, DEGs, and enrichment plots from KEGG and GO analyses. Deconvolution analysis can be performed using either the "LM22" signature matrix (for human leukocyte cell types) or Derm22 (for skin-specific cell types). The single-cell workflow provides results including quality control metrics, UMAP clustering, gene expression plots/tables, and cluster annotation using CellTypist. Comprehensive details on methods and tutorials are available in the GitHub repository. DISCUSSION/SIGNIFICANCE OF IMPACT: Although multiple workflows are available to process bulk and single cell RNA-Seq data along with deconvolution methods to bridge the gap between the two, this is the first online interface to provide the capability to explore and analyze data from all three approaches in one place, without requiring strong computational expertise or resources.

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A CTS team approach to leveraging EHR data for predicting necrotizing enterocolitis in NICU*

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OBJECTIVES/GOALS: This research aims to harness electronic health records (EHR) combined with machine learning (ML) to predict necrotizing enterocolitis (NEC) in preterm infants using data up to their first 14 days of life. We aim to provide interpretable results for clinical decisions that can reduce infant mortality rates and complications from NEC. METHODS/STUDY POPULATION: Through a retrospective cohort study using data from the

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