forms of peripheral neuropathy. DISCUSSION/SIGNIFICANCE: The significance of this project is that characterization of the relationship of clinical symptoms, non-invasive imaging and expression of NfL will lead to better diagnostic and prognostic algorithms in the treatment of compressive and traumatic peripheral neuropathies.

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Digital Spatial Profiling of Allograft Loss in Kidney Biopsies with Chronic Allograft Dysfunction

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OBJECTIVES/GOALS: Assess molecular and cellular mechanisms of allograft loss in kidney biopsies using digital spatial profiling and clinical outcomes data. METHODS/STUDY POPULATION: Patients with chronic allograft dysfunction (CGD), enrolled in the Deterioration of Kidney Allograft Function (DeKAF) study, with or without eventual allograft loss, were included. CGD was defined as a >25% increase in creatinine over 3 months relative to a baseline. Kidney biopsy tissue was assessed by Nanostring GeoMX digital spatial profiling (DSP) after staining with anti-pan-cytokeratin, anti-CD45, anti-CD68, Syto-13, to identify specific cell populations, and Nanostring's Whole Transcriptome Atlas (WTA), to quantify the distribution of transcripts across the biopsy. Up to 14 regions of interest (ROIs) were selected, with or without glomerulus. CIBERSORT was used to perform cell deconvolution. Clinical and outcomes data were from the DeKAF study and United States Renal Data System. RESULTS/ANTICIPATED RESULTS: Macrophage (M1) cell population abundance was significantly different in ROIs with glomerulus between graft loss and no graft loss. Principle component analysis of differentially expressed genes resulted in transcriptomes in ROIs that cluster together by clinical outcome of graft loss or no graft loss. There were 203 DEGs in ROIs with glomerulus that were different by graft loss or no graft loss. By pathway analysis, these 203 DEGS were enriched in the T-cell activation, integrin signaling and inflammation pathways. DISCUSSION/SIGNIFICANCE: DSP of kidney allograft biopsies allows for the identification and quantification of specific cell types, such as macrophages and molecular transcripts as potential drug targets. This data can be used to understand mechanisms of kidney allograft loss and may lead to improved immune suppression in kidney transplant recipients.

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From discovery to the clinical laboratory: a methodological appraisal of untargeted metabolomics platforms to characterize inborn errors of metabolism.

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OBJECTIVES/GOALS: Untargeted metabolomics platforms are powerful biomarker discovery tools. However, the absence of uniform study design, data analysis, and reporting standards limits translation of this research into the clinical lab. The goal was to critically appraise existing untargeted metabolomics platforms that analyzed inborn errors of metabolism. METHODS/STUDY POPULATION: A search strategy was conducted in MEDLINE via PubMed from January 16, 2013, to January 16, 2023. The search strategy was limited to primary literature articles written in English that evaluated human subjects with inborn errors of metabolism (IEMs). Articles that performed targeted metabolomic analysis or analyzed non-human samples were excluded. Information on patient cohorts analyzed, sample types, and method design were extracted using a template. Categorical data are summarized as frequencies and percentages. RESULTS/ANTICIPATED RESULTS: A total of 96 distinct IEMs were evaluated by the different untargeted metabolomics methods included in this review. However, most IEMs (55/96, 57%) were evaluated by a single platform, in a single study, with a limited cohort size. Only one study validated their results using a separate, validation cohort. There was considerable diversity in the separation techniques and mass spectrometry instrumentation used by the studies to create their untargeted metabolomics methods. Slightly over half (59%) of the studies identified at least some of the metabolites detected in their samples with the highest level of confidence. Importantly, most of the included studies reported adherence to quality metrics, including use of quality control material (65%) and internal standards in their analysis (61%). DISCUSSION/SIGNIFICANCE: Future studies analyzing IEM patient samples with untargeted metabolomics platforms should progress beyond single-subject studies and evaluate the reproducibility of the research using a prospective, or validation cohort as well as confirm metabolite annotations with reference metabolites standards to generate clinically useful data.

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Examining the clinical utility of dance to support social connection - Explorations at the level of the brain, heart, and body

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OBJECTIVES/GOALS: Social isolation/loneliness is a public health crisis and one that is unlikely to be solved through pharmacology. Nonpharmacological approaches, such as dance, are needed. The objective of this study is to investigate the physiological correlates of dance-induced improvements in social connection. METHODS/STUDY POPULATION: Participants were randomly assigned to participate for 4 weeks (2 times per week, 90-minute sessions) in either 1) improvisational dance training (experimental group; n=7); or a 2) dance movie watching experience (control group; n=7). Before and after the intervention, using mobile brain-body imaging techniques, participants and their instructor had their brain (via electroencephalography) and body physiology (via photoplethysmography) recorded during a series of verbal and nonverbal interactive experiences. Participants were also video recorded via 4 surrounding cameras for later motion capture analysis. Neuropsychological assessments were also conducted before and after the intervention. RESULTS/ANTICIPATED RESULTS: We found that dance significantly increased social skills including empathy, interpersonal skills, emotional regulation, mindfulness, and attention. Additionally, we found that dance significantly increased interbrain synchrony during nonverbal experiences including theta (4-8 Hz), beta (12-35 Hz), and gamma

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