**William S. Noble**

R01 HG011466 (Noble) 2/01/21–1/31/26
NIH $1,549,944
**Deep tensor genomic imputation**
This project develops machine learning approaches to predicting various types of genomic experiments before they are performed by leveraging big, heterogeneous compendia of existing data.
Role: PI

R25 HG012337-01 (Dobra, Noble) 07/01/22–04/30/27
NIH/NHGRI $1,260,275
**University of Washington Genomics Research Training for Data Scientists**
In support of the NHGRI Strategic Plan to Diversify the Genomics Workforce, we propose the University of Washington Genomics Training for Data Scientists program (UWGRTDS). This interdisciplinary program provides masters students in data science from underrepresented minority (URM) backgrounds with paid research experiences in genomics research laboratories at UW.
Role: Multi-PI

2245300 (Noble) 6/1/2023–5/31/27
NSF $1,199,760
**DMS/NIGMS 2: Deep learning for repository-scale analysis of tandem mass spectrometry proteomics data**
The primary technology driving the rapid growth of proteomics is tandem mass spectrometry. In addition to technological advances in mass spectrometry hardware, accurate and efficient analysis of the complex data produced by a tandem mass spectrometer requires increasingly sophisticated computational tools. The proposed project will develop these tools.
Role: PI

U01 HG013198 (Weng, Kundaje, Noble) 9/1/2023–5/31/28
NIH/NHGRI $408,426 (Noble Lab)
**Multi-Omics DACC: The Data Analysis and Coordination Center for the collaborative multi-omics for health and disease initiative**
The overall goal of the Multi-Omics for Health and Disease Consortium is to explore the use of multiomics data to detect and assess molecular profiles associated with healthy and disease states, coalescing these data into a multi-dimensional dataset that is available to the research community
Role: Multi-PI

R01 HG013321 (Wang) 09/17/2024–06/30/2029
NIH/NHGRI $2,445,545
**Deep integrative analysis of Hi-C data**
This project will develop machine learning methods to integrate timecourse Hi-C data and RNA-seq data, co-embed genome sequences, and low-coverage contact data for resolution enhancement, and translate between Hi-C and ATAC-seq.
Role: Co-I

R01 AI188634 (Le Roch) 12/1/2024–11/30/2029
NIH/NIAID $836,557 (Noble Lab)
**Decoding the Role of Non-Coding RNAs in Gene Regulation**
The main goal of this project is to identify the molecular factors that control chromatin organization and gene regulation in P. falciparum with a specific focus on long non-coding RNAs (lncRNAs). We will elucidate their importance in parasite development, virulence, and sexual differentiation, and determine whether they can be targeted by novel therapeutic intervention.
Role: Co-I

R01 HL169156 (Doulatov) 7/1/2023–5/31/27
NIH/NLHBI $615,675 (Noble lab)
**The role of lamin B1 in normal and myelodysplastic hematopoiesis**
Role: Co-investigator

I, PD/PI or other senior/key personnel, certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.

Signature: William
Date: October 9, 2025