Resource Summary Report

Generated by NIF on Apr 21, 2025

Noble Research Lab

RRID:SCR_007204
Type: Tool

Proper Citation

Noble Research Lab (RRID:SCR_007204)

Resource Information

URL: http://noble.gs.washington.edu/

Proper Citation: Noble Research Lab (RRID:SCR_007204)

Description: Our research group develops and applies computational techniques for modeling and understanding biological processes at the molecular level. Our research emphasizes the application of statistical and machine learning techniques, such as hidden Markov models and support vector machines. We apply these techniques to various types of biological data, including DNA and protein sequence data, as well as gene expression data from microarray experiments. We are currently developing methods for analyzing shotgun proteomics data, for characterizing protein function, structure and interactions, and for understanding the structure and regulatory influence of chromatin.

Synonyms: Noble Lab

Resource Type: laboratory portal, portal, organization portal, data or information resource

Funding:

Resource Name: Noble Research Lab

Resource ID: SCR_007204

Alternate IDs: nlx_45779

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250421T053615+0000

Ratings and Alerts

No rating or validation information has been found for Noble Research Lab.

No alerts have been found for Noble Research Lab.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Schreiber J, et al. (2021) Prioritizing transcriptomic and epigenomic experiments using an optimization strategy that leverages imputed data. Bioinformatics (Oxford, England), 37(4), 439.

Ramachandran S, et al. (2021) FPTMS: Frequency-based approach to identify the peptide from the low-energy collision-induced dissociation tandem mass spectra. Journal of proteomics, 235, 104116.