

Genome-wide association studies (GWAS) have enabled the discovery of new gene-disease relationships through a paradigm of simultaneous, unbiased testing of multiple associations. Similar approaches have been used to discover new associations between diseases and environmental exposures in environment-wide association studies (EWAS) and between a single genetic variant and multiple phenotypes in phenome-wide association studies (PheWAS).

In contrast, modern epidemiologic approaches have not used this paradigm in the discovery of new predictors of health outcomes. This is partly due to the fact that data sources that would contain relevant information on exposures relevant to health are difficult to find and analyze on a large scale. Clinical notes contain a rich description of numerous epidemiologic exposures that can be unlocked using natural language processing software. Studying the links between thousands of epidemiologic exposures in clinical notes and health outcomes amounts to a set of natural experiments on the grandest scale. Discovering associations based on the clinical narrative carries the added complexity of an open cohort, where patients may enter and leave the cohort at various time points and may be lost to follow-up or experience competing events.

In this talk, I will present a new methodology, which I have termed a concept-wide association study (CWAS), for examining relationships between several thousand concepts extracted from clinical notes with the development of 2 health outcomes: kidney failure and medication non-adherence. We will critically examine and discuss how to interpret its findings as well as its limitations.

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