

New method extracts information on psychiatric symptoms from electronic health records

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Researchers at Massachusetts General Hospital and Harvard Medical School have developed a new method to extract valuable symptom information from doctors' notes, allowing them to capture the complexity of psychiatric disorders that is missed by traditional sources of clinical data. The study, published in *Biological Psychiatry*, was led by co-senior authors Tianxi Cai, Sc.D., and Roy H. Perlis, M.D. A second study published in *Biological Psychiatry*, also led by Dr. Perlis, applied the new method in a proof-of-concept study to identify genes associated with psychiatric symptoms.

"Many efforts to use clinical documentation in [electronic health records](#) for research aim to identify individual symptoms, like the presence or absence of psychosis," said Thomas McCoy Jr., M.D., co-first author with Sheng Yu, Ph.D. But this approach misses the complex overlap of symptoms between different mental disorders. "My co-authors and I developed a method that instead captures symptom dimensions, or sets of symptoms, informed by the National Institute of Mental Health Research Domain Criteria," continued Dr. McCoy.

The method extracts the relevant symptoms from the wealth of information in the detailed narrative notes taken by clinicians in patients' electronic health records. Dr. McCoy and colleagues used the method to characterize 3,619 adults with psychiatric hospitalizations across a range of disorders, including schizophrenia, anxiety, major depressive

disorder, and posttraumatic stress disorder.

Characterizing the patients based on symptom dimensions could predict the length of hospital stay and time to hospital readmission better than the use of more structured data alone, such as health billing information, that is based on the categorization of disorders. The symptom dimensions were also associated with scoring of notes by expert clinicians and with neurocognitive testing, validating the results.

The idea of symptom domains rather than disease categories also extends to the neurobiology of mental illness. "The recognition that the genetic basis of psychiatric illness crosses traditional boundaries has encouraged efforts to understand psychopathology according to dimensions, rather than simply presence or absence of symptoms," said Dr. McCoy.

In the second study, Dr. McCoy and colleagues demonstrated the application of this new method to examine the association between symptom dimensions and common genetic variation in psychiatric disease. They compared the information on the symptom dimensions extracted from the narrative hospital discharge notes of 4,687 adults with the patients' genomic information. The researchers identified four areas of interest, or loci, in the genome, highlighting two genes which have not previously been identified with existing methods.

"The ability to combine large DNA data sets with meaningful psychiatric information from the electronic health record is an important step in facilitating large scale medical genetics research in psychiatry," said John Krystal, M.D., Editor of *Biological Psychiatry*.

The authors suggest that the method offers a new approach to understand brain function in mental illness. Other researchers can apply the method to different sets of patients with hospital-linked genomic records, and identification of the same loci would strengthen the support for their role

in [psychiatric symptoms](#).

"We are making the scoring software freely available and hope this work will enable transdiagnostic dimensional phenotypes to be used in efforts to achieve precision psychiatry," said Dr. McCoy.

More information: Thomas H. McCoy et al, High Throughput Phenotyping for Dimensional Psychopathology in Electronic Health Records, *Biological Psychiatry* (2018). [DOI: 10.1016/j.biopsych.2018.01.011](#)

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