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New method extracts valuable information on psychiatric symptoms from electronic health records

Two reports published in Biological Psychiatry demonstrate an approach to use electronic health records to investigate the biological basis of neuropsychiatric symptoms

Philadelphia, February 26, 2018 – 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.

Notes for editors

The articles are "High throughput phenotyping for dimensional psychopathology in electronic health records," by Thomas H. McCoy Jr, Sheng Yu, Kamber L. Hart, Victor M. Castro, Hannah E. Brown, James N. Rosenquist, Alysa E. Doyle, Pieter J. Vуйjk, Tianxi Cai, and Roy H. Perlis (<https://doi.org/10.1016/j.biopsych.2018.01.011>) and "Genome-wide association study of dimensional psychopathology using electronic health records" by Thomas H. McCoy Jr, Victor M. Castro, Kamber L. Hart, Amelia M. Pellegrini, Sheng Yu, Tianxi Cai, and Roy H. Perlis (<https://doi.org/10.1016/j.biopsych.2017.12.004>). They appear in *Biological Psychiatry*, published by Elsevier.

Copies of these papers are available to credentialed journalists upon request; please contact Rhiannon Bugno at Biol.Psych@UTSouthwestern.edu or +1 214 648 0880. Journalists wishing to interview the authors may contact Thomas H. McCoy, Jr., M.D., at thmccoy@partners.org.

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The authors' affiliations and disclosures of financial and conflicts of interests are available in the article.

John H. Krystal, M.D., is Chairman of the Department of Psychiatry at the Yale University School of Medicine, Chief of Psychiatry at Yale-New Haven Hospital, and a research psychiatrist at the VA Connecticut Healthcare System. His disclosures of financial and conflicts of interests are available [here](#).

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The journal publishes novel results of original research which represent an important new lead or significant impact on the field, particularly those addressing genetic and environmental risk factors, neural circuitry and neurochemistry, and important new therapeutic approaches. Reviews and commentaries that focus on topics of current research and interest are also encouraged.

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