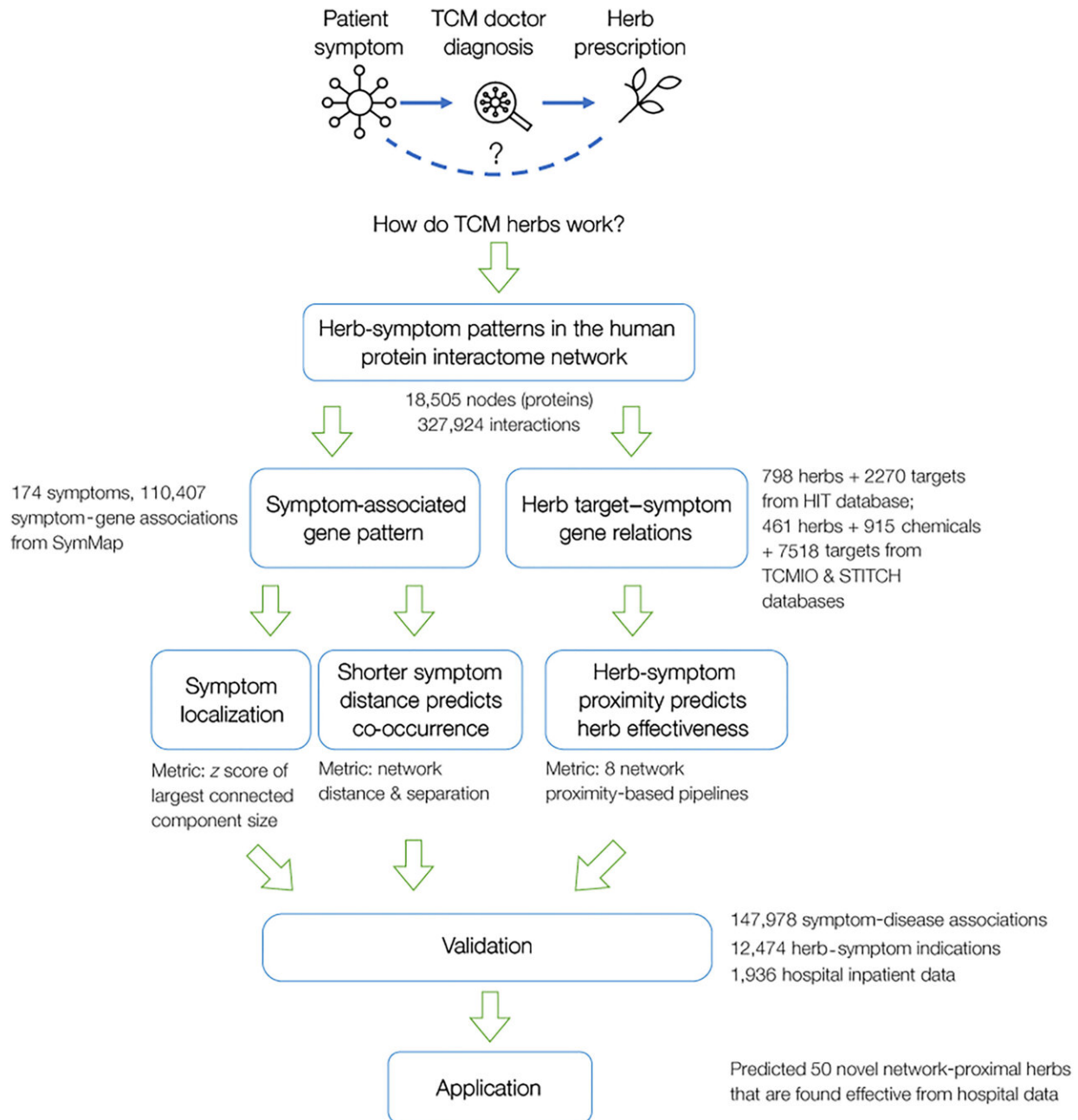


A framework for predicting the general effectiveness of traditional Chinese medicinal herbs

November 1 2023, by Bob Yirka



To explore the mechanisms of how TCM treats disease/symptoms, we develop a generic framework that characterizes TCM mechanisms as the network-based relation between symptom-associated proteins and herb targets in the human PPI. After collecting the symptom-associated proteins and herb-target data, we designed multiple network-based metrics to unveil the network patterns connecting them, including symptom localization, symptom-symptom relation, and herb-symptom proximity. We validated these relations by showing that our

network-based framework captures symptom-disease relations and herb-symptom effectiveness, leveraging online public databases and a hospital inpatient dataset. We highlight the potential application of our work in predicting herb-symptom treatments. Credit: *Science Advances* (2023). DOI: 10.1126/sciadv.adh0215

A large team of medical researchers affiliated with a host of institutions in China and the U.S. has developed a framework for predicting the general effectiveness of traditional Chinese medicine (TCM) herbs. In their paper [published](#) in the journal *Science Advances*, the group describes how they used a multi-pronged approach to build a tool that might be used to test the efficacy of traditional Chinese medicinal herbs.

Prior research has shown that some traditional Chinese herbs can be effective in treating some ailments—qinghao, for example, has been shown to be effective for treating malaria. But thus far, because of the very large numbers of TCM herbs and their reputation as mythological remedies, such herbs have not been well studied with modern technology to find out if they are useful therapies.

For this new research, the team did not set out to test whether TCM herbs are effective treatments, but instead focused on creating a tool to test them in a more general way. Such a tool, they note, could be used in a methodical way to test a wide variety of TCM herbs.

To create the framework, the researchers started by compiling a list of human genes that are known to be behind the generation of symptoms of diseases—fever, for example, or insomnia. They narrowed the gene list down to just 20 that have been associated with 174 symptoms. They then mapped the associated symptoms onto a model that shows how 18,505 proteins interact. They added data for proteins that are targeted by TCM

herbs for comparison purposes.

The researchers then used their compilation to create a framework that generated a score based on the estimated effectiveness of a given [herb](#) (or combination of herbs) against certain symptoms—based on protein generation. Next, they compared scores generated by the framework against a Chinese pharmacopeia to see how well they matched. They also applied the system to records of patients being treated at a traditional Chinese medicine–based hospital in Wuhan.

In studying the results of these comparisons, the research team found reason to be optimistic about the effectiveness of their new framework. They found instances where it scored highly for herbs that had been used for thousands of years to treat certain ailments and that did indeed offer some therapeutic benefit. They suggest more work needs to be done to test their [framework](#) to prove that it can correctly perform its intended purpose.

More information: Xiao Gan et al, Network medicine framework reveals generic herb-symptom effectiveness of traditional Chinese medicine, *Science Advances* (2023). [DOI: 10.1126/sciadv.adh0215](https://doi.org/10.1126/sciadv.adh0215)

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