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Predicting Aspects of Translational Biomedicine

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Introduction

Fundamental scientific advances can take decades to translate into improvements in human health. Shortening this interval would increase the rate at which scientific discoveries lead to successful treatment of human disease. One way to accomplish this would be to identify which advances in knowledge are most likely to translate into clinical research. Translational progress in biomedicine can therefore be assessed and predicted in real time based on information conveyed by the scientific community's early reaction to a paper. Much of the recent discussion of bench-to-bedside research has appropriately been focused on how best to allocate limited resources in support of the science that gives rise to transformative clinical impact. Making these decisions is complicated by the fact that it can take decades for a fundamental discovery to translate into improvements in human health. Characterizing these pathways of knowledge flow, defined as the movement of information from cited articles to citing articles, might have the additional benefit of identifying otherwise unnoticed discoveries that are good candidates for bench-to-bedside translation. In the past, tracking knowledge flow from bench to bedside has required manual curation by subject matter experts. Although informative, those types of analyses are time intensive and thus cannot be used to analyze large data sets. This limitation is disappearing due to recent advances in algorithm development and data availability, which now present the opportunity to measure the progress of biomedical research at scale. The extension of this approach to high-throughput, multidimensional analyses has the potential to identify commonalities shared by past discoveries that had clinical impact, which in turn could be leveraged to determine the likelihood that a recent discovery will have future translational success. A priori, any attempt to determine the translational potential of a recent discovery faces 2 key challenges. First, although it is a subject of some debate, individual scientific advances are generally considered to be unpredictable. We report here the development of a method to predict translational progress computationally at the article level. We trained machine learning models on a binary output—whether or not a clinical trial or guideline (hereafter referred to collectively as clinical articles) eventually cited the article of interest, recognizing that most of these translational "shots on goal" do not directly "score" an improvement in human health.

Before attempting to predict translation, we first needed to define it. Citations by published clinical articles are the most commonly used measure of translational progress; however, the relationship between early scientific discoveries and the cures to which they eventually lead is complex. One facet of this complexity is that important early steps in translation may appear topically distinct from their clinical descendants, raising the possibility that this method of evaluating the movement of ideas from bench to bedside might undervalue the subset of transformative biomedical research that lacks a direct link to human health.

Using citations by clinical articles as evidence of translational progress therefore does not disadvantage transformative discoveries that have laid the foundation for later clinical work; when they impact human health, papers describing those discoveries are recognized and cited directly by clinical researchers. The prediction of future clinical citations based on past citation history can only be successful if that history follows detectable patterns. While this is a reasonable hypothesis, to our knowledge it has not previously been tested.