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Challenges and promises for translating computational tools into clinical practice

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Computational modeling and associated methods have greatly advanced our understanding of cognition and neurobiology underlying complex behaviors and psychiatric conditions. Yet, no computational methods have been successfully translated into clinical settings. This review discusses three major methodological and practical challenges (A. precise characterization of latent neurocognitive processes, B. developing optimal assays, C. developing large-scale longitudinal studies and generating predictions from multi-modal data) and potential promises and tools that have been developed in various fields including mathematical psychology, computational neuroscience, computer science, and statistics. We conclude by highlighting a strong need to communicate and collaborate across multiple disciplines.

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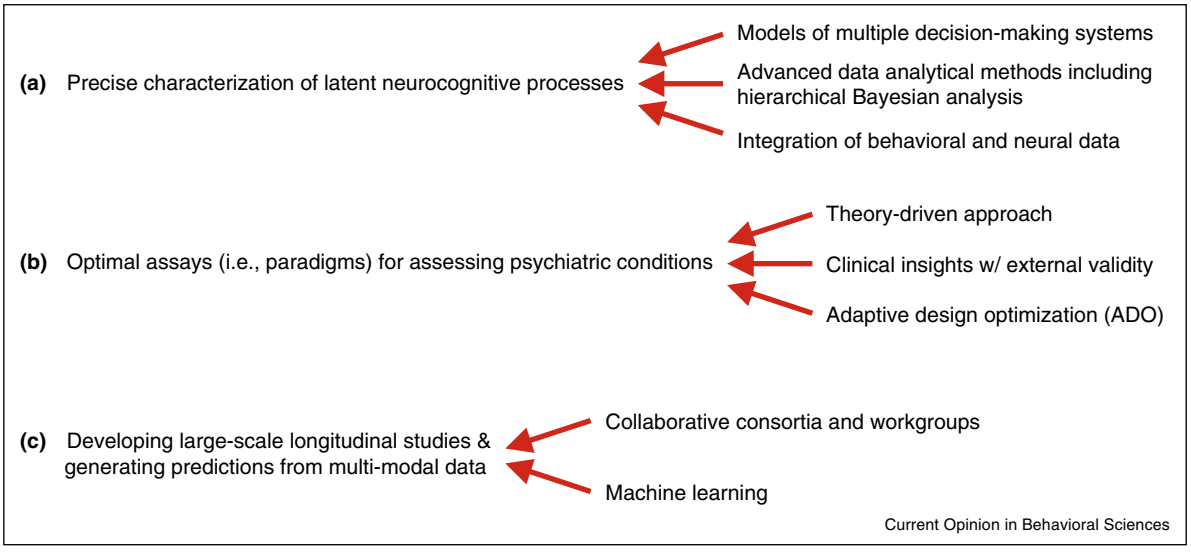
Introduction

Computational modeling has greatly contributed to understanding cognitive processes underlying our decision-making. By providing a mechanistic account of the processes, computational modeling allows us to generate quantitative predictions and test them in a precise manner. Computational modeling also provides a framework for studying the neural mechanisms of complex behaviors. Ever since reinforcement learning models were shown to well describe phasic activity changes in midbrain dopamine neurons [1], computational modeling has been widely combined with electrophysiological data and human functional magnetic resonance imaging (fMRI) signals to identify brain regions implementing specific cognitive processes [2,3]. A systematic line of research based on the computational framework suggests that the brain has multiple systems for decision-making [4,5]: the Pavlovian system, which sets a strong prior on our actions when we are faced with rewards or punishments and the instrumental system, which is further divided into habitual (i.e., model-free; efficient but inflexible) and goal-directed (model-based; effortful but flexible) systems. While the Pavlovian system has been traditionally regarded as purely model-free, new ample evidence suggests Pavlovian learning might also involve model-based evaluation [6].

There is a growing consensus that computational modeling can also be helpful to understand psychiatric disorders. Computational models can break maladaptive behaviors into distinct cognitive components, and the model parameters associated with the components can be used to understand the latent cognitive sources of their deficits. Therefore, computational modeling can provide a useful framework in understanding comorbidity among psychiatric disorders in a systematic way. Such a framework can specify psychiatric conditions with basic dimensions of neurocognitive functioning and offer a novel approach to assess and diagnose psychiatric patients [7–9,10•].

Despite the growing enthusiasm, no computational assays or methods have influenced clinical practice yet. There remain several major methodological and practical challenges that need to be solved for translating computational modeling tools into clinical practice. In this article, among many others, we focus on the following challenges as summarized in Figure 1: (A) precise characterization of latent neurocognitive processes, (B) development of optimal assays for assessing psychiatric conditions, (C) development of large-scale longitudinal studies and generating predictions using multi-modal and multi-dimensional data. In the following sections, we provide a general overview of each challenge and discuss how we can potentially address them. Our review focuses on computational modeling of human decision-making and fMRI studies, which are most relevant to the challenges we consider. We also briefly review how mathematical psychologists and computational neuroscientists have independently attempted to understand psychiatric disorders using computational methods. We hope this article will help researchers in each field identify strengths of the other field and stimulate further communication and interaction between the fields. There are some important topics that are not addressed in this article including biophysically based models and readers can refer to

Figure 1



Promising approaches to address three major changes for translating computational tools into clinical practice.

existing review papers on the topics [11•,12•,13]. Because of space limit, our review excludes a survey of model comparison methods and mathematical details of Bayesian data analysis, which are covered in other reviews [14,15•,16•].

A. Precise characterization of latent neurocognitive processes

Early applications of computational modeling to psychiatric populations were initiated by mathematical psychologists. Traditionally they focused on identifying cognitive processes embedded in a cognitive or decision-making task. Mathematical psychologists including Batchelder, Townsend, Ratcliff, Neufeld, and Treat advocated as well as empirically demonstrated that computational modeling can be used to assess clinical populations [17•]. The computational approach began to receive additional attention as Busemeyer and Stout [18] developed the Expectancy-Valence Learning (EVL) model for the Iowa Gambling Task (IGT) and apply the EVL to several clinical populations [19]. The model has been subsequently revised to improve its performance, which led to a newer version called the Prospect Valence Learning (PVL) model [20,21]. Despite criticism on the IGT for its complicated design and performance heterogeneity [22], the PVL model showed good model-fits and simulation performance (e.g., [23•]) and it has been applied to several populations with substance dependence (for a review and detailed findings see, [24]). For example, modeling approaches on the IGT revealed reduced loss aversion among heroin users compared to healthy individuals, which was robust across all models we tested [23•]. Computational models have also been used to decompose performance of clinical populations on the Balloon Analogue Risk Task (BART) [25], the Go/Nogo task [26], and speeded choice-response time tasks [27].

Independently, computational neuroscientists including Montague, Dayan, Dolan, Friston, and colleagues have put efforts to build computational accounts of (ab)normal cognition and its biological underpinnings (a.k.a. *Computational Psychiatry*) [8,28,29]. They built computational frameworks and used the method called model-based fMRI [3] or model-based electroencephalography [30] (among other methods) in which internal states predicted by computational models are used to identify brain regions that presumably implement a particular cognitive/computational process. Many applications to psychiatric disorders [31–34] have been built around the Bayesian decision framework that offers a Bayesian account of decision-making [35]. In addition, recent studies using model-based fMRI significantly enhanced our understanding of the neurobiological mechanisms underlying reinforcement learning and decision-making in the brain (for recent reviews see [12•,36]).

Once we build a computational model, the next important step is parameter estimation. Getting accurate estimates of the key model parameters is critical for phenotyping computational processes precisely. Currently the state of the art for parameter estimation is hierarchical Bayesian analysis (HBA) that pools information across individuals and captures similarities and differences among individuals in a hierarchical way [15•,37]. Hierarchical methods are particularly useful when the amount of information is small or insufficient for precise parameter estimation at