

Empirical Evidence from Neuroimaging Data for a *Standard Model of the Mind*

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Abstract

In a recent paper, Laird, Lebiere, and Rosenbloom (2017) highlight how 40 years of research on cognitive architectures has begun to yield a dramatic convergence of different approaches towards a set of basic assumptions that they called the “Standard Model of the Mind” (SMM), in analogy to the Standard Model of particle physics. The SMM was designed to capture a consensus view of “human-like minds”, whether from AI or cognitive science, which if valid must also be true of the human brain. Here, we provide a preliminary test of this hypothesis based on a re-analysis of fMRI data from four tasks that span a wide range of cognitive functions and cognitive complexity, and are representative of the specific form of intelligence and flexibility that is associated with higher-level human cognition. Using an established method (Dynamic Causal Modeling) to examine functional connectivity between brain regions, the SMM was compared against two alternative models that violate either functional or structural assumptions of the SMM. The results show that, in every dataset, the SMM significantly outperforms the other models, suggesting that the SMM best captures the functional requirements of brain dynamics in fMRI data among these alternatives.

Keywords: Cognitive architectures; fMRI; Effective Connectivity

Introduction

In a recent paper, Laird, Lebiere, and Rosenbloom (2017) have argued that, over the course of four decades, cognitive architectures have slowly converged onto a set of shared core assumptions, which they have tentatively named the “Standard Model of the Mind” (henceforth, SMM) in analogy to the “Standard Model” of particle physics.¹ The SMM is articulated as a series of assumptions about the nature of specific components and computations that are common to “human-like minds”; i.e., minds sufficiently similar in structure and function to human minds. These assumptions cover (A) structure and processing, (B) memory and content, (C) learning, and (D) perception and motor. Figure 1 is a visual illustration of the fundamental components and their architecture.

¹The “Standard Model of the Mind” has since been renamed the “Common Model of Cognition” after input from interested scientists attending a Fall symposium on the topic.

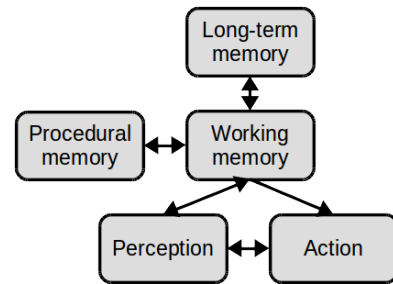


Figure 1: A graphical representation of the Standard Model of the Mind, as proposed by Laird et al. (2017)

Although the convergence was specifically illustrated in the case of the three architectures most closely associated with the co-authors—Soar (Laird, 2012), ACT-R (Anderson, Fincham, Qin, & Stocco, 2008), and Sigma (Rosenbloom, Demski, & Ustun, 2016)—the same case can be convincingly made for similar approaches as well.

This convergence likely reflects a number of factors, most notably the cumulative lessons learned from design of intelligent systems in AI and robotics, continual progress in cognitive psychology, and advancements in neuroscience. Because of the different nature of the forces that have driven this convergence, the authors have postulated that the SMM reflects a common architecture for intelligent, human-like behavior, which can be implemented in a biological or artificial system.

Evidence for the SMM

Despite the compelling theoretical arguments outlined in the paper, human beings remain the only known species capable of intelligent, general-purpose behavior, and data from humans remains the primary non-functional test-bed for the SMM. Also, irrespective of what is true of non-biological intelligent systems, it *must* be true *at least* of the human brain. That implies that the SMM must be reflected, to a certain de-

gree, in the functional architecture of the human brain.

Although an examination of the architecture of the human brain might seem an incredibly speculative project, it need not be so. Functional architectures of human brains are routinely proposed and examined, and ACT-R has been offered as a general architecture for the brain (Anderson et al., 2008).

In this paper, we show that the SMM can in fact be compared to other alternative architectures by examining the patterns of *effective connectivity* across cortical and sub-cortical regions in four neuroimaging datasets from different domains, and show that, in all cases, the SMM provides a better explanation of the data than alternative architectures of comparable complexity.

Designing an Empirical Test of the SMM

The SMM is made of several predictions, concerning the number and function of the central modules; their relative connections, and details on how information flows between modules; the format of the information that is shared between modules and its associated metadata; and the algorithms governing learning in the system.

In this paper, we focus on the most general tenets of the SMM, those concerning the specific components and their functional relationships. The central idea is that the specific components outlined in Figure 1 can be put into correspondence with specific brain circuits, and that the functional arrows in the diagram then correspond to the functional connectivity between these circuits, that is, the preferred way in which information is shared between difference circuits.

Testing Connectivity With DCM

Of these two aspects, the identification of SMM components with particular brain circuits or regions is perhaps the least controversial. In many cognitive architectures, e.g., specific modules have been mapped onto specific brain regions.

The examination of the functional connectivity between regions, however, requires special care. Here, we have chosen to examine the functional connectivity between regions using Dynamic Causal Modeling, or DCM (Friston, Harrison, & Penny, 2003). DCM is a mathematical method to estimate functional connectivity between network “nodes” that correspond to specific brain regions. It can be thought of as a more complex version of traditional General Linear Model (GLM) analysis of neuroimaging data, in which, rather than identifying the best fitting parameters for the time series of activity in every voxel, what is modeled is the time series of neural activity in a subset of regions (the network’s nodes). While in GLM analysis the time series of a voxel \mathbf{y} is estimated from the product of a matrix of parameters β and a matrix of experimental conditions \mathbf{x} (that is, $\mathbf{y} = \beta \times \mathbf{x} + \epsilon$), in DCM the time series of data in a node is fitted by a dynamic system state equation:

$$\frac{dy}{dt} = Ay + \sum_i x_i B(i)y + \sum_j y_j D(j)y + Cx \quad (1)$$

Where A , B , C , and D are four matrices that define, respectively the intrinsic connectivity between different regions (A); which regions are directly affected by task inputs, such as special stimuli or conditions (C , akin to “factors” in canonical GLM analysis); the modulatory effects that task conditions have on the connectivity between regions (B); and, finally, the modulatory effect that a network node can have on the connectivity between two other network nodes (D).

DCM has several advantages that make it the instrument of choice in our analysis. The first is that it is an explicitly top-down analysis method, which works best for testing and comparing a-priori hypotheses rather than for exploratory data analysis. This is, of course, exactly the type of approach needed. Another advantage is that DCM explicitly focuses on effective and directional *connectivity*, rather than on simple correlations between different timeseries. This makes it ideal to examine the directionality of the arrows in Figure 1. In this sense, DCM is superior to alternative approaches, such as Granger Causality (Friston, Moran, & Seth, 2013), because it better handles the temporal distortions introduced by the sluggish neurovascular coupling response, which determines the BOLD signal recorded in fMRI and which might vary substantially between regions (in GLM-based analyses, these differences can be ignored). The “Causal” in the acronym refers to the explicit directionality of the models. Yet another advantage of DCM is that parameter estimation is thoroughly conducted through a hierarchical Bayesian approach, thus giving each model the best chance to fit the data, while penalizing unreasonable physiological parameters. The use of Bayesian estimation is key to the possibility of directly comparing models, which is the goal of this paper. Finally, DCM has the advantage of being modality-independent; network dynamics are first modeled in terms of simplified neuronal activity, and then translated into the specific modality. This means that the same model can be used to fit both fMRI data (with high spatial resolution, low temporal resolution, and 3D spatial distribution of observations) and EEG data (with low spatial resolution, high temporal resolution, and surface distribution of observations). Thus, DCM provides the ideal starting point for a series of different analyses.

As with every method, DCM is not immune to criticisms (Lohmann, Erfurth, Müller, & Turner, 2012). However, most of the objections (for instance, the problems of specific parameter estimation) do not apply to the way this technique is used in this paper. Furthermore, when the underlying model is well specified, DCM does converge towards correct network parameters and successfully identifies underlying generators of neural activity (David et al., 2008).

Implementing the Standard Model in DCM

To proceed with the test, we first need to translate the SMM into a network of interconnected regions. In turn, this process requires establishing which regions are mapped to the SMM components, and how the connectivity between regions reflects the principles of the SMM.

Mapping Modules to Brain Regions In its formulation, the Standard model is made of five different “modules”. Given the fact that all of the tasks herein require manual responses, the *action module* can be uncontroversially identified with the motor regions of the brain (Brodmann Area 1). Because the four tasks examined here differ in the complexity of the visual inputs, we chose to identify the *perception module* with the primary visual cortices (Brodmann Area 18). This approach yielded a remarkably similar and stable location across tasks. Following a large amount of literature (Kane & Engle, 2002), the *working memory module* was localized within the dorsal prefrontal cortex (DLPFC), a region that is similarly implicated in maintaining and updating temporary representations. The *long-term memory module*, on the other hand, is specialized for creating and maintaining stable representations over long intervals of time—a process that can be identified with the function of the hippocampus and the medial temporal lobe (Squire, 1992). Finally, the *procedural memory module* can be identified with the basal ganglia, a set of nuclei similarly involved in the acquisition of procedural skills and action selection (Stocco, Lebiere, & Anderson, 2010).

Intrinsic Connectivity Most of the arrows in Figure 1 can be straightforwardly translated into connections between the corresponding brain regions in the DCM implementation of the SMM. The sole exception is the arrow between the model’s procedural and working memory modules, which must be interpreted in light of the special function of the procedural module in the SMM. There are two assumptions about the procedural module that have important implications for effective connectivity. Assumption *B3a* states that global control is provided by procedural knowledge in terms of rule-like conditions and actions, while assumption *B3b* states that the firing of procedural rules drives the Standard Model’s *cognitive cycle* by modifying the contents of working memory. In other words, the procedural module controls the transfer of signals to the global working memory space. In terms of effective connectivity, this function of procedural knowledge can be captured by assuming that the striatum modulates the connectivity from the other regions to the DLPFC (dashed arrows in Figure 2), rather than directly affecting the DLPFC (solid arrows in Figure 2). A similar approach has been previously suggested for DCM models of the basal ganglia (Prat, Stocco, Neuhaus, & Kleinhaus, 2016), and is compatible with contemporary neural network models of the circuit (Stocco et al., 2010). The final implementation of our model is represented in Figure 2A. In the figure, the boxes represent the SMM components, and their positions represent the (approximate) locations of the corresponding brain circuits over the outlines of a standard brain template. The solid black arrows represent the directional information channels of Figure 1, while the dashed lines terminating in circles represent the modulatory effects of the procedural module (i.e., the basal ganglia).

Evaluating the DCM Implementation

The SMM captures lessons learned from developing general-purpose, intelligent cognitive architectures. As such, it does not represent an optimal architecture system for a specific task. Rather, it represents the best single functional architecture that can successfully perform a large variety of tasks of different complexity. For this reason, the best way to test the SMM is not by providing a statistical fit against a specific dataset, but by comparing it over a variety of tasks against alternative architectures of similar complexity (that is, with a similar number of modules). If the SMM is correct, its corresponding DCM implementation should provide a comparably superior fit than other, alternative models of the neural data. In this paper, we will compare the SMM network against two alternative models of effective connectivity between the same regions. As a preliminary evaluation, these two models do not provide an exhaustive search of the possible architectures. They do, however, provide meaningful comparisons as they lay on opposite sides of the space of possible architectures.

The Structural Model In the *structural model* (Figure 2B), the modulatory connections of the basal ganglia are replaced by direct connections between the procedural module and the working memory module. Thus, this model implements a version of the SMM that reflects the general communication pathways in Figure 1, but does not reflect the special functional role of the procedural module, as defined by assumptions *B3a–b*. This model provides an interesting comparison for the SMM because of its similarity and greater simplicity, which provide an advantage in terms of Bayesian model comparison. In other words, the comparison between the SMM and the structural model reveals whether the functional assumption about the role of procedural knowledge is necessary to capture the flow of activity in the human brain.

The Fully Connected Model In the *fully connected model* (Figure 2C), all brain areas are bidirectionally connected to all others. This model serves as a theoretical counterpart to the structural model, and implements an opposite view of the nature of brain function. While the structural model assumes that constraints on the directionality between brain regions are sufficient to explain patterns of network activity, this model embodies the opposite viewpoint that there is no true “architecture” that is invariant across tasks, and that the brain’s ability to perform multiple tasks arises from the fact that all regions are in principle connected, rather than by means of a functional organization. In other words, there is no invariant architecture, only task-driven activity.

Testing Across Multiple Tasks

To capture the generality of the SMM, the three models above were compared across a spectrum of tasks that cover a broad range of cognitive capabilities, from relatively simple stimulus-response mappings to unstructured, fluid problem solving.

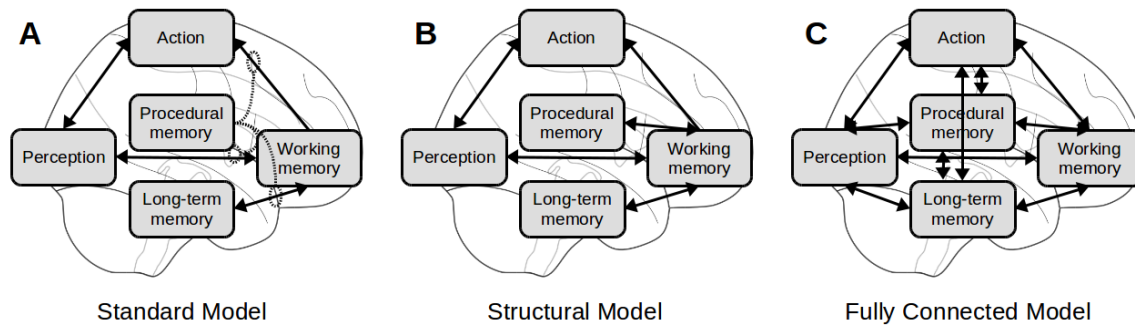


Figure 2: The three model architectures used in this analysis

Materials and Methods

Datasets and Tasks

Four functional MRI datasets were used for this analysis, all from either published studies or the first author’s laboratory. The four tasks were chosen to be representative of the spread of high-level cognitive abilities in humans. Table 1 summarizes the technical specifications of the four datasets.

The Flanker task In the Flanker task (Eriksen & Eriksen, 1974), participants respond to a central arrow-like symbol (e.g., “<”) with the hand corresponding to the symbol’s direction (e.g., left). The central symbol, however, is surrounded by four distractors, or “flankers”, that either point in the same direction (*congruent* trials, e.g., “<<<<<<”) or in the opposite direction (*incongruent* trials, e.g., “<<<><<”). Incongruent stimuli require additional control to manage the interference caused by the flankers. This task is perhaps the simplest of the experimental paradigms used to study cognitive control and executive functions, requiring minimal processing of the stimulus and depending on natural stimulus-response mappings. The dataset used is from the OpenfMRI public repository, and has been described and used by Kelly, Uddin, Biswal, Castellanos, and Milham (2008).

The Stroop task In the Stroop task (MacLeod, 1991) participants indicate through a manual response the color a word is printed in. Interference arises because the words are themselves color names, thus giving rise to congruent (e.g., “BLUE” in blue) and incongruent (e.g., “BLUE” in red) stimuli. This specific dataset is from the OpenfMRI public repository, and has been described and used by Verstynen (2014).

Rapid Instructed Task Learning (RITL) RITL is a paradigm recently developed to study cognitive flexibility and dynamic control of behavior (Cole, Laurent, & Stocco, 2013). Participants perform a different task each trial. To make this possible, each trial is divided into an “instruction” phase (where the task is communicated in a simple, predefined notation) and an “execution” phase, during which the instructions are applied to a specific stimulus. Tasks of comparable difficulty are created by combining basic mental op-

erations (such as arithmetic or semantic operations) in predefined ways. Mental flexibility is measured by comparing entirely new tasks against a subset of tasks that have been practiced in advance (Cole et al., 2013). This specific data comes from an unpublished study conducted by the first author. However, a different dataset with an identical paradigm had been previously published and described in detail by Stocco and Prat (2014).

Raven’s Advanced Progressive Matrices (RAPM)

RAPM is one of the most widely-used non-verbal tests of fluid intelligence and fluid reasoning abilities. Each problem consists of a 3-by-3 matrix. Eight cells of the matrix contain a figure made of different elements, while the bottom-right cell is empty. The visual features (such as color or orientation) of each figure vary across rows and columns according to specific but undisclosed rules. Participants must infer the rules and correctly identify the figure that completes the matrix within an array of four possible options. This specific dataset comes from what is, to the best of our knowledge, the only fMRI study that uses standard RAPM problems instead of simplified versions (Stocco, Prat, & Graham, submitted).

Task Implementation in DCM

Although the general architecture of the DCM models can be defined independently of the task, model estimation requires an explicit definition of how different stimuli affect the regions. To make the estimation and comparison procedures as general as possible, we used a uniform scheme to represent the experimental conditions across the four different tasks. In this scheme, every stimulus that is presented is encoded as an input to the visual cortex. In certain tasks, visual stimuli can differ significantly in nature. For example, in RITL (Stocco & Prat, 2014), stimuli can be either three-word instructions or two one-digit numbers, while in RAPM, stimuli can be either a 9-cell complex visual problem or a set of 4 possible 1-cell solutions. To account for this variability, different categories of stimuli are represented by separate types of inputs.

All tasks also share a basic comparison between an “easy” and a “difficult” condition, the latter of which requires additional processing. This is the case, for example, of incongru-

Table 1: Details of the four datasets. RAPM = Raven’s Advanced Progressive Matrices; RITL = Rapid Instructed Task Learning; Slices = Number of oblique axial slices; TR = Repetition time; TE = Echo time; N = Number of participants per dataset.

| Task | Publication | Scanner | Functional Imaging Parameters | Slices | N |
|---------|---------------------------|-----------------|-------------------------------|--------|-----|
| Flanker | Kelly et al. (2008) | Siemens Trio | TR = 2.0 s, TE = 20 ms | 40 | 26 |
| Stroop | Verstynen (2014) | Siemens Trio | TR = 1.5 s, TE = 30 ms | 29 | 28 |
| RAPM | Stocco et al. (submitted) | Philips Achieva | TR = 2.0 s, TE = 20 ms | 36 | 24 |
| RITL | Stocco and Prat (2014) | Philips Achieva | TR = 2.0 s, TE = 30 ms | 36 | 25 |

ent stimuli in the Flanker task (i.e., “<<><<”, as opposed to “<<<<<”). As a technique, DCM is agnostic about the nature of the stimuli. Thus, the fact that certain trials or conditions require additional processing needs to be explicitly encoded. In this study, we made the choice of including an additional input to the working memory region to mark the additional demands for processing for stimuli in the “difficult” conditions.² This decision reflects the rather uncontroversial assumption that the greater processing of certain stimuli would be accompanied by greater working memory load. Note that this assumption remains still fairly general, since it does not take into account the specific ways in which the “difficult” trials might be different across tasks.

Results

To compare the three models across the four datasets, we used a group-level Bayesian model selection algorithm, originally described in Stephan, Penny, Daunizeau, Moran, and Friston (2009). Figure 3 shows the results of the model comparisons. To make a relative comparison across a common scale, the plots use relative log-likelihood, while the labels above the bars are true log-likelihood values from the analysis.

Across all four datasets, the SMM model provides the best explanation for the data. To put this result in perspective, we can examine the quantitative differences in log-likelihood between the models. Because DCM calculates priors (also taking into account model complexity), the differences in log-likelihood can be used to derive posterior probabilities of one model being better than the others. Across all comparisons, the posterior probability of the SMM being the best explanation of the data was $p \geq 0.99$. Assuming, instead, uninformative priors (that is, no initial preference between models), log-likelihood differences can be interpreted as Bayes factors; thus, a difference of d in favor of model M_1 over model M_2 means that M_1 is e^d times more probable than M_2 . According to the standards established by Kass and Raftery (1995), values of $d > 30$ provides “strong evidence” for one model over the other. As shown in Figure 3, the SMM model has an advantage of at least $d > 124$ against the structural model, and at least $d \geq 30$ against the fully connected model across all tasks. Thus, across all datasets, we can conclude that the SMM is supported by strong empirical evidence.

²Note that in DCM, unlike in canonical GLM analysis, task factors do not need to be orthogonal with each other.

Discussion

This paper has provided a preliminary test of the hypothesis that human cognition depends on functional and architectural constraints that are common to every intelligent system. This hypothesis, known as the “Standard Model of the Mind”, was proposed by Laird et al. (2017) on the basis of a comparative analysis of cognitive architectures. Our preliminary study provides the first direct empirical support to this hypothesis by showing that the SMM is a reliable explanation for the patterns of data found in four human neuroimaging studies, and, furthermore, can be favorably compared against other models. More importantly, and perhaps surprisingly, our results demonstrate that the tenets of the SMM hold across a large number of participants (for a combined $N = 103$) and across four different tasks that vary greatly in terms of complexity. It is worth noting that, while the SMM was consistently selected as the best model, the relative rank of the other two models varied across tasks. In particular, the Fully Connected model surpassed the Structural model in the RITL paradigm, which requires a greater variety of mental operations and their combination. This suggests that our findings are not tied to any of the models having *a priori* less chance to fit the data. Although encouraging, these results are still preliminary, and future work is still needed. In particular, the validity of the SMM should be tested against a larger set of alternative models that covers a larger portion of the space of possible architectures. It would be valuable to replicate these analyses across more datasets that span a more diverse set of domains, including, for example, long-term memory, decision-making, and language tasks. Finally, it would be important to integrate connectivity analysis with other types of analysis that tests other assumptions of SMM; for instance, using Representational Similarity Analysis (Kriegeskorte, Mur, & Bandettini, 2008) to investigate assumptions about knowledge representations. Existing large-scale neuroimaging databases, such as the Human Connectome Project, provide perhaps the most exciting venue to further this project.

Acknowledgments

This work was sponsored by the W. M. Keck Foundation, the Air Force Office of Scientific Research (award FA9550-15-1-0157), the U.S. Army (contract W911NF-14-D-0005), the Army Research Laboratory (contract W911NF-10-2-0016), and the Office of Naval Research (awards N00014-15-1-2468, N00014-15-12151, N00014-12-C-0638, and N00014-

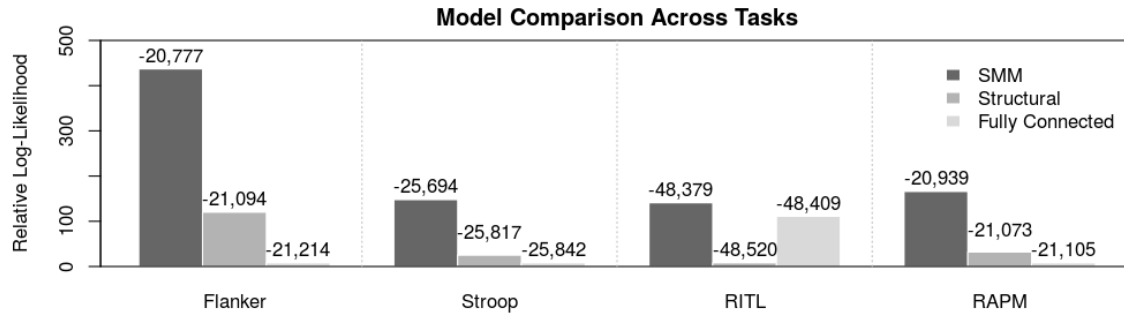


Figure 3: Bayesian model comparison across tasks. Bars represent relative and labels indicate absolute log-likelihoods

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