Social structure, endogenous diversity, and collective accuracy

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ARTICLE INFO

ABSTRACT

Markets, democracies, and organizations rely on accurate aggregate predictions to function properly. A large literature explains how accuracy can arise from diverse predictive models, typically captured as independent or non-perfectly correlated signals. Yet, that literature largely ignores how the diversity of models arises and is maintained. In this paper, we derive equilibrium levels of model diversity as a function of social structure, population size, the probability of experimentation, and the number of available models by building on a theoretical framework used to study biodiversity. We then link model diversity to collective accuracy by generalizing the bias-variance decomposition formula. Assuming equally accurate models, we find that for large populations collective accuracy depends primarily on the diversity of available models and that for small populations, social structure and rates of experimentation also matter. We then show, contrary to intuition, that dividing a population into isolated sub groups does little to increase equilibrium diversity levels. We also extend the model to allow for heterogeneity in accuracy and selection effects.

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1. Introduction

Democracies, markets, and organizations require collections of individuals to make accurate aggregate forecasts of future events and values in order to function properly (Ober, 2008; Von Hayek, 1945). These forecasts or predictions need not be exact, but they do need to lie within reasonable bounds. When predictions miss the mark by wide margins, costly consequences ensue. Capital is misallocated, firms fail, markets crash (Reinhart and Rogoff, 2009), and the masses can even fall prey to illogical ideas (Whyte, 1989; Le Bon, 1895).

The logic that underlies the possibility of collective accuracy is formalized in the Condorcet Jury Theorem. If individuals receive independent signals, their errors will cancel out.[2] More elaborate models extend that core insight and demonstrate that collective accuracy depends on (i) the difficulty of the predictive task, (ii) the level of uncertainty, (iii) the extent of social influence, (iv) the amount of model diversity, (v) the rule or mechanism used to aggregate predictions (Armstrong,

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[2] See Grofman et al. (1983) for a survey.

2001; Piketty, 1999; Lamberson and Page, 2012) (vi) whether or not forecasts are weighted,[3] and (vii) whether individuals behave strategically (Feddersen and Pesendorfer, 1997).

The extant literature on collective accuracy, though vast, takes the distribution of model and signal accuracy to be an exogenous feature of the world (Page, 2008).[4] In this paper, we demonstrate that it is possible to endogenize the distribution of signals. Specifically, we derive the equilibrium level of predictive model diversity as a function of social structure, rates of experimentation, the number and accuracy of possible models, and the extent of selection. We then show that this equilibrium diversity level is a sufficient statistic for collective accuracy by generalizing the familiar bias-variance decomposition formula.

In our model, we assume a population of individuals embedded in a social structure. Each individual relies on a model to make a prediction about some future event. Individuals can copy models from others or draw new models from a set of possible models. The accuracy of the population at any moment will depend on the diversity of models in use. We intend for this framework to approximate many real world situations. For example, within a group of doctors evaluating a patient, there will exist multiple predictive models for the cause of some symptom, and among economic forecasters, there will exist multiple predictive models for the future path of the economy. The same is true in other domains such as fashion, politics, sports, and the arts. In each case, there will exist a set of plausible models distributed across the relevant population in some way.

To solve for equilibrium diversity, we apply and extend theoretical frameworks developed for the study of diversity dynamics in biological systems (Kimura and Crow, 1964; Hartl and Clark, 1997; Hubbell, 2001). Those frameworks capture the forces that shape the diversity and distributions of biological variants, be it the diversity of genotypes in a population or species in an ecosystem. Specific models show how diversity levels are shaped through introduction of novelty (i.e. through mutation/speciation), the effects of sampling error in a finite system that dissipate diversity from a system (i.e. drift), and differences in fitness among variants (i.e. selection). Here, we take a similar approach to study the forces shaping the diversity of predictive models in a social group.

Reinterpreting biological models with social contexts is not novel. Evolutionary game theory has been applied to the dynamics of competitive types in both biology and economics for decades (Maynard Smith, 1982; Friedman, 1998). To date though, most models have emphasized selection. A large class of biological models, called *neutral models*, do not assume selection. These models are used to explore the diversity levels that arise and are maintained when dynamics are governed by mutation and drift (Kimura, 1984; Hubbell, 2001).[5]

Neutrality also applies to socio-economic systems. It does so in contexts when there exist multiple signals or models of approximately equal accuracy or when the ability to discern model accuracy is insufficient to choose among models. In both cases, there exists a set of equally plausible models circulating in the population, and the social learning process exhibit *neutral drift* where changes in population distribution result from sampling errors and stochastic fluctuations. Selection plays no role.

Neutral drift does not imply that all models are equally likely to spread in a population. Social structure can advantage some models. Empirical analyses of how people think about the world and what models they use find that individuals often borrow the models and ideas of their friends.[6] It follows that in hierarchical societies, the models adopted by high influence individuals proliferate with higher probability. In other words, the source may be as important as the content.

To account for the fact that in many social contexts selection does occur, we later extend the model to allow for different accuracy levels as well as selection. We find that selection is a double edged sword. It selects better models but reduces diversity. The former effect improves accuracy while the latter reduces it.

In the initial model, we assume an exogenous set of available predictive models. Initially, individuals randomly draw a predictive model from this set. Over time the distribution across the models evolves according to a social process that includes *experimentation*, in which an individual randomly draws a new model from the set of possible models, and *conformity*, in which an individual copies the predictive model of someone else in the population. Varying the rates of experimentation and conformity alters the equilibrium level of diversity. As would be expected, more experimentation produces more diversity and, as a result, greater collective accuracy.

The rate of experimentation can be interpreted as how often individuals form their own opinions, and the rate of conformity can be interpreted as capturing social influences, with experimentation introducing diversity into the population and conformity purging it. Though here we consider predictive models as our unit of analysis, the same formalism could be applied to the study of cultural traits or behaviors (Bentley et al., 2004; Bednar et al., 2010; Page, 2014). The mechanism through which people copy can also be made more elaborate. Individuals could, for example, refer back several periods rather than copy a current model (Ormerod, 2012; Bentley et al., 2011).[7]

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[3] See Armstrong (2001), Ashton (1986), Batchelor and Dua (1995), Lamberson and Page (2012), Breiman (1996) and Welinder et al. (2010).

[4] Variation in the realizations of signal values are typically explained by environmental variation, noise, or complexity of the inferential task (Page, 2008).

[5] We make no claims to the originality of the idea that social and biological processes may exhibit similar dynamics. See for example Cavalli-Sforza and Feldman (1981).

[6] See, for example, Huckfeldt et al. (2004) for an analysis of how voters change their ideas and opinions.

[7] Our approach differs from papers that study the spread of innovation (Young, 2009). By definition, innovations improve outcomes (provided there exist enough adopters). That's not to say that we do not consider similar questions. For example, Young (2011) shows how social structure in the form of tighter clustering allows innovations to spread more quickly through a population.