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Towards a genetically informed approach in the social sciences: Strengths and an opportunity

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ABSTRACT

Researchers agree that heritable effects influence almost all traits of interest for social science. A corollary of ubiquitous heritability is that measurement and control of genetic differences is essential for basic and applied social science. Despite this, remarkably few studies in the social sciences use genetically informative samples. Here we discuss how complex-trait behavior genetics can be used more effectively to address a range of social science questions, including multivariate genetic modeling, discordant twin designs, studies of gene-environment interaction, and adoption studies. We next advocate a concerted effort to build a new openly accessible resource to increase the utilization of genetically informative designs in social science research. Specific criteria for this proposed resource are defined and include full coverage of socio-economic status, multiple and complementary family, environmental, and genetic relationships, an open and extensible method for low–cost testing, and an open-access data repository. We suggest the cost would be moderate and returns high, generating benefits for many hundreds of researchers, maximizing impact for funders, and increase the rate of scientific progress in social science.

1. Introduction

The talk from which this paper grew was written to highlight two ideas regarding behavior genetics and social science. Firstly, most if not all behavior of relevance to societal well-being and improvement, from early development through education into workplace and economic behavior, contain heritable variation (Turkheimer, 2000). As such, behavioral genetic research is required if we are to test (almost all) social science theories, even those that do not explicitly include genetic effects. Despite this, however, behavior genetic methods are surprisingly under-utilized in social science research.

Secondly, although a good deal of research investigating heritable influences on single traits has been undertaken, study designs with multiple variables, designs utilizing discordant twins to examine causal effects of the environment, and gene-environment interaction ($G \times E$) designs that allow more sophisticated questions concerning genetic and environmental influences to be answered, are much less common. Many traits have yet even to be examined let alone different measurement instruments compared, or interactions and genetic correlations studied. Even for traits such as intelligence, the number of $G \times E$ studies remains under a dozen despite over 20 years of interest in the topic (Hanscombe et al., 2012).

After the talk, numerous researchers contacted us, asking how they could incorporate these designs in their research. It became clear that insuperable concerns over the funding and methodology required to execute these studies constitute an obstacle for the great majority of social scientists. In this paper, therefore, we not only recapitulate the argument for a substantial increase in complex behavior genetic research, but put forward a proposal for solving this need – a social-science equivalent to CERN (the European Organization for Nuclear Research; a particle physics enterprise which pools the resources of several European countries to support uniquely powerful research tools) – in the form of a genetically informative resource open to researchers. With internet and phone-based testing, the ability to easily aggregate previously collected data, and with many hundreds of researchers and students able to analyze the data, studies can be completed quickly and much more cheaply than would be the case if each researcher required an in-house research team, lacked access to already-collected data, and required a full grant application to generate the funds for the stand-alone project. To be clear, we are not suggesting that existing samples are not excellent, nor that behavior genetics lacks collaboration: Behavior genetics researchers are, in our experience, exemplary in their openness and willingness to share data and resources. Rather, we feel that creating a system which ensures that important phenotypes are studied in multiple

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behaviorally informative designs would have large and longstanding benefits to the scientific community and beyond.

The paper is organized in three main sections. The first section outlines the nature of causal inference problems in social science, and how behavior genetics can help to tackle these issues. The second section outlines a selection of powerful, but often underutilized tools which modern behavior genetics brings to social science, with concrete examples of genetically informative designs answering important social science questions. In the third and concluding section, we focus on barriers preventing many hundreds (perhaps thousands) more scientists bringing these tools to bear on their own questions, concluding that the time is ripe to build a shared, open-access, rapid turnaround capacity for behavior genetics, with a concrete suggestion for achieving this goal.

2. Why genetically informative designs are needed in social science

The need for genetically-informative designs in social science can be illustrated with the following hypothetical scenario: A researcher wishes to understand whether certain rearing environments predict offsprings' later-life anti-social behavior. As such, a study is commissioned to examine the quality of mothers' interactions with their children and from this data an association is observed linking negative maternal responses with subsequent anti-social behavior in the child. How should one interpret these findings? While it may be intuitive to conclude that this effect is environmental in origin, it must be noted that mothers provide more than just environments for their offspring: they also provide genes. It is possible, then, that the observed association between maternal response and child anti-social behavior is genetic in origin. Thus, the critical role of genetically informative designs (such as twin and family studies: described in more detail in the next section), which allow the researcher to estimate relative effects of genetic and environmental influences and so distinguish between these competing explanations, is illustrated.

While most studies of environmental influences on behavior still do not include genetic controls and thus confound environmental and genetic effects (Plomin, 2011), researchers may feel that such designs (i.e. non-genetically informative designs) can generate reliable and non-confounded conclusions by control of covariates or other statistical techniques. However, the missing information about genetic causes cannot be recovered analytically. While experimental studies are capable of producing large numbers (perhaps even a majority) of false findings due to factors as diverse as small studies, the search for small effects, and the possibility for researchers to select tested relationships ex-post facto as well as financial and other interests (Ioannidis (2005), health and social research studies searching for effects in large samples are vulnerable to additional confounds to which experimental research is not prone. This is particularly true for the effects of confounding and reverse causality; that is, misinterpreting effects as causes (Lawlor, Hart, Hole, & Davey Smith, 2006). Aggregation across studies is often thought to bolster credibility, and for experimental designs this is true. Pereira and Ioannidis (2011), for instance, examined the true-positive probability of conclusions based on a population of four hundred sixty-one meta-analyses of experimental clinical trials. They reported that of findings given meta-analytic support, while many effects were likely inflated, around 75% of findings were credible based on subsequent studies. However, if designs are not randomized and experimental, but rather observational and confounded, then reliable replication of an effect does not raise the credibility of the finding, as each study suffers the same fundamental weakness.

Another widely used strategy in social research is statistical control of correlated variables such as education and social class. Statistical control of variables in a regression framework, however, can mask the effects of a causal variable, and, perhaps worse, can introduce false associations between traits (Glymour, Weuve, Berkman, Kawachi, & Robins, 2005). More sophisticated models are possible using the same structural equation modeling (SEM) framework which underlies behavior genetics, and a substantial body of theory has placed the conclusions that can be drawn from SEM on a firm mathematical footing. This work shows that while SEM models can test causal hypotheses, many designs cannot test valid competing hypotheses, even in principle (Pearl, 2000). Moreover, and unlike the randomized control trial design, increased sample size does not dilute the effect of mistaken causal assumptions in observational designs (Pearl, 2011). Other authors too have highlighted just how critical and limiting is this conclusion for the interpretation of almost all epidemiological data (Davey Smith, 2010b), concluding that without experimental control in social and health science we are likely to keep on seeing headlines along the lines that "Taking Vitamin C reduces car accidents by 40% ..." (Davey Smith, 2010a). When subsequent experiments fail to support these false findings, the effect is corrosive of public credulity and support. Coupled with an urgent demand from people and their social organizations for breakthroughs to raise outcomes in areas as diverse as educational success, mental health, and community coherence, and the problem of contemporary social science is cast into sharp relief: Solutions are urgently needed if we are to avoid the Scylla and Charybdis of despair and false hope. Such study designs, thankfully, are available, and in the next section some of these designs are outlined, along with their ability to deliver powerful and revealing insights into the origins of complex and socially-relevant issues.

3. Behavior genetic design solutions in social science

Behavior genetic studies typically use biological relatedness between family members and patterns of co-habitation to delineate the relative influence of genetic and environmental influences on a given measure(s). For example, in the classical twin design researchers take advantage of a remarkable natural experiment afforded by the knowledge that twins come as one of two types. Identical, or monozygotic (MZ), twins are genetic clones (arising from a single fertilized egg splitting into two shortly after conception and thus producing two identical zygotes), and as such share all of their genetic matter (with the exception of any de novo mutations that arise after conception; Machin, 2009). In contrast, fraternal, or dizygotic (DZ), twins share approximately half of their variable genetic matter. (Note: we are all genetically identical to the order of c. 99.5% of our genetic matter: It is this residual variable component that DZ twins are half alike on). This biological knowledge affords researchers key information concerning the influence of genes and environments for any given trait: In short, if MZ twins are more similar to each other than are DZ twins, given the broadly identical rearing environments (i.e. same womb, age, home life, culture, etc.), this greater concordance is taken as evidence for the presence of heritable factors at work.

As with most (if not all) scientific methods, certain assumptions and constraints on interpretation must be met: For instance, a violation of the equal environments assumption would occur if MZ twins were found to be treated more similarly (as compared to DZ twins) in a manner that related to the trait under investigation. In such a situation, the heritability estimate will be inflated as the MZ twins will be more similar to each other than DZ twins for both genetic *and* environmental reasons. In addition, the common notion that heritability estimates reflect a fixed/immutable number is also incorrect: Heritable effects can differ as a function of environmental factors (e.g. parental socio-economic status) as we

discuss in more detail in a later section. Both of these issues, among other prominent topics of relevance to behavior genetic methods, have been discussed in great length elsewhere, and so instead of simply regurgitating what has been said well elsewhere we refer the reader to several excellent reviews (e.g. Martin, Boomsma, & Machin, 1997; Medland & Hatemi, 2009; Plomin, DeFries, & McClearn, 2008).

We begin the coverage of the utility of behavior genetic designs for social science by focusing on how these data can inform us about the role of the environment in influencing behavior. We then show how a suite of multivariate models, such as the common pathway model, can be used to test complex psychological theories. This is followed by a brief survey of the effects of shared environment, discordant twin designs, multivariate genetic models, gene-environment (G × E) interaction designs, and adoption studies.

3.1. A primary role of behavior genetics is in understanding the environment

As Bronfenbrenner and Ceci (1994) note, "Heritability coefficients provide the best scientific tool presently available for assessing the extent to which particular environments and psychological processes foster or impede the actualization of individual differences in genetic potential for effective development." (p. 570). A major reason for using behavior genetic designs, somewhat paradoxically then, is for the benefits they convey in understanding the influence of the environment.

One such example of behavior genetics elucidating effects of the environment is the finding that between-family effects (i.e., differences in shared environment) typically decline sharply with increasing age (Rowe, 1994). In other words, rather than the effects of exposure to parents, social status, and neighborhoods cementing and amplifying their effects, instead they appear to diminish over time. Thirty years after the appearance of Plomin and Daniels (1987) iconic article "Why are children in the same family so different?" this observation remains a considerable challenge to theories of human development (Plomin, 2011). Yet it is not known even to what class of behaviors such effects are restricted, or what the precise mechanisms of change are. Acquisition of science knowledge, for instance, appears to reverse this trend (Haworth, Dale, and Plomin (2009), with between-family differences growing in magnitude in adolescence. Such effects need more study if we are to apply such knowledge.

3.2. Discordant twins and environmental influences

Along with estimating the relative importance of the environment on development and behavior, a major goal in social science is deducing causal mechanisms among environmental activities. For instance, it might be thought that fruit is good for health (Boffetta et al., 2010), but commonly used epidemiological designs are multiply confounded, and the results may not be causal (Ioannidis & Siontis, 2011): For example, eating fruit may be correlated with a specific genetic architecture, which in turn is predictive of the health outcome. In this case, then, a study finding an association between fruit consumption and health outcomes would be spurious: Genetic factors would be the confounding third variable. One model that allows genetic effects to be effectively controlled is the discordant twin design: Here, identical twins discordant on a measure of interest (e.g. health) are investigated to determine whether a proposed protective factor (e.g. fruit consumption) is predictive of this discordancy. The strength of this study design lies in the fact that as the identical twins share all of their genetic makeup, discordant effects cannot be confounded by genetic factors (with the exception of de novo mutations acquired during development; cf. Machin, 2009), and so provides revealing insights into the role of environmental factors.

One example of the information that can be gleaned from discordant twins comes from work examining the association between exercise and lower levels of depression. People with depression also exercise less than people without depression, but is this association causal? In an initial study, De Moor, Beem, Stubbe, Boomsma, and De Geus (2006) examined this cross-sectionally in 19,288 individuals in The Netherlands Twin Registry study on lifestyle and health. Along with effects of sex and age, exercisers had modestly lower levels of anxiety and depression, and were less neurotic, more extraverted, and higher in sensation seeking as compared to non-exercisers. Experimental interventions, though often small, and confounded with compliance and non-exercise specific side-effects, such as social contact, suggest that these effects may perhaps be causal: That is, if you do exercise you will (all things being equal) lower your risk of depression. For instance, Mota-Pereira et al. (2011) examined the effects of exercise on depression in 33 treatment-resistant (non-remitting after 9–15 months of pharmacotherapy) subjects selected from 150 available patients. 22 patients were asked to walk for 30–45 min a day, 5 days per week for 12 weeks, with 1 walk per week accompanied by the researchers. Compared to 11 subjects who remained on pharmacotherapy but were not asked to engage in walking, remission rates differed (non-significantly) at the 12-week follow-up.

De Moor, Boomsma, Stubbe, Willemsen, and de Geus (2008) examined this question of causality in a genetically informative design. As one component of a multi-method twin and family study of more than 8000 individuals, they compared the subset of monozygotic twins who reported exercising more than their (genetically identical) co-twin, and tested whether these more-active individuals displayed fewer depressive symptoms than their more sedentary co-twin (see Fig. 1). The authors concluded that the small phenotypic association of exercise to depression was best accounted for by a common (pleiotropic) genetic factor influencing propensity to exercise and having opposite effects on depression; moreover, they found no significant evidence of a positive effect of exercise on depression independent of this inverse genetic association. Of course, the method can also reveal significant effects of environmental interventions. For example, in a study of 63 pairs of monozygotic twins discordant for self-reported regular vigorous exercise Johnson and Krueger (2007) reported scores .4 SDs higher on a latent factor of mood,

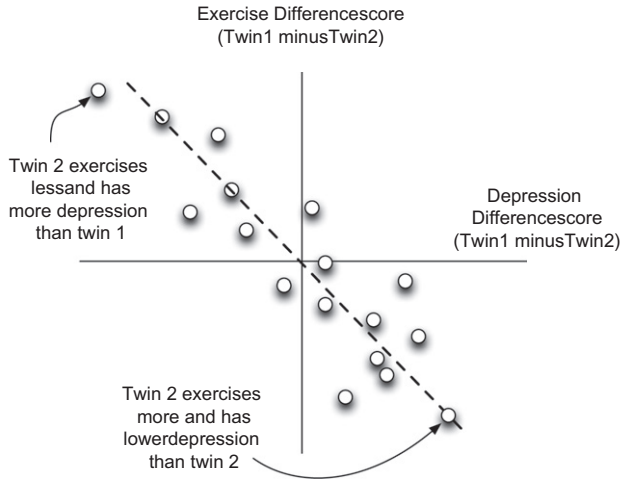

Fig. 1. Discordant MZ twin test of the effects of exercise on depression (Adapted from De Moor et al., 2008).

optimism, control over life, and social behaviors in the twins reporting higher-levels of regular vigorous exercise.

3.3. Testing social science theory using genetic models

We next turn from studies of the environment, to the use of behavior genetic designs to test complex social science theories of the structure and relationship of traits such as personality, or complex social behaviors such as in-group favoritism (Kurzban, Tooby, & Cosmides, 2001). At the simplest level, multivariate genetic studies can establish the number of distinct genetic and/or environmental factors in a dataset and so provide the means to test trait architecture. As an example, we recently used multivariate modeling to test predictions that basic needs for community integration and existential uncertainty account for the heritable bases of religiosity (Lewis & Bates, under review): In other words, in such a study design one is able to assess whether genetic and/or environmental factors between different measured traits overlap. This was the case for the heritable bases of religiosity, which in this study could be explained by genetic variation underpinning community integration and existential uncertainty.

In a similar vein, Kendler, Heath, Martin, and Eaves (1987) developed the common pathway model as powerful statistical tool in order to test theories that proposed a common underlying mechanism for a given set of behaviors. This model works as shown in Fig. 2. A common mechanism necessarily requires that all effects, be they genetic or environmental, are exerted via this common pathway, creating a "bottleneck", with the relative effects of genes and environments on this common factor able to be ascertained using a twin design. In our research we successfully applied this model to race prejudice. Here, two broad theories had emerged: The first suggested that race favoritism arises as a manifestation of broader "us vs. them" mechanisms and not race-specific processes per se (Kurzban et al., 2001). An alternative model, however, argued that race favoritism emerges via specific modules for "living kinds" or species detection (Gil-White, 2001). The common pathway model allowed us to discriminate between these theories through the predicted patterns of genetic and environmental influences on in-group favoritism (Lewis & Bates, 2010).

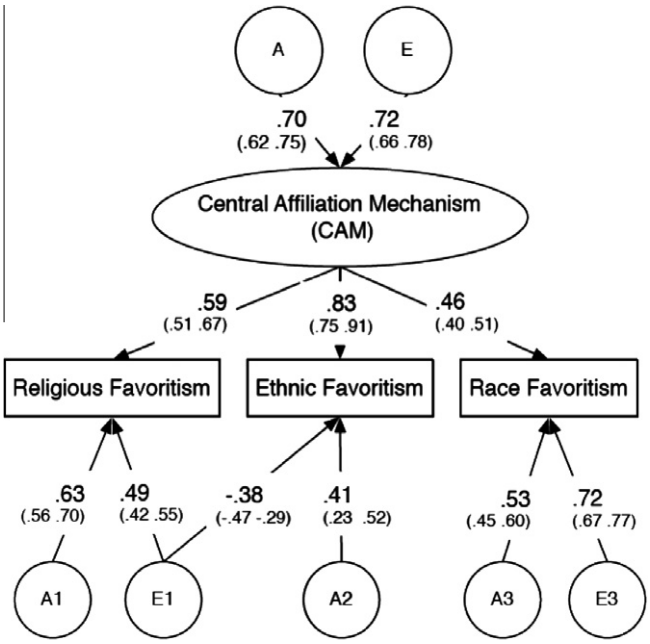

Fig. 2. Common pathway model as a test of two theories of in-group favoritism (from Lewis & Bates, 2010).

3.4. Gene-environment interaction: modeling the complexity of developmental mechanisms

The recognition that heritability (and, indeed, environmental effects) may vary under exposure to different levels of environmental moderators such as social status is not new (Plomin, Defries, & Loehlin, 1977). This perspective, however, has become more influential in recent times as models have been developed to interpret the interactions of environment and genes in terms of mechanisms, such as for translating genetic potential into achieved intelligence (Bronfenbrenner & Ceci, 1994). Progress in addressing these interactions has, however, been much too slow: Far too few studies with the ability to test models proposed by authors such as (Ceci, 1996) and Anastasi (1958) have been undertaken.

Positive (or negative) G × SES interactions are prima-facie evidence for the mechanisms via which genetic potential is realized (Bronfenbrenner & Ceci, 1994; Bronfenbrenner & Evans, 2000). As such, funding such studies is a pressing issue. Two examples of novel knowledge flowing from such designs must suffice. Tucker-Drob, Rhemtulla, Harden, Turkheimer, and Fask (2011) recently demonstrated that G × SES interactions for IQ emerge as early as 3 years of age, with high levels of between-family factors influencing variance in the development of intellectual potential among the lowest SES groups. This research is now flowing into a search for specific, likely remediable factors which this research demonstrates vary between these families.

A second high-impact finding emerged from researchers capitalizing on the number of twins naturally present in the Florida elementary school population, and the creation of a State-Level Progress Monitoring and Reporting Network archiving data on pupil progress from school staff. This natural experiment in reading pedagogy – that is, differences in teaching ability between teachers – coupled with the natural experiment afforded by twins revealed that the heritability of reading ability is highly sensitive to teacher quality (Taylor, Roehrig, Soden Hensler, Connor, & Schatschneider, 2010): More able teachers (as indexed by their ability to increase the reading ability of children they taught other than the probands) were found to maximize the genetic potential of children in their classroom.

3.5. Adoption studies

While G × E designs can reveal developmental non-linear relationships of genetic and environmental effects on measured environmental variables, other designs can inform us about the extent and effects of gene-environment covariation. Gene-environment correlation occurs, for instance, when parents pass on both genes and rearing environments in a coordinated fashion. This creates an ambiguity as to the cause of similarity in siblings. Adoption studies are one design which has the potential to attenuate or remove this correlation between genes and environment. The nature of information flowing from adoption studies is dependent on the degree to which placement is made independent of the genetic characteristics of the adoptees, but the design has distinct advantages which make it well worth while meeting these criteria. For instance, while it is often thought that twin studies have supported effectively zero levels of family impact on development, in fact the relatively few adoption studies undertaken suggest that systematic environmental influences on behavior may account for 14–22% of variance across domains ranging from IQ to personality (Buchanan, McGue, Keyes, & Iacono, 2009). Data on similarities among adopted children and their non-biological siblings and/or adopted co-twins reveal not only the effects of family environment, but also cast light on the role of gene-environment covariation on twin similarity as well as shedding light on the effects of family environment independent of otherwise covarying genetic potential in siblings and

between parent and child (Plomin et al., 2008). While adoption studies of the environment have been conducted (e.g. Loehlin & Defries, 1987), only a handful of suitable studies exist and more are needed.

Adoption studies, which reduce shared environment between adopted siblings, can also shed light on modes of inheritance. For instance, adoption designs reduce the effect of shared environment on sibling similarity. This highlights the relative importance of additive genetic effects (which have linear effects on MZ and DZ similarity) and epistatic or gene × gene interaction effects which have much larger effects on MZ similarity compared to their effects on DZ similarity. Recent studies suggest that this information will be extremely valuable for understanding whether genetic effects are predominantly additive or if they show complex non-additive effects where trait levels reflect not the sum of allele effects but rather some non-linear function of a set of alleles (Zuk, Hechter, Sunyaev, & Lander, in press).

It may not be thought realistic to pursue adoption studies due to changes in the rates of adoption compared to earlier decades and challenges with regards to legislation. Adoption designs, however, remain possible, as evidenced by the continued generation of new studies – for instance the Early Growth and Development Study (Leve, Neiderhiser, Scaramella, & Reiss, 2010). Incorporating these multiple methods into behavior genetic studies reduces the number of causal assumptions which need to be made, allows others to be tested, and increases the types of causal question that can be addressed by researchers (Plomin et al., 2008).

3.6. Additional approaches

While a brief article such as this cannot remotely substitute for a textbook presentation on behavior genetics, it is important to highlight the importance of the use of multiple types of genetically informative design to generate genetic and environmental contrasts under a range of different conditions, and to make possible the testing of more realistic models of development. Moving to more complete models of development requires the inclusion of more complex systems of relationships – for instance the "extended twin" design which includes parents, siblings, and other relatives (Keller, Medland, & Duncan, 2010; Maes et al., 2009). Such models begin to allow researchers to simultaneously incorporate assortative mating, dominance effects, shared environment, and to examine cultural transmission and homogamy (Maes et al., 2006; Vinkhuyzen, van der Sluis, Maes, & Posthuma, 2012). Likewise, longitudinal growth models are powerful tools for determining the origins and continuity of developmental causes (Neale & McArdle, 2000). For instance, where behavior genetic studies often suggest very high levels of genetic continuity in traits across time, recent work on depression suggests (perhaps surprisingly) that this disease might have a genetically distinct etiology in adolescence compared to middle-age (Martin, 2010).

In summary, we are not suggesting that any single study is magically definitive if it merely includes twins or some other genetic design: Replication remains important, and researchers must identify the correct variables to resolve causal mechanisms. We are, however, emphasizing that studies of appropriately ascertained genetically informative subjects afford the possibility of testing the causal assumptions underlying observed correlations. We next examine how such designs can be made more accessible for greater numbers of researchers.

4. How we can move forward: a proposal

Currently, researchers lack diverse genetically informative samples with open-access and nimble turn around. Imagine if you could test your favorite hypothesis in a month, with no need for a specific stand-alone grant proposal. Or could access a wealth of longitudinal genetically controlled data in your field of interest? Here we briefly sketch a research proposal for an informative and open genetically informative resource.

The potential for rapid advances based on the acquisition of comprehensive behavioral phenotypes in a range of samples with complementary genetic informativeness is clearly enormous. We propose a concerted effort, broadly engaging researchers across the social sciences to establish this resource. The proposal does not require breakthroughs in measurement or analysis. The proposal simply creates a system for open-access data collection and distribution with rapid turnaround based on high-throughput testing. The project does not involve costs out of scale with the existing funding structure, but, like other large infrastructure resources, generates benefits for an entire research community, where few individual projects could, on their own, justify the investment. The project could also complement and build on other active arms of research such as brain imaging. These modalities might use the panel subjects, and also profit from a genetically informative and incredibly well phenotyped subject pool. As time progresses, the dataset becomes naturally longitudinal, generating new information from developing children of twins, actualized social relationships, and inter-generational transfers of cultural informational (such as education) and material resources. These additional measurement projects and novel relationships will be integrated into existing data, with rich connectivity allowing multi-level modeling of such factors as economic externalities, effects of schooling variables, and effects of changing policies. The project is inexpensive when projected against the gains it offers for research efficiency and capability, enabling all researchers to access pools of subjects, and rich covariates that are currently unavailable.

4.1. Operating principles: the bazaar not the cathedral

Just as in physics and astronomy social scientists must collaborate, pooling resources in order to generate experiments on the scale needed to progress our field. Without national-level pooling, funding must otherwise be restricted to levels too-small for anyone to undertake the studies required to answer these pressing questions with greater clarity and precision. Rather than individually generating 1000 requests a year for the £200,000 required to support a lab with just a single post-doc, we must collaborate to gain efficiencies of scale, and transfer costs out of our institutions, with their overheads. If good science is cheaper, we can do more of it.

The value of open-access publication, and the data lying behind it is widely recognized in government (Department for Business Innovation, 2011), as well as by the heads of research councils for instance in biology and medicine (Kell, 2009). Progress is being made toward ensuring harmonized data formats are used (Sansone et al., 2012), and there are very successful examples of open approaches to large-scale data sharing – the Autism Genetic Resource Exchange (Autism Speaks, 2012) to cite just one example. The importance of legal infrastructure supporting open access in the intellectual property domain has also been recognized (Hargreaves, 2011). It was clear from this latter review that data "*should be accessible for non-commercial research purposes and not restricted by the out-dated copyright system. Much of this information is already well used in this way, but we must ensure that everything of academic value that might be used, can be*" (Kell, 2011). In addition to opening access to data already collected, and ensuring that new data are open for access, it is suggested here that the collection of data can also be enhanced by provision of a powerful resource (a large sample with multiple genetically informative relationships) with the ability for researchers to request novel phenotypes for collection, and a peer-review

system for approving these, in roughly the turn-around time of a journal, and at no cost to the researcher (who would also gain no privileged access to the data: It would be open for all researchers).

4.2. Sample

The paradigms introduced in Section 2 make clear that a new resource should combine not only twins reared together, but adoptees (and pedigrees, which have their own benefits: Luciano et al., 2010). Outside genetic informativeness, too much research is conducted on opportunity samples, which too often are WEIRD – an acronym coined by Henrich, Heine, and Norenzayan (2010) to encapsulate the dependence of too many studies on people who are White, Educated, Industrialized, and reside in Democratic nations – and ignore also the vast range of difference even within neighborhoods (Nettle, Colleony, & Cockerill, 2011). A prerequisite, then, is that the samples are representative of the diversity of genetic relationships, decoupled from environments, and more capable of capturing the full range of within and between-family effects.

4.3. Measures

As the designs should be chosen to resolve live debates, so too phenotype measures must include the factors predicted to be important by actively debated theories. This might be thought to open a Pandora's Box: A plethora of overlapping and ill-validated vanity scales, which would swamp any subject panel, no matter how well run and incentivized. Here we take a Jeffersonian approach: To give democracy a chance. If some 100–500 active researchers were to cooperate well-enough to make a successful grant to generate this enduring and open sample, it may be that they can also find efficient methods to agree on a modest required set of measures, resolving choices between measures competing for the same phenotype and competing phenotypes via a combination of mechanisms. Again, for reasons of space we will outline just one possible solution.

For choosing phenotypes to include, one possibility is the generation of a collaborative web site, similar to Wikipedia, but allowing researchers to create pages for open research questions. These would allow competing positions to generate "knowns and unknowns" papers (Neisser et al., 1996), ending in a list of community-agreed competing hypotheses, and linked to specific measures required to arbitrate between these competing models. Some of these would gain almost universal agreement: All subjects, for instance, would be assessed on the major domains of personality, with both peer and self-report forms. Likewise, it would be crucial to include core measures of intelligence and self-control, as well as extensive demographics, and health outcome measures. The conventional procedure involves mounting a specific bid for a large in-house project, which is assessed by a small panel of peers, and typically runs over a 3–5 year period. We suggest a more efficient system, with researchers continuously collaborating on referencing the important questions in their area, listing measures required to answer these, and proving the reliability and validity of these by citations or by running the competing measures off against each other on a very low-cost data-acquisition system such as Amazon's Mechanical Turk, which are known to be effective (DeScioli, Christner, & Kurzban, 2011). For final access to the large subject panel, we suggest researchers simply vote – that is, rank all proposed measures in terms of their scientific importance.

4.4. Costs

To take a UK perspective, an ambitious initiative to recruit, test, and retain a diverse sample of twins, parents, siblings, adoptees, and children of twins sample on the order of 15,000 subjects might cost around .5–1% of the current RCUK budget: £15–30 million of a total of £3 billion (Research Councils UK, 2012). This is not insignificant, and the work of identifying, recruiting, testing and retaining subjects for the spectrum of designs envisaged would, it is acknowledged, be a significant task, although one that we feel would be worthwhile undertaking given the ultimate scientific and social payoff.

4.5. What next?

As funding agencies are simultaneously seeking efficiencies and demanding solutions to pressing problems, we hope that as researchers we may be at a point in time where supporting and organizing this project is seen as a realistic and compelling prospect. Of course, putting together the research proposal to our funding agencies to enable this will require collaboration to conduct the detailed planning and documentation required, but this too will be beneficial for the community. We look forward to receiving comments on this proposal, and, hopefully, to implement it.

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