Application for grants within the area of Economy (E42/15)

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Area of research: Economy
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Grant manager:
Stiftelsen Institutet för Näringslivsforskning
802001-5692

Principal investigator
David Cesarini
PhD
IFN

Leveraging New Technologies to Advance Social-Science Genomics.

Nyligen har ett antal studier börjat påvisa genetiska effekter på sociala beteenden och attityder publicerats. För att ta detta spirande forskningsfält till nästa nivå krävs dock nya ansatser, såväl empiriskt, metodologiskt som teoretiskt. Det föreslagna består av flera delprojekt med fokus på ett antal för samhällsvetenskaperna centrala beteenden, attityder och personlighetsdrag. På basis av helgenomassociationsstudier (GWAS) kommer vi att undersöka i vilken mån miljontals genetiska markörer (”snippar”) är relaterade till olika ekonomiska och sociala beteenden och attityder. Vidare avser vi att utnyttja den kvasiexperimentella variation som olika policyreformer (exempelvis skolreformer) har gett upphov till för att på ett betydligt mer stringent sätt skatta hur genetiska effekter varierar tvärs olika sociala och institutionella betingelser. En viktig lärdom från tidigare forskning på området är att studier av denna typ kräver urvalsstorlekar som är tio- eller hundrafalt större än vad som är gängse inom den empiriskt orienterade samhällsvetenskapen. Med anledning av detta har vi inlett samarbeten med ett antal biobanker med vars hjälp vi kan nå mycket stora urval individer för vilka genetisk information redan finns tillgänglig. En central del i projektet är att via webb- och mobilbaserade enkäter få information om de centrala beteenden och attityder vi avser att studera för dessa individer.

Information about the grant manager

Organisation's corporate number/Personal identity number: 802001-5692
Name: Stiftelsen Institutet för Näringslivsforskning

Principal investigator contact details

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Year of disputation: 2010

Area of research

Economy

Subject

Economics

Project title

Project title

Leveraging New Technologies to Advance Social-Science Genomics.

Grant period start

2016-07-01

Grant period end

2020-07-01

Lay summary

Nyligen har ett antal studier börjat påvisa genetiska effekter på sociala beteenden och attityder publicerats. För att ta detta spirande forskningsfält till nästa nivå krävs dock nya ansatser, såväl empiriskt, metodologiskt som teoretiskt. Det föreslagna består av flera delprojekt med fokus på ett antal för samhällsvetenskaperna centrala beteenden, attityder och personlighetsdrag. På basis av helgenomassociationsstudier (GWAS) kommer vi att undersöka i vilken mån miljontals genetiska markörer (”snippar”) är relaterade till olika ekonomiska och sociala beteenden och attityder. Vidare avser vi att utnyttja den kvasiexperimentella variation som olika policyreformer (exempelvis skolreformer) har gett upphov till för att på ett betydligt mer stringent sätt skatta hur genetiska effekter varierar tvärs olika sociala och institutionella betingelser. En viktig lärdom från tidigare forskning på området är att studier av denna typ kräver urvalsstorlekar som är tio- eller hundrafalt större än vad som är gängse inom den empiriskt orienterade samhällsvetenskapen. Med anledning av detta har vi inlett samarbeten med ett antal biobanker med vars hjälp vi kan nå mycket stora urval individer för vilka genetisk information redan finns tillgänglig. En central del i projektet är att via webb- och mobilbaserade enkäter få information om de centrala beteenden och attityder vi avser att studera för dessa individer.

Budget year 2016

Personnel costs

Salary earner	HEI/Organisation	Department	LKP in %	Monthly salary full time in SEK	Work time in project, % per year	Requested sum in SEK.
David Cesarini (PhD) , david.cesarini@ifn.se	Institutet för Näringslivsforskning		50%	70,000:-	25%	315,000:-
Sven Oskarsson (PhD) , sven.oskarsson@uu.se	Uppsala universitet	Statsvetenskap	46.7%	50,000:-	25%	220,050:-
				120,000:-	50%	535,050:-

Other costs

Item	Requested amount in SEK.
Research Assistant, App Development, Surveying and Data, Travel and Meetings	1,200,000:-
	1,200,000:-

Budget year 2017

Personnel costs

Salary earner	*HEI/Organisation*	*Department*	*LKP in %*	*Monthly salary full time in SEK*	*Work time in project, % per year*	*Requested sum in SEK.*
David Cesarini (PhD) , david.cesarini@ifn.se	Institutet för Näringslivsforskning		50%	70,000:-	17%	214,200:-
Sven Oskarsson (PhD) , sven.oskarsson@uu.se	Uppsala universitet	Statsvetenskap	46.7%	50,000:-	25%	220,050:-
				120,000:-	42%	434,250:-

Other costs

Item	*Requested amount in SEK.*
Research Assistant, App Development, Surveying and Data, Travel and Meetings	1,200,000:-
	1,200,000:-

Budget year 2018

Personnel costs

Salary earner	HEI/Organisation	Department	LKP in %	Monthly salary full time in SEK	Work time in project, % per year	Requested sum in SEK.
David Cesarini (PhD) , david.cesarini@ifn.se	Institutet för Näringslivsforskning		50%	70,000:-	17%	214,200:-
Sven Oskarsson (PhD) , sven.oskarsson@uu.se	Uppsala universitet	Statsvetenskap	46.7%	50,000:-	25%	220,050:-
				120,000:-	42%	434,250:-

Other costs

Item	Requested amount in SEK.
Research Assistant, App Development, Surveying and Data, Travel and Meetings	1,200,000:-
	1,200,000:-

Budget year 2019

Personnel costs

Salary earner	HEI/Organisation	Department	LKP in %	Monthly salary full time in SEK	Work time in project, % per year	Requested sum in SEK.
David Cesarini (PhD) , david.cesarini@ifn.se	Institutet för Näringslivsforskning		50%	70,000:-	17%	214,200:-
Sven Oskarsson (PhD) , sven.oskarsson@uu.se	Uppsala universitet	Statsvetenskap	46.7%	50,000:-	25%	220,050:-
				120,000:-	42%	434,250:-

Other costs

Item	Requested amount in SEK.
Research Assistant, App Development, Surveying and Data, Travel and Meetings	1,200,000:-
	1,200,000:-

Budget year 2020

Personnel costs

Salary earner	HEI/Organisation	Department	LKP in %	Monthly salary full time in SEK	Work time in project, % per year	Requested sum in SEK.
David Cesarini (PhD) , david.cesarini@ifn.se	Institutet för Näringslivsforskning		50%	0:-	17%	0:-
Sven Oskarsson (PhD) , sven.oskarsson@uu.se	Uppsala universitet	Statsvetenskap	46.7%	50,000:-	25%	220,050:-
				50,000:-	42%	220,050:-

Other costs

Item	Requested amount in SEK.
Research Assistant, App Development, Surveying and Data, Travel and Meetings	1,200,000:-
	1,200,000:-

Totalt requested amount

8,057,850:- (excluding indirect costs and direct rental costs - these are calculated by the Foundation)

Proposal

Introduction

The widespread availability of inexpensive genetic data is transforming how medical research is conducted and is beginning to impact social science research (1). Large datasets have begun to genotype their respondents, and research has begun to identify specific single-nucleotide polymorphisms (SNPs) (sites in the genome where the base pairs carried by distinct individuals may differ) that account for some of the heritable variation in anthropometric traits and common diseases (2, 3).

Studies led by this proposal's applicants have also begun to identify genetic associations with behavioral outcomes such as educational attainment, personality and subjective well-being. This proposal seeks funding for a number of studies that will advance our understanding of the specific genetic variants associated with these and other "phenotypes." As we have outlined elsewhere (1, 4), there are several ways in which such discoveries may ultimately prove valuable for economics:

1. Directly measured genotypes could advance empirical analysis by providing better measures of preferences and abilities. These measures are key parameters in many models but are often unobserved.
2. Economists might be able to use genetic data to more effectively address economic questions with no direct connection to genetics. For example, genotype data can be used to improve the precision of an estimated treatment in a randomized controlled trial.
3. Genetic information may also be valuable for learning about how policy factors can amplify or dampen genetic risk (so-called "gene-by-environment" (G*E) interactions).
4. Identifying genetic differences that predict heterogeneity in behavior may provide an empirical basis for decomposing – even rearranging – crude concepts such as risk aversion and discounting into more primitive attributes with biological microfoundations.

Alas, there are some formidable challenges to the realization of these promises. A major hurdle is what we have dubbed the "power problem." Any true association between a complex economic trait and a genetic marker is likely to be extremely small. As a result, very large samples of genotyped respondents with measures of the behavioral phenotypes are needed to credibly identify genetic associations.

In this proposed research, we focus on attaining large sample sizes and will only conduct well-powered analyses.
In particular, we propose new ways of gathering behavioral data in large samples of genotyped respondents via smartphone Apps and internet surveys, technologies that are much more cost-effective than traditional approaches based on interviews or paper-and-pencil surveys. (Because the primary goal of most existing studies is the study of medical outcomes, they often lack high-quality measures of many behavioral traits.)

For each outcome of interest, we plan to address three primary research questions, which are relevant for realizing the eventual contributions to social science listed above:

1. Can particular SNPs associated with each trait be identified?
2. To what extent can we predict an individual's trait based on that individual's measured SNPs?
3. How do environmental circumstances moderate genetic effects (i.e., can we identify G*E interactions)?

Survey

Around 2009, we began our efforts to identify specific SNPs associated with behavioral traits measured in existing datasets. Our early papers documented that most claims in the social-science genetics literature about such associations should be viewed skeptically (5–7).

Today, this conclusion has gained widespread acceptance.

Currently, the best practice in medical genetics is a genome-wide association study (GWAS), which systematically examines the association between the outcome of interest and each of the millions of SNPs measured in "dense SNP data." To understand GWAS, it is helpful to begin with a simple model in which the outcome of interest is determined as follows:

Yi = m+Beta1*gi1+…+BetaJ*giJ+ei

where i indexes individuals, SNPs are indexed from 1 to J, m is a constant, gij is the number of reference alleles individual i is endowed with at polymorphism j and Betaj is the effect of polymorphism j (interpreted as the result of a hypothetical experiment in which the number of reference alleles is increased by 1 at conception). Given that around J = 20 million SNPs (after imputation) can be observed reliably with data from modern genotyping platforms, the sample analog of this equation cannot be estimated because the number of regressors would exceed the number of individuals in the sample. Instead, in GWAS, a regression equation is estimated separately for each SNP that passes standard "quality control filters." Typically, these tests for association include controls for sex, age and several principal components (PCs) of the genotypic data. The PCs are included to account for "population stratification," a confound present whenever the frequency of an allele is correlated with unobserved determinants of the outcome being studied. Due to the multiple hypothesis testing inherent in GWAS, the "genome-wide significance" threshold of p<0.00000005 is used.

A few years ago, it was common to (mis)interpret the fact that GWAS up to that time had identified only a small number of SNPs as evidence that GWAS is a flawed approach. Within medical genetics, today it is increasingly understood that an ever-increasing number of SNPs associated with complex phenotypes are being identified as the sample sizes have grown. For example, the first study of schizophrenia identified one SNP (8), but the most recent published study is up to 108 (3). Early studies of height identified 10-20 SNPs (9–11), whereas new research by the GIANT consortium (2), based on a sample of 250,000 individuals, identifies 700.
In addition to identifying SNPs, the GWAS results can be used to construct a polygenic score: a predictive variable for the phenotype constructed as a linear combination of genotypes. For example, a polygenic score from the 700 SNPs explains around 16% of the variance in height in independent samples.

SSGAC

The medical genetics community was able to attain sufficiently large sample sizes by forming "consortia" to meta-analyze GWAS results from multiple cohorts. To enable large samples in studies of behavioral traits, the applicants followed the same research strategy by developing a research infrastructure, the Social Science Genetic Association Consortium (SSGAC). The SSGAC was launched in 2011 and is now a fully functional research consortium. The consortium website (www.thessgac.org) contains a catalog of ongoing initiatives, updates on recent publications, and posted results (to facilitate replication and follow-up work). The SSGAC has an Advisory Board comprising prominent researchers across a variety of disciplines.

In addition to coordinating major GWAS efforts, we are coordinating the collection of harmonized preference measures for GWAS analyses. We have substantial survey-design experience and are leveraging this expertise to help cohorts participating in the SSGAC to implement new surveys to collect harmonized behavioral data. We had previously designed and implemented the Swedish Twin Registry's SALTY survey on risk preferences, trust, and political orientations, but to achieve sufficient power, additional data from other cohorts needs to be collected. The SALTY questions are a template for these efforts.

The SSGAC's first major study, a GWAS of educational attainment ("EA1"), was based on what as at the time a record-shattering N = 125,000 subjects from 57 cohorts. The study, published in Science (12), identified three independent loci that were associated with EA at the genome-wide level of significance and showed that all three replicated in an independent sample. Shortly after its publication, we published a follow-up study in PNAS on cognitive performance (13).

Since the publication of EA1, we have completed two additional large-scale GWA studies. The first is a follow-up study of educational attainment based on a discovery sample of nearly 300,000 subjects (14). This paper, EA2, identifies 74 SNPs that reach the threshold of genome-wide significance and shows that the SNPs replicate well in an independent sample (N 111,349). EA2 is currently revise-and-resubmit (third round) at Nature.

The second study (15), under review at Science, reports GWAS of three genetically correlated phenotypes: subjective well-being (SWB, N = 298,420), depressive symptoms (DS, N = 161,460) and neuroticism (N = 170,910). At genome-wide significance, we identify three SNPs associated with SWB, two with DS, and eleven with neuroticism. Many SNPs that reach genome-wide significance in the analysis of one trait (e.g. SWB) are nominally associated with the other traits (e.g. neuroticism and DS) in independent samples. SWB, DS, and neuroticism are all traits for which identifying SNPs has proven elusive. Our results illustrate the value of studying the traits jointly and in large samples.

The SSGAC has a number of procedures in place to facilitate follow-up studies by other researchers. The SSGAC website posts the GWAS results from all completed papers immediately upon publication; SSGAC researchers or contributors have no proprietary or privileged access to these data after publication. The SSGAC efforts have already substantially influenced how social-science genetics research is conducted; we are aware of over 20 ongoing follow-up studies using polygenic scores constructed from EA1 results to examine issues as diverse as the role of genetic factors in the intergenerational transmission of social status and lifecycle variation in cognitive skills and wages.

Cost-Effective Phenotyping

To date, we have been limited to studying behavioral traits available in existing datasets. Despite our ongoing efforts to gather harmonized phenotypic measures of a richer set of behavioral traits, the samples remain too small for well-powered analyses. During the 4-year period of this grant, we believe this state of affairs will change, for two reasons.

First, very large cohorts have started to become available for some behavioral phenotypes. For example, the UK government has funded a birth-cohort study of 500,000 Brits. UK Biobank ("UKB") participants have provided biological specimens for genotyping and have undergone extensive physical and mental examinations. The full data are scheduled to be released in April 2016 and will contain high-quality measures of many interesting behavioral phenotypes, including measures of cognitive function, risk attitudes, subjective well-being and neuroticism.

Second, we propose to make progress by making creative use of new technologies to measure behavioral phenotypes of interest in large cohorts of genotyped individuals. For example, we have begun a major collaboration with the 23andMe, a direct-to-consumer genetic testing company with over 1,000,000 genotyped customers. 23andMe collaborates with a limited number of academic partners, but over the past years, we have developed a strong working relationship with them. They collaborated with SSGAC on a (successful) replication study of the EA1 findings (16) and contributed data to our ongoing GWA studies on EA, SWB and fertility.

23andMe have expressed interest in letting us survey their existing customer database at a cost that is a fraction of the cost of conventional paper-and-pencil surveys. Recently, 23andMe also invited the SSGAC to be one of their academic partners as they launch a new research platform through which their customers will be able to participate in research studies via their smartphones. With one million customers, even a modest response rate to a survey will attain a sample size that as little as a few years ago would have been unthinkable.
We have developed a prototype app for iPhone built on the Apple Researchkit infrastructure (see Appendix A). The prototype, called "AskMe", currently contains four surveys (measuring trust, risk tolerance, optimism, altruism) and three games (two memory games and one logical reasoning game). In early 2016, 23andMe will announce the collaboration to their customers. We will analyze the responses of customers who download and use the app, and give informed consent for us to analyze their phenotypic and genetic data. The prototype app is designed so that it is easy to expand the number of games and surveys.

We anticipate that in the coming years, many similar opportunities for cost-effective phenotyping will materialize. One of the most promising is the Estonian Biobank, whose deputy directory, Tonu Esko, is a key SSGAC collaborator who has agreed to work with us to gather data via the App. The Estonian Biobank is on track to complete genotyping of 54,000 respondents during 2016 (with approximately half already completed), and during the grant period, an additional 200,000 subjects will be genotyped.

Projects

During the 4-year grant period, we plan to pursue two types of research projects: GWAS of behavioral traits and quasi-experimental studies of G*E.

GWAS of Behavioral Traits

Like our previously published studies, the GWAS we propose will be conducted using (constantly evolving) best methodological practices designed to (i) ensure that any observed associations are not spurious or technical artefacts and (ii) explore the behavioral and biological mechanisms underlying any observed genetic association (see the SI in EA2 for a detailed overview of the analyses that are currently considered state-of-the-art).

While the list below is not meant to be exhaustive, some of the proposed analyses are:

Project #1. Risk Aversion. A survey-based measure of general attitudes toward risk is available for around 500,000 genotyped UKB respondents. Additionally, the SALTY survey's question on risk attitudes has been gathered in a number of SSGAC cohorts (including 23andMe). Excluding any additional data gathered via AskMe, the release of the UKB data next year should give us a combined sample size of N = 600,000.

Project #2. GWAS of Subjective Well-Being (SWB2). Our current GWAS of SWB is based on a sample of 300,000 subjects, 60,000 of whom are from an early release of the UKB data. Once full UKB data are released next year, we will be able to increase the sample size to 430,000. SWB is also a prioritized phenotype for additional phenotyping via AskMe and internet-based surveys, so we are optimistic that the final sample will be even larger.

Project #3. GWAS of Educational Attainment (EA3). We anticipate that EA will be the first phenotype for which we will be able to attain a discovery sample-size of one million individuals. A polygenic score generated from the coefficient estimates in such a study are projected to have an out-of-sample R2 greater than 10% (17) – a level of predictive power at which many social-science applications become realistic. We will also use the data on the various facets of cognitive performance, measured via AskMe and UKB, to perform detailed follow-up studies of mechanisms through which the identified variants impact EA.

We also plan to gather phenotypic data on other behavioral traits, including creativity, trust, agreeableness, optimism, time preferences, typically using the SALTY questions as a template. Since these are not measured in the UKB data, we view these efforts as investments to eventually build up a sufficient sample size for GWAS.

Quasi-Experimental Studies of G*E Interactions

Researchers studying gene-by-environment (G*E) interactions must wrestle with two major methodological challenges. First, whenever G is a single SNP, its effect size (both "main effect" and interactions) is likely to be very small, implying that most existing studies, which are based on at most a few thousand individuals, are dramatically underpowered (1, 18). A second challenge is providing evidence for a causal relationship since most existing research is correlational. The first challenge can be addressed by using polygenic scores as measures of G; and the second, by importing quasi-experimental research strategies from economics.

Project #4. After WWII, Swedish educational reforms extended compulsory schooling from 7 to 9 years, delayed ability tracking, and introduced a national curriculum. A series of important papers beginning with Palme and Meghir (19) have exploited the gradual rolling-out of the reform to obtain credible estimates of the aggregate effects of the reform on earnings, schooling, and health, and to test for heterogeneous effects by family background and ability. This project, led by co-applicant Sven Oskarsson, will examine if the reform effects were heterogeneous by genotype. Preliminary results suggest that the reform led to a more equal the distribution of educational outcomes.

Research Team

David Cesarini (2010 PhD from MIT) is an Assistant Professor of Economics at NYU and affiliated with the Research Institute for Industrial Economics (IFN). He is one of the co-founders and co-directors of the SSGAC. In grant Year 1, he will be based in Sweden, and for the remaining years, he will spend at least three months per year on the project. His research on social-science genetics has appeared in numerous outlets, including QJE, JF, Management Science, JEP, Annual Review of Economics, Psychological Science, APSR, Science (2 articles), Nature Neuroscience, PNAS (6 articles).

Sven Oskarsson (2002 PhD from Uppsala University) is Associate Professor in Political Sciences, Uppsala University. He has published a number of papers applying behavior-genetic methods to political variables. These papers have appeared in APSR, the American Journal of Political Science, Behavior Genetics and numerous other outlets. Oskarsson co-led the work on G*E analyses reported in EA2, and has worked on several studies that exploit the Swedish schooling reforms to estimate the causal impact of schooling on political participation and attitudes.

The research team includes several additional Swedish researchers for whom we are not requesting salary support. Two key collaborators are Magnus Johannesson (Stockholm School of Economics) and Patrik Magnusson (the Swedish Twin Registry (STR)). Johannesson launched Swedish research on social-science genetics; he designed the economics and politics questions on the Swedish SALTY survey, coauthored the early behavior-genetic studies on the heritability of economic outcomes, and has played a key role in the development of the SSGAC infrastruture. Magnusson is the deputy director of STR, was PI of the SALTY survey, and has overseen several of STR's genotyping efforts.

Many of the projects will involve additional collaborators who have contributed to past SSGAC projects. Key collaborators are: Daniel Benjamin (economics, USC), Christopher Chabris (psychology, Union College), Tõnu Esko (bioinformatics, University of Tartu and Harvard University), David Laibson (economics, Harvard University) and Tino Sanandaji (Stockholm School of Economics).
Dan Benjamin is co-founder of the SSGAC and, along with Cesarini and Johannesson, developed the AskMe prototype. Chabris is a cognitive neuroscientist and scientific adviser to the company knack.it, which develops original apps custom-designed to measure cognitive abilities, personality traits, and preferences. Tino Sanandaji is an expert in the measurement of entrepreneurship and creativity, and designed the entrepreneurship questions included in SALTY. Laibson is an economist with extensive experience of research on the measurement of economic preferences. Chabris, Laibson and Sanandaji will provide the research team with advice on expansions of the functionality of the AskMe app in their areas of expertise.

Timeline

The GWAS on risk attitudes and SWB will be completed in Year 1, since the relevant UKB data will become available in April 2016. For Project 3, we anticipate reaching the target sample size of one million individuals in Year 2. We plan to pilot AskMe in early 2016 and gradually expand the number of surveys and games included. Though our current prototype runs on iPhone, future versions will be compatible also with Android phones, and the programs and games accessible also via web browsers. Even under a pessimistic scenario where AskMe is only used in the 23andMe customer database and the Estonian Biobank, we estimate that these efforts will provide us with phenotypic data in 200,000 subjects. However, it is of course our intention to enroll as many cohorts as possible.
Budget Justification

We are requesting funding primarily to help us develop and administer the new technologies for phenotype collection. The other requested funding is for some personnel time and for workshops in Sweden that will help push forward many of the project activities and provide training in social-science genomics to Scandinavian researchers.

Salary Support. Cesarini During Year 1, Cesarini will be on sabbatical from NYU and entirely based in Sweden. During the sabbatical, he is entitled to ¾ of his base 9-month salary from NYU and expected to cover remaining salary from grants. He and Oskarsson are each requesting 3 months of funding for each year of the grant.

Research Assistant. We are requesting funds for one RA to assist with collection and analyses of data performed as part of the projects described in this proposal.

App Development. The pilot App developed for the 23andMe collaboration was designed in collaboration with two professional App developers who charge an hourly rate of 375 SEK ($45) for their services. For each year of the grant, we have budgeted 667 hours of consulting time to pay for software development. The annual cost is therefore 250,000 SEK.
Surveying and Data Costs. 23andMe's academic pricing schedule charges a fixed fee of $60,000 per survey. 23andMe surveys have historically yielded about 60,000 respondents, implying a cost of $1 per completed survey. The exact cost cannot be forecast with certainty, but is virtually guaranteed to be lower by an order of magnitude lower compared to costs of traditional pen-and-paper surveys. We are requesting an annual budget of 500,000 SEK for data purchases. We will spend these funds wherever we deem their marginal impact to be highest.

Travel and Meetings. Team meetings are critical for expediting the work because of its highly collaborative nature. Historically, we have held annual meetings in Sweden and hope to continue to do so. We will schedule these so they either follows or precedes a training workshop in social-science genomics open for PhD students and junior faculty in Scandinavian countries (see letter from Magnus Henrekson). Historically, these workshops have cost about 250,000 SEK per year, but given the added training component we are requesting 350,000 SEK.

Ethics

All Swedish Twin Registry's surveys of SALTY data have been approved by the Medical Ethics Review Board in Stockholm. The international data are subject to similar approvals. The data collection for analyses of data collected via apps will undergo approval by institutional review boards before the research commences. We are also committed to communicating transparently about the work in a way that minimizes the risk of understanding. In conjunction with the publication of EA1, we released a Q&A document on the SSGAC website that addressed, in plain, easy-to-understand language, key questions about the study and the interpretation of the study's findings. The document was cited approvingly in an editorial published in Nature on best practices in the communication of genetics research (Nature 2013). With the help of the bioethicist Michelle Meyer, who serves on the SSGAC Advisory Board, we will continue to publish FAQs for all major publications.

1. D. J. Benjamin et al., Annu. Rev. Econom. 1, 627–662 (2012).
2. A. R. Wood et al., Nat. Genet. 46, 1173–1186 (2014).
3. S. Ripke et al., Nature. 511, 421–427 (2014).
4. J. Beauchamp et al., J. Econ. Perspect. 25, 57–82 (2011).
5. C. L. Apicella et al., PLoS One. 5, e11153–e11153 (2010).
6. C. F. Chabris et al., Psychol. Sci. 23, 1314–1323 (2012).
7. D. J. Benjamin et al., Proc. Natl. Acad. Sci. U. S. A. 109, 8026–8031 (2012).
8. S. M. Purcell et al., Nature. 460, 748–752 (2009).
9. D. F. Gudbjartsson et al., Nat. Genet. 40, 609–615 (2008).
10. M. N. Weedon et al., Nat. Genet. 40, 575–583 (2008).
11. H. Lango Allen et al., Nature. 467, 832–8 (2010).
12. C. A. Rietveld et al., Science. 340, 1467–71 (2013).
13. C. A. Rietveld et al., Proc. Natl. Acad. Sci. U. S. A. 111, 13790–13794 (2014).
14. A. Okbay et al., "Education-associated SNPs are enriched for brain function and disorders" (2015).
15. A. Okbay et al., Genetic Associations with Subjective Well-Being Also Implicate Depression and Neuroticism. bioRxiv (215AD), pp. 1–
16. C. A. Rietveld et al., Psychol. Sci. 25, 1975–1986 (2014)

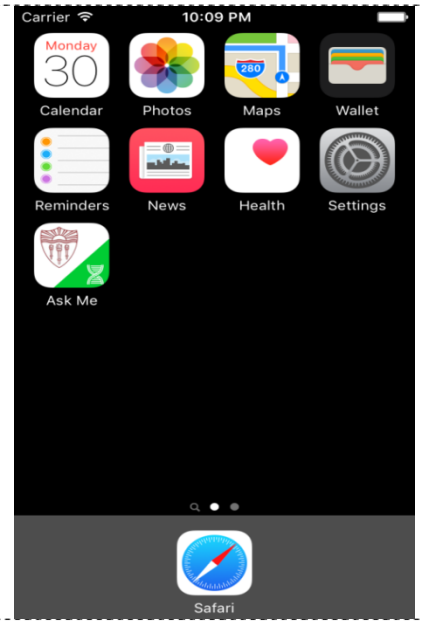
CV

CVs.pdf 123 kb

Attachments to the proposal

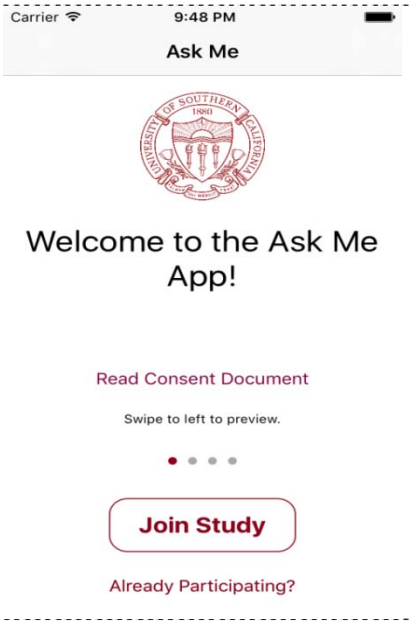
Other.pdf 387 kb

Overiew of Protype AskMeApp



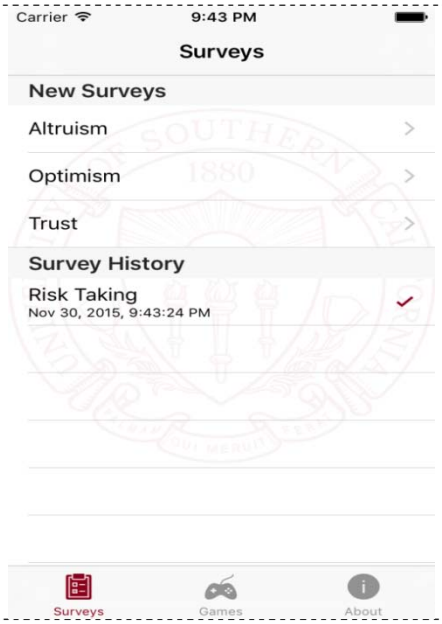
#1. Iphone Screen

AskMe app depicted on third row.



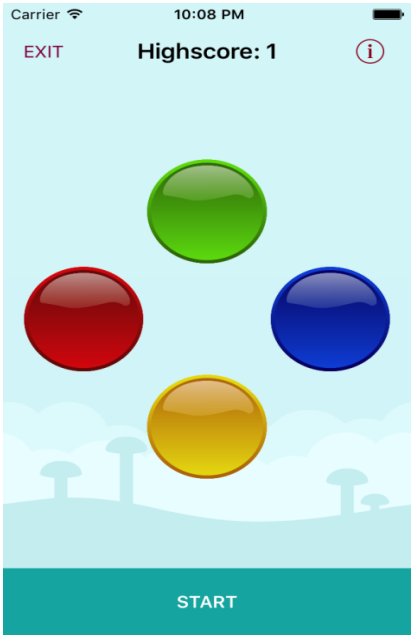
#2. Welcome Screen

Asks first-time users for basic demographic information and to read and approve consent document.



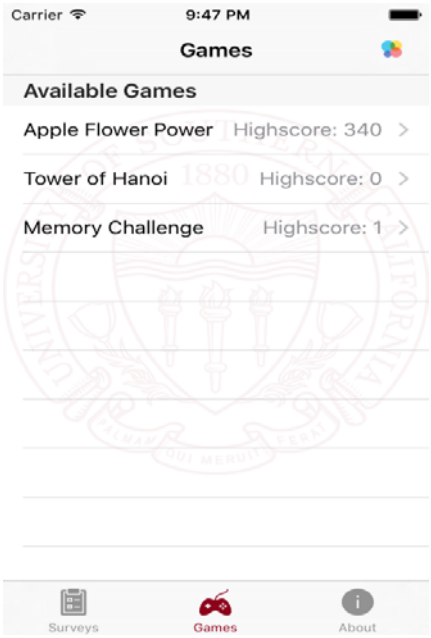
#3. Main Survey Screen

Participants can review completed surveys, take new ones, or navigate to Games or study information ("About")



#4. Sample Game ("Memory Challenge")

Short-term memory game where the goal is to reproduce a random sequence of flashing lights.



#5. High Scores

Participants can view their high scores and compare them others' (a similar feature is available for surveys).

#6. Sample Survey ("Risk")

Adapted from SALTY survey; originally from German Socioeconomic Panel.

RESEARCH INSTITUTE OF INDUSTRIAL ECONOMICS

Stockholm, December 1, 2015

Ragnar Söderbergs stiftelse
Box 7079
103 87 STOCKHOLM

Dear Committee,

I am writing to affirm the IFN's strongest institutional support for the project proposal "Leveraging New Technologies to Advance Social-Science Genomics."

The IFN has long been supportive of David's work at the intersection of economics and biology. He first visited IFN in 2009. He subsequently joined the institute as an affiliated researcher and has spent a substantial amount of time with us every year since, including much of his sabbatical year in 2013. Some of his most well-known papers, including the two papers in the Quarterly Journal of Economics and the landmark paper in Science, were written in large part during visits to the IFN.

David was recently awarded (jointly with Daniel Benjamin) a grant from the Russell Sage Foundation to teach a summer course in social-science genomics for PhD students. The course, which will be given in the US, was inspired by and will be modeled on the highly influential summer school in behavioral economics funded by the foundation for many years (taught by David Laibson and Matthew Rabin).

Under David's proposal, he and Daniel Benjamin would offer similar training to Swedish PhD students and postdocs. I believe (as the Russell Sage Foundation evidently also believes) that the work David and his collaborators are doing is likely to prove foundational. A course taught by two social scientists who have quickly established themselves as leaders in this nascent field would help secure Sweden's continued status at the vanguard of social-science genomics. Offering the course to PhD students and junior researchers from multiple disciplines and institutions ensures that more individuals will have the opportunity to receive training in state-of-the art method and helps promote interdisciplinary dialogue.

We would be delighted to support such a course in any way we can, including advertising, organization and administrative support.

Yours sincerely,

Magnus Henrekson
CEO, Professor

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