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(Article begins on next page)
Research Conducted Using Data Obtained through Online Communities: Ethical Implications of Methodological Limitations

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Strong claims regarding the benefits of research using these resources are often made in order to encourage individuals to provide personal (health) information. For example, 23andWe, the research arm of 23andMe “gives customers the opportunity to leverage their data by contributing it to studies of genetics. With enough data, we believe 23andWe can produce revolutionary findings that will benefit us all” [1]. PatientsLikeMe tells patients that sharing personal stories and health data does not only enable individuals to “put your disease experiences in context and find answers to the questions you have” but also gives “the opportunity to help uncover great ideas and new knowledge” [2]. But how valid are these claims? Can online data collection lead to major breakthroughs in health research? We worry that overstating the conclusions that can be drawn from these resources may impinge on individual autonomy and informed consent. Just as researchers must take care to accurately convey direct benefits to study participants (which, we argue, in these situations are often small), they should also describe the likely outcomes and known limitations of observational studies conducted using volunteers. Clarity regarding the benefits of research using solicited personal data is particularly important when the data collected are also used for other purposes (e.g., PatientsLikeMe may sell members’ information to pharmaceutical and insurance companies [2]), lest the allure of participation in a scientific study be used as a Trojan horse to entice individuals to part with information they might not otherwise volunteer.

“Revolutionary” Findings?

As early examples of such initiatives, 23andMe and PatientsLikeMe have already published their first scientific results. Using self-reported phenotypic data provided by their customers, 23andMe reported that they replicated over 100 genetic associations from the catalogue of genome-wide association studies (GWAS) of the National Human Genome Research Institute’s Office of Population Genomics [3], identified genetic associations for miscellaneous traits long suspected of having a genetic basis [4], and identified two novel loci and a substantial genetic component for Parkinson disease [5]. And in a study of 447 patients, PatientsLikeMe showed that lithium carbonate did not affect the rate of progression in amyotrophic lateral sclerosis (ALS) [6].

But how valid and new are these findings? One of the loci for Parkinson disease that 23andme discovered was confirmed in collaboration with the International Parkinson Disease Genomics Consortium [7], but the other loci need further replication [8,9], and

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also the newly identified associations for various traits still need to be replicated in independent samples [4]. The replication of 180 associations concerned 144 out of 392 attempted associations in case-control and quantitative phenotypes from the GWAS catalogue and 39 out of 106 attempted associations with phenotypes that were in weak correspondence with those in the catalogue. In both instances, the observed percentage of replications was less than expected based on the statistical power for each of the phenotypes tested [3]. And finally, as acknowledged by the authors, the absence of an association between lithium carbonate and ALS progression reported by PatientsLikeMe was in line with earlier observations and two prematurely stopped randomized clinical trials [10,11]. Still, it is not clear that the absence of a statistically significant finding of this particular study can be interpreted as the absence of a true effect, given the methodological limitations in online data collection. Using self-reported data from self-selected individuals is subject to several known biases in the presence of which reported frequencies, prevalences, and associations can be over- or underestimated. Table 2 lists the sources of bias in observational studies that are commonly observed but particularly relevant for studies using self-reported data from self-selected individuals [12]: selection bias, information bias, and confounding.

Sources and Implications of Bias

The first source of bias, selection bias, occurs when the study population does not represent the target or sampling population, for example when customers of personal genome tests are healthier, higher educated than the general population [13], or when participating patients are more motivated, literate, and empowered [14,15]. Selection bias is also observed when participation in a study by cases is related to a certain risk factor and participation amongst control individuals is unrelated to that factor, e.g., when depressed people are less likely to join online communities. In that example, the validity of studies in psychiatric, neurological, and geriatric diseases might be reduced, because the frequency of the risk factor in cases and its impact on disease risk are likely underestimated. Statistical techniques, such as inverse-probability sample weighting, can correct the effects of selection bias, but these require that the sampling population is known. The fact that the sampled population is unknown is a major shortcoming in studies that recruit online through participant self-selection.

The second source of bias, information bias, concerns any systematic error in the collection of data. Errors in exposure reporting that are unrelated to the phenotype being studied (“non-differential misclassification”) cannot create an association when none truly exists, although they can attenuate the estimated size of a true association. Of greater concern, errors that are related to the phenotype being studied (“differential misclassification”) can create spurious associations where none exist, or over- or underestimate the size of true associations. For example, individuals with a disease may recall their exposure history differently than those without (reporting and recall biases), especially if the exposure is widely suspected to be linked to the disease.

Misclassification of outcome typically occurs for outcomes that apparently follow from certain exposures (detection bias). In studies with continuous online data collection, outcome misclassification may be particularly troublesome because participants may report their phenotype status after learning about their risk factors and

Table 1. Examples of online research initiatives.

<table>
<thead>
<tr>
<th>Initiative</th>
<th>Aims and Claims</th>
</tr>
</thead>
<tbody>
<tr>
<td>PatientsLikeMe.org</td>
<td>“To provide a better, more effective way for you to share your real-world health experiences in order to help yourself, other patients like you and organizations that focus on your conditions.”</td>
</tr>
<tr>
<td>23andMe.com</td>
<td>“Our research arm, 23andWe, gives customers the opportunity to leverage their data by contributing it to studies of genetics. With enough data, we believe 23andWe can produce revolutionary findings that will benefit us all.”</td>
</tr>
<tr>
<td>Personal Genome Project (personalgenomes.org)</td>
<td>“The mission of the Personal Genome Project is to encourage the development of personal genomics technology and practices that are effective, informative, and responsible; yield identifiable and improvable benefits at manageable levels of risk; and are broadly available for the good of the general public.”</td>
</tr>
<tr>
<td>DIYgenomics.com</td>
<td>“A non-profit research organization founded in March 2010 to realize personalized medicine through crowdsourced health studies and apps.”</td>
</tr>
<tr>
<td>Genomera.com*</td>
<td>“We’re crowd-sourcing health discovery by helping anyone create group health studies.”</td>
</tr>
<tr>
<td>CureTogether.com*b</td>
<td>“Bringing patients into research as active partners is one of our big missions at CureTogether.” [21]</td>
</tr>
</tbody>
</table>

Quoted information was downloaded from the organizations’ websites on July 1, 2012.

*Beta version.

*Acquired by 23andMe.

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Table 2. Biases in observational studies and their potential effect when using self-report data from self-selected individuals [12].

<table>
<thead>
<tr>
<th>Bias</th>
<th>Problem When</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection bias</td>
<td>Bias occurring in the selection of the population: population studied is not representative for target population</td>
</tr>
<tr>
<td>Ascertaintment bias</td>
<td>Inappropriate definition of the eligible population</td>
</tr>
<tr>
<td>Non-participation bias</td>
<td>Non-participation is related to the outcome or risk factors investigated, e.g., depression</td>
</tr>
<tr>
<td>Healthy volunteer bias</td>
<td>Participants are healthier than general or target population</td>
</tr>
<tr>
<td>Information bias</td>
<td>Bias occurring during data collection: systematic measurement error</td>
</tr>
<tr>
<td>Misclassification bias</td>
<td>Imperfections in procedure to classify exposures or disease status</td>
</tr>
<tr>
<td>Detection bias</td>
<td>Presence of risk factors increases probability that disease is diagnosed</td>
</tr>
<tr>
<td>Recall bias</td>
<td>Recall of risk factors differs between individuals patients and nonpatients</td>
</tr>
<tr>
<td>Reporting bias</td>
<td>Reporting of risk factors differs between patients and nonpatients, e.g., patients with lung cancer may underreport smoking status</td>
</tr>
<tr>
<td>Hawthorne effect</td>
<td>Awareness of being observed influences outcome of the study, e.g., participants complete exposure/disease status on the basis of observed associations</td>
</tr>
<tr>
<td>Confounding</td>
<td>Observed risk factor is correlated with unmeasured risk factor</td>
</tr>
<tr>
<td>By indication</td>
<td>Prognostic factors influence treatment decisions</td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pmed.1001328.t002

their impact on the phenotype [4,16]. 23andMe suspected this source of bias for several traits, including athletic performance [4]. They observed that self-report of athletic status, i.e., performance in sprint or endurance races, was more in line with the observed genotype-phenotype association among customers who had viewed their genotype status prior to completing the questionnaire. Information bias might also be a problem when openness of data is encouraged such as with PatientsLikeMe. Patients can view risk factors and symptoms of other individuals before they complete their questionnaire, which may lead to biased representation of the clustering of symptoms. In general, self-reported data are known to be subject to misclassification of outcome because lay people are less aware of formal definitions and diagnostic criteria. Misclassification in the outcome variable is a serious concern, particularly when epidemiological associations are expected to be small, such as in genetic studies in multifactorial diseases.

The third source of bias, confounding, occurs when two variables are associated because both are associated to a third that might explain the association between the two. Confounding can be effectively dealt with using stratified or multivariable regression analyses when the confounding variables are measured. An advantage of online data collection is that additional questions can be asked of participants, but there are sources of confounding that cannot be solved this way. It is difficult to reliably assess confounders retrospectively and to correct bias that is caused by confounders that affect the probability of participation. Examples of potential confounders that may be associated with the probability of participation in online studies are socio-economic status and health literacy.

**Opportunities for Research**

While these biases can greatly affect the interpretation and generalizability of what can be done with self-reported data collected from volunteers, there are many situations where these data may prove useful. First, analyses can be done on risk factors and outcomes that are less susceptible to misclassification because the phenotype definition or methods of assessment are straightforward, such as for demographic information and for diseases that less likely remain undiagnosed, e.g., cancer, Parkinson disease, and ALS. Second, the data can be used for analyses where the selection of individuals is the preferred study design. Many gene discovery studies are performed using so-called extreme group comparisons, i.e., comparing patients with screened controls or comparing patients with a family history of disease with unscreened controls. Screening controls on the absence of any symptoms related to the disease of interest may compensate for potential misclassification of the outcome. And third, the data can still be used in analyses for which the presence of bias does not affect the conclusion of the study—analyses where bias may affect the magnitude of association, but not the presence of association. When expected associations are large or when the sample size is large, associations may still be significant in the presence of misclassification. But other than these, the opportunities for research are limited, as the results obtained using self-reported data from self-selected individuals may not easily withstand skepticism about the biased approach.

**Concluding Remarks**

The new initiatives of public participation in science (citizen science) by online and continuous data collection have changed our views on how to most efficiently and effectively conduct scientific studies [17], and their greatest value may be in that area. These initiatives can speed up scientific research by facilitating the recruitment of participants in a relatively easy way, which is particularly relevant for rare diseases such as ALS and Parkinson disease. PatientsLikeMe has a trial search tool, linked to clinicaltrials.gov, through which patients can see which trials are still recruiting [2]. And with their rich data collections and online opportunities for fast data updates, they can quickly put new topics on the scientific agenda and question published observational studies and trials. An excellent example was provided by 23andMe. Within a week of the high-profile publication of a putative genetic predictor of longevity, 23andMe showed that the predictor did not replicate in their data. After re-examination of their study protocol and data analysis, the authors of the longevity study retracted their initial publication [18,19]. Nevertheless, the biases in the design and data collection of the citizen science organizations warrant that most conclusions from their studies need further replication.

Initiators of online data collections are strong advocates of openness and trans-
progression, will patients discontinue treatment? Will they still trust their doctors when they were prescribed a drug that apparently does not work? Researchers should clearly explain the limitations of their approach and their findings and stress that participants should not change their medical regimens without consultation of their doctor (Table 3).

We have focused on the ethical implications of methodological limitations of research involving self-reported data from self-selected participants. Research using data obtained through online communities faces new dilemmas in relation to old issues, which require further ethical analysis and public debate, including the provision of adequate consent, the safeguard of public trust, disclosure of commercial development of research results, and the sale of participants’ data to third parties [17]. Only a responsible approach with realistic expectations about what can be done with and concluded from the data will benefit science in the long run.

**Author Contributions**

Wrote the first draft of the manuscript: ACJWJ PK. Contributed to the writing of the manuscript: ACJWJ PK. ICMJE criteria for authorship read and met: ACJWJ PK. Contributed to the writing of the manuscript: ACJWJ PK. Wrote the first draft of the manuscript: ACJWJ PK.

**References**