

The Adoption of Genomic-Related Innovations by Family Physicians

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The speed of genomic discovery has left little time for health professionals to acquire an understanding of the implications for practice. We examine the factors influencing receptivity to genomic education and adoption of the genetics-informed optimal family history (OFH) among US family physicians (FPs). We test a model based on Rogers' theory of innovation diffusion using data from a sample of 1035 FPs who completed a web-based survey. The pathways of influence are analyzed using structural equation modeling.

As opposed to Rogers' theory of innovation diffusion, we find that multiple pathways influence FPs' receptivity to the adoption of genomic-related innovations. Their inclination to be innovative, and to resist a structured practice approach, is a significant initial indicator of receptivity for both paths. In Pathway 1, this inclination is associated with FPs' increased comfort using genetic information, and in turn increased response to family history and subsequent use of the OFH and intent to undertake genomic education. In Pathway 2, this inclination increases the belief in the relevance of family history and genetics to common diseases. This in turn is associated with increased use of the OFH and intent to undertake genomic education.

The path to adoption of genomic-related innovations in family practice may not follow the sequential process described by Rogers. Moreover, the data suggest that interventions aimed at increasing FPs' belief in the relevance of family history and genetics to common diseases will have a greater positive impact on FPs' adoption of the OFH and willingness to undertake genetic education than interventions that increase FPs' level of comfort using genetic information by an equivalent amount. The paper is accessible to readers with an intermediate level of statistics. Prior exposure to structural equations models is useful but not strictly necessary.

Keywords: Family Physicians, Genetic, Genomic, Family History, Innovation

Introduction

Experts forecast that in the next two decades genomic discoveries will increase options for prevention and treatment of common multi-factorial health conditions such as diabetes, heart disease, and cancer (Guttmacher and Collins 2004, Manolio 2009). Genetic service delivery is likely to expand beyond the current specialty care paradigm – with focus on high risk populations - to primary care (Greendale and Pyeritz 2001, Khoury 2003, Gray and Olapade 2003). This already has begun with the availability of genetic tests for familial cancer syndromes (e.g. genes BRCA1/2, mutations of which are associated with an increased risk of breast and ovarian cancer) and direct-to-consumer marketing of some genetic tests (Gray and Olapade 2003, Wasson, Cook and Helzlsouer 2006, Gollust, Wilfond and Hull 2003). Currently, primary care clinicians lack knowledge and confidence about how to counsel or when to refer patients to genetic services. Moreover, most primary care clinicians do not see the value of genomics for primary care and thus do not perceive the need to become better educated about genomics (Greendale and Pyeritz 2001, Burke, Acheson and Botkin et al. 2002, Doukas and Phan 1999, Mountcastle-Shah and Holtzman 2000, Harvey, Fogel, Peyrot et al. 2007). These findings are similar to those recently reported for US Health Educators (Harvey, Fogel, Peyrot et al. 2007).

Family physicians (FPs), one of the largest US physician groups, are a primary source of care for the majority of Americans. Indeed, FPs could be optimal disseminators of genomic clinical innovations because they establish long-term relationships with patients, use a family-centered approach (Greendale & Pyeritz 2001), and see 23% of the U.S. office visits (see article at <http://www.cdc.gov/nchs/data/ad/ad374.pdf>). Thus, engaging FPs in genomic-related innovations could be instrumental in evaluating whether and how these services could be used to improve primary care (Collins 2004, Guttmacher, Porteous and McInerney 2007).

In recognition of this, the American Academy of Family Physicians (AAFP) made genomic medicine the topic of their 2005 Annual Clinical Focus (ACF) curriculum. This curriculum, offered eight web-cast modules to physicians. The period prior to the launch of this curriculum provided an opportunity to survey current practices and receptivity to innovations in genomic-related practice among this important target group of clinicians.

In this study, we examine family physicians' likelihood to adopt genomic-related innovations, as evidenced by their

intent to obtain genomic education, their adoption of the Optimal Family History (OFH), and the factors that might influence such likelihood. We propose a conceptual theory-based model, grounded in the diffusion of innovation theory (Figure 1). Discussions within an expert reviewer group also informed the development of this model.

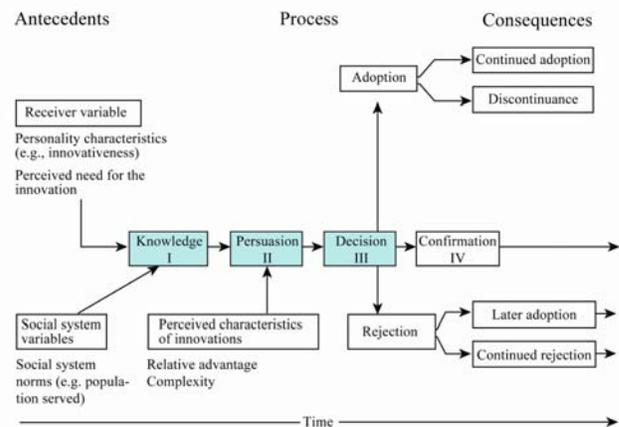


Figure 1. Stages of Innovation-decision Process
Adapted from E. Rogers, *Diffusion of Innovations* (5th edition), Free Press, 1995.

We tested the model using structural equation modeling techniques, applied to a nationwide sample of US Family Physicians. We chose structural equation modeling because it is a robust statistical technique that handles missing data efficiently, reduces type I error, simultaneously assesses all variables and their interactions as proposed in the model, and examines the fit of the hypothetical model to the empirical data (Bollen 1989, Hatcher 2005).

We sought to answer three questions: 1) What are the attitudes, current practices, and receptivity of family physicians' regarding genomic-related innovations (i.e., use of the OFH assessment as a clinical innovation and participating in genomic education)? 2) Does the proposed model adequately explain FPs' likelihood to adopt genomic related innovations? 3) Is it possible to identify specific "pathways" which might be targeted for interventions to increase FPs' receptivity to genomic-related innovations?

Materials and Methods

Instrument

Family physicians were asked to complete an online survey. The survey instrument was developed in iterative steps as follows. Measures of each domain of the

diffusion of innovation theory (Rogers 2003) were developed by our study team that included family physicians, a behavioral scientist, online survey designers, and genomics experts. These items were reviewed for clarity by outside content experts and a convenience sample of family physicians. The online survey was piloted with a second small convenience sample of FPs in the online format. At each step feedback was used to revise the instrument as needed.

The final version of the questionnaire contained 31 questions comprising the following domains derived from diffusion of innovation theory: knowledge, persuasion, and decision (described in detail below). Additionally, dispositional innovativeness was assessed as well as personal and practice-related demographics. The survey took about 30 minutes to complete. Following review and approval by the National Institutes of Health and AAFP institutional review boards, the survey was located at a portal on the AAFP home page. As an incentive to participate, physicians who completed the survey were entered in a lottery to win one of six iPods.

Participants

In January 2005, prior to the implementation of the AAFP Annual Clinical Focus on Genomics curriculum, 10,000 AAFP members were randomly selected to participate in the web-based survey. Selected physicians were sent invitation emails from the AAFP that described the purpose of the study, risks and benefits of participating, and provided participants a URL to access the survey. The sample was stratified by years since completing residency, so that half of the invitations went to physicians who had completed residency over fifteen years earlier. Invitations were sent in two groups of 5000 members each. Two reminder emails followed within two weeks of the original invitations. The survey was available online for three weeks.

Measures

Genomic-related innovations

Currently, family history (FH) assessment represents the best genomic tool available for use in primary practice (Wattendorf and Hadley 2005, Scheuner, Wang and Raffel et al. 1997, Yoon, Scheuner and Jorgensen et al. 2009). FH has been shown to have clinical utility for a wide range of health conditions (Hariri, Yoon and Moonesinghe et al. 2006, Grosse and Khoury 2006) and has been standard practice for the intake of new patients (Rich, Burke and Heaton et al. 2004). However, new and more specific recommendations in family health history assessment are emerging that may enable better

clinical characterization of inherited risks than the current standard of care (Bennett 1999, Yoon, Scheuner and Khoury 2002, Yoon, Scheuner and Peterson-Oehlke-Gwinn et al. 2002). Recommendations for collecting this “optimal” family health history (OFH) are that: 1) disease information should be collected on three generations of blood relatives, 2) among these relatives, birth defects and age of diagnosis and death from all illnesses should be collected, and 3) family history should be updated at each well-care visit (Bennett, Steinhaus and Urich et al. 1995, National Coalition for Health Professional Education in Genetics 2001) (See <http://www.nsgc.org/consumer/familytree/index.cfm>). The hope is that these additional specifications can increase family health history assessment precision in ways that increase its clinical utility (Rich, Burke and Heaton et al. 2004). However, the value of the recommended innovation represented by the OFH has not been rigorously tested against routine care, nor endorsed officially by the US Preventive Services Task Force or any national medical/advocacy groups (e.g., the American Academy of Family Physicians). Consequently, the OFH can be considered a genomic-related innovation and physicians who were currently using the OFH could be considered as early adopters of the innovation. We measure the adoption of the OFH in two ways, how often FPs use the OFH with new patients and how often they use it to update family histories of existing patients.

As already indicated, the AAFP had targeted genomic medicine for the 2005 ACF curriculum. FPs’ intent to undertake this curriculum was used as a measure of adoption for this innovation.

Diffusion of Innovation Framework

A number of factors have been suggested as critical to the successful diffusion of new practices or “innovations”. In Rogers’ (Rogers 2003) seminal theory of innovation diffusion (Figure 1), diffusion is led by a vanguard of “innovators” who familiarize themselves with the innovation (knowledge), form attitudes about whether the innovation has the potential to improve upon current practice (persuasion), decide whether or not to adopt the new practice (decision), and engage in ongoing evaluation of the utility of the adopted practice (confirmation). Innovators, often termed early adopters, are critical drivers of wide scale diffusion, modeling adoption for their social networks. As diffusion progresses, “late adopters” slowly incorporate the innovation reaching maximum diffusion.

In determining what might attract FPs to be early adopters of genomic education, Rogers suggests several factors worth considering. “Receiver” factors such as

social and dispositional characteristics, although not amenable to change, must be considered in determining who will lead innovation adoption. By comparison, factors suggested by Rogers that are amenable to intervention include awareness of the innovation, beliefs regarding whether the innovation is an improvement on current practice, and availability of opportunities to engage with the innovation.

Measures of the various domains associated with Rogers' model were developed from the items of the survey. All measures were developed or adapted specifically for this study. Table 1, in the APPENDIX, includes construct information including variables, number of sample questions, and interpretation details. Further descriptions of these measures are provided below.

Analysis

We chose structural equation modeling (SEM) as our analytic strategy (Bollen, 1989, Hatcher 2005). SEM encompasses aspects of confirmatory factor analysis and regression and consists of two parts:

- A measurement model that reflects the relationships between observed data from the survey and latent constructs reflective of Rogers' domains of knowledge, persuasion and decision. Thus, those survey items that load on each construct can be identified as a first step.
- A structural model (path model) then can be proposed that suggests an array of dependencies among the constructs to understand how each construct impacts a FP's intent to undertake genomic education and their adoption of the OFH. The path weights indicate the strength of the associated dependency.

The advantages of using this approach were twofold (Bollen, 1989, Hatcher 2005, Tomarken and Waller 2005, Muthén LK and Muthén BO 2006). First, SEM enables us to assess whether the survey items we developed actually aligns with the designated domain of Roger's diffusion model, thus offering added psychometric validity to the results. Second, SEM enables us to simultaneously estimate dependencies among multiple domains and to determine directed dependencies (i.e., directionality) of these associations and their influence on FPs' adoption of genomic-related innovations.

The measurement model

The measurement model allowed us to confirm the survey items which measured the various domains represented by Rogers' model and are described below:

- "Receiver" characteristics were assessed with a construct representing FPs' practice approach. This construct was in turn represented by two constructs:
 - preference for innovativeness; and
 - preference for less structure in their clinical practice (Jones 1997).
- The "knowledge" construct was assessed by a construct representing FPs' comfort with genetic information as measured by two constructs:
 - confidence in discussing genetics of common disease with patients; and
 - confidence in deciding what standard family history information is needed to evaluate patients' genetic susceptibility to common diseases.
- "Persuasion" was represented by a construct that indicated the relevance of FH and genetics to common diseases and was measured through five other constructs.
 - a FP's experience with using family histories; and
 - a FP's perception of the extent to which genetic risks have clinical relevance for a variety of diseases that are commonly seen in family practice. The disease constructs separate into "disease I" which includes three diseases (i.e., liver, lung, and cervical cancer), "disease II" which included three diseases (i.e., breast, colon, and ovarian cancer), "disease III" which includes four diseases (i.e., addiction, Alzheimers, asthma, and bipolar disorder) and "disease IV" which includes four diseases (i.e., coronary heart disease, diabetes, obesity, and stroke).
- The "decision" construct, represented by a FP's response to (optimal) FH was measured by items that indicated a FPs' perception of the value of the OFH to their clinical practice and patient care.

The path model

The path model linked the domains from the measurement model and the items representing adoption of the innovations, namely adoption of the OFH and intention to participate in the genomic education as was suggested in Rogers' model.

Results

A total of 1,035 physicians completed the web-based surveys, yielding a 10% response rate. Physicians with incomplete data or who reported spending 10% or less of their time with patients were excluded yielding a final sample of 912 physicians. We discuss the research questions in turns.

Question 1. The first question was about the attitudes, current practices, and receptivity of family physicians' (FPs) regarding use of an "optimal" family health history (OFH) assessment as a clinical innovation. Respondent characteristics are displayed in Table 2.

The majority who completed the survey was male and preferred an innovative approach to clinical practice. Almost all perceived genetics of common diseases to be important for primary care, but less than half felt comfortable referring patients to genetic services for common diseases. The FPs surveyed reported being comfortable using standard family history to make clinical decisions; however, only one quarter had used the optimal family history approach or intended to pursue the genomic education provided by the AAFP.

Table 2. Characteristics of Family Physicians in the Sample (n=912)

Variable	Percent (N)
Male	67 (611)
Practice in teaching/training environment	30 (269)
<15 years since residency	55 (503)
Prefer innovative practice approach*	61 (557)
Prefer structured practice approach*	51 (465)
Comfortable using family history to make clinical decisions	69 (631)
Have updated family history in existing patients	59 (537)
Comfortable referring patients to genetic services for common diseases	42 (380)
Perceive genetics of common disease to be important for primary care	95 (865)
Have used optimal family history approach	23 (212)
Intend to pursue AAFP genetic curriculum	24 (222)

Question 2. Second, we asked whether the proposed model adequately explain FPs' likelihood to adopt the genomic-related innovations represented by participation in genomic education and adoption of the OFH. Confirmatory factor analysis was used to establish the relationships between the questionnaire data and the various constructs in the measurement model. The structural equation model was fit using MPLUS version 4.1 (Muthén LK and Muthén BO 2006) to accommodate the questionnaire's skip patterns along with a multiple imputation algorithm (Schafer and Olsen 1998) for missing data. Statistical testing of the measurement model and original path model represented in Figure 1 led to the final structural model shown in Figure 2. The fit of the overall structural equation model shown in Figure 2 was assessed using a variety of fit measures.

As expected, given the large sample size, the traditional chi-squared goodness of fit measure ($\chi^2 = 1770.5$ with 752 degrees of freedom; $p < .0001$) indicated that the model did not fit the data. The other measures, the

comparative fit index (CFI=.93, greater than .9), the Tucker Lewis index (TLI=.92, greater than .9), the root mean square error of approximation (RMSEA=.039 with a 90% confidence interval [.036, .042], less than .08), and the standardized root mean square residual (SRMR=.056, less than .1) all indicated that the model provided an adequate fit to the data. The estimated standardized path weights shown in Figure 2 were all highly significant ($p < .001$).

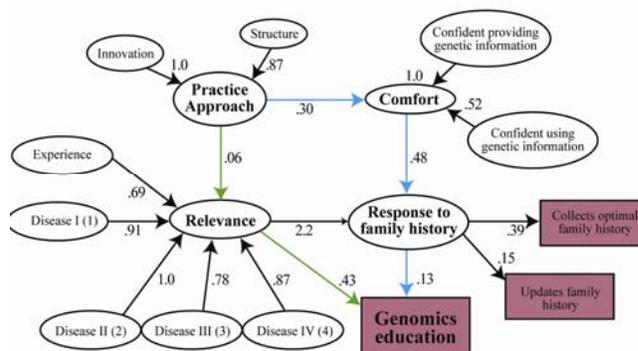


Figure 2. Structural Model to Predict Update of Genomics Education

- Disease I = liver, lung, and cervical cancer
- Disease II = breast, colon, and ovarian cancer
- Disease III = addiction, Alzheimer's, asthma, and bipolar disorder
- Disease IV = coronary heart disease, diabetes, obesity, and stroke

Question 3. Third, we asked whether it was possible to identify specific "pathways" which might be targeted for interventions to increase FPs' receptivity to genomic-related innovations. The final model indicates two pathways through which FPs became adopters of genomic-related innovations (see Figure 2), as opposed to Rogers' theoretical model which would suggest only one. The first pathway indicates a strong and significant association between "practice approach" and "response to family history" via "comfort." In this pathway those who preferred an innovative approach and resisted a structured approach to practice had greater comfort giving information to patients about common disease genetics and using standard family history assessments ($B = .3, p < .001$); that in turn increased their perception of the value of collecting an OFH ($B = .48, p < .001$). It was via this pathway that FPs became 'adopters' of innovations such as genomic education ($B = .13, p < .001$) and OFH ($B = .39, p < .001$ and $B = .15, p < .001$).

A second significant pathway to predicting adoption of the OFH and genomic education was via the influence of "practice approach" on "relevance," so that FPs who preferred innovative approaches to practice and resisted structured approaches were more likely to perceive family history assessment as clinically important and to see the relevance of genetics to clinical practice for several

groupings of common diseases ($B=.06$, $p<.001$), and thus to perceive greater value in collecting an OFH ($B=2.2$, $p<.001$). This again led to adoption of the OFH ($B=.39$, $p<.001$ and $B=.15$, $p<.001$) and intent to participate in genomic education ($B=.13$, $p<.001$). This path highlighted another difference with the underlying model proposed by Rogers. For the innovation representing the intent to undertake genomic education, there is a direct path from relevance ($B=.43$, $p<.001$) as well as the direct path from the response to family history already noted. This could be a reflection of the nature of the difference in the innovations represented by intent to participate in genomic education and by adoption of the OFH and could suggest that the structure of the Rogers model may depend on the type of innovation.

The size of the path weights provide additional insight regarding the different paths to the adoption of each of the innovations considered. In particular, if we consider the intent to participate in genomic education, the path from relevance is much stronger (.72; .43 on the direct path and .29 on the indirect path) than the path from comfort (.06 on an indirect path). This would suggest that, to influence FPs to undertake genomic education, interventions that raise the level of relevance will have a stronger impact than innovations that increase comfort by the same amount. A similar result is observed for adoption of the OFH in that the paths from 'relevance' to adopting the OFH have weights .85 and .33 respectively which are larger than the weights from 'comfort' (.18 and .07 respectively).

These results suggest that it may be easier to influence adoption of genomic-related innovations by focusing on 'relevance' issues as opposed to 'comfort' issues. The results also suggest that it may be easier to influence the adoption of an innovation such as intent to undertake education than it is to influence the adoption of an innovation such as the OFH which represents a more substantial investment in changing existing practices.

Discussion

It is well recognized that the dissemination of clinical innovations presents challenges. Educational efforts are needed to equip primary care clinicians with a knowledge base to evaluate emerging technologies and enable them to participate fully in shaping these technologies to increase their potential to improve clinical care (Burke et al. 2002, Collins 2004). Systematic conceptual approaches are increasingly being recommended as key to planning and studying integration of clinical improvements (Grol et al. 2007). The majority of respondents to our on-line survey preferred an innovative practice approach and indicated comfort using

standard family history approaches in their practice (69%). However, relatively few were routinely using optimal family history assessment approaches or were interested in genomic education offered by their national professional association.

Structural equation modeling to consider the multivariate pathways suggested by innovation diffusion theory indicated a best fitting model that had two possible pathways for increasing the receptivity of family physicians to two genomic-related innovations. The results suggest that there are different paths by which one can influence the adoption of innovations as opposed to Rogers' conceptual model that would suggest a linear sequential path. Results also indicate that the nature of the innovation may influence the strength and nature of the path to adoption. This has definite implications for the introduction of future genomic-related innovations to FPs. In particular, it would appear that influencing the perception of relevance would have a stronger influence on innovation adoption than influences to comfort with the innovation.

FPs' inclination to be innovative was an initial catalyst in both pathways. In the first, those with greatest comfort in collecting family history were most receptive to considering refinements in these assessments and seeking genomic education. Academic detailing regarding standard family history assessment and how improvements could be achieved via the greater specificity of the "optimal family health history" approach could be another strategy to engage physicians in genomic-related innovations. Providing physicians with the opportunity to utilize newly available family history tools (e.g., CDC Family Healthware™ tool (Yoon, Scheuner and Jorgensen et al. 2009)) might increase comfort with these assessments. Possible avenues include low demand professional development and continuing education opportunities to interact with general clinical innovations that occur in routine practice as a strategy to keep the clinical work force open to new technologies (i.e., grand rounds, CME credited seminars at national meetings, Internet-based CME, publications; point of care resources).

Another avenue through which FPs became interested in continuing education about genomics was via their perception of the relevance of genetics to common diseases. Indeed, those who were most interested in continuing genomic education perceived the value of genetics for several groupings of diseases that are routinely seen in primary care settings (Acheson, Stange and Zyzanski 2005). One way to enhance recognition of this value may be to focus genomic education around groupings of diseases that FPs' perceive to have a

common thread of relevancy to each other and genomics. For example, including genomic content in presentations (e.g., via case presentations or scenarios) related to familial cancers (e.g., breast, colon, and ovarian), or mental health conditions (e.g., Alzheimers, addictions, bipolar disorder) could provide an organizing framework for helping physicians see the relevancy of genomics and enhance adoption of genomic education.

Implementing models for fostering openness to innovation among primary care clinicians (Stanley, Hoiting and Burton 2007), and identifying and grooming “innovators” as early as medical school and residency could be an avenue to engage FPs in the diffusion of genomic education. Early adopters could lead efforts to introduce their colleagues to genomic innovations such as improvements in family health history assessment which would help others see the relevancy of these improvements for day-to-day clinical care.

Limitations

These results should be interpreted cautiously. The proposed pathways have not been replicated. The response rate was limited although the survey respondents demographics (67% male, 55% less than 15 years since residency and 30% practicing in a teaching/training environment) were fairly representative of the membership of American Academy of Family Physicians (68% male, 61% less than 15 years since residency and 38% practicing in a teaching/training environment). The survey respondents may not be representative of the general population of family physicians. The majority of the sample was inclined towards being innovative in their practice and again, may not represent FPs generally. Given this, it is noteworthy that only 24% indicated interest in the AAFP genomic curriculum. This suggests that issues of comfort and relevancy may present even greater challenges for the broader population of primary care physicians. Our sample of respondents included fewer under-represented minorities and women than the general population, which is reflective of the family medicine profession generally.

Despite these limitations, insights gained from this study will add to the limited literature in this area. To our knowledge this is the first effort to simultaneously consider the complexity of factors that influence family physicians engagement with genomic education. Moreover, no other studies have utilized the diffusion of innovation theory to confirm pathways which provide practical information about what efforts might influence primary care physicians’ participation in genomic education and practice change. Growing concern is

being expressed about the disconnect between the emerging tsunami of genomic discovery and the lack of a prepared workforce (Hunter, Khoury and Drazen 2008, Institute of Medicine 2008). Direct-to-consumer marketing of new tests that have yet to be evaluated for clinical utility are putting primary care providers in awkward interactions with patients who get tested (Hogarth, Javitt and Melzer 2008). New approaches to engaging the clinical workforce are sorely needed. Recognition of the value of genomic knowledge to clinical practice may be the most influential starting point to improving clinical care for all.

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Abbreviations

American Academy of Family Physicians (AAFP)
 Centers for Disease Control and Prevention (CDC)
 Family history (FH)
 Family physicians (FPs)
 National Coalition for Health Professional Education in Genetics (NCHPEG)
 National Human Genome Research Institute (NHGRI)
 National Institutes of Health (NIH)
 "Optimal" family health history (OFH)

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APPENDIX

Table 1: Model Components

Diffusion of Innovation Variable	Corresp. Model Construct	Model Construct Sub-Factors	# of Survey Items	Sample Questions	Interpretation
Knowledge	Comfort	Confident providing genetic information	7	How confident are you that you can provide information about the availability of genetic testing for common diseases?	Higher values indicate greater confidence.
		Confident using genetic information	3	How confident are you that you can use family history information to make treatment decisions for patients who have common diseases?	Higher values indicate greater confidence.
Persuasion	Relevance	Experience	4	In the past three months, how often have you used family history information when making clinical decisions or recommendations for your patients?	Higher values indicate greater experience using family history in practice.
		Disease I	3	From the perspective of family medicine, to what extent do you think that genetic risk has clinical relevance for liver cancer?	Higher values indicate greater extent.
		Disease II	3	From the perspective of family medicine, to what extent do you think that genetic risk has clinical relevance for breast cancer?	Higher values indicate greater extent.
		Disease III	4	From the perspective of family medicine, to what extent do you think that genetic risk has clinical relevance for bipolar disorder?	Higher values indicate greater extent.
		Disease IV	4	From the perspective of family medicine, to what extent do you think that genetic risk has clinical relevance for diabetes?	Higher values indicate greater extent.
Decision	Response to family history		3	How favorable or unfavorable do you feel about the proposed "optimal" family history?	Higher values indicate stronger belief about the value of OFH.
Receiver characteristics	Practice approach	Innovation	4	Please indicate how often the statement reflects your personal approach to work. I like to implement new ideas.	Higher values indicate more innovative.
		Structure	3	Please indicate how often the statement reflects your personal approach to work. My ideas challenge established views.	Higher values indicate greater resistance to structure.
Adoption			3	Do you intend to participate in the 2005 ACF genomics curriculum? In the past three months how often have you collected an OFH from a new adult patient? In the past three months how often have you updated a family history (using an OFH) for a continuing patient?	Higher values indicate stronger intent. Higher values indicate greater adoption. Higher values indicate greater adoption.