Personalized Medicine Implementation with Non-traditional Data Sources: A Conceptual Framework and Survey of the Literature

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Summary

Objectives: With the explosive growth in availability of health data captured using non-traditional sources, the goal for this work was to evaluate the current biomedical literature on theory-driven studies investigating approaches that leverage non-traditional data in personalized medicine applications.

Methods: We conducted a literature assessment guided by the personalized medicine unsolicited health information (pUHI) conceptual framework incorporating diffusion of innovations and task-technology fit theories.

Results: The assessment provided an overview of the current literature and highlighted areas for future research. In particular, there is a need for: more research on the relationship between attributes of innovation and of societal structure on adoption; new study designs to enable flexible communication channels; more work to create and study approaches in healthcare settings; and more theory-driven studies with data-driven interventions.

Conclusion: This work introduces to an informatics audience an elaboration on personalized medicine implementation with non-traditional data sources by blending it with the pUHI conceptual framework to help explain adoption. We highlight areas to pursue future theory-driven research on personalized medicine applications that leverage non-traditional data sources.

1 Introduction

Personalized medicine is becoming more informed by non-genetic factors with the explosive growth in availability of health data captured using non-traditional sources such as online social networks (e.g., Twitter, online health forums) [1, 2], consumer health wearables, and medical devices (e.g., FitBit, smart phone apps) [3-5]. For personalized medicine applications, these health data are promising to complement genetics data in the development of novel algorithms and risk scores that provide a more complete view of patient health and wellness. This is particularly true for complex polygenic diseases that are especially difficult to predict. For those diseases, combining multiple factors such as clinical, demographic, environmental, and genetic data can offer more precise risk predictions [6]. For example, genetic risk scores developed based solely on multiple contributing genetic variants leading to common conditions such as coronary heart disease [7], may be combined with more traditional factors (e.g., family history, conventional risk scores) including from non-traditional sources such as mobile devices to improve the accuracy of risk estimates.

The success of emerging approaches combining genetic and non-genetic factors to advance personalized medicine will depend on our capacity to deploy tools that leverage non-traditional data sources in a timely manner [8]. Mobile data capture has potential to augment traditional approaches such as questionnaires to collecting social factors (e.g., habits and preferences), high frequency data (e.g., movement) and unstructured data (e.g., online activity). Within clinical research, mobile devices are already increasingly deployed to gather patient-reported outcomes and to associate behaviors with clinically informative biomarkers.

There are three areas where approaches that leverage multiple data types are having an impact on personalized medicine. First, healthy individuals are increasingly receiving health data (e.g., direct to consumer genetic testing) that indicate a risk for poor outcomes (e.g., diseases or adverse drug reactions). When health data collection is initiated outside of the clinical setting ("person-generated data" [9, 10]), from a clinician's perspective they can be characterized as "unsolicited health information." Health care providers will need to ensure that results from unsolicited health information are handled prudently, by addressing the receipt of the results, workflow challenges, and liability issues. Second, combining data from multiple sources has potential to provide a more complete view of the relationship between how health is managed (therapies, lifestyles, etc.) and health outcomes (response to therapy, disease burden, etc.) when assessing risk compared to risk assessments accounting for a single data type alone [6, 11]. Solving the problem of integrating data from multiple sources in risk assessments will have a major impact on personalized medicine by providing a more complete assessment of individual risk for poor outcomes. Third, health assessments based on innovative technologies can lead to population samples that contain bias [12, 13] and that can contribute to misestimating health risks in those populations (e.g., GWAS data for genetic risk

scores [14]). In order to minimize bias, data collection strategies that minimize over or under sampling of a given population (sample disproportionality), especially among racial and ethnic populations, are needed.

The success of personalized medicine depends on translational research of tools based on algorithms and risk scores, including the study of dissemination and implementation with evidence-based genomic applications [15]. Traditional approaches to study algorithms and risk scores draw from data-driven research. *Data-driven research* [16] involves creating or obtaining sources of data relevant to assessments of health and risk; cleaning, extracting, and annotating data streams to prepare for analyses; integrating, aggregating, and representing data to detect insights; analyzing and modeling data to place insights in context; and interpreting the insights to arrive at solutions. Traditional approaches fail, however, to assess the implementation and dissemination of those solutions with respect to healthcare settings. *Implementation science* is the study and application of methods to promote adoption of research findings into practice [17]. *Dissemination science* is the study of how the outputs of implementation science (i.e., evidence-based practices, programs, and policies) can be best communicated to potential adopters and implementers to produce effective results [18]. In order to evaluate implementation and dissemination of new and emerging tools that leverage non-traditional data sources in personalized medicine, theory-driven research is required. *Theory-driven research* [16] involves: deriving research questions from existing or extended theory; formulating hypotheses to address the questions; designing studies to minimize confounding effects; collecting data using appropriate instruments; and analyzing data to draw inferences.

The objective of this paper is to provide a review of what kinds of theory-driven analyses are being applied to study tools that use non-traditional data sources and their translation into personalized medicine applications. In order to address this objective, we conducted a systematic and concept-centric review of the biomedical literature. We analyzed eight publications in terms of constructs from a conceptual framework for technology adoption that we call the personalized medicine unsolicited health information (pUHI) framework. This allows us to understand and structure existing work, as well as to derive future research directions.

2 Personalized Medicine Unsolicited Health Information Conceptual Framework

With a focus on implementation and dissemination of personalized medicine solutions that use non-traditional data sources, different models can be drawn from to explain the adoption of information technology. Commonly used to assess technology in health care, are the Technology Acceptance Model (TAM) [19-21] and the Unified Theory of Acceptance and Use of Technology (UTAUT) [22, 23]. The previously used personalized medicine unsolicited health information (pUHI) framework we developed [24] was used to guide the literature review. While other models solely focus on technology adoption, the pUHI framework draws from two theories that allow the investigation of both effective communication of health information and technology: diffusion of innovations (DOI) [25] and task-technology fit (TTF) [26] (see Figure 1). This framework was previously used to guide our study that explored the acceptance of electronic health record (EHR)-embedded clinical decision support to deliver pharmacogenomics information to physicians [24].
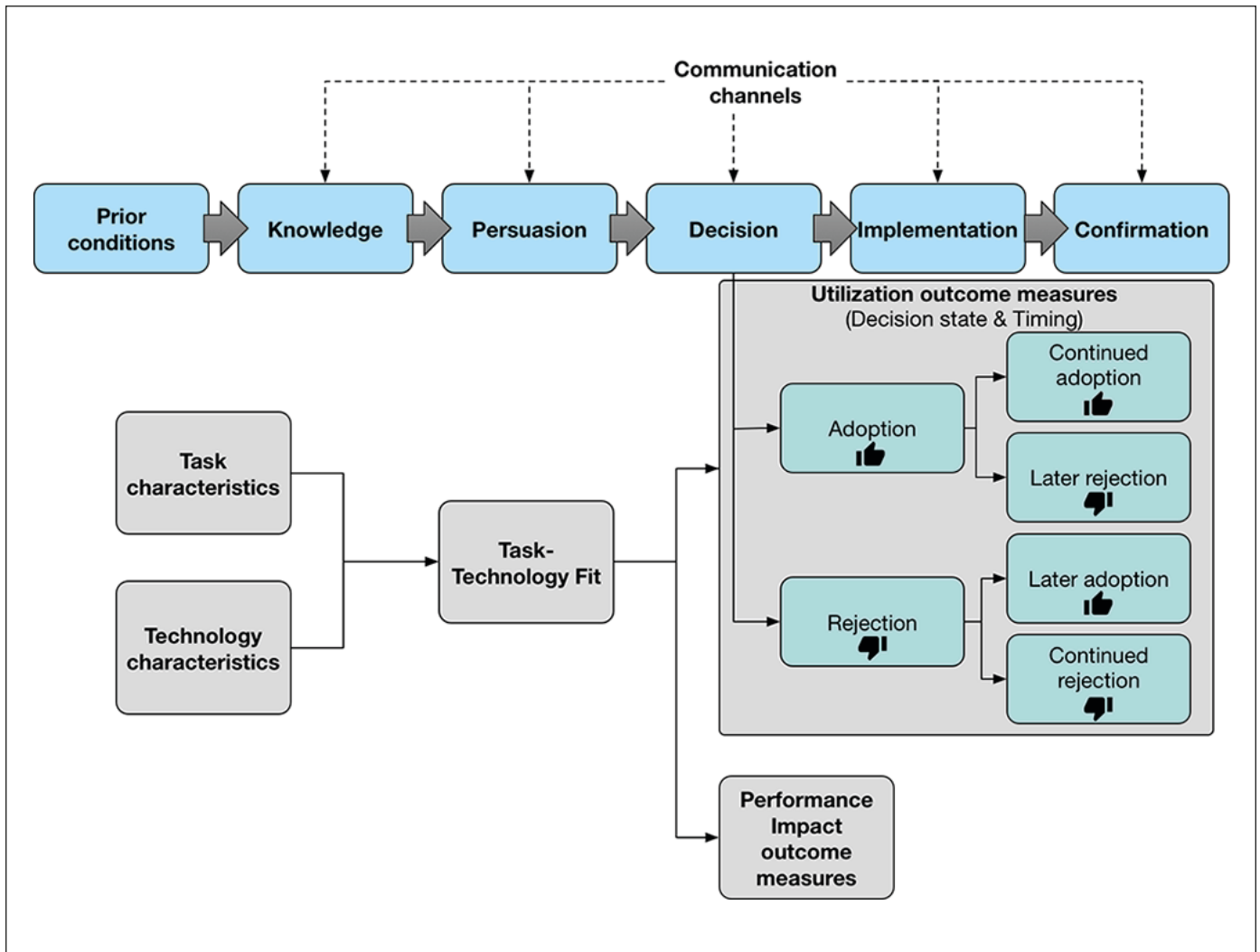
Diffusion of innovations [25] theory seeks to evaluate the rate of technology adoption using four key elements to help to explain the "Innovation-Decision Process": innovation (a solution that leverages health data from non-traditional sources), communication channels (processes enabled by the proposed solution), time (when the solution is adopted or rejected and the rate of adoption), and social system (individuals and groups involved in implementation and dissemination strategy decisions for a solution). TTF [26] theory suggests that task-technology fit is achieved by both the tasks the user performs and the character-

istics of the technology used. Fit, in turn, leads to utilization and performance impact.

Use of pUHI framework offers many advantages including the ability to identify how, when, and in whom important variables from DOI and TTF theories were measured; the ability to determine what potential sources of variance were evaluated and controlled for; and the ability to extract how and when solutions are successful. Furthermore, DOI and TTF complement each other. The goal for dissemination is broad-based adoption of an intervention, and as such, both diffusion and implementation factors are important. DOI captures dissemination factors including those relevant to the innovation, adopter, social system, individual adoption-process, and diffusion system. TTF captures extent of, quality of, and individual responses to implementation. In addition, it has been highlighted that cultural differences have important implications for perceptions of TTF [27]. Whereas cultural perceptions are not explicitly part of TTF, communication channels and social system elements from DOI can capture those perceptions. For these reasons, we used the pUHI framework to develop the search strategy for the biomedical literature review.

3 Methods

Our review is made of three phases. First, we retrieved publications from PubMed that were published between 2014 and 2018 to focus on recently developed and published efforts in the clinical and biomedical literature. The broad keywords and topics used for the search are displayed in Table 1. Keywords and MeSH terms related to non-traditional data sources focused on the data collection tool itself (e.g., the survey instrument), thus, we did not include platforms such as Twitter. The inclusion criteria for screening were as follows: mention of a personal data collection tool; English article; manuscript in peer-reviewed scientific journal; research article; and human participants. The exclusion criteria for full-text reviews were as follows: no study of a tool using non-traditional data; not theory-driven in relation to the use of a tool; and no genomic medicine application.

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Fig. 1 Personalized medicine unsolicited health information (pUHI) framework to interpret theory-driven studies on tools that use non-traditional data in personalized medicine applications, relative to innovation attributes, social system, communication channels, and task-technology fit of the technologies.

Table 1 Terms and filters used in the search.

Theory-driven research	AND	Personalized medicine application	AND	Collection of non-traditional data source
Keywords: theory, construct.	AND	*PubMed Medical Genetics Search Filter Categories[28]:* diagnosis, differential diagnosis, clinical description, management, genetic counseling, molecular genetics, genetic testing.	AND	*Keywords and Mesh terms:* telemedicine, telehealth, telesurveillance, social media, blogging, crowdsourcing, mobile applications, cell phones, handheld computers, geographic information systems, global positioning systems, mobile health, mHealth, eHealth, Facebook, online social network, social networking site, chat room, chat group, short message service, Web-based questionnaire, app, personal digital assistant, cell phone, cellphone, cellular phone, cellular telephone, mobile phone, mobile telephone, smart phone, smartphone, mobile phone, mobile device, wearable sensor, wearable device, wearable technology, surveys, questionnaires, momentary assessment, self report.

Second, we coded the identified literature along six dimensions from the pUHI framework (see Table 2): attributes of innovation, social system, communication channel, time, task characteristics, and technology characteristics. We also included one additional dimension to capture the theory being used in the research. Last, we analyzed the literature by using a concept matrix to assess the current state of theory-driven analyses being applied to study tools that use non-traditional data sources and to derive directions for future studies.

4 Results

A total of 702 references were retrieved from the PubMed search and entered into the selection process. Results of the screening process are described in the Figure 2 flow diagram. First, after review of publication titles and abstracts, 430 publications were considered irrelevant and were excluded from further review. Publications were considered irrelevant according to our screening inclusion and exclusion criteria. Second, the full-texts of the remaining 272 publications were reviewed against the criteria (a *study* of a tool that used non-traditional data sources, the research was theory-driven in relation to the tool, and there was a personalized medicine application), which excluded another 264 publications. One exception was that randomized controlled trials for which study participants were randomized to use of a technology was considered theory-driven in relation to the technology. Overall, the search of the literature identified eight articles that reported theory-driven research on the use of a technology or instrument that uses non-traditional data sources for a personalized medicine application.

A concept matrix was created to summarize insights gained from the literature (Table 3). In the following, we present the details of our analysis that led to the creation of Table 3. With regard to the *attributes of innovation*, we considered Roger's characteristics on the adoption of an innovation [25]: relative advantage, compatibility, complexity, trialability, and observability of the innovation were described. For two of the articles [29,

Table 2 Coding dimensions informed by theoretical domains from the pUHI framework.

Theoretical domain	Analysis categories	Characteristics within the categories
Diffusion of innovations	Attributes of innovation	Relative advantage, compatibility, complexity, trialability, and observability of the innovation [25]
	Social system	Socioeconomic characteristics, norms, expectations, or potential consequences of an innovation
	Communication channel	Patient portal, cell phone, FitBit, blog, etc.
	Time	Speed of adoption
Task-Technology Fit	Task characteristics (genomic medicine application)	Genetic test ordering, cancer treatment planning, etc.
	Technology characteristics (non-traditional data collection approach)	Genetic testing turn-around time, cancer treatment pre-visit education, etc.
Other	Theory used	Task-technology fit theory
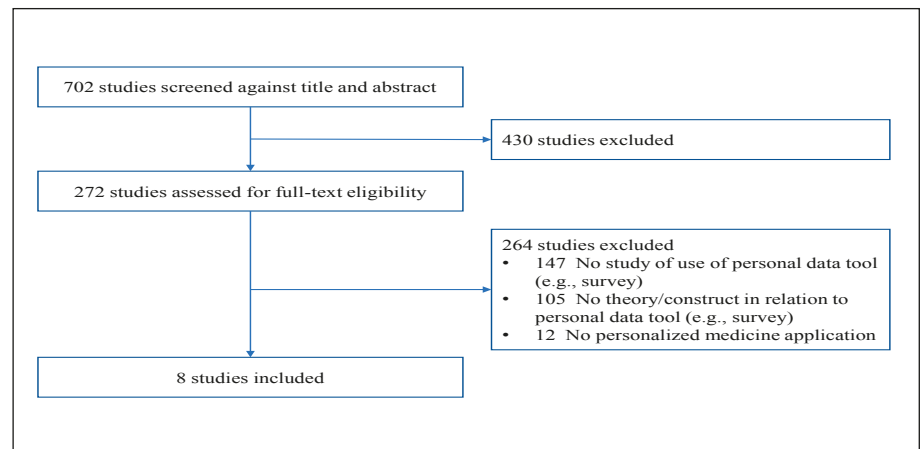
Fig. 2 Flow diagram of the search strategy.

30] a description of attributes was the outcome of the study, five of the articles [31-35] provided a general description of attributes, and one article [36] provided a reference to a description published elsewhere. Concerning the *social system*, all but one article [29] studied the influence of social system on outcomes. Among those articles, two articles [30, 32] studied social system in relation to adopting a tool. *Communication channels* represented among the eight studies were questionnaires [30, 34], telephone [33, 36], interactive presentation [31], pre-test counseling [32], online risk calculator [35], and

online discussion forum [29]. *Time* to tool adoption was not assessed for any of the reviewed articles. For two articles [30, 32], however, tool adoption was studied as a specific outcome. *Task characteristics* included tasks for tool use and were targeted to healthcare providers for one article [30], to patients for six articles [29, 31-33, 35, 36], and one article did not have a target end-user [34]. The healthcare provider task was to identify at-risk relatives [30]. Patient tasks included communicating risk to family members [31], making decisions around genetic testing and screening [32, 36], understanding genetic

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test results/assessments of risk [33], and making decisions around care coordination [29]. *Technology characteristics* included technology design characteristics of three tools that were informed by behavior and/or communication theories [31, 33, 36]. Four tools were used to directly characterize personal health status [32, 34, 35] or the health status of relatives [30]. One tool enabled unstructured communication [29]. The *theory-driven approaches* used in the reviewed studies included randomized controlled trials [31, 36], Normalization Process Theory (NPT) [30], Multidimensional Measure of Informed Choice (MMIC) [32], Self-Regulation Model of Health Behavior (SRTHB) [33], Rasch Unidimensional Measurement Model [34], Theory of Planned Behavior [35], and Planning Theory of Communication [29].

5 Discussion

The goal of this biomedical literature analysis was to examine the current state of theory-driven research on tools that collect and use non-traditional data in personalized medicine applications and to provide direction for future work. The PubMed search was limited to articles published between 2014 and 2018 to focus on recently developed and published efforts. Nonetheless, there may be relevant publications before 2014 or in other databases (e.g., ACM digital library) that were missed. For example, our approach identified studies that use theory-driven approaches such as NPT, but we did not identify studies that used popular technology acceptance theories such as TAM. In order to confirm if a gap exists, a complementary survey of the literature might study published articles that specifically use technology acceptance theories to measure the adoption and use of personalized medicine applications more broadly (without the focus on collection and use of non-traditional data).

In addition, our search strategy did not identify some studies due to our focus on the direct application of theory to study the adoption of tools. For example, one effort of relevance that was missed is the NIH National Human Genome Research Institute

(NHGRI)-funded Implementing GeNomics In pracTicE (IGNITE) Network that supports the development of strategies to incorporate genomic information into clinical care, and also the exploration of methods for effective implementation, diffusion, and sustainability of those strategies in diverse clinical settings [37]. Through the Network, sites have adopted the Consolidated Framework for Implementation Research (CFIR) [38] to guide their evaluation of genomic medicine interventions and have identified common strategies to address implementation challenges [39, 40]. They do not assume specific relationships between individual constructs and outcomes so that commonalities and differences in implementation strategies across projects that have diverse outcomes can be identified.

Another limitation of our approach is that there are some concepts relevant to adoption that may have been missed by the proposed pUHI framework. For example, while DOI theory provides several innovation-related constructs that are relevant to healthcare technology adoption such as relative advantage and compatibility [41], trust is an important element of adopting personalized medicine applications that is not covered. Indeed, it is well-known that trust plays an important role in both adoption of healthcare technologies by clinicians (e.g., due to a perceived threat to their professional autonomy [42]) and by patients (e.g., due to privacy concerns [43]). Extensions of the pUHI framework should be considered to include trust as well as other factors as the role on end-user acceptance is clarified.

Overall, we found only eight publications that fit our criteria. Given our use of PubMed, this may indicate a lack of work published in biomedical journals that study the adoption of personalized medicine applications that use non-traditional data. This is not surprising given our targeted search and also that previous characterization of the scientific literature and federally funded grants found that the majority of genomic research falls within the translational research discovery phase (T0) and the phase where candidate genomic applications are characterized and developed (T1) [44]. Less than 2% of research falls within phase 2-4 research (T2-4) that attempts to translate genomic discovery into

real-world settings and improve population health outcomes [45]. Furthermore, a recent systematic review of T2-4 research found that very few studies incorporated implementation science theoretical models [46]. Similarly, when assessing studies that evaluated IT-based applications in healthcare, most did not discuss a specific theory being applied [47].

In addition, the few articles that fit our criteria may also reflect a lack in the use of non-traditional data sources for personalized medicine research and practice. In order to enable personalized risk assessments from non-traditional data sources, there were several challenges, largely due to the reliability of those data that should be overcome. Many potential sources for more data-driven applications (artificial intelligence and machine learning algorithms) were highly unstructured and had variable quality depending on the source (e.g., online health forums). Moreover, properly describing the environment context for such applications remains a challenge. Proposed solutions to this problem included incorporating the review of input data by domain experts given that those data can contain biases; conducing prospective clinical trials with diverse patient populations to help address potential racial bias due to the use of historical data; and continually calibrating models with human feedback [48].

We also found that while articles covered in this review had personalized medicine applications, the majority of the approaches did not involve the direct collection and use of genetic data. This is consistent with the view that collection of genetic data clinically is still inhibited by cost and availability of facilities required to handle the clinical genomic sequencing of the large number of patients needed to impact population-level risk modeling [49]. There are, however, several large efforts that are studying the value of clinical genomics with other data types such as the NIH-funded *All of Us* program that is obtaining access to electronic health records and collecting personal genetic, lifestyle, and environmental data to determine relationships to health and disease [50].

Based on our assessment, we propose four directions for future research (Table 4):
a) We need more studies on the influence of innovation and of societal structure on the adoption of strategies that use non-tradi-

Table 3 Concept matrix.

Article	Attributes of innovation	Social system	Communication channels	Time	Task characteristics	Technology characteristics	Theory-driven approach
[30]	Experiences and views about using S-FHQ to refer relatives to genetic services (Focus groups)	Experiences and views about taking family history, approaching relatives of affected individuals, and referring these relatives to genetic services (Focus groups)	Questionnaire	Not studied (Note: outcomes related to the tool was primary care professionals' views about using the S-FHQ)	Identify at-risk relatives of patients with genetic conditions	Seven-item family history questionnaire (S-FHQ)	Normalization process theory (NPT) [65-67]
[31]	KinFact intervention design description	Demographics and other measures (birthdate, race, ethnicity, highest educational level, personal cancer history)	Review of individualized breast/colon cancer risk, and interactive presentation about cancer and communication	Not studied (Note: outcomes related to the tool was whether participants reported collecting family history, shared cancer risk information with relatives, and the frequency of communication with relatives)	Enhanced family communication about cancer risk	20-minute KinFact intervention based on communication and behavior theory	Randomized controlled trial
[32]	Description of information on Non-invasive prenatal testing (NIPT) given to women during pre-test counseling	Knowledge, Attitude, Deliberation (Interviews drawing from MMIC); Decisional Conflict Scale; State Trait Anxiety Inventory (STAI-6); questions to explore motivations for testing and preference for test attributes; questions on parity and socio-demographic questions (Questionnaires)	Pre-test counseling	Not studied (Note: outcomes related to the tool was uptake of NIPT)	NIPT for aneuploidy following Down's syndrome screening	Non-invasive prenatal testing (NIPT)	Multidimensional measure of informed choice (MMIC) [68, 69]
[36]	Description of telephone counseling intervention	Demographic characteristics (gender, age, race, ethnicity, education, risk level, household income, health insurance status, regular doctor status); Baseline characteristics related to colorectal cancer screening (e.g., past screening history, knowledge of guidelines, intentions to screen, risk perception, barriers to screening) (Phone interviews)	Telephone	Not studied (Note: outcomes related to the tool was adherence to colonoscopy in members of high-risk families)	Developing an individualized action plan based on readiness for colorectal screening	Tailored telephone counseling intervention grounded in behavioral theory	Randomized controlled trial
[33]	Description of telephone disclosure communication protocol	Participant characteristics (age, race, education, marital status, history of cancer, treatment decision, status of known mutation in family, genetic test [BRCA 1/2] results)	Telephone	Not studied (Note: outcomes related to the tool included psychological distress, satisfaction with genetic services, and opinions and experiences regarding telephone disclosure post-disclosure)	Communicating BRCA1/2 (breast cancer) test results	Theoretically grounded protocol for telephone disclosure	Self-Regulation Model of Health Behavior [70, 71] (to study patient and provider open-ended responses on advantages and disadvantages to telephone disclosure)
[34]	Description of questionnaire development	Basic characteristics (age, gender, duration of illness, stage of FAP, and having had a liver transplantation or not)	Questionnaire	Not studied (Note: outcomes related to the tool was measurement precision)	Detecting activity and participation restrictions in patients with Familial Amyloid Polyneuropathy (FAP)	FAP Rasch-built overall disability scale (pre-FAP-RODS); and FAP-specific symptoms inventory questionnaire (FAP-SIQ)	Rasch Unidimensional Measurement Model (RUMM2030) [72, 73] to determine whether model expectations would be met
[35]	Description of the Diabetes Association (ADA) Diabetes Risk Factor Survey tool	Demographic characteristics (age, gender, BMI group); Attitude toward controlling diabetic risk factors, subjective norm, peer influence, perception of the difficulty performing preventive behavior	Online risk calculator	Not studied (Note: outcomes related to the the tool was likelihood of preventive behavior)	Increasing knowledge of risk factors for diabetes	ADA Diabetes Risk Factor Survey tool that calculates a risk score	Theory of Planned Behavior [74]
[29]	Description of how communication occurs on online forums	Not studied	Leukemia-focused online patient forum	Not studied (Note: outcomes related to the tool was how the tool was used)	Deliberating goals and plans for leukemia care coordination	American Cancer Society Cancer Survivors Network (CSN)	Planning theory of communication [75]

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tional data in personalized medicine applications. We found that few studies measure attributes of innovation at baseline. According to pUHI framework, such characteristics influence how rapidly an innovation can be adopted. In addition, while the majority of studies we identified collected data on social system, only two studied social system in relation to adoption. Indeed, the adoption of technologies that collect and use non-traditional data sources for personalized medicine (e.g., FitBit for quantified self-tracking, social networks for physician Q&A) will be strongly influenced by social system (e.g., social value systems, status [e.g., socio-economic levels], cultural backgrounds, etc). As evidenced by others, such factors can lead to variations in adoption and use, which in turn can shape social inequalities in health [12]. These contextual variations due to social system highlight a need to capture how various technologies are accessed and used. These are important aspects of data context [51] that are important for measuring the quality of personalized medicine applications leveraging those data. There is also a need to provide multiple channels of communication to account for a range of societal structures.

b) We need new study designs that allow flexible communication channels while still preserving the ability to study health outcomes of interest. Effective communication can help to answer questions, build familiarity and increase the appeal of an innovation or new strategy. Enabling multiple communication channels can influence how quickly a strategy is shared in different communities and can improve adoption. One such study is the NIH-funded IMA-Gene (Individualized Medicine through Application of GENomics) clinical trial [52] that is evaluating genomic screening in Ashkenazi Jewish and Hispanic communities. In order to find the best way to communicate information about genetic screening, study participants can decide if they want to use self-guided learning via mailed paper and DVD, or web-portal education. Participants can switch at any time and always have access to a genetic counselor. The value of measuring adaptation is already evident as it relates to health IT adoption

[53]. Similarly, enabling the flexibility to adapt communication processes allows different approaches to be tested and has potential to maximize adoption. With new study designs, tracking the progress of how effective different communication channels are, can make a greater impact by providing lessons that others can draw from when establishing implementation and dissemination strategies with similar interventions.

c) Third, we can become active in personalized medicine implementation and dissemination by creating and studying interventions in healthcare settings. Health information systems such as computer-based patient records, EHRs, telemedicine, and decision support systems are common areas of biomedical informatics research [47]. Furthermore, these technologies are changing patient-provider communication by enabling patients to ask questions, request medication refills, and obtain test results electronically. While there is recognition that such systems can be of value to accelerate personalized medicine practices, there have been few studies that demonstrate integration into clinical settings in a scalable way (e.g., genomic clinical decision support [54]). Drawing from the work of others studying the adoption of health information systems

[55], in order to avoid deploying systems that are not feasible or acceptable for use in practice, studies should also provide a forum for end-users to play a role.

d) Translational informatics scholarship can make a greater impact if it goes beyond data-driven research to conducting theory-driven research with interventions based on algorithms and risk scores that combine genetics and non-genetics factors. Research in this area involves more engagement with health care practice in order to understand the consequences of using those interventions across contexts and time. One area for more theory-driven research is in comparing outcomes and acceptability of different formats for delivering clinical guidance based on algorithms and risk scores. This is an area of importance highlighted by three main trends: *(i)* the goal for interventions to reach diverse populations that may have varying levels of comprehension in response to different delivery formats [56]; *(ii)* the recent move to alternative models to provide genomic information to patients [57-59]; and *(iii)* a growing focus on outcomes that are of most value to patients [60]. Such efforts would contribute to the growing literature reporting findings from studying the return of genetic test results [61-64].

Table 4 Research directions and rationale.

Direction	Description	Rationale
(a) Investigate attributes of innovation and of societal structure.	Study the interaction of attributes of innovation with the adoption of strategies that use non-traditional data sources.	No study investigated attributes of innovation, and only two studied societal structure in relation with outcomes.
(b) Conduct studies that compare and contrast communication channels.	Allow more flexibility in communication channels to enable the formulation of design principles for implementation.	Two studies investigated multiple communication channels as part of a randomized controlled trial. No study enabled study participants to choose their preferred communication channel.
(c) Create and investigate personalized medicine interventions in healthcare settings.	Explore interventions within healthcare settings in order to shed light on patient and provider perceptions (e.g., access to providers) and impact (e.g., provider workload).	Only one study of a tool targeted to healthcare providers and assessed within a healthcare setting. None targeted to both healthcare providers and patients.
(d) Conduct theory-driven research with data-driven interventions.	Expand research on data-driven interventions to also include theory-driven implementation and dissemination research.	Only one study involved the use of a calculation with measures from multiple sources.

6 Conclusion

This work offers two contributions. First, we introduced to an informatics audience an elaboration on personalized medicine implementation with non-traditional data sources by blending it with the personalized medicine unsolicited health information (pUHI) conceptual framework to help explain adoption. We believe that this supports a new line of informatics inquiry that will enable gaining a richer understanding of how personalized medicine interventions disseminate. Second, we highlighted the need for: more research on the relationship between attributes of innovation and of societal structure on adoption; new study designs to enable flexible communication channels; more work to create and study approaches in healthcare settings; and more theory-driven studies with data-driven interventions. With the explosive growth in availability of health data captured using non-traditional sources, these are areas where biomedical informatics scholars can increase their influence on personalized medicine as it becomes more informed by those data sources.

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