# EVALUATION OF A TAILORED WEBSITE TO SUPPORT INTERPRETATION OF GENETIC TEST RESULTS FOR LYNCH SYNDROME

by

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# STATEMENT OF THESIS APPROVAL

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# ABSTRACT

Patients find genetic test results hard to interpret. Information about testing colon cancer (CRC) patients for Lynch syndrome (LS) is particularly complex as it involves several laboratory tests and has to be interpreted along with family/ personal health history information. In this study, the example of LS was used to explore methods of presenting information to patients. Specifically, the tailoring of information was compared to the general didactic presentation in a web-based format for communicating genetic test results to patients.

Ninety volunteers, aged 50-75, with ability to read and write English and familiarity with using the Internet were recruited from the Osher Lifelong Learning Institute at The University of Utah and through ResearchMatch.org. Healthcare professionals/ students, people with a professional medical background and the University faculty were excluded. This study was a postintervention, two-group randomized controlled trial. For evaluating the website, a vignette of a typical CRC patient being tested for LS was designed and participants were asked to imagine that they were the patient described in the scenario. They were then asked to interpret the test reports and answer a survey. The primary outcome was genetic knowledge based on interpretation of the test results. The other outcomes were task completion (correct/ incorrect), time to complete the task, usability and usefulness of the website.

The two groups showed no statistically significant difference in total knowledge score, task completion and usefulness outcomes. Inconsistent differences were found between groups for individual knowledge questions. Time data had to be excluded from our analysis as there were inconsistencies in reporting time. Usability was rated significantly higher for the nontailored website.

Our study has demonstrated that online tailored communication of genetic test results is possible and effective, although it could not determine conclusively if tailoring is more effective than nontailoring methods for conveying complex genetics-based testing information to patients. Future research on evaluating the website for its usability through cognitive response methods with actual CRC patients is necessary to get more insights into how the users actually process information and clarify these results.

Dedicated to my parents who taught me the beauty of hard work.

TABLE OF CONTENTS

LIST OF TABLES

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# CHAPTER 1

# INTRODUCTION

## 1.1 Introduction

As the role of genetic information in health care decisions increase, patients will be expected to understand their genetic test results. The Internet is growing in importance as a source of health information for patients. Genetic information is particularly complex and including genetic information in websites is particularly challenging. The current study proposes that personalized tailoring of information is an effective methodology for educating patients about their diagnostic test results. This thesis focuses on the development and evaluation of an online tailored intervention to support interpretation of diagnostic test results for a genetic disease called Lynch syndrome (LS).

In this chapter, the objectives of the study are presented first, followed by the challenges of communicating genetic test results and the rising use of the Internet for health communication. Later, the concept of tailoring is presented and compared with other forms of health communication in terms of theory and prior research. The subsequent topics in the chapter will focus on the example of Lynch syndrome where we will first speak about Lynch syndrome, followed by the challenges of interpreting diagnostic test results for LS, and consumer health education in cancer. Finally, the chapter concludes with a summary.

## 1.2 Objectives of the study

The objective of this study is to improve the ability of patients and their families to interpret and learn complicated genetics-based disease-related information. Using an example of diagnostic test results associated with Lynch syndrome, we developed and evaluated a tailored website for colorectal cancer (CRC) patients and their families. A randomized trial was used to compare the tailored website information with a non-tailored format. Following are the specific research questions for this study:

1) What is the impact of a tailored website design on patient's genetic knowledge where information is tailored to the individual patient as compared to a generic presentation?
2) What is the impact of a tailored website design on patient's perception of usability and usefulness as compared to a generic presentation?

## 1.3 Background

### 1.3.1. Challenges of communicating genetic test results

Personalized medicine is a rapidly growing field that is challenging the usual patient education and care delivery processes. With the growing responsibility of the patients/consumers for managing their own health, there is a need for them to understand their genetic test results for improved health outcomes. However, patients are finding it difficult to make sense of genetic tests and the implications of testing [1]. In the Mayo Clinic Proceedings of 2005, it was mentioned by Ensenauer et al. that, "It would be illusionary to assume that dealing with a gene test result is as simple as obtaining a straightforward negative or positive test result."[2] Added to the complexity of the problem,

one-on-one education with a genetic counselor is not possible in all situations. Hence, new methods of communicating genetic test results efficiently to patients need to be investigated.

### 1.3.2. The Internet for health communication

The Internet is viewed as a medium with great potential for addressing complex health information needs. With the proliferation of the Internet, patients are becoming active consumers of health information [3]. In a report on online consumer health information seeking behavior, the 2011 Pew Internet and American Life Project noted that 80% of Internet users look for health information online. They ranked "Searching for health information" as the third most popular online activity for all Internet users 18 and older. People search online for information on a variety of health topics like specific disease or medical problem, certain medical treatment or procedure, food and drug safety, medical test results etc. Hence, a growing area of research is to find effective methods of communicating genetic test information via the Internet.

### 1.3.3. Tailoring and other forms of health communication

Traditionally, health messages have been generic, personalized, targeted or tailored in nature. *Generic communications* aim to provide as much information as possible within a single communication (or finite number of communications) [4]. They fail to consider any specific characteristics of the potential users of the information and typically aspire to be "all things to all people." In using generic messages, it is not assumed that all the people have the same informational needs but rather that people can

and will disregard parts of the message that are nonrelevant to them in order to focus on information that is personally relevant to them.

*Personalization* is presenting a standard message with the recipient's name on it [5]. In a personalized communication, a person's name is used to draw attention to an otherwise generic message. A *targeted* message is also standardized but aimed at a population subgroup who share a common demographic character, such as adults aged 50-75, all women etc [6]. There is some evidence that both these techniques are effective in bringing about a behavior change[7-9]. However, targeting cannot address variations between individuals on factors that are not demographic in nature and often a personal identifier or demographic data alone would not be sufficient to understand an individual's health-related decision [5,10].

Compared to the above methods, a more advanced method is *tailoring*. Tailoring has been defined as a process for creating **individualized** communications; a process of presenting information to a specific person based on characteristics that are unique to that person, related to a given health outcome and has been derived from an individual assessment [10,11]. In a tailored communication, data regarding a health behavior of an individual is collected and processed through some decision-making rules or algorithms and then presented to the individual. Thus, the message presented to each person can be highly individualized.

### 1.3.4. Advantages of tailoring in health communication

The advantage of tailoring is that it allows educators to present health information customized to the needs of a unique person. Through the process of tailoring, we can

collect and process an individual's data related to a specific health outcome and use that data to determine the most appropriate information necessary to meet that individual's unique health needs. Compared to generic messages, tailored messages are more likely to be read and remembered [12,13], be saved [14] and be discussed with others [14]. They are more likely to be perceived by readers as interesting and considered as having been written especially for them [14]. Tailored information increases user's attentiveness and the user is more likely to view it as personally relevant [15]. Compared to personalization and targeting, tailoring has the added advantage of presenting information based on data related to a health behavior not just personal identification and demographic data. Since health behavioral data of an individual can be collected through tailoring methods, we can develop personal plans in order to bring about a complex health-related behavior change by addressing the individual's motivation and beliefs [16].

### 1.3.5. Theoretical rationale for tailoring

The theoretical framework underlying the concept of tailoring is provided by the Elaboration and Likelihood Model (ELM) of persuasion developed and validated by Petty and Cacioppo [17]. The ELM states that there are two routes to persuasion—the central route and the peripheral route. The central route processing occurs when there is enough motivation and ability to deeply process the information. When the central route is taken by a person, the ideas and content of the message are more extensively scrutinized (high elaboration) than when the person takes the peripheral route.

According to this model, elaboration is the process of deeply attending, scrutinizing and thoroughly processing of arguments contained in a message by an

individual. Elaboration on a message varies on a spectrum from no thought about the message to completely processing every argument in the message. People relate the new message to related information they have encountered in the past and integrate these elaborations into a comprehensive cognitive and attitude schema. The ELM provides the rationale for tailoring by stating that people process information more thoughtfully (i.e., more elaborately) if they consider it to be personally relevant than if they do not. And as mentioned above, the process of tailoring increases personal relevance.

Previous studies have found that tailoring is a promising strategy for communicating health information to consumers and leads to improved health behaviors in areas such as smoking cessation [18-20], diet and nutrition [12,14,21], cancer screening [13], health risk appraisal [20], cholesterol management[20], childhood immunizations [22], physical activity [23,24] etc. Ettar et al. conducted a study on the use of the Internet for smoking cessation and compared the mass-level dissemination of automatised, individualized counseling on the Internet to the Industrial Revolution, when skilled craftsmen working in small shops were replaced by huge plants [25]. A study in 2005 which reviewed Diabetes websites mentioned that, "Websites need not be merely electronic versions of a pamphlet or a flyer," [26]. Thus, previous research recommends that tailoring may be explored in health education websites in order to take full advantage of the Internet[26-29].

### 1.3.6. Lynch syndrome: A special case

In this study, the impact of tailoring for presenting genetic test results to patients for evaluation of Lynch syndrome is explored. In the following sections of this chapter, Lynch syndrome will be presented as well as the challenges of interpreting diagnostic test

results for LS, consumer health education in cancer and why we think tailoring may be effective for LS evaluation.

1.3.6.1. About Lynch syndrome

Lynch syndrome (LS) or Hereditary Nonpolyposis Colorectal Cancer (HNPCC) is the most common hereditary form of colon cancer [30]. In addition to colon and rectal cancers, predisposed individuals have increased risk of developing cancers of other organs, including cancers of endometrium, ovaries, renal pelvis, ureter, stomach, small bowel, bile duct, pancreas, brain, and skin [31,32]. LS is caused by germ-line mutations in the DNA mismatch-repair genes, mostly MLH1, MSH2, MSH6 and PMS2[31]. It is inherited in an autosomal dominant pattern.

1.3.6.2. Statement of the problem

Lynch syndrome accounts for 2-5% of all colorectal cancers (CRCs)[33]. Genetic testing is available to detect mutations causing Lynch syndrome and test results can guide screening recommendations[34]. Providing information to patients about their genetic test results will help patients in overcoming skepticism, misconceptions and fears associated with genetic testing and cancer and improve care [1]. However, there are no tools tailored to the needs of CRC patients to adequately explain genetic testing associated with Lynch syndrome.

1.3.6.3. Challenges of interpreting diagnostic test results in LS evaluation

It is important to evaluate CRC patients for LS because early detection can be life-saving for them. However, testing CRC patients for LS is not straightforward. It

entails several laboratory tests [Microsatellite instability by Immunohistochemistry or by Polymerase chain reaction, DNA methylation analysis, BRAF mutational analysis, gene sequencing, and deletion/duplication analyses] along with family history evaluation. Expression of the disease in multiple organ systems, overlap of the phenotype with other hereditary cancer syndromes, lack of sensitivity and specificity of the family history-based diagnostic criteria[35], ambiguous risks to patients and their family members, involvement of multiple genes and complex testing methodology make it difficult for lay people to understand the test implications. Hence, educating these patients about their results can be challenging.

1.3.6.4. Consumer health education in cancer

Many websites have been built previously to promote online consumer education regarding genetic tests for cancer patients. The Genetics Home Reference website developed by NLM educates the public about genes, mutations, inheritance, genetic counseling and genetic testing (http://ghr.nlm.nih.gov/). The NCBI-developed website, genetests.org, is a comprehensive source of information on genetic testing. The above two websites also provide information about Lynch syndrome genes and testing done to detect mutations causing LS. However, the information contained in them is generic.

Some elements of tailoring are known to exist in health education websites developed for cancer patients. The E-Info Gene website was designed to provide computer-tailored information and question prompts to breast cancer patients prior to genetic counseling[36]. Another site, cancercarelinks.org, embeds an education program tailored to the needs of newly diagnosed breast cancer patients[37]. This website explains

pathology reports in general, but not genetic test reports. This site has interactive flow charts for patients to see the entire trajectory of care.

Tailored health messages are also prevalent in Health Risk Assessment websites. These websites collect mortality risk data from an individual and provide individualized cancer risk estimates. For example, the Harvard "Your Disease Risk Index" is a web-based interactive tool that calculates cancer (of colon and other organs) risk and provides personalized tips for cancer prevention[38]. In 2004, the Centers for Disease Control and Prevention developed Family Healthware, a web-based tool that assesses familial risk for colorectal cancer and other cancers based on data collected on health behaviors, screening tests, and disease history of a person's first- and second-degree relatives and provides personalized recommendations for lifestyle changes and screening for cancer prevention[39]. These websites, however, are not meant for LS evaluation.

Though websites with information on testing for Lynch syndrome are available for CRC patients, to the best of our awareness, only nontailored websites have been developed so far. The information found in these websites is presented in a generalized manner, without tailoring to the specific needs of the patients. In this study, we take a novel approach in elucidating the results of diagnostic tests for Lynch syndrome to lay people by exploring tailoring. The results of this evaluation can have implications for similar diseases where the complexity of the disease and its management necessitates enhanced methods for communicating information to patients.

1.3.6.5. Why tailoring for communicating results of Lynch syndrome evaluation

In the evaluation of Lynch syndrome, the results of tumor tissue tests are analyzed along with the individual's family health history. Tailored genetic information is

expected to enhance learning of the patients about their diagnostic test results as research has proven that tailored information is more likely to be read and remembered [12,13]. A tailored intervention allows us to gather data on family history and any prior test results of an individual. Based on the user input, testing recommendations can be provided, making the information personally relevant. Thus, the implications of the results of the specific test(s) undergone by the patient can be conveyed to him/her directly instead of presenting an electronic document with the entire testing information in one location. The latter format can be overwhelming to the patient.

## 1.4 Conclusion

With an increasing role of patients in managing their health, along with the rise of personalized medicine, patients are increasingly expected to master complex genetic information. As genetic test results are hard to interpret, new methods have to be explored for conveying the testing information to patients. In this context, the Internet is seen as an effective medium for communicating health information to patients. Prior theoretical and empirical research evidence suggests that tailoring of genetic information on the Internet would be especially effective and worth investigating.

With this perspective, the current study is designed to explore tailoring as a method for communicating results of diagnostic tests for LS to CRC patients through the Internet. The outcome should help inform development of other websites for communicating complex health information to patients and their families.

# CHAPTER 2

# MATERIALS AND METHODS

## 2.1 Overview

A website presenting tailored information about diagnostic test results to CRC patients for evaluation of Lynch syndrome was constructed for this study. Two versions of the website were created, a tailored and a nontailored website. They were pilot-tested and evaluated in terms of impact on patient's knowledge and perceptions of usability using a randomized control trial. This chapter provides a detailed explanation of how the research study was conducted. The description includes the study design, setting, the subjects, the process of developing the interventions. In addition, the development of a Lynch syndrome patient scenario is described as well as the survey instrument. Then a step-by-step description of the actual study procedures will be there. Finally, the statistical methods used to analyze the study outcomes will be described.

## 2.2 Methods

### 2.2.1. Study design

This study utilized a posttest only, two-group randomized controlled trial design. The study participants were randomized to one of the two groups—tailored or the nontailored intervention (website).

### 2.2.2. Setting

The study was conducted online and the study subjects were recruited through two organizations: the Osher Lifelong Learning Institute (OLLI) of The University of Utah (http://continue.utah.edu/osher/index.php) and ResearchMatch.org (https://www.researchmatch.org/). The OLLI was chosen as this institute offered separate study programs for people over 50 years old. ResearchMatch.org is a Clinical and Translational Science Awards (CTSA) registry for recruiting participants. It took about 4 months, from March, 2011 to June, 2011 for recruiting the subjects.

### 2.2.3. Subjects

#### 2.2.3.1. Inclusion/exclusion criteria

Our inclusion criteria were: people aged 50-75, with ability to read and write English and familiarity with using the Internet. The reason for recruiting people aged 50-75 was that the US Preventive Task Force recommends that people should be screened for colorectal cancer starting at age 50 and continuing until age 75[40]. For recruiting participants through ResearchMatch.org, “healthy” volunteers were selected. These were the people who registered on ResearchMatch and selected “No” to the following question: "Have you been diagnosed with a health or medical condition". Only “healthy” people were considered because people with some health condition could be mentally or physically challenged.

Healthcare providers, health educators and other healthcare professionals or students and people with a professional medical background were excluded from our study. University faculty members were also excluded as they have a higher education

level compared to the general population. Cancer patients were also not recruited because we do not want to worry them by informing about a health condition (LS) in which there is increased risk of multiple cancers as these people are already emotionally burdened with the diagnosis of a cancer. We also wanted to be relatively sure that our participants were not already educated about cancer, as might be more likely with cancer patients.

2.2.3.2 Participant selection and recruitment

The study was approved by the Institutional Review Board (IRB), University of Utah in January, 2011. Two fliers were designed for participant recruitment. One had the study URL which provided access to the tailored website, while the other had the URL which provided access to the nontailored website. Study participants were first recruited from The University of Utah OLLI as this institute offered separate study programs for people over 50 years of age. The concerned authority at The University of Utah OLLI randomized the study population into two groups and emailed our study fliers to them.

Our initial plan was to recruit all the participants from the OLLI. However, the number of participants from the OLLI was not enough to satisfy our projected subject population. As a result, additional participants were recruited through ResearchMatch. After receiving an amendment approval from the IRB, we queried this registry for people who met our study criteria and sent out our recruitment message to the eligible people through ResearchMatch. ResearchMatch then provided us with a list of people who expressed interest in our study. These people were then randomized into two groups and our study fliers were emailed to them.

2.2.3.3. Informed consent

The study was designed using REDCap (Research Electronic Data Capture) survey software [41]. Study data were collected and managed using REDCap electronic data capture tools hosted at the School of Medicine, University of Utah. REDCap is a secure, web-based application designed to support data capture for research studies, providing: 1) an intuitive interface for validated data entry; 2) audit trails for tracking data manipulation and export procedures; 3) automated export procedures for seamless data downloads to common statistical packages; and 4) procedures for importing data from external sources. When a participant opened the study URL, the survey software first took him/her through the informed consent process. There was an option for the participants to save a copy of the form for their records.

2.2.3.4. Sample size estimation

The study sample size was estimated based on a previous study that performed a randomized controlled trial to compare the effect of an interactive decision aid with a standard audio-booklet version of the decision aid [42]. The difference between the group mean knowledge scores detected in this study was 6.7 ($SD$ = 9). Using these values, sample size estimation was done at $\alpha$ (2-sided) = 0.05 level and $\beta$ = 0.2 (power=0.8) level and it was found that we would need 30 subjects per group. Allocating for 30% dropout, 90 people total, i.e., 45 per group had to be recruited.

### 2.2.4. Description of intervention

#### 2.2.4.1. Website design

For the purpose of this study, we developed a website that explains the results of diagnostic tests for Lynch syndrome to CRC patients and their family members. Initially, the Internet was explored for existing websites that explain health conditions to consumers. Our search was further narrowed down to cancer and colon cancer websites, especially websites that contained information about testing for LS. This search provided us the incentive to identify the initial content of our website. **The content of the website was written based on the 2009 NCCN (National Comprehensive Cancer Network) guidelines for evaluating CRC patients for Lynch syndrome and the letters written by the genetic counselors to CRC patients.**

Website design consisted of several phases. In the ground phase, two subject experts were consulted to understand the nature of the health problem. The subject matter expertise of the genetic counselor who is also a member of our research group was used to clarify the process of care and the information needs of the patients, especially the difficulties patients face in interpreting the test results. Meetings with two pathologists and two genetic counselors helped us identify the problems patients face in interpreting the test reports. These talks focused on what information has to be obtained from the user in order to give tailored feedback messages. Essentially, the focus was on the questions to be presented for the assessment and the response choices to each question so that the assessment would not be burdensome for the user.

With this groundwork, the initial draft of the website was created and the content was reviewed by the genetic counselor. The entire web content was also reviewed and

edited by a health educator in order to attain a 7th-8th grade reading level. While constructing the website, we also ensured that the website was easy to use for older adults. We focused on assuring that the layout, the text font and color, pictures, navigation buttons and the language would be easy to read and understandable. With the initial draft of the website, a pilot study was done (described later) in order to assess usability. Based on the feedback received in the pilot study, changes were made to the website prior to the actual study.

2.2.4.2. Content and architecture of the website

In the final website, the entire web content was organized into six sections, and one web page was allotted to define the content under each section. Thus, a main menu was created with six buttons: "About Lynch syndrome," "Causes and inheritance," "Testing for Lynch syndrome," "Interpret your test results," "Genetic counseling and disease management" and "Additional resources." These buttons were displayed in a row on top of each web page to provide access to each of these six sections. When a user pointed the mouse over a button in the main menu, the topics in that section would be shown in the submenu to facilitate easy navigation. Figure 1 shows a screen shot of the website containing the main menu and a submenu. On top of each section was a text box showing the context of the section so that users could read or skip that section. The content of each section is described in the following paragraphs.

The section "**About Lynch syndrome**" contained a brief introduction to Lynch syndrome, its prevalence and the potential red flags in a family history for Lynch syndrome. The increased risk of multiple cancers in LS was depicted using a graph and a

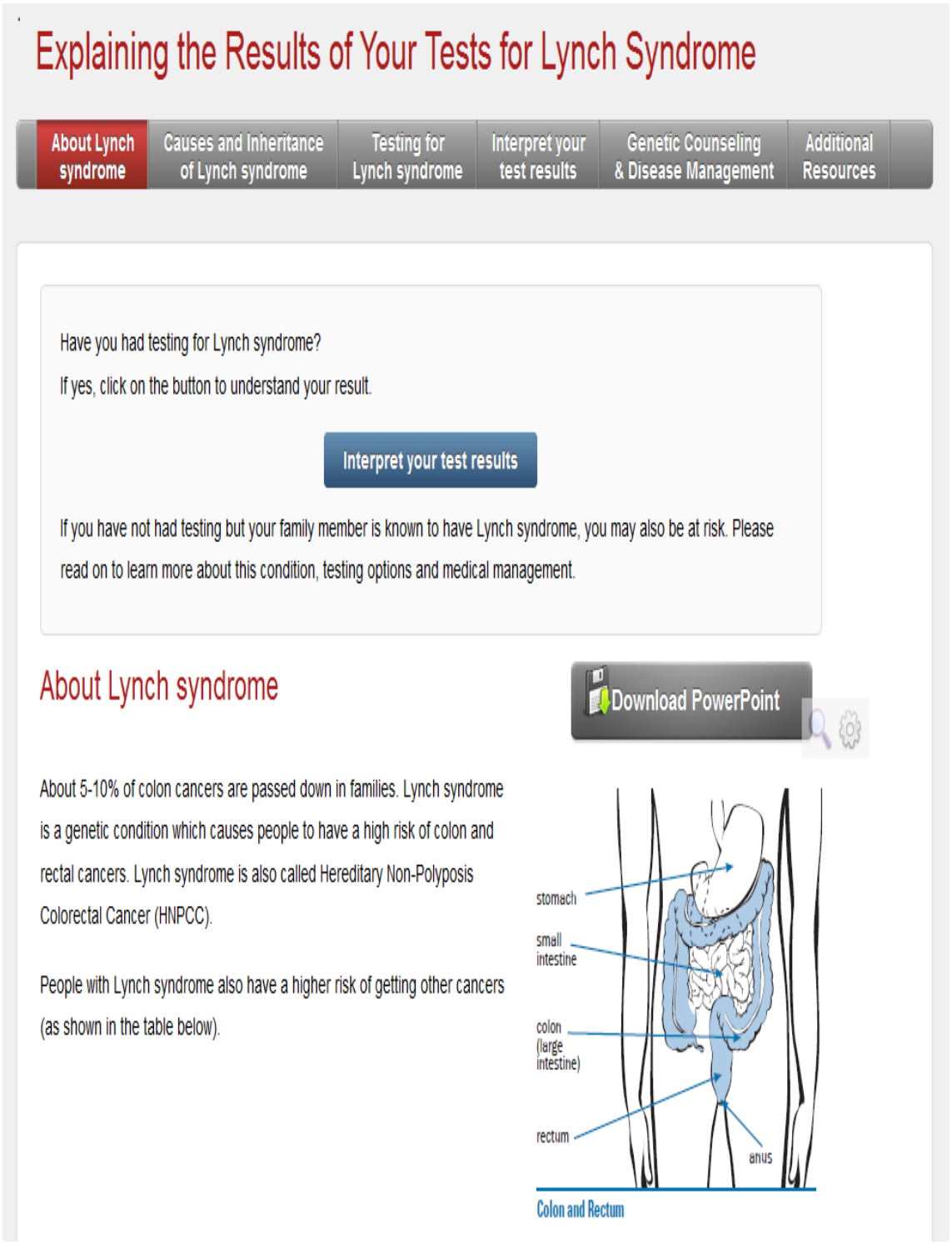



Figure 1. Screen shot of the website showing the main menu and a submenu

table. This section also contained a Microsoft PowerPoint presentation containing an overview of Lynch syndrome. In the "**Causes and inheritance**" section, genes, mutations, and how genes causing LS can be passed on in a family was explicated in order to facilitate contextualization.

In the third section, "**Testing for Lynch syndrome**," screening strategy for LS, which included both tumor tissue testing (which comprised Microsatellite Instability testing through Polymerase Chain Reaction and Immunohistochemistry) and genetic testing, were briefly explained.

The "**Interpret your test results**" section provided explanation for interpreting the results of diagnostic tests currently used for evaluating CRC patients for LS. A detailed explanation about this section is described under the next heading.

The fifth section, "**Genetic counseling and disease management**" contained information about genetic counseling and how one can prepare for an appointment with a genetic counselor. Two separate tables were used: one to present a list of questions patients may want to ask the genetic counselor and another to present a list of reports that patients can take with them when they meet with their doctor or genetic counselor. In the latter half of the same section, disease management was explained; this part also mentioned how LS patients can prevent colon, endometrial and other cancers and screening recommendations for the children of LS patients.

The last section, "**Additional resources**," provided links to important external resources for LS patients and their family members. Throughout the website there were guided instructions for the users to navigate easily through the website. Pictures were

used wherever needed for better understanding. The website was developed in HTML and JavaScript.

2.2.4.3. Tailored and nontailored versions of the LS website

In order to test our hypothesis, two versions of our website were developed: tailored and nontailored. **The two versions differed only in the "Interpret your test results" section.** The layout and content were kept exactly the same for other sections. In the tailored version, "Interpret your test results" provided tailor-made information to each user. A user would be presented with a series of multiple-choice questions about the testing undergone by him/ her. For example, a user would be asked to choose the name of the test performed and all the possible results for the test name chosen would be displayed as options. Based on the option chosen, feedback, explanation of the test result and recommendations would be provided for the user. Figure 2 shows a screen shot of the interpretation section of the tailored website. There were buttons for the users to click and view sample reports of Microsatellite Instability testing through Polymerase Chain Reaction or Immunohistochemistry (if they had a PDF Reader installed). Four questions on family/personal health history were also incorporated. Based on the family history and the tumor tissue testing results a user would input, recommendations would be provided. If the Immunohistochemistry result of a user indicated that a protein is missing, he/she would be shown the options for genetic test results.

Figure 3 shows a screen shot of the interpretation section of the nontailored website. In the nontailored version, the interpretation section consisted of tables of information about diagnostic tests for LS, with one table allotted for each test, i.e., a table

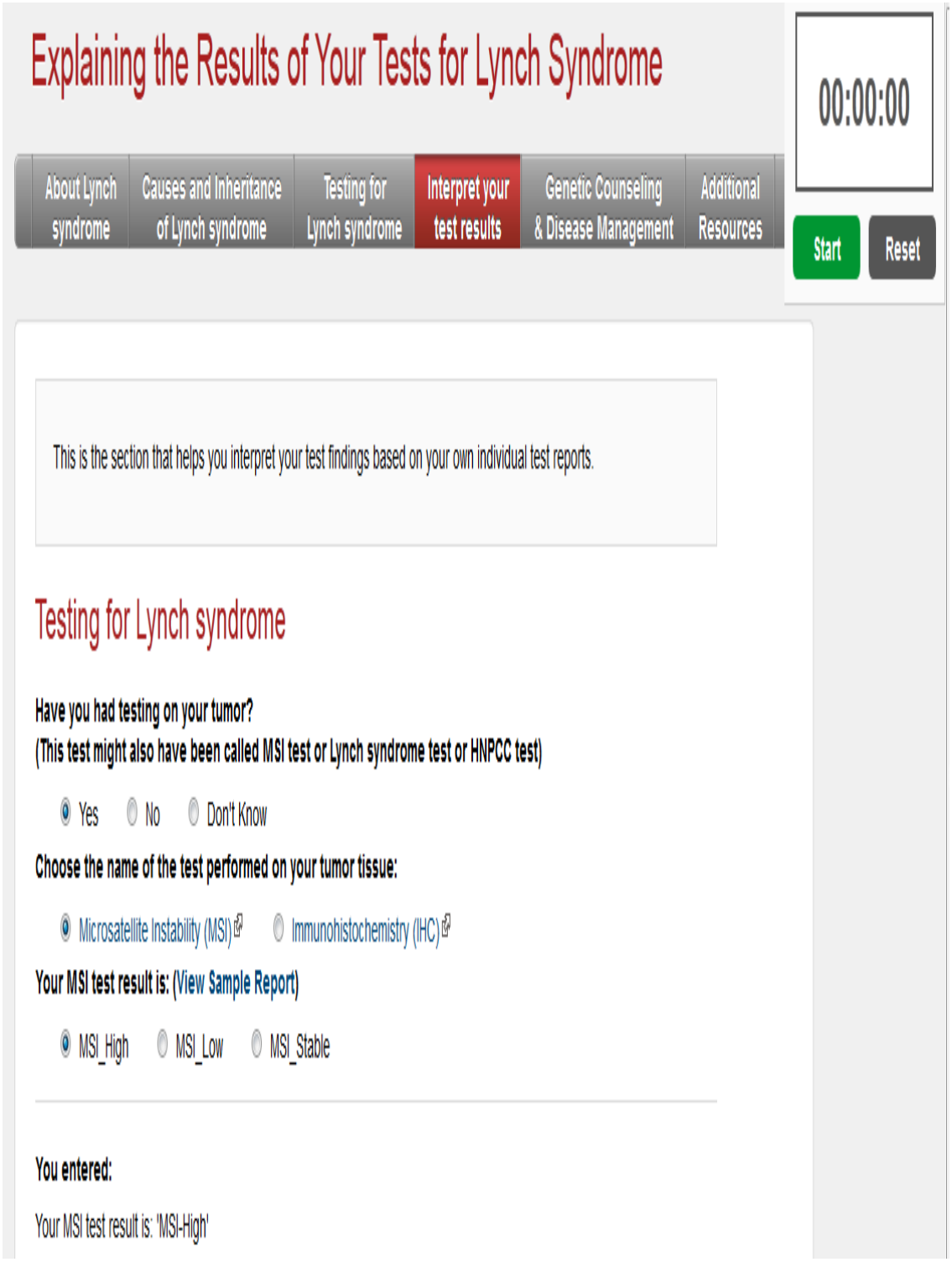



Figure 2. Screen shot of the interpretation section of the tailored website

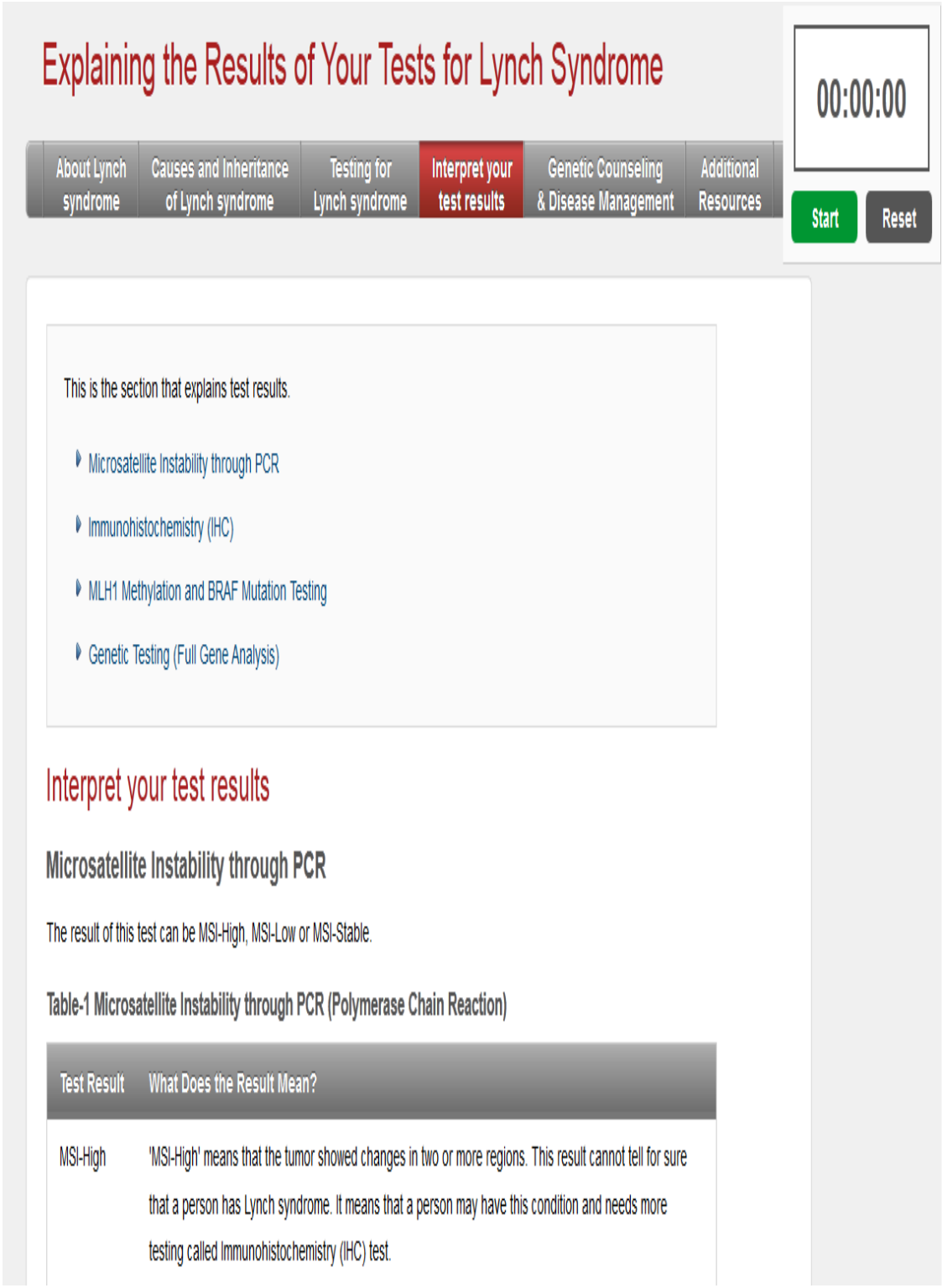



Figure 3. Screen shot of the interpretation section of the nontailored website

explained all the possible results of a test. The explanation of each test was provided first, followed by the table(s) explaining the results of the test. The text box placed on top of this page contained the names for each test and the user could click on a test name to navigate to the information on that test. Users could navigate to the top of the section by clicking on the "Back to Top" link placed at the end of each table. In this version, family history information was also displayed as generic text in the table that explained the Immunohistochemistry test result "Normal."

In both the versions, explanation of the test result and recommendations were the same except for the "tailoring" part. Both the versions were tested in the pilot study before they were used in the actual study. See Appendix A for more detail.

### 2.2.5. Development of scenario

For evaluation of our website, a scenario of a typical colon cancer patient named Susan, who was being evaluated for LS, was developed. Susan was described as a 55 year-old woman who was operated on for colon cancer. Tumor tissue testing indicated a missing DNA mismatch repair protein (MSH6) and genetic testing found a mutation in the MSH6 gene. She was in a situation where she was unsure about how she can inform her family members about the discovery of the mutation because this would have important implications for their health. Her genetic counselor suggested that Susan and her family view the website.

Since recruiting CRC patients was not an option for the study, this scenario was developed and the study participants were asked to imagine themselves to be like the Susan character described in the scenario. Along with Susan's scenario, a copy of her

tumor tissue test (Immunohistochemistry) report was also presented to the participants. See Appendix B.

### 2.2.6. Development of survey instrument

The survey consisted of sociodemographic information (age, sex, highest education level) and four sections, described below. The first section contained questions about participants' Internet usage. These questions were about their comfort level in using the Internet and how often they use the Internet and, in particular, if and how often they search for online health information.

The second section of the survey had 12 questions measuring knowledge about the interpretation of the test results for Susan (the woman described in the scenario). These questions were modified and adapted from previous questionnaires measuring knowledge on cancer risk assessment and Lynch syndrome [43-45]. The questions were modified to focus on the main points which the genetic counselor thought that Susan and her family members should know.

In the third section, 8 out of 10 Nielsen's usability heuristics[46] were used to measure the usability of our website. These questions collected participants' opinions of these criteria about our website on a 1 to 7 Likert scale.

Questions eliciting overall impressions about the usefulness of the website were placed in the last section. These questions were adapted from previous work done by Densie et al. to evaluate the Genetics Home Reference website [47]. Participants were also asked to provide comments at the end of the survey. The questions in the first, second and fourth sections were all multiple-choice questions.

The questionnaire was tested for its clarity and understandability in a pilot study (explained in the next section) performed before the actual study, though it was not validated it in order to ensure that the instrument was consistent and accurate. See Appendix C.

### 2.2.7. Description of pilot work

The pilot study was done to accomplish three aspects of the research process: (1) usability analysis of the website; (2) a test of the study procedures; and (3) an assessment of the survey questions. The pilot study was conducted with three people: one genetic counselor, one undergraduate, and one individual aged 50+ with less than a graduate level of education. The genetic counselor was chosen for the pilot study as she was the subject expert. The other two people were selected to see if the website can be used by people with lower education levels and elderly people, potential users of the website.

Usability analysis was done to get insight into how the users may actually use our website and to see if our website worked as intended. Usability testing of the initial draft of the website was done using the "think aloud" method with MORAE usability testing software developed by TechSmith Corporation[48]. In the "think aloud" method, the subject is assigned a task and is instructed to keep talking aloud while performing the task [49]. The subject's onscreen activity along with his/her speech can be video/audio taped for later analysis. This method was chosen in order to capture directly any problems that a user might face while interacting with our system. For our study, verbalizations and on-screen activities of the participants were captured using MORAE recorder as they were thinking

aloud. Usability script read out to the participants was adapted from Steve Krug's Rocket Surgery Made Easy, 2010 [50].

After the informed consent process, the participants were at first comforted that we were evaluating the website and not themselves. A few questions were asked to ascertain their usage of the Internet. Then they were asked to open the Google Maps site and search for the nearest airport while thinking aloud. This was done in order to let them practice the "think aloud" method. Next each participant was asked to skim through the first page of the website for about 2 minutes and give his/her first impressions of likes and dislikes for the website. A scenario of a CRC patient being evaluated for LS was drafted for evaluating the website and each participant was presented with three sequential tasks pertaining to the patient described in the scenario. Printouts of the scenario and the tasks were handed to the participants while they were also read aloud to them. Participants were asked to perform the tasks using the website while thinking aloud. Problems that the participants faced while they were accomplishing the tasks were noted.

After doing the usability testing, each participant was asked to perform our actual study procedures. This was done to detect any unforeseen problems with our study design. Finally, the participants were asked to answer the questions in the survey instrument in order to assess the clarity and interpretability of the questions being used to measure the outcomes.

Based on the feedback in the usability testing, changes were made to the initial draft of the website. The tailored website was edited based on the results of usability testing. Then the nontailored website was made by creating exactly the same copy of the

tailored website except for the “Interpretation of the test results” section. This section was created separately explaining the test results in tables. Finally, all the procedures in the pilot study were repeated with both tailored and nontailored versions with the help of a few colleagues in our department.

The scenario used for usability testing was different from the scenario used in the actual study, though both the scenarios illustrate CRC patients being evaluated for LS. See Appendix D.

2.2.7.1. Results of the pilot study

Many changes were made to the website based on the feedback from the participants in the pilot study:

- Font size was increased.
- Some of the topics were reorganized. For example, the topic “Potential Red Flags in a Family History for Lynch syndrome” was removed from the “Testing for Lynch syndrome” section and placed in the first section because of its high significance.
- Guided instructions were added to facilitate easy navigation. For instance, in the beginning of the testing section, a message was added saying, “This section explains technical information about tumor tissue testing. If you are curious read on. If not, proceed to 'Interpret your test results' section.”
- The explanation about genes and mutations was further simplified in order to facilitate easy understanding.
- The diagram showing the screening strategy for LS was simplified.

- The Immunohistochemistry test results were explained more clearly by using the terms “Stable (Normal)” and “Unstable (Abnormal or Missing Proteins)” in place of “Negative” and “Positive” to avoid confusion.

A few changes were also made to the actual study procedures and the survey instrument:

- Some of the study procedures had to be rearranged.
- The instructions for starting and stopping the timer were edited to measure the time for accomplishing the task more accurately.
- A few questions were edited in the survey for one of the following reasons: the answer was obvious, an answer could be guessed from a previous question, or the question was not clear.
- Participants in the pilot study found it difficult to understand the Nielsen’s usability heuristics that we used in the questionnaire. In the final questionnaire, a sentence explaining the heuristic was added below each heuristic to clarify them.
- It was decided to conduct the study online as it would be time-consuming to do the study in person with 90 participants. Hence, the study was drafted online using REDCap survey software and was tested with a few colleagues in our department.

### 2.2.8. Study procedures

#### 2.2.8.1. Overview

This study was conducted entirely online through REDCap survey software. The study participants were presented with a vignette of a typical colon cancer patient (Susan) being evaluated for Lynch syndrome and were asked to pretend to be Susan and interpret

the findings of her test report using the “Interpret your test results” section of the website. They were assigned a task related to the interpretation of her test reports. Time to accomplish this task was measured using a timer in the “Interpret your test results” section of the website built for the purpose of the study. In the end, they were required to answer the questions in the survey instrument which measured knowledge about their interpretation of the test results and also elicited their opinion on the usability and usefulness of the website.

2.2.8.2. Explanation

After the informed consent process, study instructions were displayed and the participants were asked to have a PDF reader installed in order to view our study documents. There were four steps that the study participants were required to do as shown in Table 1.

In the first step, the survey software displayed to them the URL of our website. Participants in the control group received the URL to the nontailored website while those in the intervention group received the URL to the tailored website. Participants were asked to open the website in a browser and explore it for about 3 minutes so that they become comfortable using the website.

After completion of the first step, in step two, participants were shown two documents- 1) Susan’s scenario and 2) her Immunohistochemistry test report. They were directed to read the scenario and simulate Susan’s experience as described in the scenario. Participants were instructed to leave these documents open until they complete the study.

Table 1. Overview of study procedures

| Steps | Procedures | Outcomes measured |
|---|---|---|
| Step 1 | Open the URL of the website<br>Explore the website for 3 minutes | |
| Step 2 | Click on links to Susan's scenario and her Immunohistochemistry test report<br>Read Susan's Scenario | |
| Step 3 | Navigate to 'Interpret your test results' section of the website<br>Start timer<br>Complete the task and stop timer<br>Note down time | Time |
| Step 4 | Close the website<br>Answer the questionnaire | Demographics<br>Internet usage<br>Knowledge<br>Usability<br>Usefulness |

For completing step three, participants were asked to use only the "Interpret your test results" section of the website. In this step, they were assigned an information search task and were asked to note down the time they take to finish the task using the timer in our website. They were limited to 15 minutes to complete the task. An instruction was displayed saying that they were being asked to record time just to make sure that they do not exceed 15 minutes. This was to make them less apprehensive about being tested and to make sure that they read the content presented in the "Interpret your test results" section. The "task completion" question assigned to them assessed their understanding of the risk for Susan's children. This task was chosen because understanding risk for children is one of the most important implications of the test findings. Participants were allowed to refer to Susan's test report and her scenario as they accomplish the task.

In step four, participants had to answer the questionnaire and were limited to 10 minutes to complete it. They were instructed to close our website while answering the questionnaire. At the end of the study, participants were asked to enter their name and contact information, if they wanted to be compensated.

### 2.2.9. Description of participants

A total of 252 people accessed the online survey, with 90 responding (a 39.6% response rate). Of the 90 people who completed the survey, data from 2 participants were excluded from analysis. One participant was excluded from the nontailored group as he/she could not access the test results due to technical reasons. Another participant belonging to the tailored group was excluded as the participant did not follow the study instructions. After excluding these 2 participants, data were prepared for analysis using R.

### 2.2.10. Statistical analysis

Data analysis was done using R statistical package, version 2.10.1 [51]. See Appendix E. Baseline characteristics of the participants in the tailored and nontailored groups were compared. All the tests were two-tailed and statistical significance was estimated at alpha = 0.05 level.

For all demographics (except age) and Internet usage variables, counts and percentages were computed and Fisher's exact test was used to compare the tailored and the nontailored groups. The Shapiro-Wilk test was used to assess the normality of the continuous variables (age). As age showed nonparametric distribution, median and

interquartile ranges were reported and Wilcoxon signed rank test was used to compare the groups.

Time taken to accomplish the task was measured but had to be excluded from analysis as more than one-third of the participants in each group could not note down time accurately. The reasons for excluding time data from analysis will be explained in the next chapter.

For the task completion question, counts and percentages of correct responses were calculated. The two groups were compared through Chi-squared test (with Yates continuity correction applied).

A total knowledge score (kscore) was computed for each participant by assigning a score, 1, for each correct answer and summing up the total number of correct answers. A kscore can range between 0 and 12. A blank or "Don't know" or incorrect response was evaluated as a wrong answer. The Shapiro-Wilk test was applied to detect the normality of kscore. As the kscores showed a nonparametric distribution, the Wilcoxon rank sum test was used to compare the kscores of the two groups. For analyzing each knowledge question, the percentages of correct responses in the tailored and nontailored groups were compared using the Chi-squared test. Bar plots were used to visualize the performance of the groups on the knowledge questions. To detect the effect of the baseline characteristics (except age) on kscore, the Kruskal-Wallis test was applied. Simple linear regression was used to analyze if age was associated with kscore. A stepwise linear regression with kscore as the dependent variable and all the baseline characteristics and group (tailored/ nontailored) as the predictor variables was conducted in order to find the best individual predictor of kscore.

Usability variables, which were rated on a 1-7 Likert scale (1 = bad, 7 = good), were analyzed as ordinal data. For each of the eight variables, group mean and sd was computed. Welch two sample t-test was done to compare group means for each variable and also the overall usability.

Usefulness variables were recoded (1 = Strongly Disagree to 5 = Strongly Agree) and analyzed as ordinal data. The group means for each variable and also the overall usefulness were compared via Welch two sample t-test.

The next chapter presents a detailed report of the results of the data analysis.

# CHAPTER 3

# RESULTS

## 3.1. Overview

This chapter describes the results of the research study. First, the characteristics of the study participants in the tailored and nontailored groups will be presented. Then the performance of the groups on the task completion question, the reasons for excluding time data from analysis and the results of the comparison of the two groups on knowledge, usability and usefulness will be discussed.

## 3.2. Results

### 3.2.1. Baseline characteristics of the included participants

Table 2 describes the baseline characteristics of the included participants in the tailored (T group) and nontailored group (NT group). There was no significant difference in the baseline characteristics of the study participants belonging to the two groups expect for age.

As age failed the Shapiro-Wilk test for normality ($p < 0.05$), nonparametric measures were computed. The two groups showed a marginally significant difference in age ($p = 0.05$). As indicated in Table 2, the median and interquartile range are higher for the T group.

Table 2. Baseline characteristics of the included participants

| **Baseline characteristic** | **Group = NT (N=44)** | **Group = T (N=44)** | ***p-value** |
|---|---|---|---|
| | **No (%)** | | |
| **Median age** (Interquartile range) | 55 (52, 60) | 58 (54, 63.25) | 0.050, Significant |
| **Gender** | | | 0.326, NS |
| Male | 9 (20.5) | 13 (29.6) | |
| Female | 35 (79.6) | 29 (65.9) | |
| **Highest Education Level** | | | 0.295, NS |
| Less than high school | 0 | 0 | |
| High school graduate or equivalent (GED) | 3 (6.82) | 9 (20.46) | |
| Vocational / technical school degree/ certificate | 5 (11.36) | 5 (11.36) | |
| College graduate | 16 (36.36) | 14 (31.82) | |
| Postgraduate/professional degree | 20 (45.46) | 15 (34.09) | |
| **Choose how comfortable you are with using the Internet** | | | 0.721, NS |
| Very uncomfortable | 9 (20.5) | 7 (15.9) | |
| Somewhat uncomfortable | 3 (6.8) | 1 (2.3) | |
| Neutral | 1 (2.3) | 2 (4.6) | |
| Somewhat comfortable | 8 (18.2) | 6 (13.6) | |
| Very comfortable | 23 (52.3) | 27 (61.4) | |
| **On average, for how many hours do you use the Internet daily?** | | | 0.733, NS |
| Less than one hour | 2 (4.6) | 3 (6.8) | |
| One to three hours | 23 (52.3) | 19 (43.2) | |
| More than three hours | 19 (43.2) | 21 (47.7) | |
| Do not use the internet | 0 | 0 | |
| **How often do you use the Internet to find information about your health or the health of your family members?** | | | 0.237, NS |
| Very frequently | 11 (25) | 12 (27.3 ) | |
| Somewhat frequently | 18 (40.9) | 18 (40.9) | |
| Never | 0 | 0 | |
| Very infrequently | 1 (2.3 ) | 5 (11.4) | |

*****All p-values are from Fisher's exact test, except for age which is from Wilcoxon signed rank test. NS: Nonsignificant at 0.05 level
Sum of values does not always equal the # of participants due to missing values

In the T group, two subjects did not report gender and one person did not mention the education level. Data were analyzed after excluding the missing values. Overall, females constitute a majority of the study participants (72.73%). Males are more in the T group (29.6%) than in the NT group (20.5%). College graduates and postgraduates together constituted ~82% of the subjects in the NT group and ~66% in the T group. However, no significant difference was detected between the two groups in gender ($p = 0.326$) or highest education level ($p = 0.295$).

3.2.1.1. Internet usage variables

One participant did not answer any of the three questions on Internet usage in the survey. Hence, he/she was excluded from analysis of the Internet usage questions.

No significant difference was detected in comfort with using the Internet (comfort with Internet) between the groups ($p = 0.721$). A high percentage of participants in either groups indicated they are "somewhat" or "very" comfortable with using the Internet (NT group = 70.5%, T group = 75.0%).

There was also no statistically significant difference in the average number of hours spent daily with the Internet (hours spent daily using the Internet) by the participants in the two groups ($p = 0.733$). More than 90% of the participants in both groups reported using the Internet daily for "One to three hours" or "More than three hours." Similarly, there was no significant difference between groups regarding the frequency of using the Internet to find information about their health or the health of their family members (frequency of Internet use for health information, $p = 0.237$).

### 3.2.2. Task completion

Figure 4 shows the comparison of the correct and incorrect responses for the task completion question by the two groups. Task completion refers to the proportion of each group that correctly answered the family genetic question (the chance of Susan passing a copy of the gene with the mutation to her son).Thirty-five (79.55%) participants in the NT group and 29 (65.91%) participants in the T group answered the task question correctly. There were no missing values in either group. Chi-squared test could not detect any significant difference between the two groups ($\chi[1] = 1.4323$; $p = 0.231$).

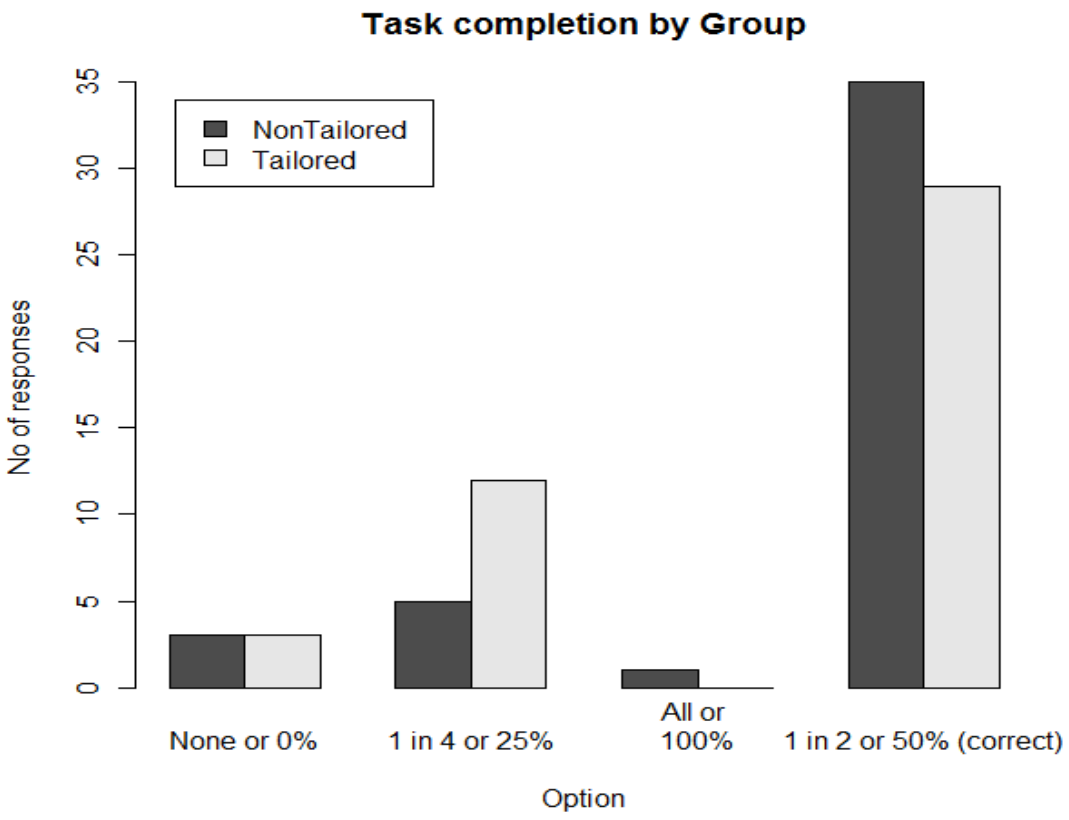



Figure 4. Bar plot of task completion by group

### 3.2.3. Time

Table 3 shows the reasons for excluding time from analysis. Part of the study plan was to measure the time to accomplish the information search task and compare the times noted by the two groups. However, time had to be excluded from our analysis as more than one-third of the participants in each group could not note the time shown in the built-in timer of the website accurately. These participants did not note the time at all or times noted were hard to interpret or indicated that there was a problem with the timer.

Table 3. Reasons for excluding time from analysis

| **Group** | **Reason for excluding** | **No of participants** |
|---|---|---|
| Nontailored | Reported problems with timer | 3 |
| | Mentioned time as "50%" (might have given the task completion answer here) | 1 |
| | Time noted was hard to interpret<br>(Times noted by subjects as they are: 0.27, 5, 12, 2, :22, 4.05, 10:00:00, 50, 00:00.9, 30, 1, 2.01, 24) | 14 |
| | | |
| Tailored | Reported problems with timer | 5 |
| | Did not mention time | 3 |
| | Indicated time as am and pm | 7 |
| | Time noted was hard to interpret<br>(Times noted by subjects as they are: 0:12, 0:16, 0:57, 50, 1, 2, 20, 14, 5, 0.5, 0.58, 0.02) | 12 |

### 3.2.4. Knowledge

Group comparison on the knowledge assessment was done in two ways. The total knowledge score was compared as well as the scores on individual knowledge questions.

#### 3.2.4.1. Analysis of total knowledge score

Total knowledge score (kscore) ranged from 6 - 12 in the NT group and 5 – 12 in the T group. The Shapiro-Wilk test indicated that kscore was not normal ($p < 0.05$). A Wilcoxon rank sum test found no significant difference in kscores between the groups ($p = 0.835$). The median kscore was 10 in both the groups with overlapping confidence intervals (95% CI = 9.5, 10.5).

#### 3.2.4.2. Analysis of individual knowledge questions

For this analysis, percentages of correct responses in the two groups were compared for every question. As shown in Figure 5, the groups performed similarly on most of the questions. Both the groups scored at least 65% in all the questions. Overall, there were many questions where the percentage of correct answers were very high (e.g., in the mid-90%), thus creating a possible ceiling effect that would limit the usefulness of statistical analyses. As indicated in Table 4, Chi-squared test detected a statistically significant difference in 2 out of the 12 knowledge questions. The difference was significant for question 1 on the indication of Susan's IHC test result for LS ($p = 0.038$) with T group (88.64%) outperforming the NT group (68.18%). For question 11, (the importance of testing Susan's siblings for mutations in the LS genes), the results were significant but in the opposite direction, with 97.73% of the NT group and 79.55%

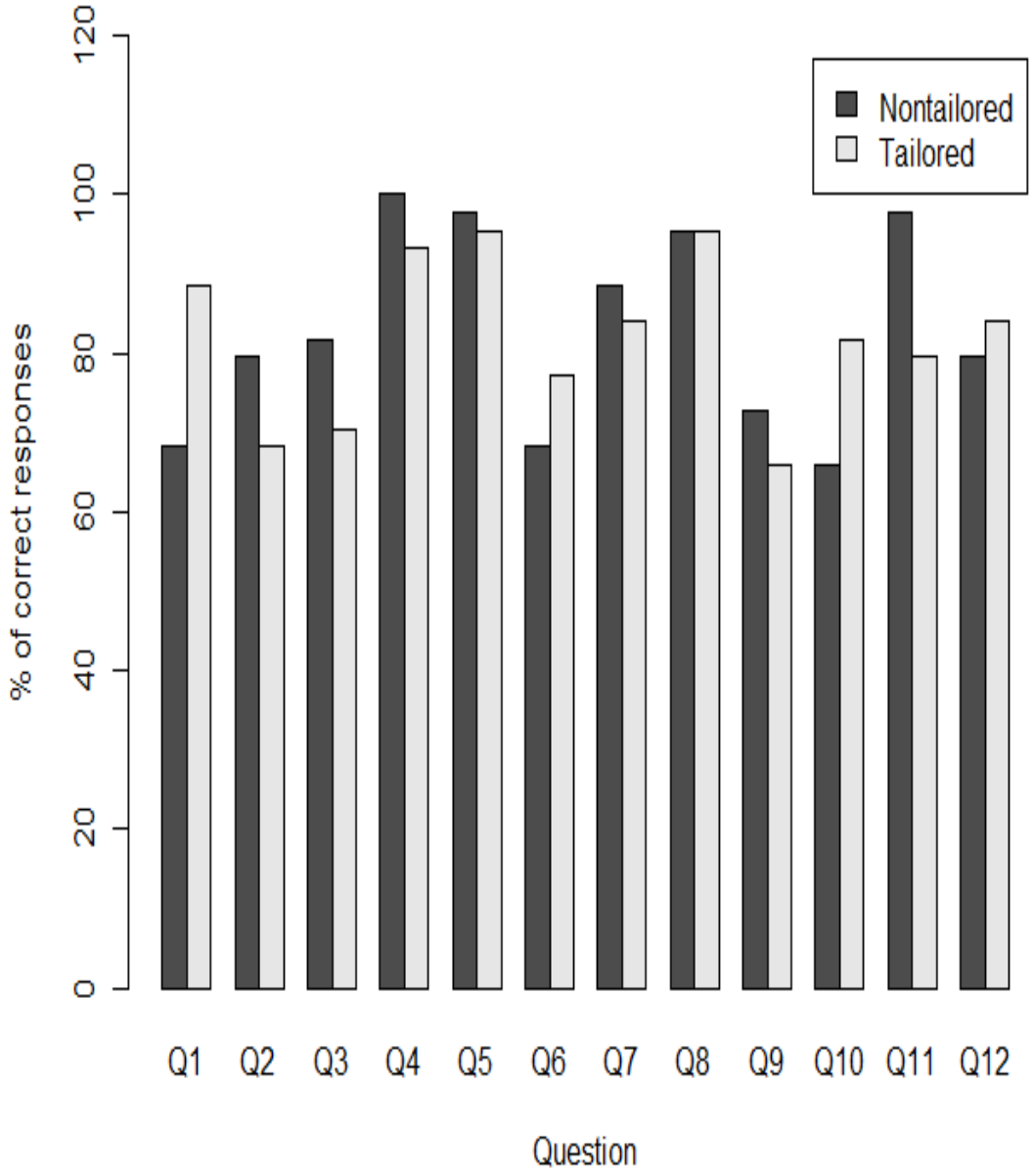



Figure 5. Group performance on knolwedge questions

Table 4. Analysis of knowledge questions

| Knowledge question | Group = NT (N=44) | Group = T (N=44) | χ[1] | *p-value |
|---|---|---|---|---|
| | No (%) correct responses | | | |
| **1. What did Susan's IHC test result indicate?**<br>(1) Susan may have Lynch syndrome<br>(2) Susan does not have Lynch syndrome<br>(3) Susan and her family members have Lynch syndrome<br>(4) Don't know<br><br>Correct answer: 1 | 30 (68.18) | 39 (88.64) | 4.296 | 0.038, Significant |
| **2. What did Susan's genetic test result indicate?**<br>(1) She will not develop colon cancer in her lifetime<br>(2) She has an increased risk of developing uterus cancer in her lifetime<br>(3) She will definitely develop uterine cancer in her lifetime<br>(4) Don't know<br><br>Correct answer: 2 | 35 (79.55) | 30 (68.18) | 0.9418 | 0.332, NS |
| **3. Why is it important to know if Susan has Lynch syndrome?**<br>(1) Her children can undergo genetic testing for Lynch syndrome<br>(2) She can undergo increased screening for colon cancer and prevent it.<br>(3) Both of the above<br>(4) Don't know<br><br>Correct answer: 3 | 36 (81.82) | 31 (70.46) | 1.0007 | 0.317, NS |

Table 4 continued

| Knowledge question | Group = NT (N=44) | Group = T (N=44) | $\chi$[1] | *p-value |
|---|---|---|---|---|
| | No (%) correct responses | | | |
| **4. How can Susan alert her family members about Lynch syndrome associated cancers?**<br>(1) by communicating about her diagnosis to her close biological relatives and alerting them.<br>(2) not telling about her diagnosis to her family members because they will be unnecessarily worried about getting Lynch syndrome.<br>(3) by communicating about her diagnosis to her close biological relatives few years later.<br>(4) Don't know<br><br>Correct answer: 1 | 44 (100) | 41 (93.18) | 1.3804 | 0.240, NS |
| **5. Testing Susan's family members for mutations in the Lynch syndrome genes can:**<br>(1) Help predict their future risk (chance) of getting colon and other types of cancer<br>(2) Tell if they have colon cancer<br>(3) Tell if they will or will not get colon cancer<br>(4) Don't know<br><br>Correct answer: 1 | 43 (97.73) | 42 (95.46) | 0 | 1, NS |
| **6. IHC test result indicated that Susan's cancer**<br>(1) could be hereditary<br>(2) is random<br>(3) is hereditary<br>(4) Don't know<br><br>Correct answer: 1 | 30 (68.18) | 34 (77.27) | 0.5156 | 0.473, NS |

Table 4 continued

| Knowledge question | Group = NT (N=44) | Group = T (N=44) | $\chi$[1] | *p-value |
|---|---|---|---|---|
| | No (%) correct responses | | | |
| **7. Who can inherit the copy of the gene with the mutation from Susan?**<br>(1) Her daughters only<br>(2) Her sons only<br>(3) Both her daughters and sons<br>(4) Don't know<br><br>Correct answer: 3 | 39 (88.64) | 37 (84.09) | 0.0965 | 0.756, NS |
| **8. Susan's children who inherit the Lynch syndrome gene**<br>(1) will get colon cancer in their life time.<br>(2) have increased risk for colon cancer compared to the general population.<br>(3) are at equal risk for colon cancer compared to the general population.<br>(4) Don't know<br><br>Correct answer: 2 | 42 (95.46) | 42 (95.46) | 0.2619 | 0.609, NS |
| **9. Genetic test indicated that Susan has a high risk for**<br>(1) colon cancer<br>(2) endometrial cancer<br>(3) both colon cancer and endometrial cancer<br>(4) Don't know<br><br>Correct answer: 3 | 32 (72.73) | 29 (65.91) | 0.2137 | 0.644, NS |
| **10. Which of the following statements about testing for Lynch syndrome is true?**<br>(1) Tumor tissue can be used in Lynch syndrome diagnosis.<br>(2) Blood sample can be used for genetic testing.<br>(3) Both (1) and (2)<br>(4) Don't know<br><br>Correct answer: 3 | 29 (65.91) | 36 (81.82) | 2.1191 | 0.146, NS |

Table 4 continued

| Knowledge question | Group = NT (N=44) | Group = T (N=44) | $\chi$[1] | *p-value |
|---|---|---|---|---|
| | No (%) correct responses | | | |
| **11. Do you think it is important to test Susan's siblings for mutations in the Lynch syndrome genes?**<br>(1) Definitely important<br>(2) Definitely not important<br>(3) May be important or may not be important<br>(4) Don't know<br><br>Correct answer: 1 | 43 (97.73) | 35 (79.55) | 5.5282 | 0.019, Significant |
| **12. Susan's children who do not inherit the Lynch syndrome gene**<br>(1) will not get colon cancer in their life time.<br>(2) have increased risk for colon cancer compared to the general population.<br>(3) will be at equal risk for colon cancer compared to the general population.<br>(4) Don't know<br><br>Correct answer: 3 | 35 (79.55) | 37 (84.09) | 0.0764 | 0.782, NS |
| *p-value is from Chi-squared test (with Yates continuity correction applied)<br>NS: Nonsignificant at 0.05 level | | | | |

of the T group answering correctly (p = 0.019). About 16% of the 44 participants in the T group wrongly opted that it may be important/ may not be important (the correct answer being definitely important) to test Susan's siblings for mutations in LS genes. The highest frequencies of correct answers in the NT group were noted for questions on alerting family members about LS associated cancers (question 4) and the importance of testing Susan's family members (question 5) and Susan's siblings (question 11) for mutations in the Lynch syndrome genes, 100%, 97.73% and 97.73%, respectively. In the T group, questions 5, 8 and 4 scored the highest frequencies of correct answers, 95.46%, 95.46% and 93.18%, respectively.

The highest number of wrong answers in the NT group was observed for question 10 (body tissue that can be used for testing LS) and 6 (if Susan's Immunohistochemistry test result indicated that her cancer is hereditary), with proportion correct of 65.91% and 68.18%, respectively. In the T group, questions 9 and 2 had the highest number of wrong answers, 65.91%, and 68.18%, respectively.

The two randomization groups scored more than 90% on questions on alerting and testing family members and colon cancer risk to children (questions 4, 5, 8). Both the groups have an equal number of correct answers (95.46%) for question 8 which was on the risk of colon cancer to Susan's children who inherit the LS gene.

3.2.4.3. Effect of baseline characteristics on kscore

As shown in Table 5, a Kruskal-Wallis test could not detect any significant effect of gender, education level or Internet usage characteristics on kscores. As the two groups showed a marginally significant difference in age, simple linear regression was done with

Table 5. Effect of baseline characteristics on kscore

| Criteria | Kruskal-Wallis chi-squared | Df | *p-value |
|---|---|---|---|
| age | | | 0.642, NS |
| Gender | 0.0997 | 2 | 0.951, NS |
| education level | 0.3437 | 4 | 0.987, NS |
| comfort with Internet | 7.2991 | 5 | 0.199, NS |
| hours spent daily using the Internet | 1.3252 | 3 | 0.723, NS |
| frequency of Internet use for health information | 1.6173 | 4 | 0.806, NS |
| *All p-values are from Kruskal-Wallis test, except for age which is from simple linear regression. NS: Nonsignificant at 0.05 level | | | |

age as the independent variable and kscore as the dependent variable to see if age had any effect on kscore. The result showed no significant association with kscore ($p = 0.642$).

A stepwise linear regression was done to regress all the demographic and Internet usage variables along with group membership on kscore. The result indicated that comfort with Internet is the best individual predictor of kscore, although the model with Internet comfort alone was not significant ($p = 0.155$, Adjusted R squared = 3.6%).

### 3.2.5. Usability

Table 6 presents the usability results of the study. The NT group has two missing values (one in consistency and another in clearly marked exits). There is one missing value in the T group (feedback about location).Usability analysis was done after excluding the missing values. On a 1-7 (1=bad and 7=good) scale, both the websites received a rating of at least 4 on all the criteria.

There was a significant difference noted in the overall usability between the two

Table 6. Usability analysis

| Heuristic | Group = NT | Group = T | *p-value |
|---|---|---|---|
| | Group Mean Score | | |
| Simple and Natural Dialogue | 5.14 | 4.96 | 0.598, NS |
| Speak the Users' Language | 5.23 | 4.59 | 0.066, NS |
| Minimize User Memory Load | 4.57 | 4.39 | 0.601, NS |
| Consistency | 5.26 | 4.93 | 0.361, NS |
| Feedback about Location | 5.16 | 4.61 | 0.102, NS |
| Clearly Marked Exits | 4.98 | 4.36 | 0.102, NS |
| Expected Functions | 5.56 | 4.59 | 0.008, Significant |
| Easy-to-navigate | 5.46 | 4.52 | 0.013, Significant |
| Average Group Mean Score | 5.17 | 4.62 | 0.001, Significant |
| *p-value is from t-test<br>NS: Nonsignificant at 0.05 level | | | |

websites, the nontailored website outperforming the tailored one ($t = -4.1479$; $p = 0.001$, $df = 12.81$). The average group mean score was 5.17 for the nontailored website and 4.62 for the tailored website. A significant difference between the groups was found only for two criteria viz. "Expected Functions" ($p = 0.008$) and "Easy-to-navigate" ($p = 0.013$).

### 3.2.6. Usefulness

Table 7 summarizes the results of the usefulness data analysis. In the NT group, questions 2, 4 and 5 have one missing value each. In the T group, there was one missing value for question 4. Usefulness data were analyzed after excluding the missing values. On a 1-5 (1 = strongly disagree to 5= strongly agree) scale, the overall usefulness was more than 3.5 for both groups, but there was no significant difference between the two groups in the overall usefulness ratings ($t_7 = 1.0098$; $p = 0.346$, $df = 7.145$) or in any of the five usefulness items.

Table 7. Usefulness data analysis

| **Usefulness Item** | **Group = NT** | **Group = T** | ***p-value** |
|---|---|---|---|
| | **Group Mean Score (1 = strongly disagree to 5= strongly agree)** | | |
| 1. The website helped me better understand the complex terminology of genetics and testing associated with Lynch syndrome. | 3.71 | 3.48 | 0.228, NS |
| 2. The website was useful in understanding test results. | 3.61 | 3.27 | 0.099, NS |
| 3. I would recommend this website to somebody who is getting tested for Lynch syndrome. | 3.75 | 3.77 | 0.912, NS |
| 4. The website adequately addressed the reasons for getting early and frequent screening if a close relative is diagnosed with a cancer. | 4.1 | 3.84 | 0.177, NS |
| 5. The information provided in the website will help Lynch syndrome patients to communicate better about their health condition with their health care provider. | 3.81 | 3.89 | 0.713, NS |
| Average Group Mean Score | 3.796 | 3.650 | 0.346 , NS |
| * All p-values are from t- test<br>NS: Nonsignificant at 0.05 level | | | |

## 3.3. Summary

There was no significant difference in the baseline characteristics of the participants belonging to the tailored and nontailored groups except for age. The difference was marginally significant for age between the two groups. The groups showed no significant difference in answering the task completion question. Time data were excluded from analysis due to inaccuracies in reporting time. Total knowledge score was similar for both the groups and except for questions 1 and 11, there were no

significant differences between groups. There were significant ceiling effects on the response ranges, making analysis difficult.

As per the usability of the website, the nontailored one received significantly better ratings than the tailored one for overall usability as well as for two of the eight heuristics assessed (“Expected functions” and “Easy-to-navigate”). With respect to usefulness of the website, there was no significant difference between them in terms of overall usefulness or any of the five usefulness items. A detailed discussion of the study results can be found in the next chapter.

# CHAPTER 4

# DISCUSSION

## 4.1. Overview

This chapter contains a detailed discussion of the study outcomes. After discussing the study results, significance of the project will be explained for 1) other online tailored health communication projects, 2) the field of Biomedical Informatics and 3) the specific usefulness of tailored websites for genetic counseling. Then limitations of the study and directions for further research will be described. Finally, we close the chapter with a brief conclusion.

## 4.2. Discussion of the study outcomes

Substantial prior research has found that tailoring has positive outcomes in health education websites[26-29]. Studies have found that tailoring is a promising strategy for communicating health information to consumers in areas like smoking cessation[18-20], diet and nutrition [12,14,21], cancer screening [13], health risk appraisal [20], cholesterol management[20], childhood immunizations [22], and physical activity [23,24], etc. Based on the results of tailoring in other health behavior studies, this study was conducted in order to explore the impact of tailored information for communicating genetic test results to patients.

To the best of our awareness, this is the first study to investigate the effect of tailoring (tailored to the individual's results) for communicating genetic test results. This study was a two-group randomized controlled trial that compared the effectiveness of tailored versus nontailored website format in conveying information about the genetic test results of a colon cancer patient who is being evaluated for LS. The two websites differed only in the manner in which the test results were presented. The outcomes were: task completion, time, knowledge, usability and usefulness.

In contrast to prior work on tailored messaging, statistical analysis from this study showed that tailoring did not impact the outcomes of interest. Overall, both groups performed very well using the website, indicating that the websites were effective and useful, regardless of tailoring. Few differences were found between groups for knowledge. Usability was rated higher for the nontailored group.

There are several possible explanations for these results. First, the manipulation of tailoring might have been not strong enough to have an impact. The inconsistent pattern of results supports this conclusion, but the fact that only one of the findings was in the predicted direction argues against this explanation. Second, the knowledge test may have not been a good measure of the impact. It may have been too easy, thereby not really providing a test of the tailored method. The subjects in both groups scored very well on the knowledge test and there were substantial ceiling effects. The knowledge test questions were created in consultation with experts in genetic counseling, but were not pretested on another population. Third, the subject pool may not have been representative of the relevant subject population. The subjects selected for this study were in the age group where colon cancer diagnoses are more relevant. However, they, themselves, did

not have a diagnosis, nor did any members of their families. Tailored communication may be particularly helpful when patients are personally involved.

At present there is limited understanding on what factors actually increase the effectiveness of tailoring [52]. Pretesting the website with CRC patients who are in different stages of evaluation for LS may help us determine on what variables the assessment could be done in order to achieve better results. Such pretesting would be especially helpful in understanding how websites might interact with the personal interaction that a genetics counselor provides. This may even help us to refine the multiple-choice questions and response choices that are in the tailored website now and make the entire assessment more comprehensible.

Usability analysis (Table 6) showed that users rated both websites at least a 4 on a 1-7 (1=bad and 7=good) scale for all of the usability criteria. These results were very encouraging to us. However, overall usability was rated lower for the tailored website, possibly due to increased effort needed to use the site (effort was not tested in this study). The nontailored website also received significantly higher ratings for two usability criteria ("Expected Functions" and "Easy-to-navigate"). These results suggest that the design of the tailored website had some aspects that the users did not expect and the tailored website was not so easy-to-navigate. One usability problem indicated by a participant in the tailored group was expressed thus: "On the website, when I was looking at interpreting the test results, it was easy to match up which gene had the defect. But when I selected the icon for genetic test, I was expecting another window to open. It took me a while to figure out I needed to scroll down". However, the decision to use or not use pop-up windows was difficult in the website design as it was thought that some

participants might face problems removing the pop-up blocker. Further refinement of the usability of screens is an important next step.

Usefulness data analysis (Table 7) showed that both the websites received similar scores in terms of overall usefulness and the participants in both groups agreed that the website (tailored/ nontailored) would be useful for LS patients. Two of the study participants commented, "A friend of mine and 3 family members were recently diagnosed with Lynch syndrome. I wish I could share this with her," "The lab results documents are very hard to read….and the information is only understandable due to the website's education." One comment made by a participant in the nontailored group worth mentioning here is, "Most people need to know only about their own specific test results, not all the ifs, ands, and wherefores."

Several participants reported difficulties with interpreting the lab report provided online for the study's use case (Susan). A few comments by the participants are included here: "The test report was virtually unintelligible to nonmedical trained person," "Lab report was not very readable and like many reports confusing," "Test results in pathology could be worded more clearly." These remarks encourage us to further explore online communication of test results. The experience of these users will be helpful in informing future website designs.

### 4.2.1 Suggested modifications to the tailoring assessment

Figure 6 shows the modifications to the tailoring assessment. In the tailored website evaluated in our study, assessment was based on the test results and family history information. However, as people are in different stages of LS evaluation i.e.,

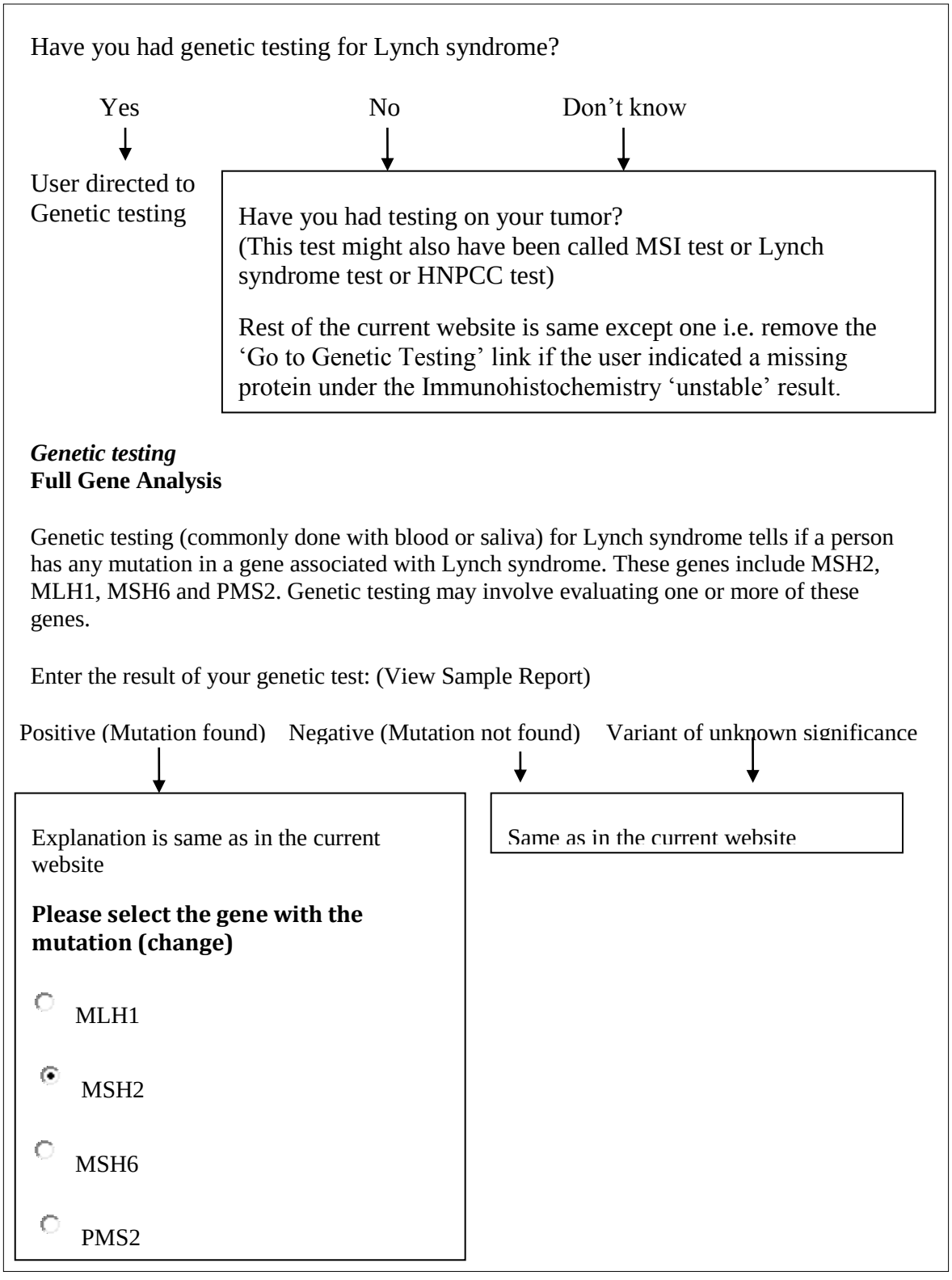



Figure 6. Modifications to the tailoring assessment

depending on whether a patient is in the tumor tissue testing stage or genetic testing stage, their information needs vary. For example, a person like Susan, for whom genetic testing detected a LS mutation could be directed to information pertinent to having a molecular diagnosis of Lynch syndrome rather than needing to first go through information about preliminary results, which indicate a possibility of Lynch syndrome and need for further testing. Hence, "stage of evaluation" is an important variable to be incorporated in the tailoring assessment.

In the current tailored website, the assessment should begin with the question: Have you had genetic testing (using a sample of blood or saliva) for Lynch syndrome? The answers would be "Yes," "No," "Don't know." If the user indicated "Yes," he/ she should be directed to genetic testing. Under genetic testing, if the user indicates that a mutation is identified, it would be apt to provide a list of the DNA mismatch repair genes and ask the user to indicate the gene for which the mutation is identified. Based on the mutated gene, tailored information (like the cancer risk based on the gene involved) can be provided.

## 4.3. Significance of the project

The significance of the project can be understood from three perspectives. First, with the growing role of patients in managing their own health, there is a pressing need for them to understand the results of their tests. Hence, people are increasingly accessing the Internet for information about medical test results. Further, with the Internet transcending all geographical boundaries, it evolves as an important medium for patient education, especially for people living with a rare health condition like LS. For a lot of

complex testing, Internet-based tools have a great potential to communicate results in ways that will be more informative to patients.

Second, the need to convey personalized genetic information is increasing exponentially. The Centers for Disease Control (CDC) advocates screening all newly diagnosed cases of CRC for LS[53]. As an increasing number of patients undergo the evaluation for LS and other genetic tests, research on online patient education tools that help in interpreting the test results gains significance. "Tailoring" for conveying complex information about colorectal cancer genetics through the Internet is one method (shown to be effective in other fields) that is worth further exploration.

Another perspective is that with the anticipated shift in US healthcare from fee-for-service to bundled payments, as in the various ACO (Accountable Care Organization) models, healthcare organizations will have to use lab tests more efficiently. This will obligate the laboratories to make the lab results more understandable, particularly to patients, because of their increasing role in clinical decision making.

#### 4.3.1. Implications to online tailored health communication projects

This project has some important implications to online tailored health communication projects. First, this project emphasizes the importance of subject matter experts in order to know the nature of the health problem before developing any health communication program. Future analysis will help identify the variables relevant for tailoring and effective communication. For example, in the very early phase of the website, the expertise of a genetic counselor was used to determine how an interactive assessment can be done. It was decided that messages could be tailored based on the

names of the diagnostic tests, the test results and the family history information.

Second, the "think aloud" method used in the study helped us to capture directly the problems that a user might face while using our website. It is very important to assign certain tasks to the users and note the problems that they face while accomplishing the task. This enables us to see first-hand how the users go about completing a task. Although tailoring has been shown to be effective in other fields, genetic counseling is so complex, future work should identify the exact ways that users interact with the website.

Third, this study employed a clinical vignette-based survey for evaluating the website. This technique can be especially useful when recruiting members of the target population is a big challenge. However, the results have to be interpreted with caution.

### 4.3.2. Contribution to Biomedical Informatics

As defined by Friedman et al., "Biomedical Informatics is the science underlying the acquisition, maintenance, retrieval, and application of biomedical knowledge and information to improve patient care, medical education, and health sciences research." [54] As laboratory genetic testing becomes available now for cancer, patients have greater need to understand the complex medical information in order to interpret the implications of the test results for themselves and their family members. Through the example of Lynch syndrome, this project has evaluated tailoring as a strategy for conveying complex information about the results of genetic tests to patients. The methods and the outcomes of our study can have implications for the development and evaluation of other online tailored health communication programs on genetic testing. We believe that this project

would be a stepping-stone for the future online tailored communication of genetic test results.

Recommendations to improve the effectiveness of tailored websites that are suggested by the results of this study include: 1) increase the usability of tailored websites; 2) pretest the tailoring assessments to determine for which variables tailoring can be done so that the impact of the tailored messages can be known; 3) evaluate website designs with people who can be the potential users of the website; and 4) explore the benefits of having the genetic counselor choose whether the patient has access to a tailored or a nontailored website.

#### 4.3.3. Tailored website for genetic counseling

A tailored intervention does not replace the work of a genetic counselor, but rather serves to complement the counseling work to improve knowledge of the patients on the interpretation of their test results. Moreover, a tailored website does not provide the direct emotional support that a counselor can provide. The key biomedical design question is how websites could be effectively designed to complement and enhance the work of the genetic counselor. However, with the advancements in technology, tailored interventions can have the ability to reach far more people than would be possible with interpersonal counseling [55].

## 4.4. Limitations of the study

One of the major limitations of our study was that the study was not conducted with actual colorectal cancer patients (CRC) being evaluated for Lynch syndrome. Our

original plan was to recruit CRC patients from the Huntsman Cancer Institute in Utah as they wait for their appointment at the cancer clinic. However, there were a couple of issues that we considered could affect our results. First, there could be newly diagnosed cancer patients who are emotionally overwhelmed with their health condition. Second, there could be patients who had already consulted with a genetic counselor and learned of Lynch syndrome. Third, some of the patients could be physically challenged to navigate through the website. After exploring a couple of places for possible recruitment of the subjects within a reasonable scope of time and resources, and without compromising on the sample size, the project committee decided that the subjects could be recruited from The University of Utah Osher Lifelong Institute (OLLI) and ResearchMatch.org.

The recruitment of healthy individuals over 50 years old for this study can be justified by three facts. First, the most common incidence of colon cancer is 50 years of age. Second, healthy, at-risk individuals undergo genetic testing to determine their cancer risk. One study which compared knowledge about HNPCC between mutation carriers and physicians, mentioned that "an increasing number of healthy, at-risk individuals now undergo genetic testing and though not formally patients, these individuals are dependent on healthcare for early cancer prevention."[45] Third, Lynch syndrome is a rare form of cancer. Hence, recruiting individuals with LS was not possible in the limited study period.

The second limitation was that the study participants were asked to simulate the experience of Susan (a colon cancer patient whose tumor was resected and the tumor tissue was being evaluated for LS) and interpret the results of her tests for LS using the tailored/ nontailored website. Though the participants were asked to pretend to be Susan,

tailored messages might not have been perceived as personally relevant by the participants and hence, the results were not as expected.

The third limitation would be the usability aspects of the website. The failure of the study to detect a significant effect of tailoring on the outcomes may be attributed to some extent to the design faults of the website. However, usability testing cannot eliminate the usability problems completely. Effort was made to minimize the problems of navigating through the website within the limits of time and resources.

The fourth limitation of the study would be that the content in the interpretation section in the nontailored website has been presented in tabulated form. Had the entire information in that section been left as plain text without organizing into tables of information, the study might have detected significant effect of tailoring on the outcomes measured. However, a tabulated form was used in order to avoid overburdening the subjects.

The fifth limitation of the study was that the knowledge questionnaire was not formally validated. However, these questions were adapted from previously validated questionnaires and the expertise of the genetic counselor was used in modifying them.

Finally, the results may have less generalizability in that the study subjects had a higher level of education than the general population. Further, since the recruitment message was sent to potentially eligible people through email, people are obligated to have email-id and could be Internet savvy compared to the general population. Since our subjects were volunteers, the motivation to participate would be high. The results of our study have to be interpreted bearing these facts in mind.

## 4.5. Future directions

The study could not determine conclusively if tailoring is advantageous over nontailoring methods in conveying complex genetics-based testing information to patients. However, participants did very well answering the knowledge questions overall. While one study cannot answer all the questions pertaining to a problem, the information obtained from this study can be used to refine further tailoring studies on patient education of genetic test information.

First, in the website we have built, tailoring was based on the assessment derived from a handful of data from a family history. It would be ideal to integrate a complete family history collection tool in order to make the entire assessment simulate a personalized counseling session that would more fully address the individual needs of the patients.

Second, further research is needed to evaluate mental models of cancer patients facing genetic testing and counseling. More in-depth cognitive task analysis using a variety of techniques would provide more clarity about how patients construct the problem of interpreting genetic test results and how they are framing their information search. Such a study could provide us with rich information about how such users actually use the website. Results of the study will also help us decide on what variables the messages could be tailored for effective communication.

Third, exploring different interactive multimedia options is worth considering as it could enhance the ability of the users to comprehend the test results. For example, integrating audio into the website could simulate an interaction with a counselor.

## 4.6. Conclusion

This project has demonstrated that online tailored communication of genetic test results is possible and effective, though no significant effect of tailoring on the outcomes measured could be determined. The tailored website was at least on par with the nontailored website on task completion, knowledge and usefulness outcomes.

Tailored health communication is still in its infancy. Future research on evaluating the website through cognitive response methods with actual CRC patients is necessary to get more insights into how the users actually process information and clarify these results.

# APPENDIX A

## SCREEN SHOTS OF TAILORED AND NONTAILORED WEBSITES

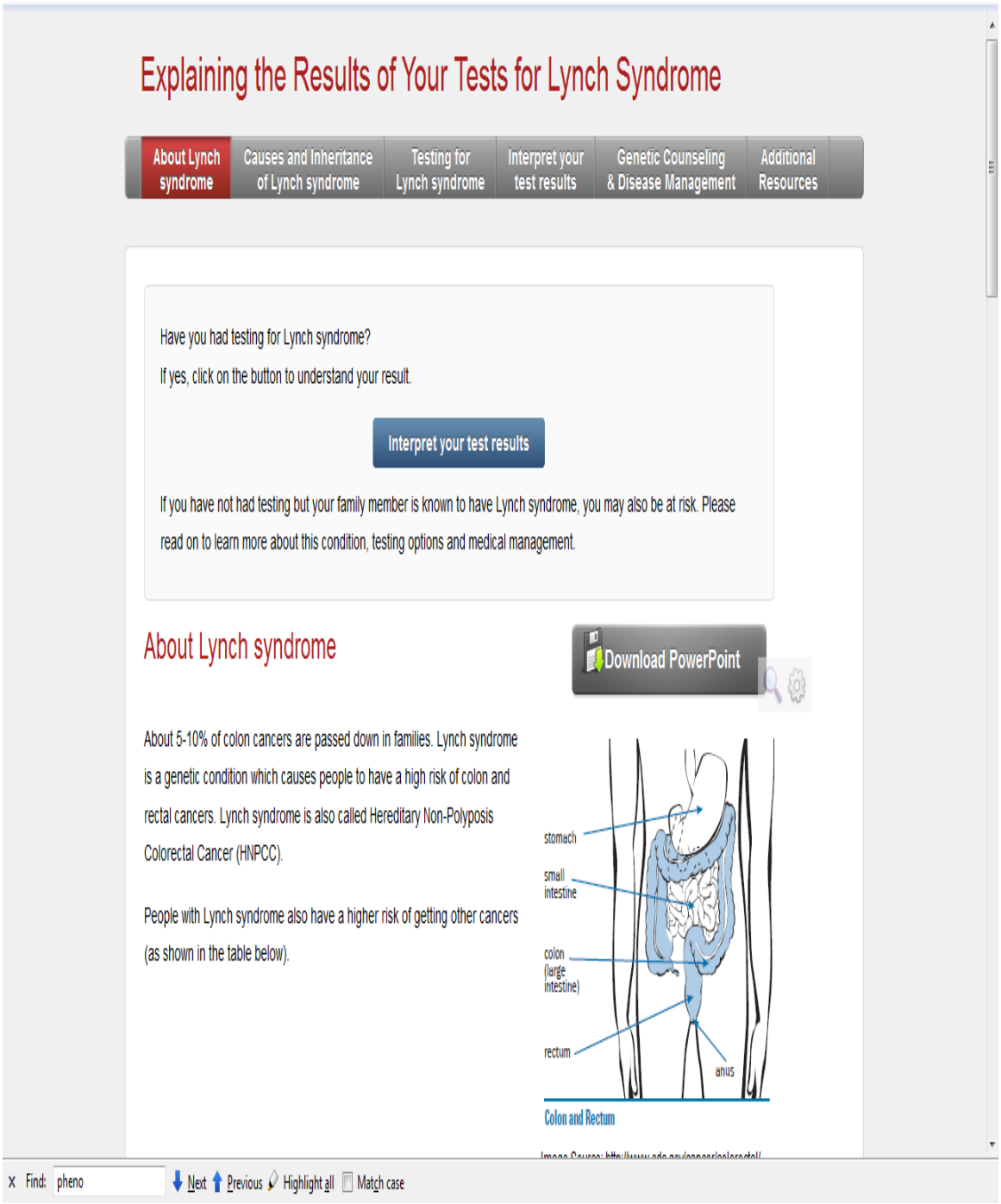



Figure 7. Screen shot of the “About Lynch syndrome” section

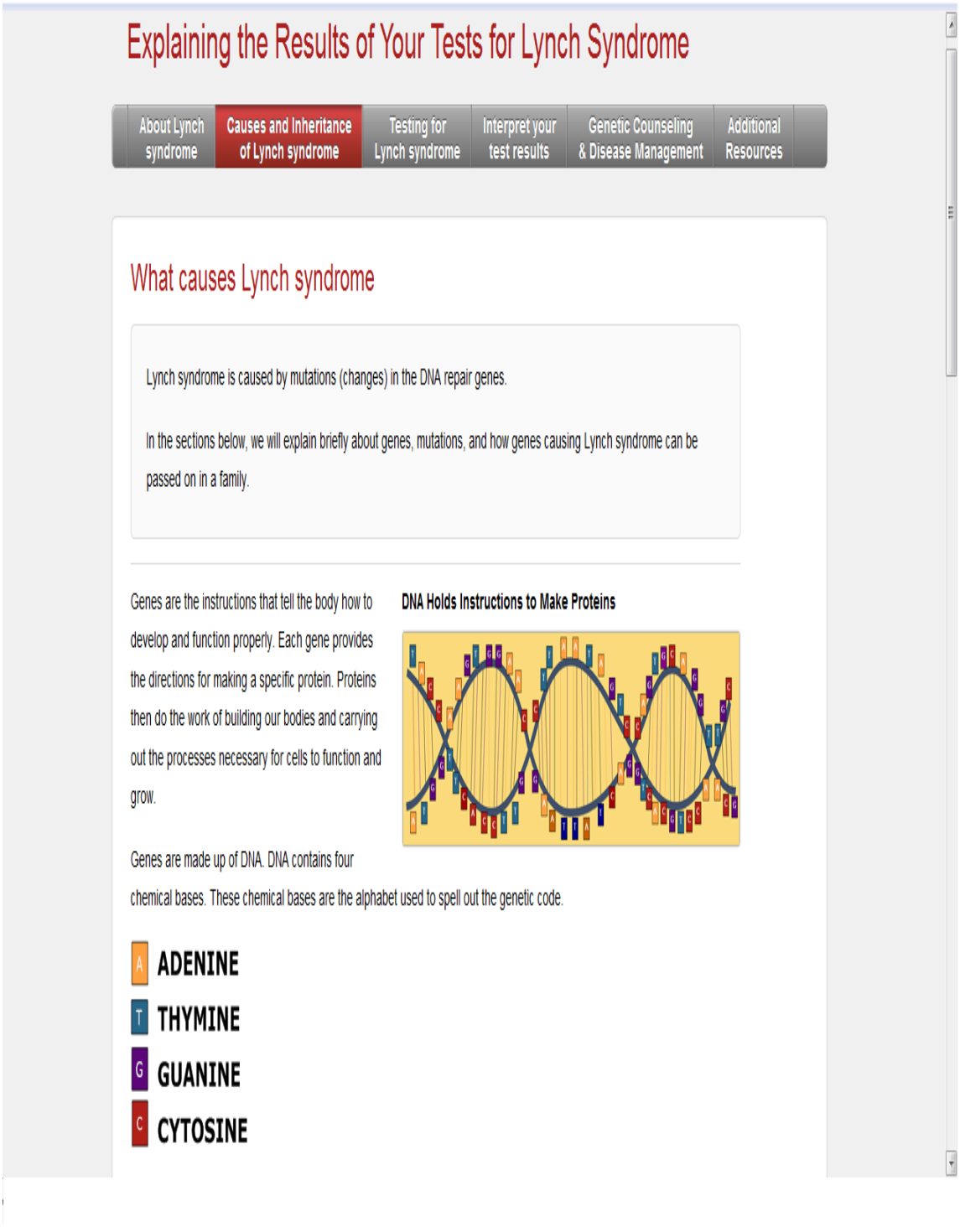



Figure 8. Screen shot of the “Causes and inheritance” section

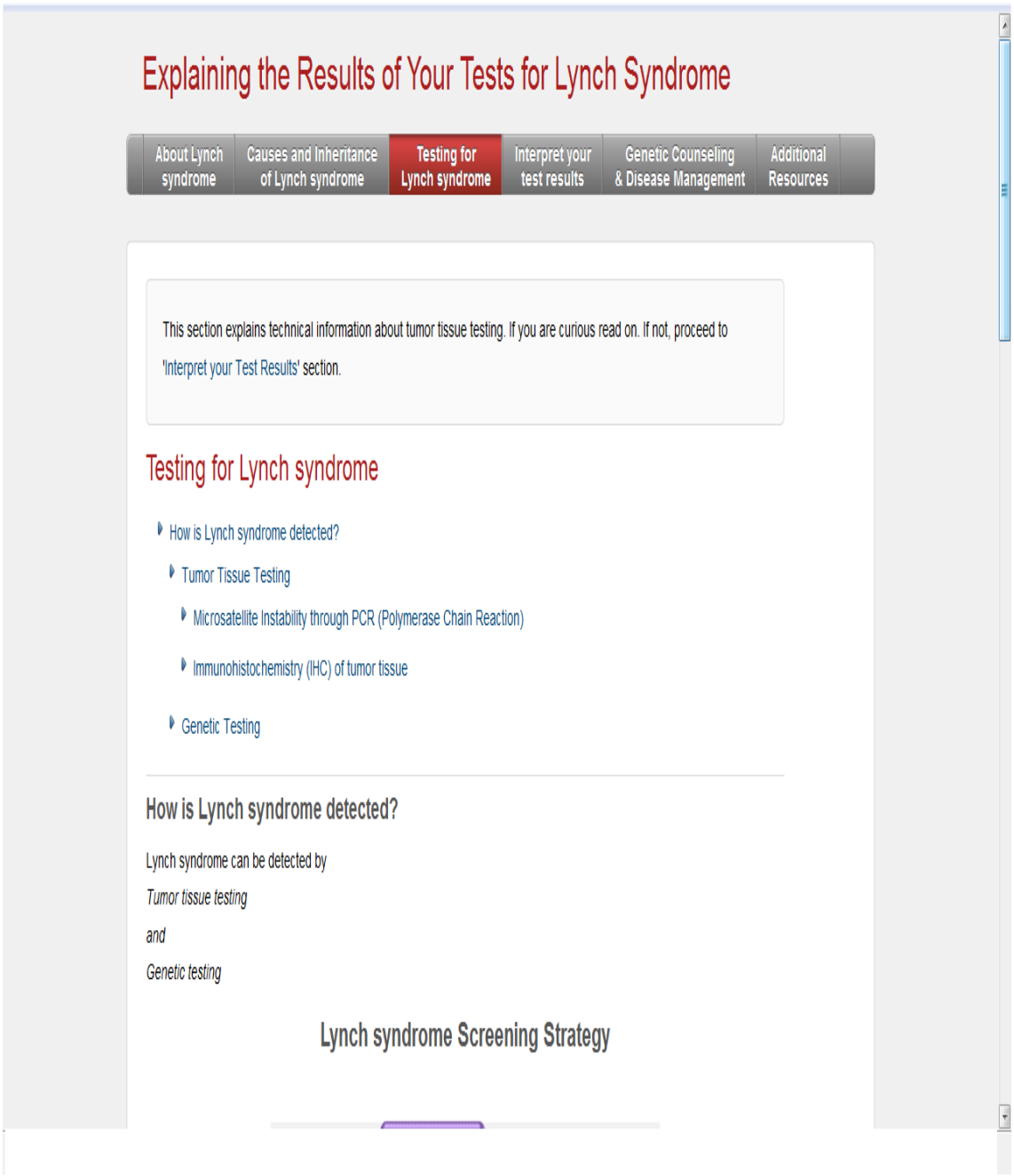



Figure 9. Screen shot of the “Testing for Lynch syndrome” section-1

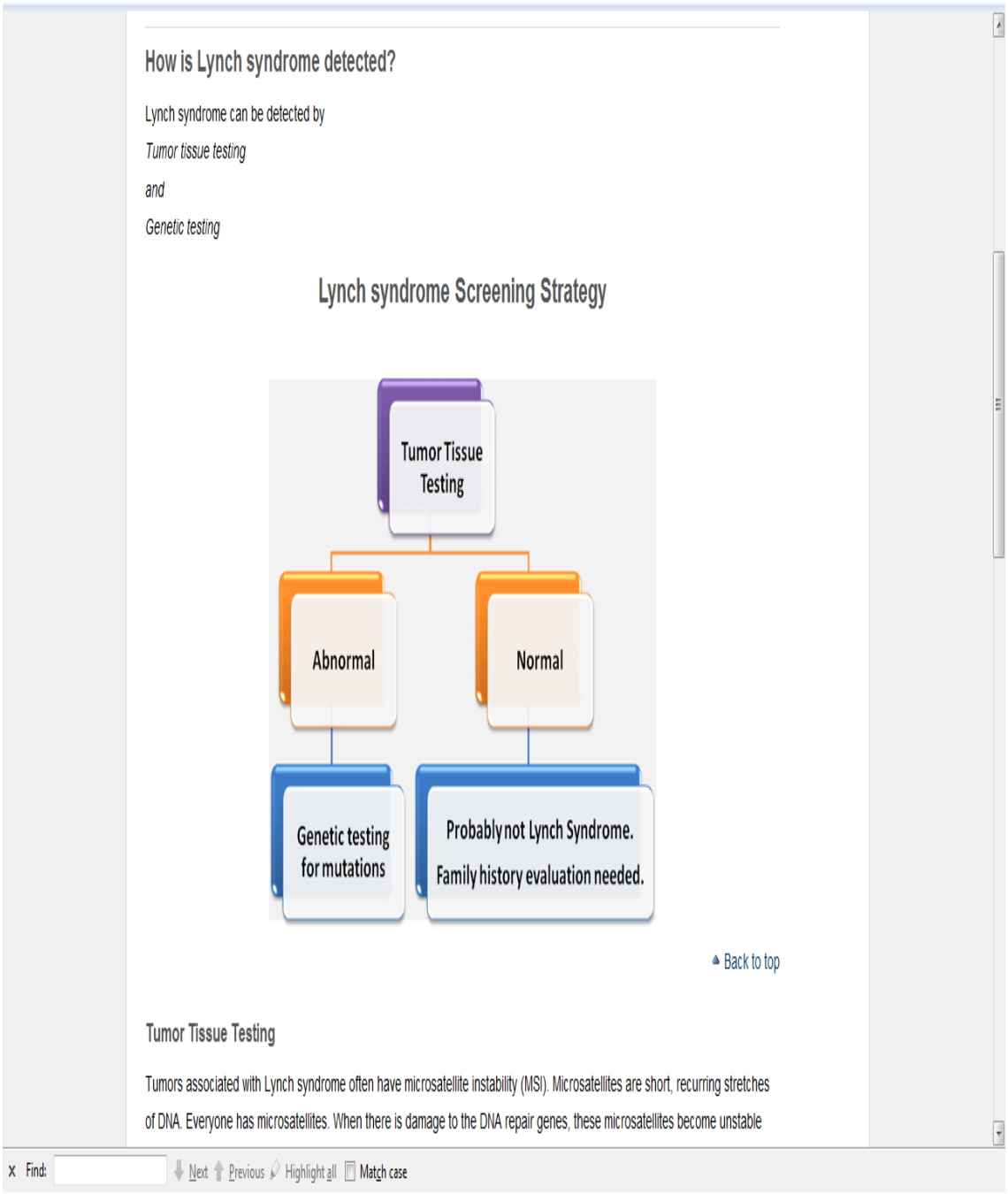



Figure 10. Screen shot of the “Testing for Lynch syndrome” section-2

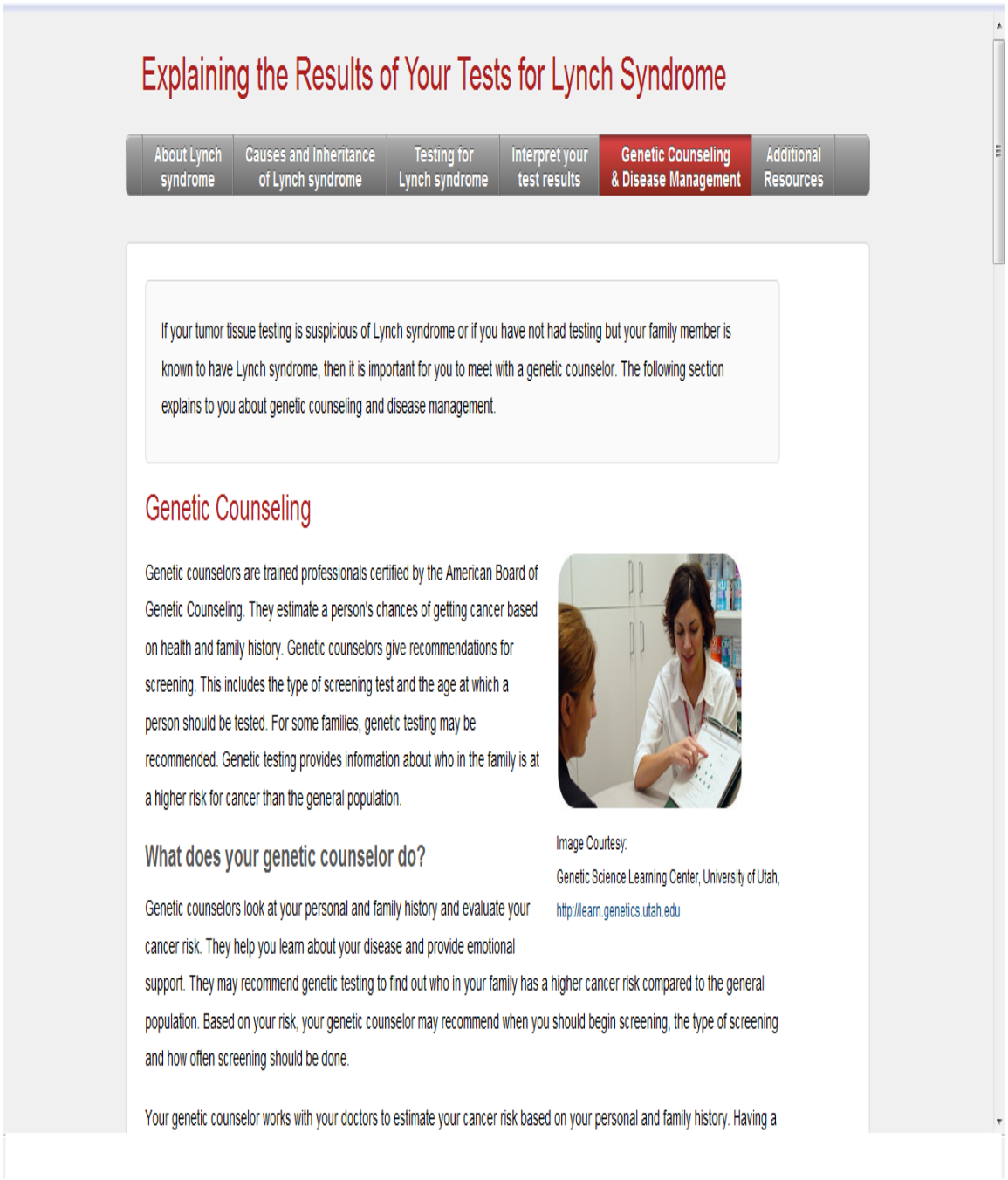
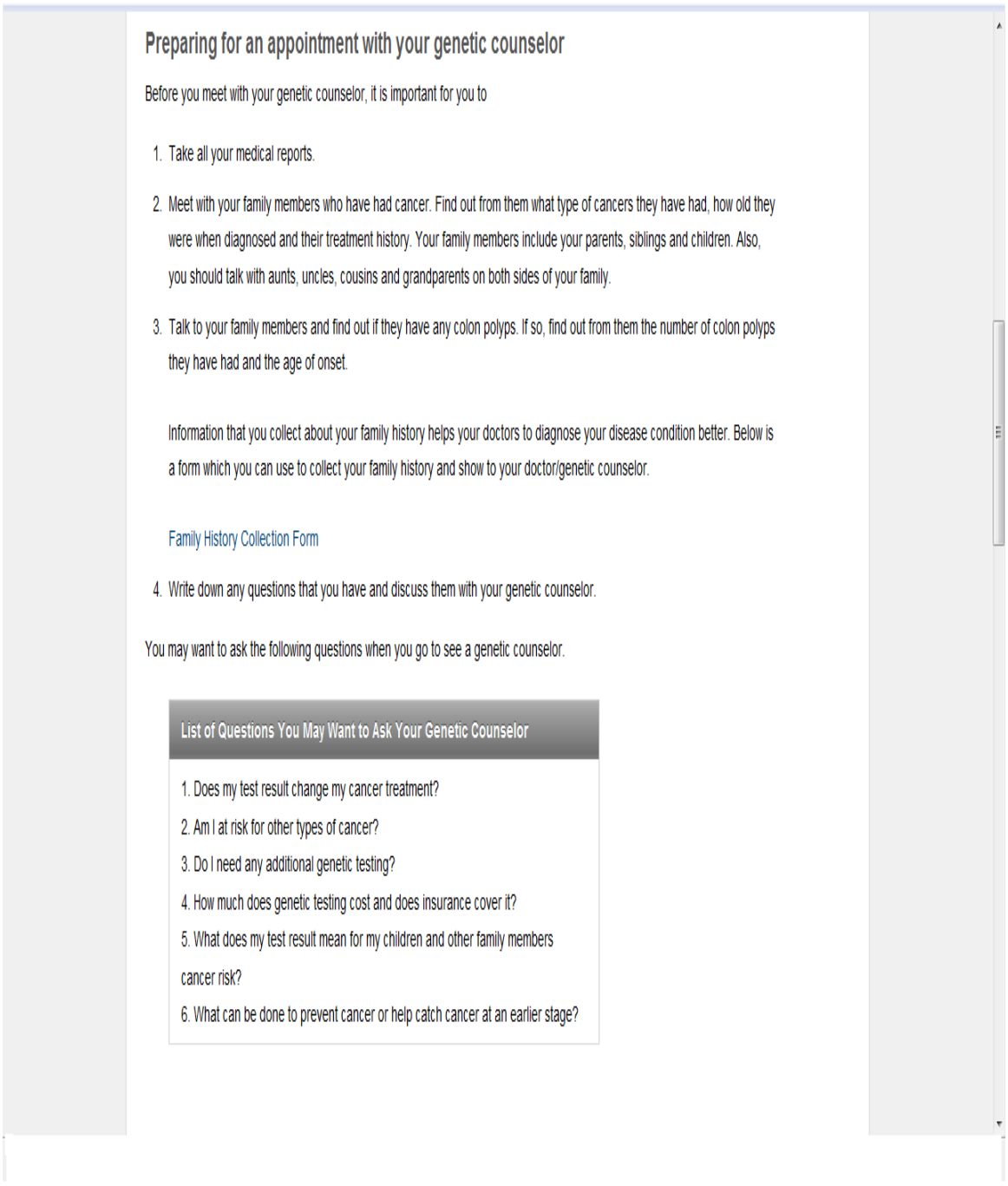



Figure 11. Screen shot of the “Genetic counseling and disease management” section-1



## Preparing for an appointment with your genetic counselor

Before you meet with your genetic counselor, it is important for you to

1. Take all your medical reports.
2. Meet with your family members who have had cancer. Find out from them what type of cancers they have had, how old they were when diagnosed and their treatment history. Your family members include your parents, siblings and children. Also, you should talk with aunts, uncles, cousins and grandparents on both sides of your family.
3. Talk to your family members and find out if they have any colon polyps. If so, find out from them the number of colon polyps they have had and the age of onset.

   Information that you collect about your family history helps your doctors to diagnose your disease condition better. Below is a form which you can use to collect your family history and show to your doctor/genetic counselor.

   Family History Collection Form

4. Write down any questions that you have and discuss them with your genetic counselor.

You may want to ask the following questions when you go to see a genetic counselor.

| List of Questions You May Want to Ask Your Genetic Counselor |
| --- |
| 1. Does my test result change my cancer treatment? |
| 2. Am I at risk for other types of cancer? |
| 3. Do I need any additional genetic testing? |
| 4. How much does genetic testing cost and does insurance cover it? |
| 5. What does my test result mean for my children and other family members cancer risk? |
| 6. What can be done to prevent cancer or help catch cancer at an earlier stage? |

Figure 12. Screen shot of the “Genetic counseling and disease management” section-2

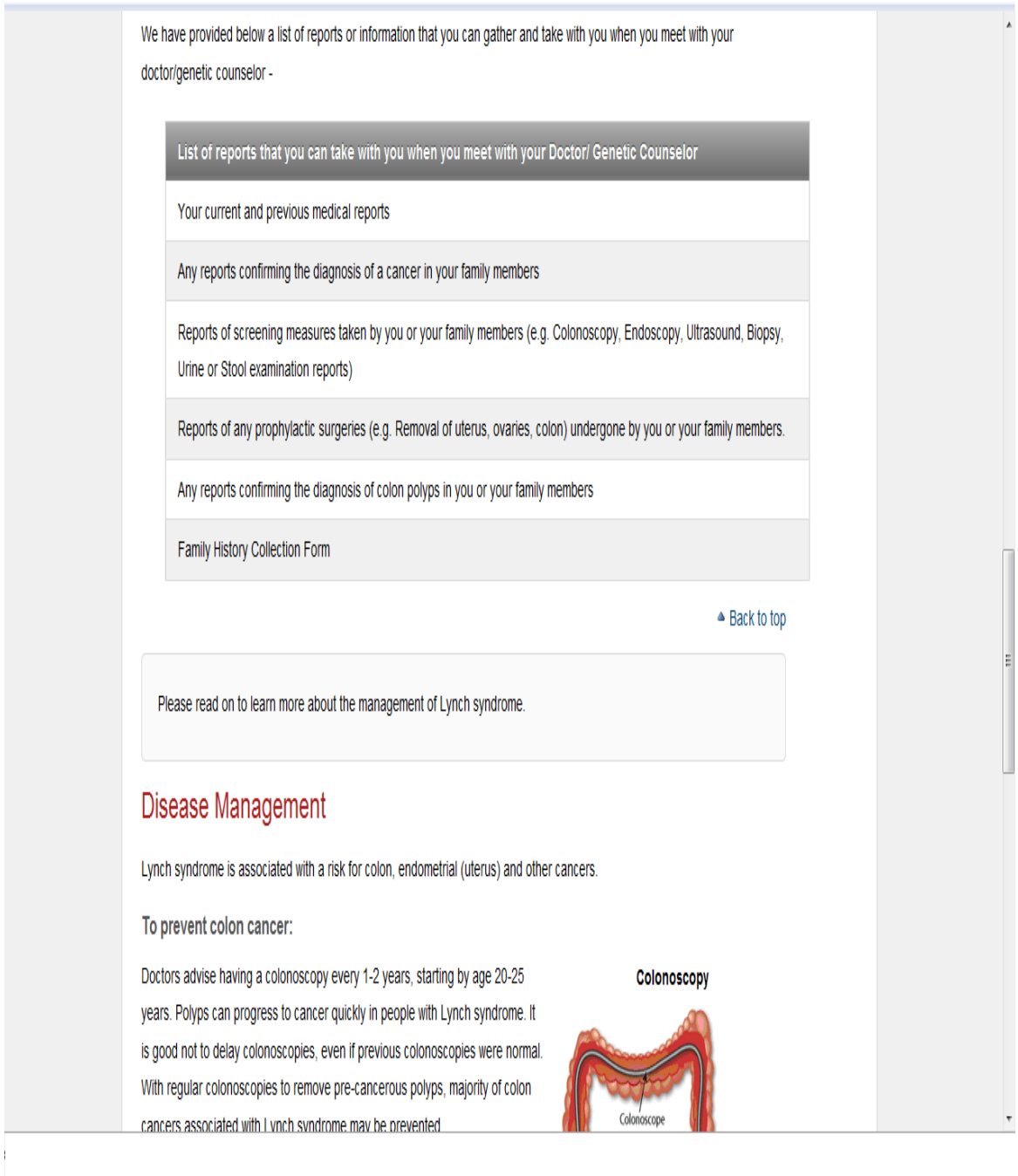



Figure 13. Screen shot of the "Genetic counseling and disease management" section-3

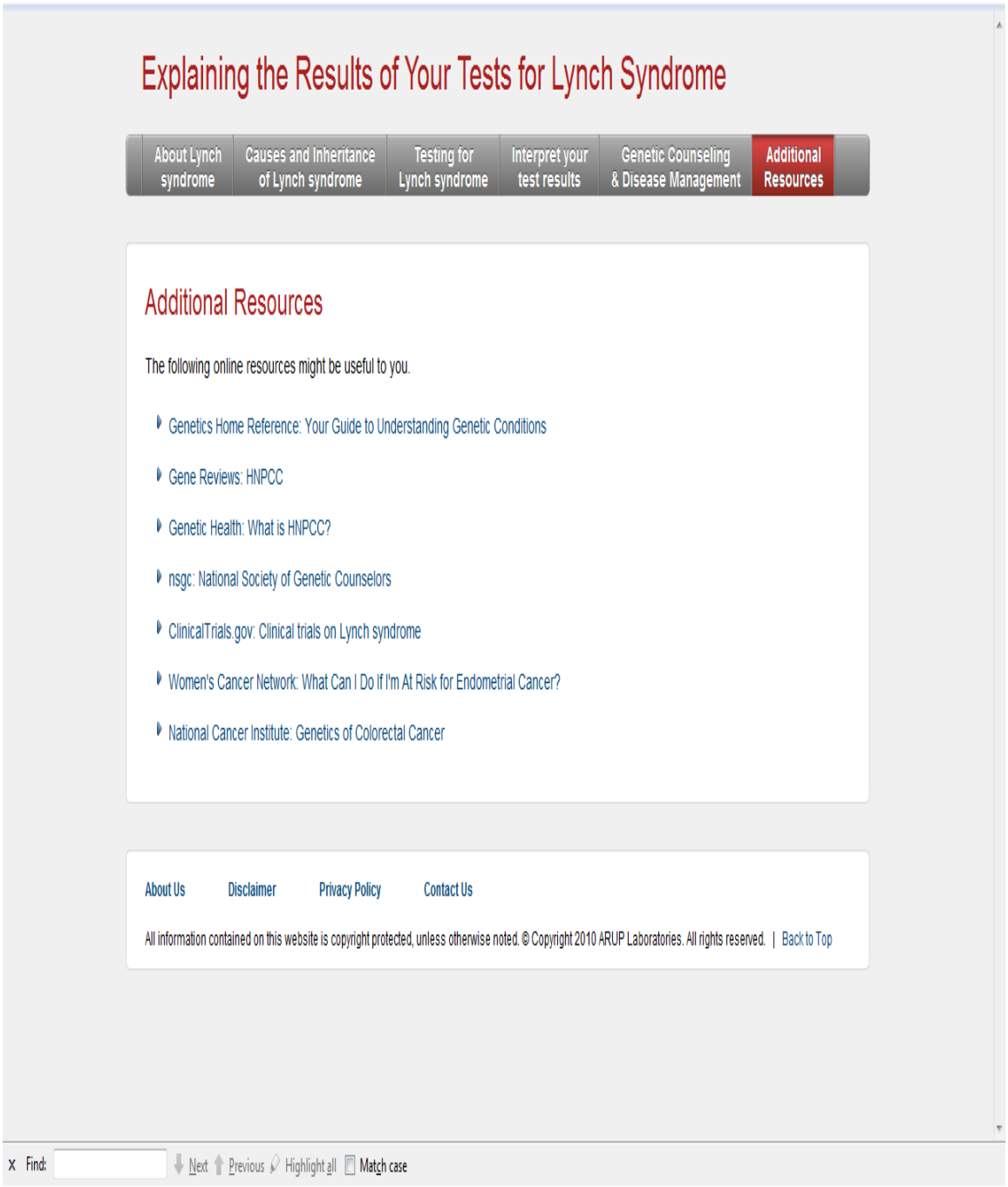



Figure 14. Screen shot of the "Additional resources" section

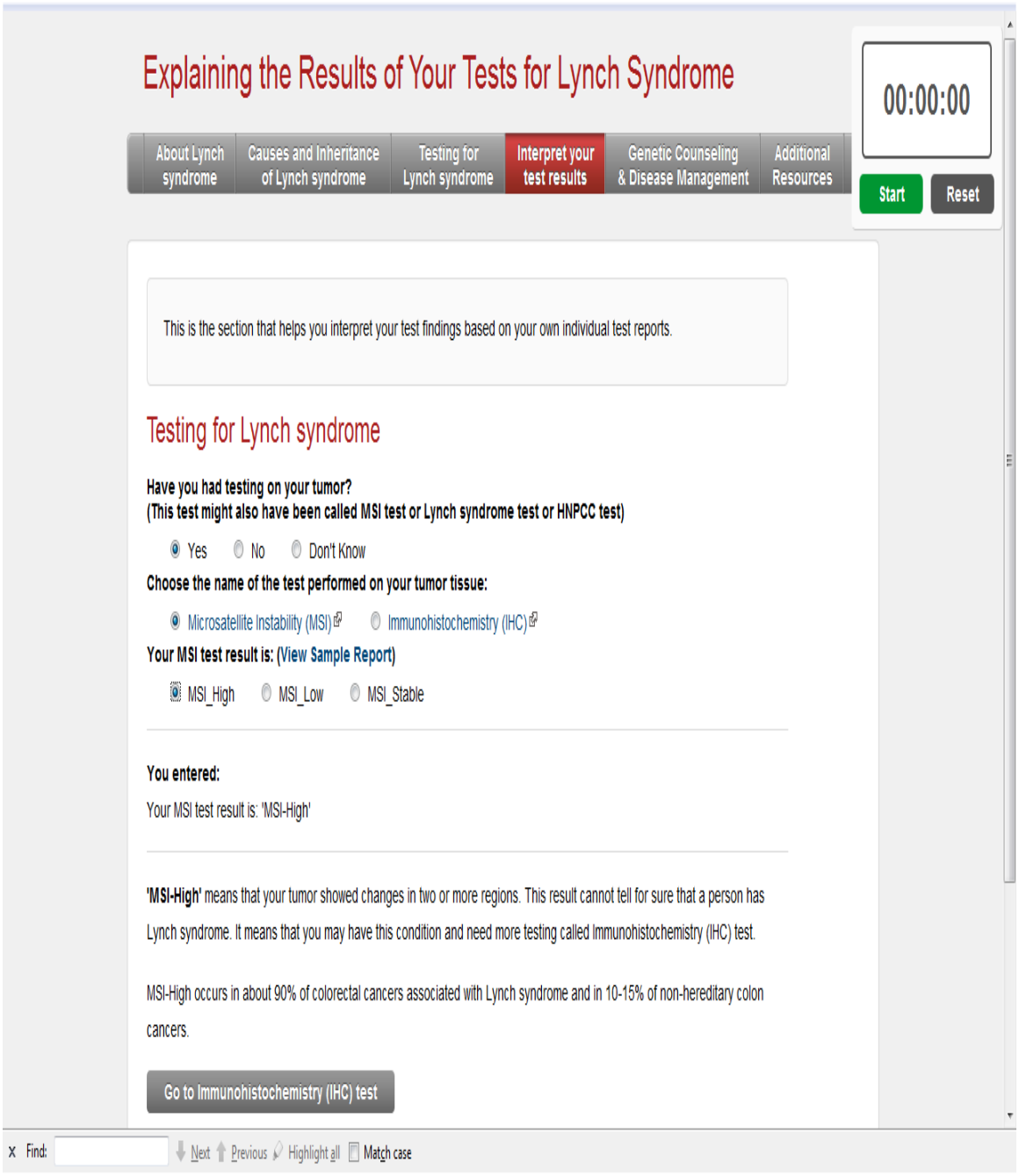



Figure 15. Screen shot of the tailored website displaying MSI test results

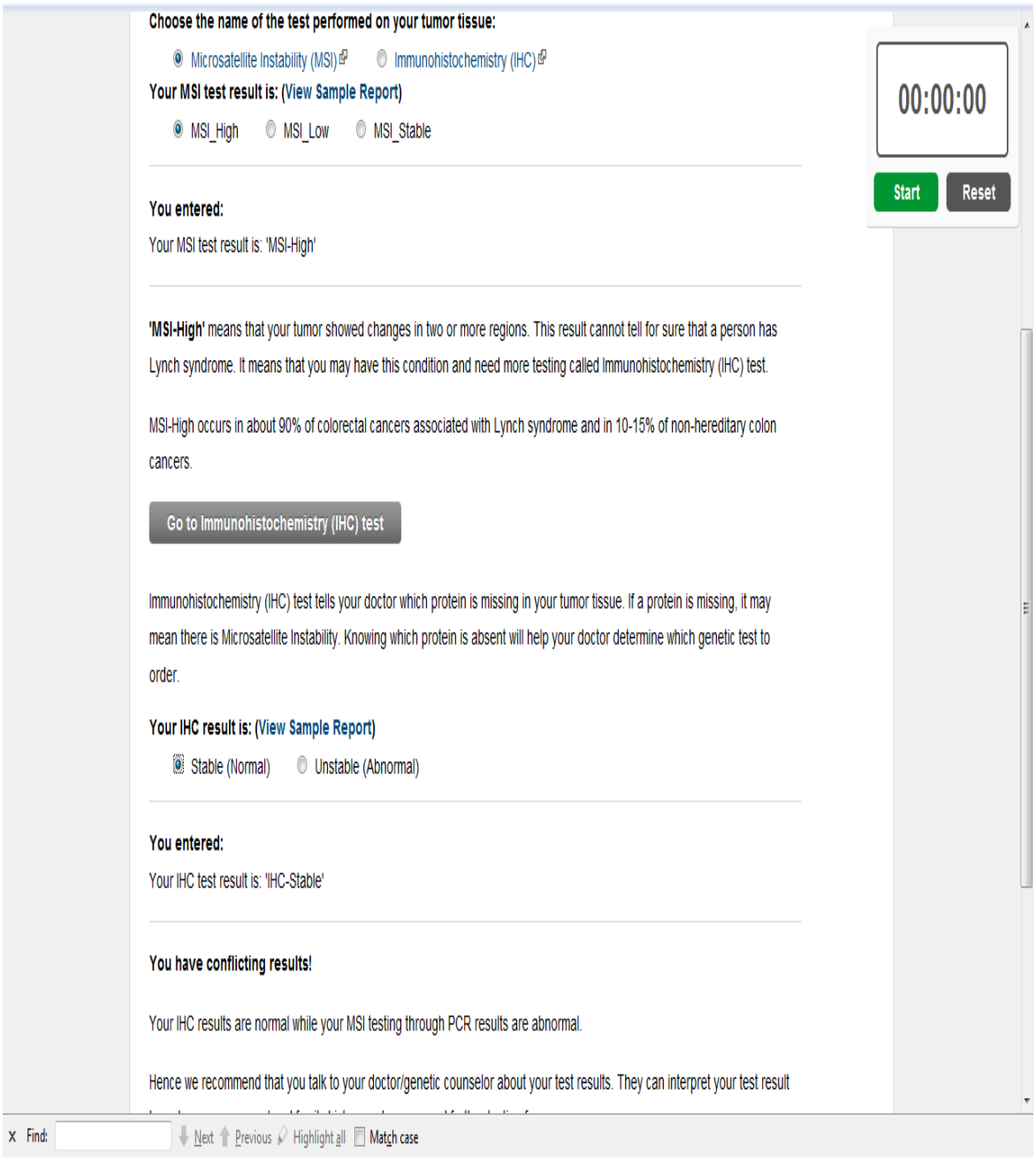



Figure 16. Screen shot of the tailored website when a user enters conflicting results

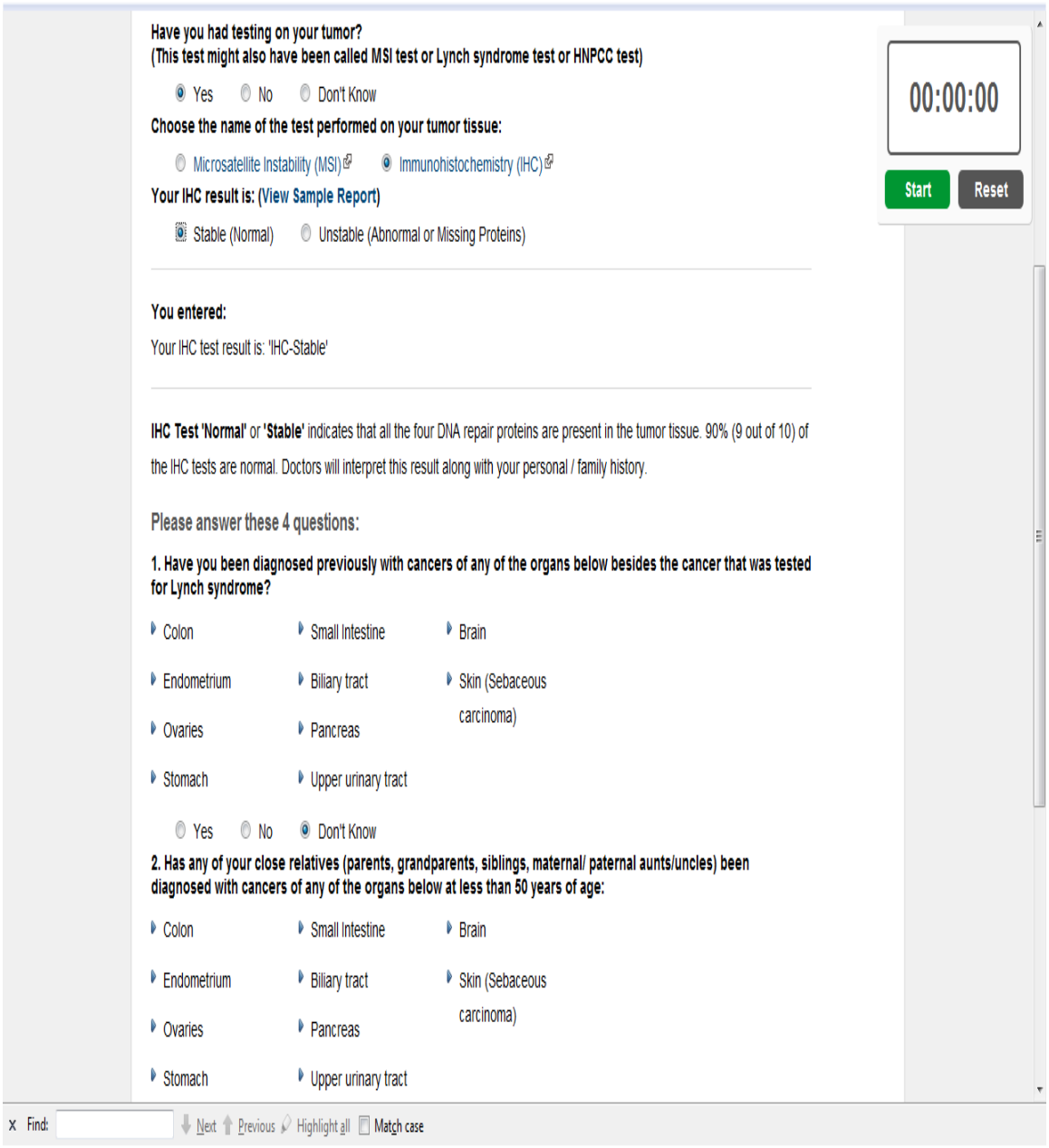



Figure 17. Screen shot of the tailored website displaying family history questions if a user selects Immunohistochemistry result "Normal"

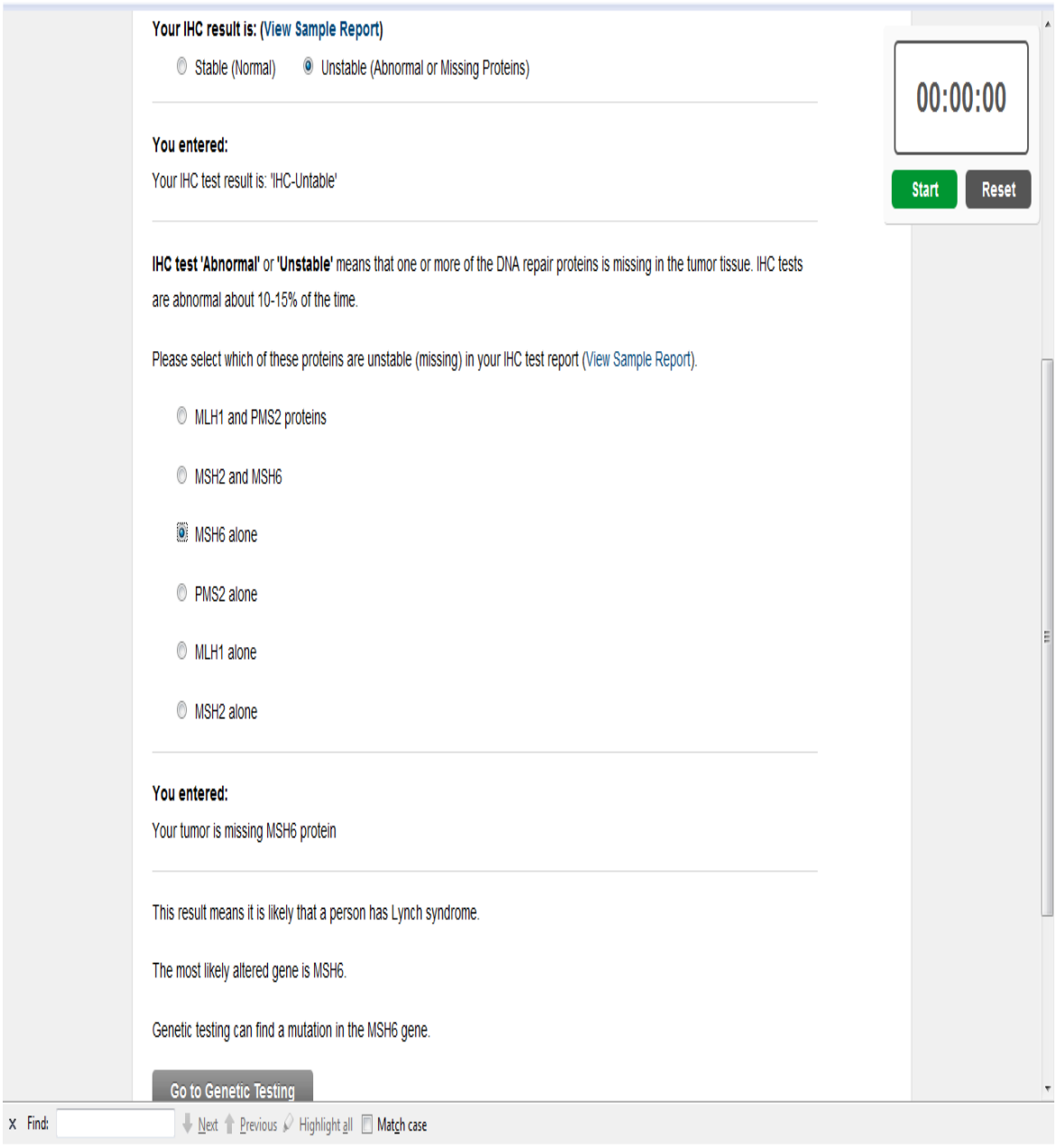



Figure 18. Screen shot of the tailored website displaying missing proteins if a user selects Immunohistochemistry result "Abnormal"

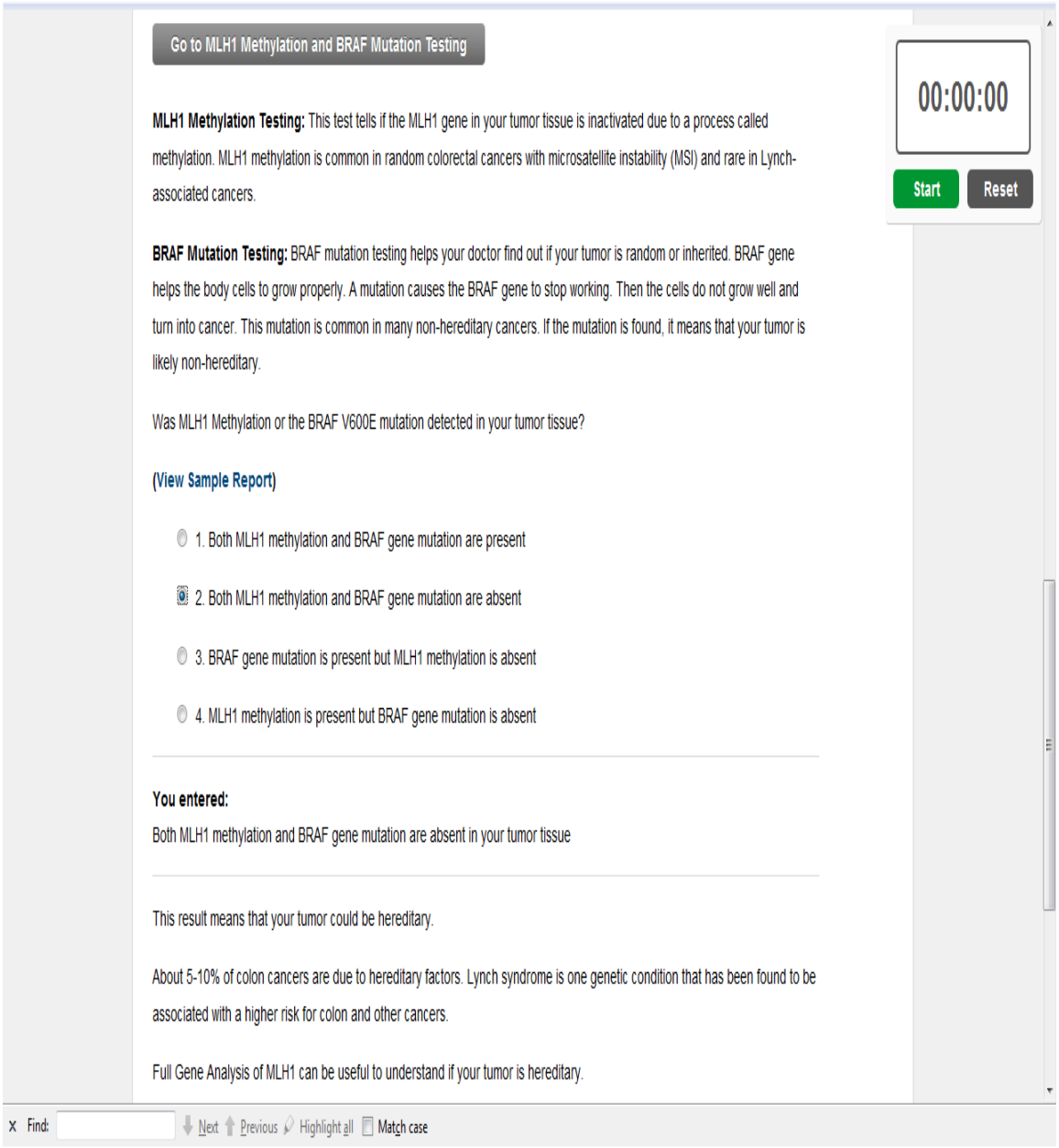



Figure 19. Screen shot of the tailored website displaying MLH1 methylation and BRAF mutation testing results

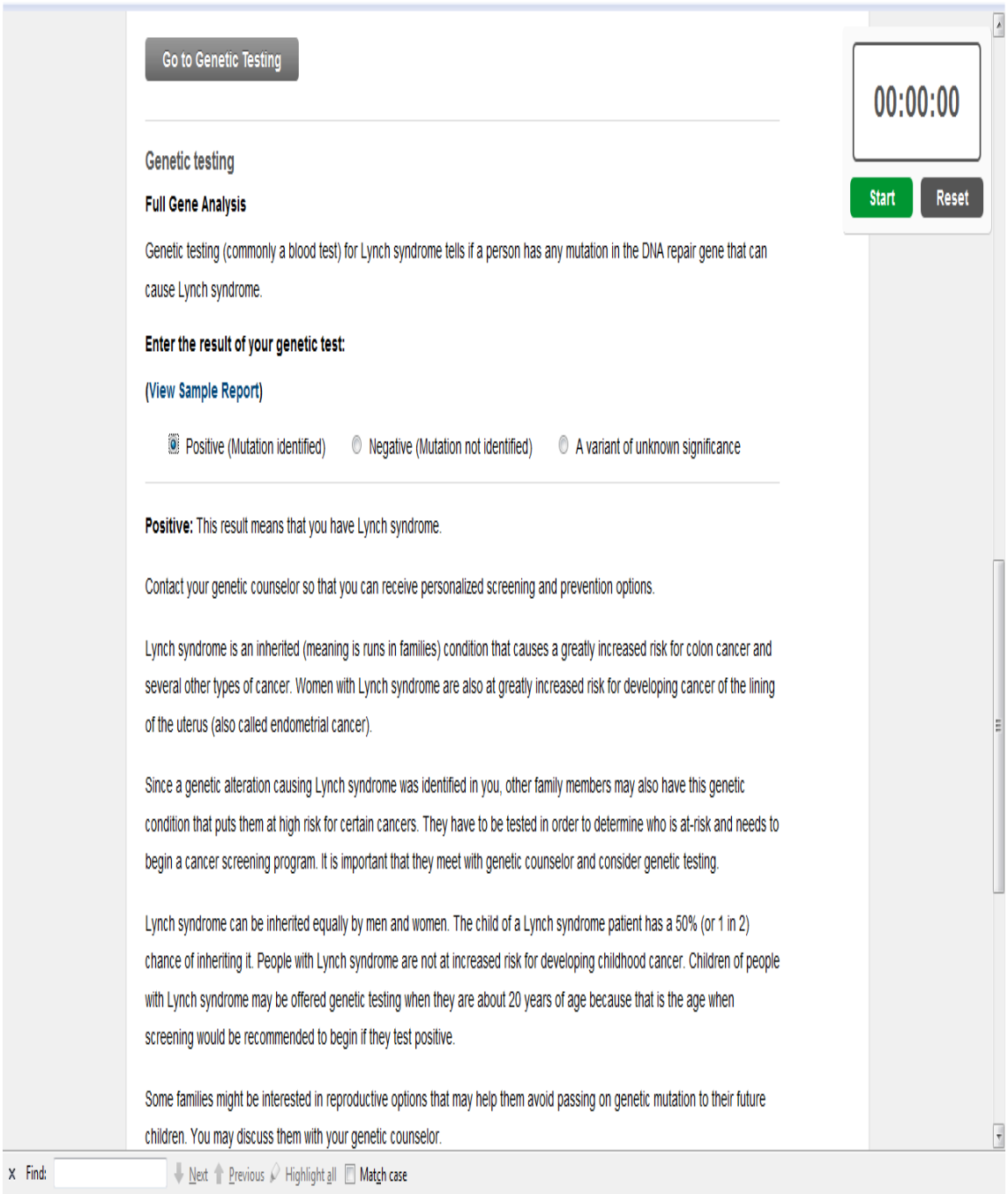



Figure 20. Screen shot of the tailored website displaying genetic test results

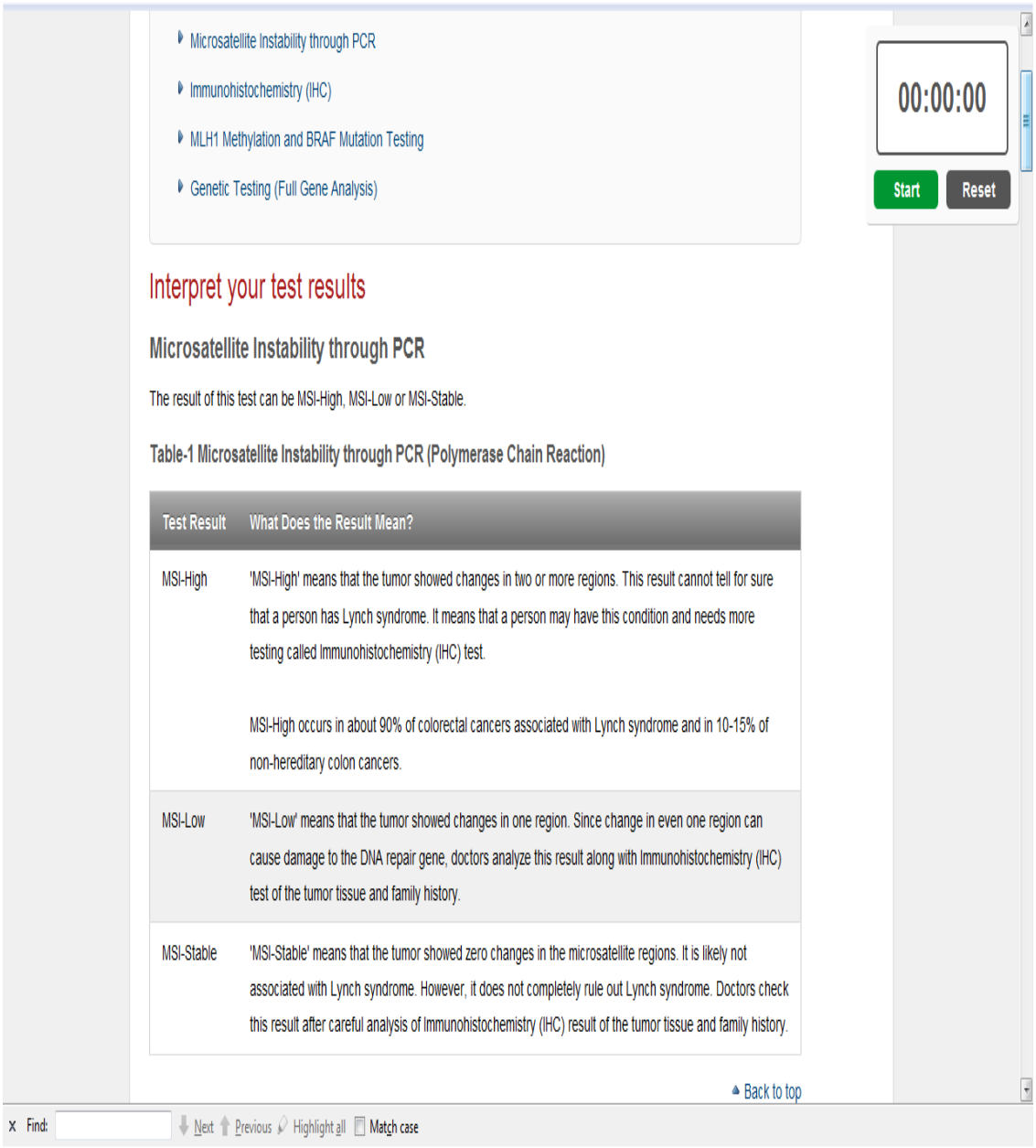



Figure 21. Screen shot of the nontailored website displaying

MSI test results

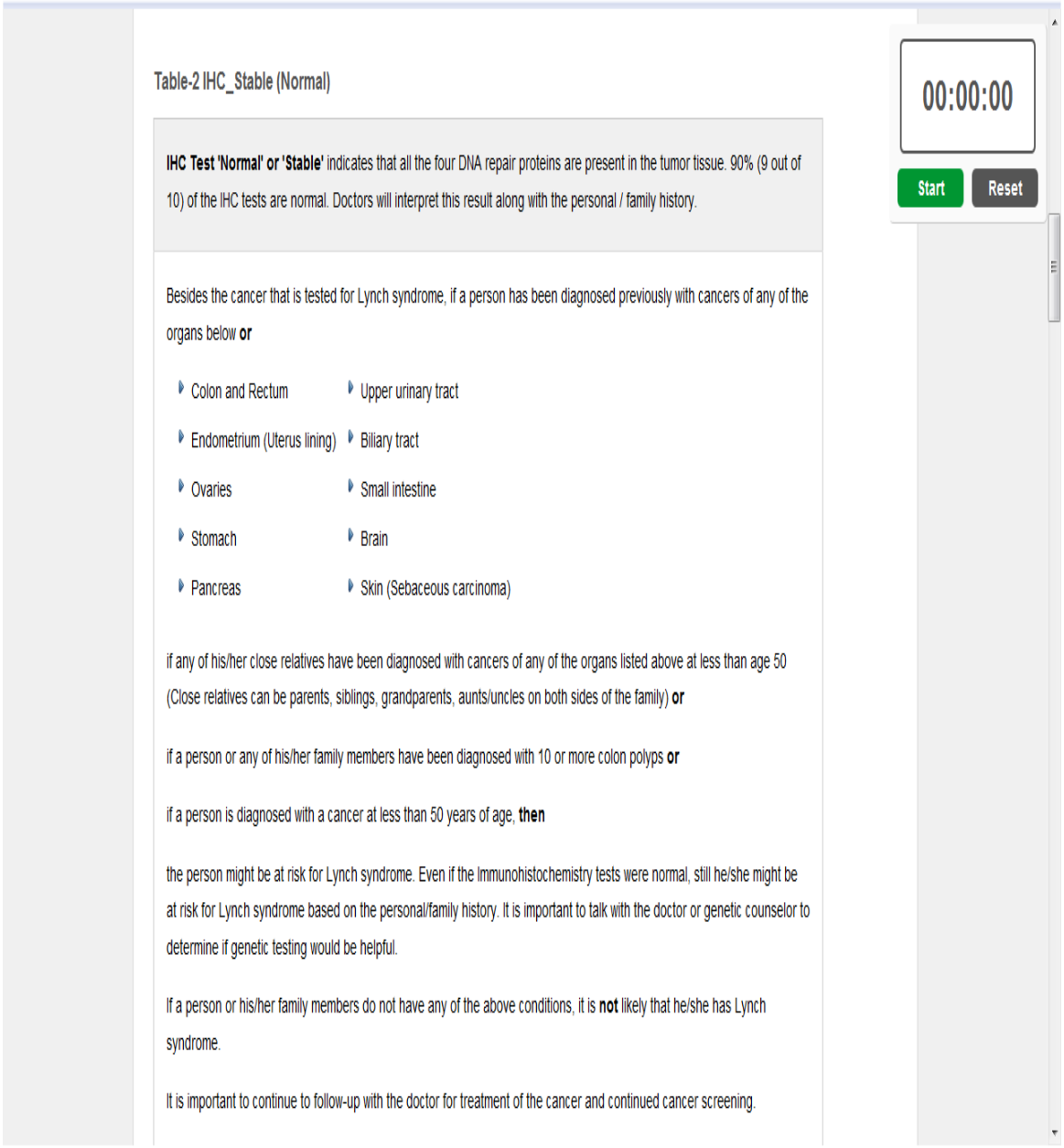



Figure 22. Screen shot of the nontailored website displaying Immunohistochemistry result "Normal"

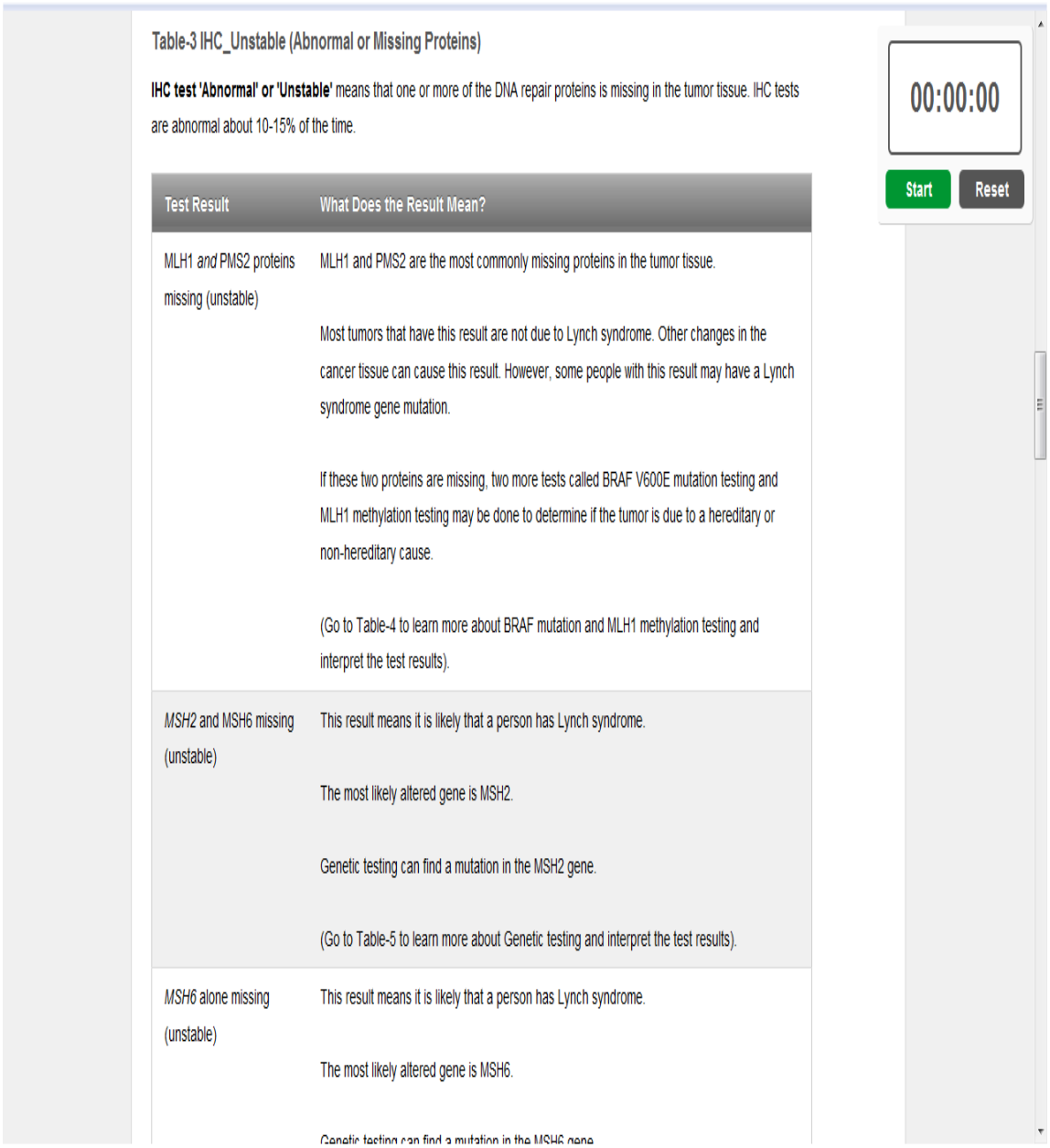


Table-3 IHC_Unstable (Abnormal or Missing Proteins)

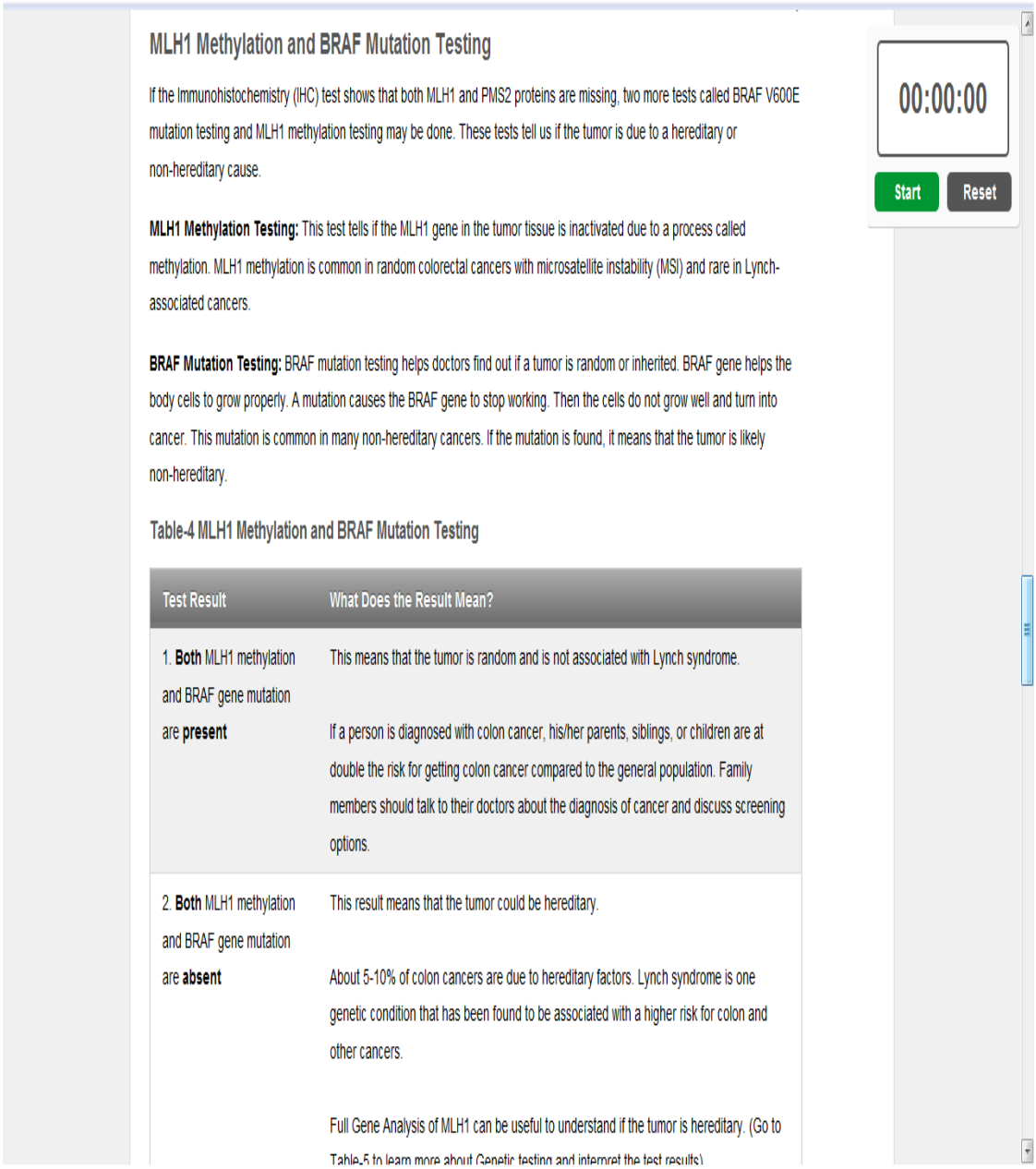
**IHC test 'Abnormal' or 'Unstable'** means that one or more of the DNA repair proteins is missing in the tumor tissue. IHC tests are abnormal about 10-15% of the time.

| Test Result | What Does the Result Mean? |
|---|---|
| MLH1 *and* PMS2 proteins missing (unstable) | MLH1 and PMS2 are the most commonly missing proteins in the tumor tissue.<br><br>Most tumors that have this result are not due to Lynch syndrome. Other changes in the cancer tissue can cause this result. However, some people with this result may have a Lynch syndrome gene mutation.<br><br>If these two proteins are missing, two more tests called BRAF V600E mutation testing and MLH1 methylation testing may be done to determine if the tumor is due to a hereditary or non-hereditary cause.<br><br>(Go to Table-4 to learn more about BRAF mutation and MLH1 methylation testing and interpret the test results). |
| *MSH2* and MSH6 missing (unstable) | This result means it is likely that a person has Lynch syndrome.<br><br>The most likely altered gene is MSH2.<br><br>Genetic testing can find a mutation in the MSH2 gene.<br><br>(Go to Table-5 to learn more about Genetic testing and interpret the test results). |
| *MSH6* alone missing (unstable) | This result means it is likely that a person has Lynch syndrome.<br><br>The most likely altered gene is MSH6.<br><br>Genetic testing can find a mutation in the MSH6 gene |

00:00:00

Start Reset

Figure 23. Screen shot of the nontailored website displaying Immunohistochemistry result "Abnormal"



## MLH1 Methylation and BRAF Mutation Testing

If the Immunohistochemistry (IHC) test shows that both MLH1 and PMS2 proteins are missing, two more tests called BRAF V600E mutation testing and MLH1 methylation testing may be done. These tests tell us if the tumor is due to a hereditary or non-hereditary cause.

00:00:00

Start Reset

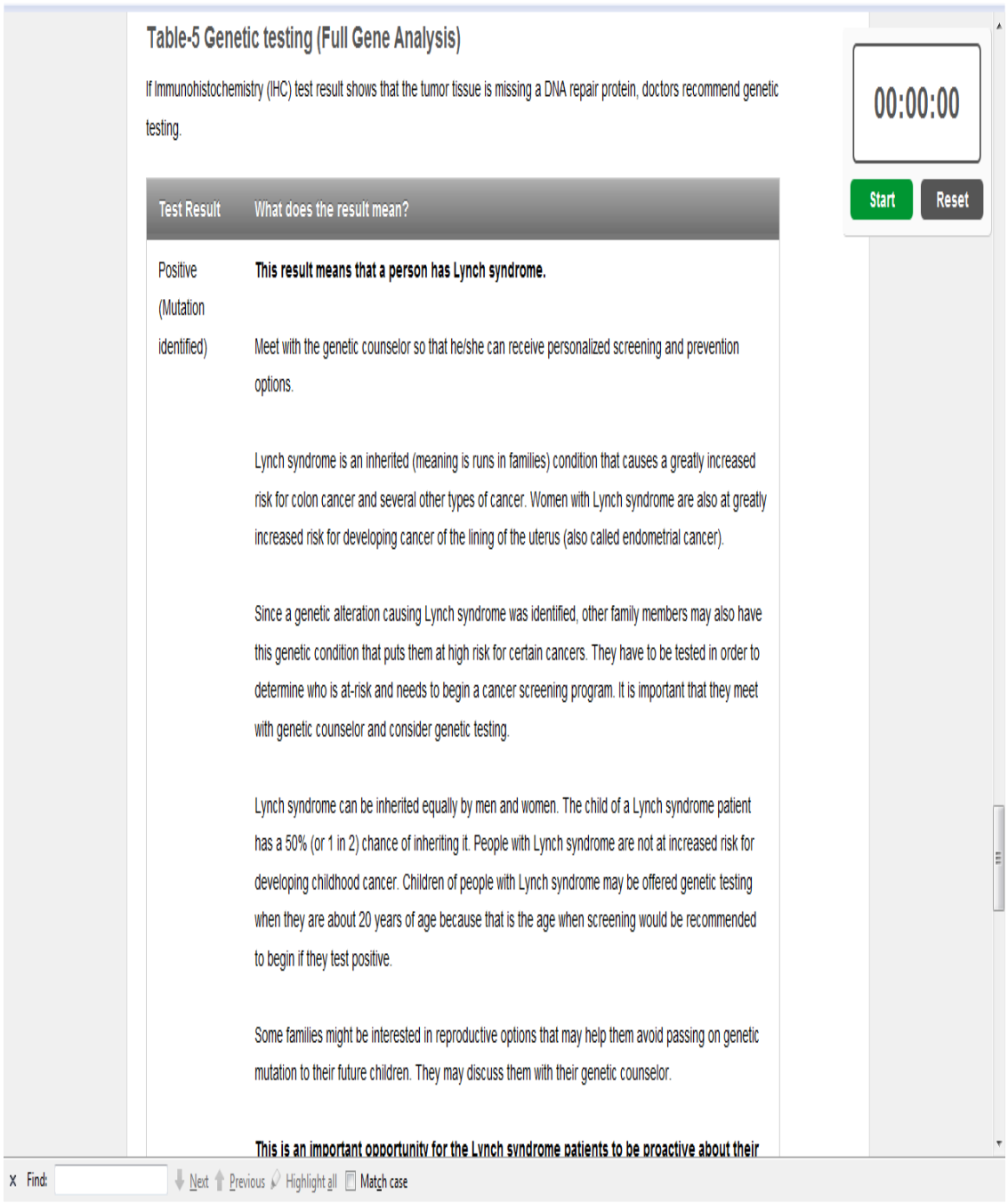
**MLH1 Methylation Testing:** This test tells if the MLH1 gene in the tumor tissue is inactivated due to a process called methylation. MLH1 methylation is common in random colorectal cancers with microsatellite instability (MSI) and rare in Lynch-associated cancers.

**BRAF Mutation Testing:** BRAF mutation testing helps doctors find out if a tumor is random or inherited. BRAF gene helps the body cells to grow properly. A mutation causes the BRAF gene to stop working. Then the cells do not grow well and turn into cancer. This mutation is common in many non-hereditary cancers. If the mutation is found, it means that the tumor is likely non-hereditary.

### Table-4 MLH1 Methylation and BRAF Mutation Testing

| Test Result | What Does the Result Mean? |
|---|---|
| 1. **Both** MLH1 methylation and BRAF gene mutation are **present** | This means that the tumor is random and is not associated with Lynch syndrome.<br><br>If a person is diagnosed with colon cancer, his/her parents, siblings, or children are at double the risk for getting colon cancer compared to the general population. Family members should talk to their doctors about the diagnosis of cancer and discuss screening options. |
| 2. **Both** MLH1 methylation and BRAF gene mutation are **absent** | This result means that the tumor could be hereditary.<br><br>About 5-10% of colon cancers are due to hereditary factors. Lynch syndrome is one genetic condition that has been found to be associated with a higher risk for colon and other cancers.<br><br>Full Gene Analysis of MLH1 can be useful to understand if the tumor is hereditary. (Go to Table-5 to learn more about Genetic testing and interpret the test results) |

Figure 24. Screen shot of the nontailored website displaying MLH1 methylation and BRAF mutation test results



## Table-5 Genetic testing (Full Gene Analysis)

If Immunohistochemistry (IHC) test result shows that the tumor tissue is missing a DNA repair protein, doctors recommend genetic testing.

00:00:00

Start Reset

| Test Result | What does the result mean? |
|---|---|
| Positive (Mutation identified) | **This result means that a person has Lynch syndrome.**<br><br>Meet with the genetic counselor so that he/she can receive personalized screening and prevention options.<br><br>Lynch syndrome is an inherited (meaning is runs in families) condition that causes a greatly increased risk for colon cancer and several other types of cancer. Women with Lynch syndrome are also at greatly increased risk for developing cancer of the lining of the uterus (also called endometrial cancer).<br><br>Since a genetic alteration causing Lynch syndrome was identified, other family members may also have this genetic condition that puts them at high risk for certain cancers. They have to be tested in order to determine who is at-risk and needs to begin a cancer screening program. It is important that they meet with genetic counselor and consider genetic testing.<br><br>Lynch syndrome can be inherited equally by men and women. The child of a Lynch syndrome patient has a 50% (or 1 in 2) chance of inheriting it. People with Lynch syndrome are not at increased risk for developing childhood cancer. Children of people with Lynch syndrome may be offered genetic testing when they are about 20 years of age because that is the age when screening would be recommended to begin if they test positive.<br><br>Some families might be interested in reproductive options that may help them avoid passing on genetic mutation to their future children. They may discuss them with their genetic counselor.<br><br>**This is an important opportunity for the Lynch syndrome patients to be proactive about their** |

x Find: Next Previous Highlight all Match case

Figure 25. Screen shot of the nontailored website displaying genetic test results

# APPENDIX B

## HEALTH SCENARIO OF SUSAN (STUDY'S USE CASE)

Susan's health scenario

Please read the scenario below, and **pretend that you are the "Susan" that is described**. In this scenario, Susan has recently had surgery to remove a colon cancer, and she has been given the following information about testing for Lynch syndrome that was performed on the cancer after it was removed.

**********

Susan is 55 years old. She was recently diagnosed with a colon cancer. The hospital that did the surgery for Susan tested her tumor tissue to see if her cancer is associated with Lynch syndrome. A few days later Susan received a letter from the hospital which informed her that the **"Immunohistochemistry (IHC) test performed on your colon cancer indicated that the tumor tissue is missing the DNA repair protein called MSH6 protein".** A visit with a genetic counselor was recommended.

Susan was surprised to hear that she was being recommended to see a genetic counselor. Her paternal grandmother had cancer of the uterus (also called endometrial cancer), but no other family members had colon cancer.

During her appointment with the genetic counselor, **Susan is recommended to have a genetic test (a blood test) to look for mutations in the MSH6 gene. Her blood sample is sent to a laboratory, and a mutation is identified in the MSH6 gene.** The genetic counselor tells Susan that it is important to notify family members about the discovery of this mutation because this will have important implications for their health. Susan asks if there are any resources that can help her explain the testing she has had to her family members. The genetic counselor suggests that Susan and her family view this website.

# APPENDIX C

## SCREEN SHOTS OF THE SURVEY


Figure 26. Screen shot of the survey displaying the link to the Lynch syndrome website

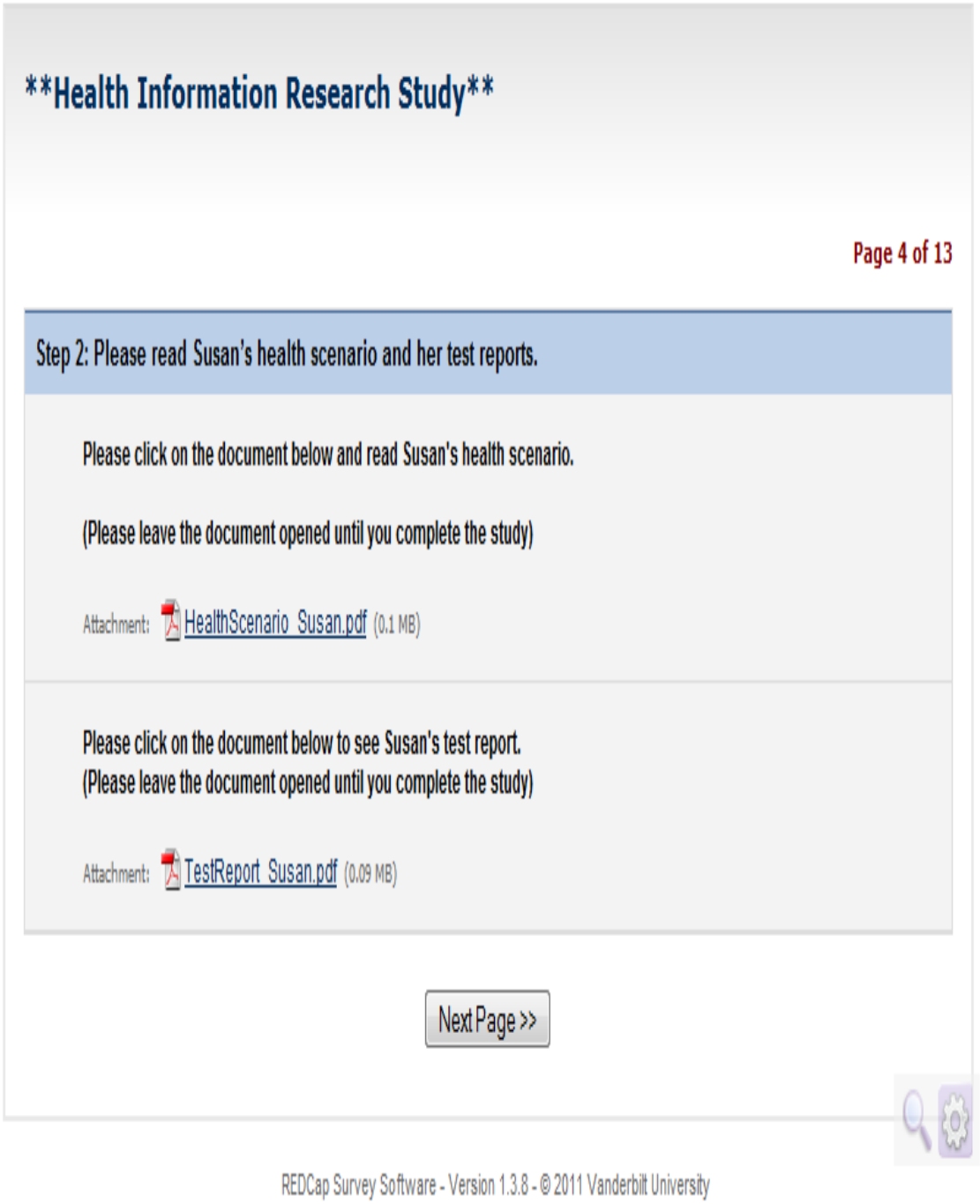



Figure 27. Screen shot of the survey displaying Susan's health scenario and her test report documents

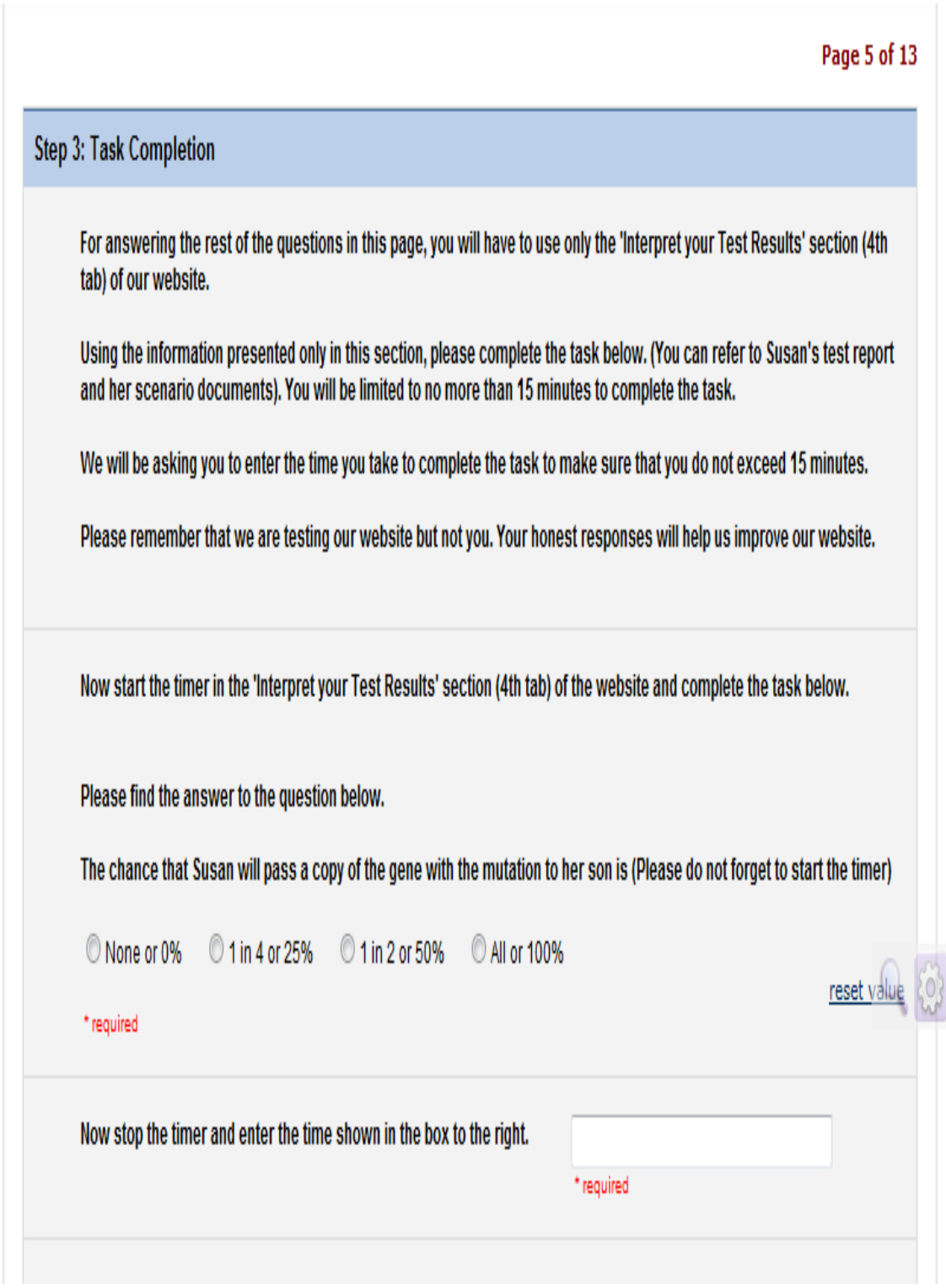



Figure 28. Screen shot of the survey displaying the task completion question

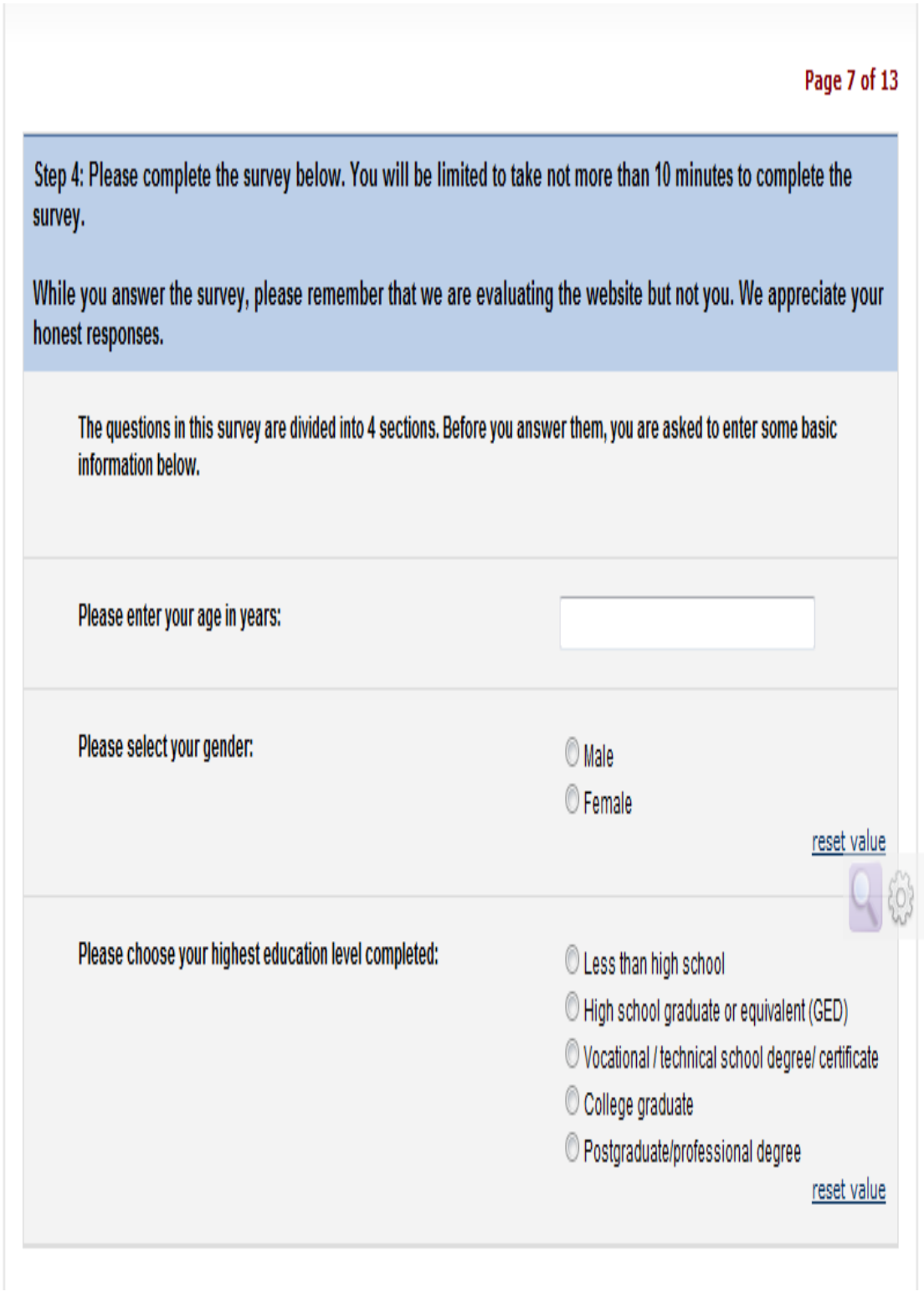



Figure 29. Screen shot of the survey displaying questions on demographic information

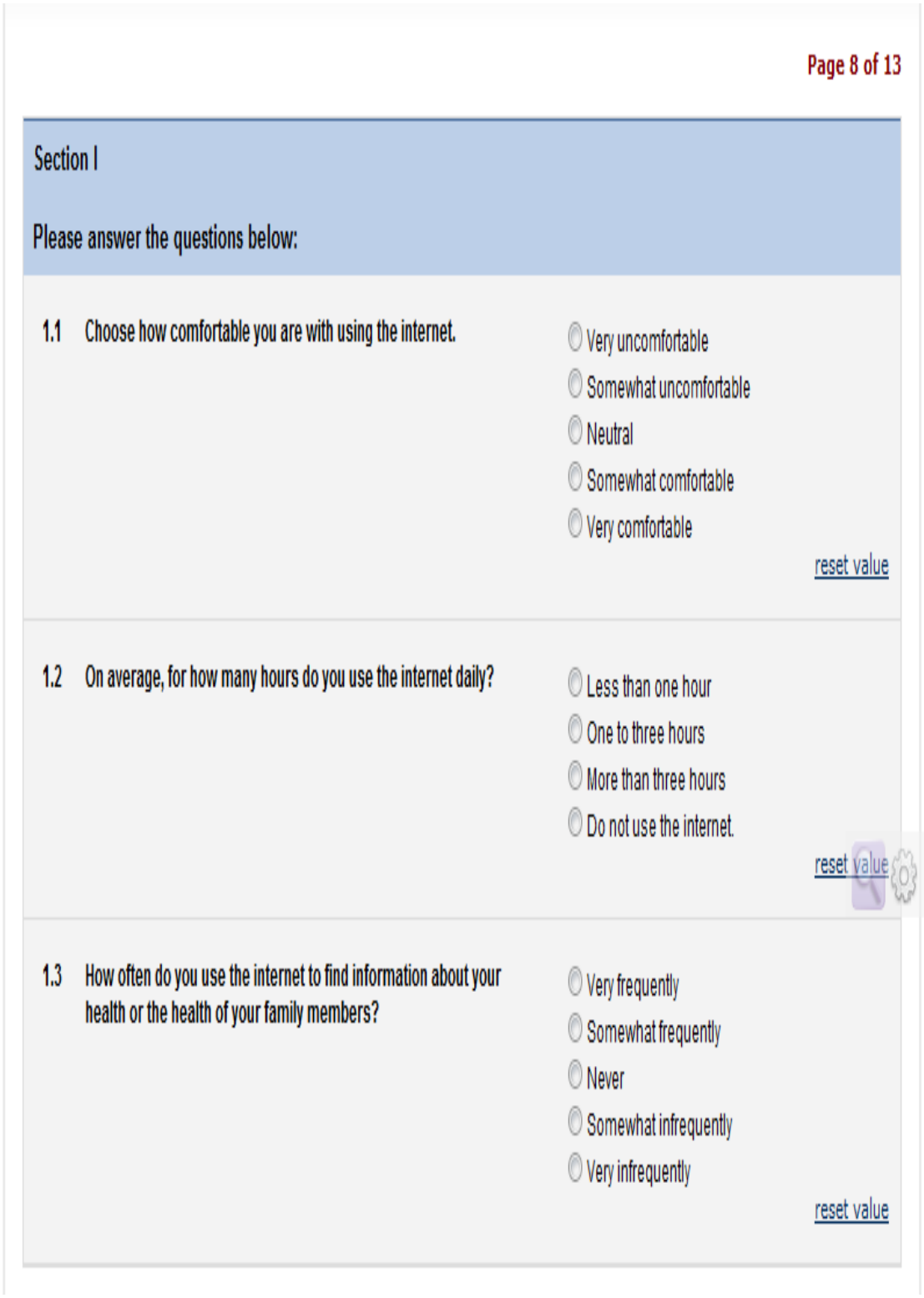
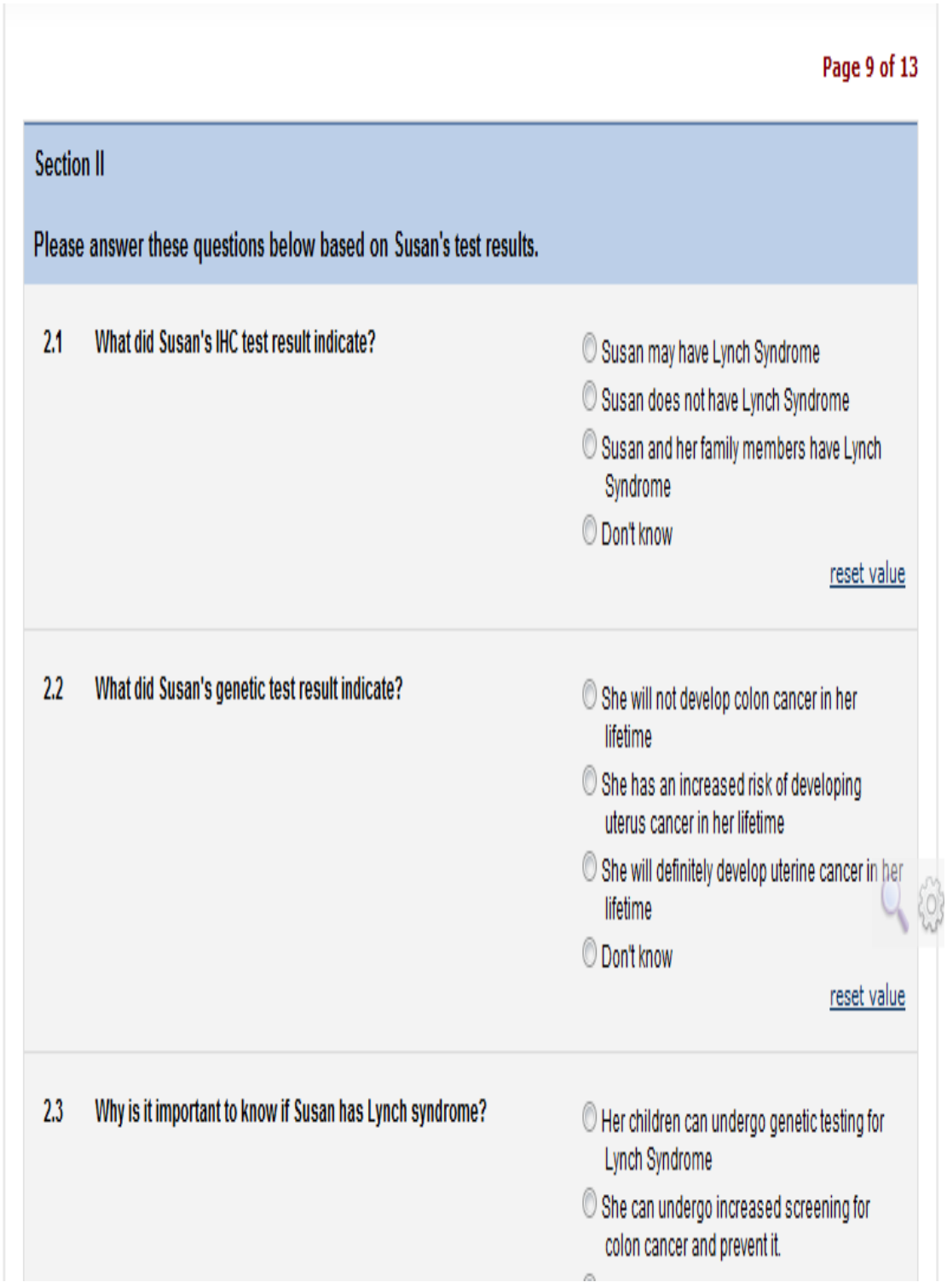



Figure 30. Screen shot of the survey displaying questions on Internet usage



Page 9 of 13

Section II

Please answer these questions below based on Susan's test results.

2.1 What did Susan's IHC test result indicate?

- Susan may have Lynch Syndrome
- Susan does not have Lynch Syndrome
- Susan and her family members have Lynch Syndrome
- Don't know

reset value

2.2 What did Susan's genetic test result indicate?

- She will not develop colon cancer in her lifetime
- She has an increased risk of developing uterus cancer in her lifetime
- She will definitely develop uterine cancer in her lifetime
- Don't know

reset value

2.3 Why is it important to know if Susan has Lynch syndrome?

- Her children can undergo genetic testing for Lynch Syndrome
- She can undergo increased screening for colon cancer and prevent it.

Figure 31. Screen shot of the survey displaying knowledge questions

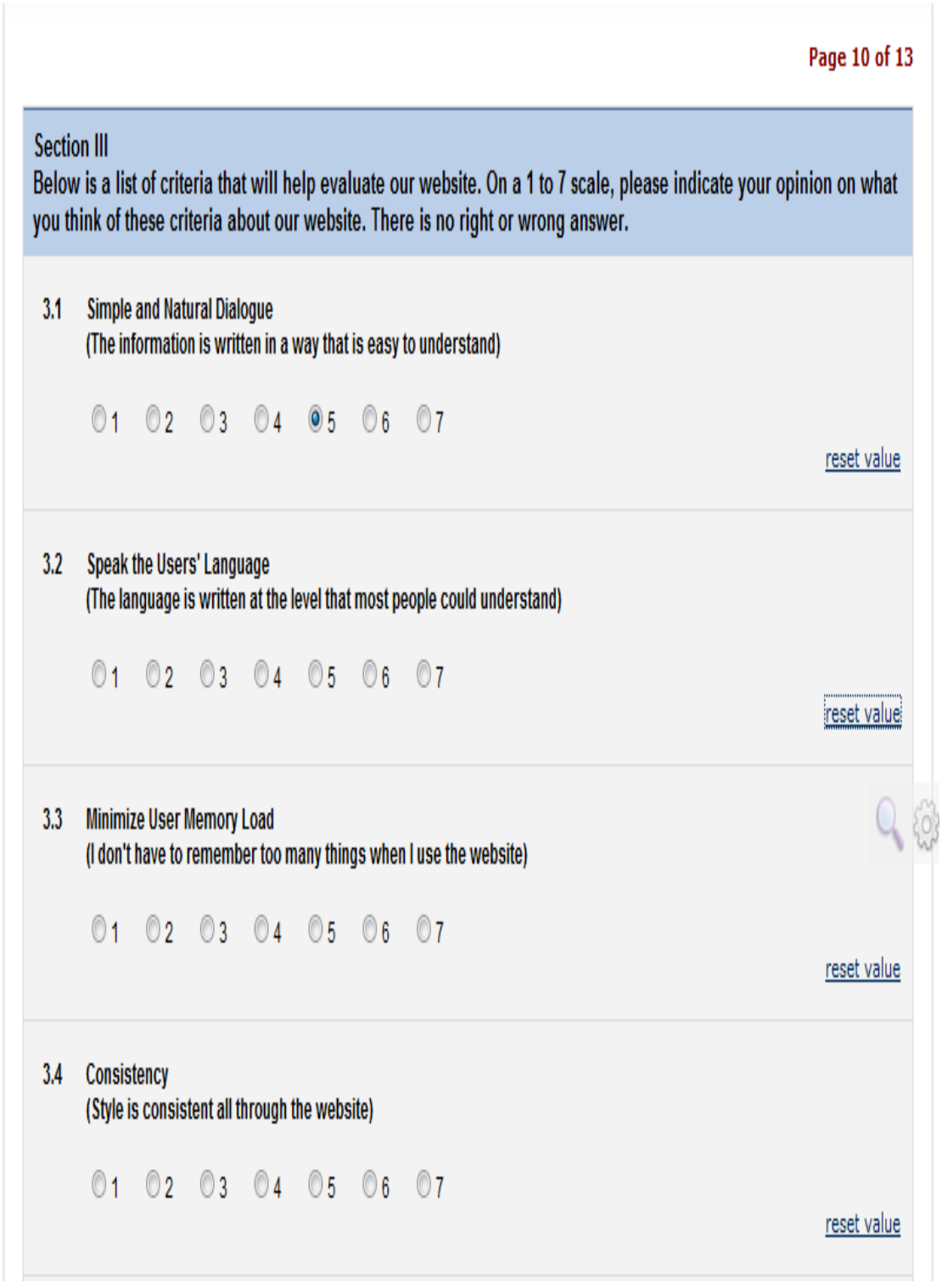



Figure 32. Screen shot of the survey displaying questions on usability of the website

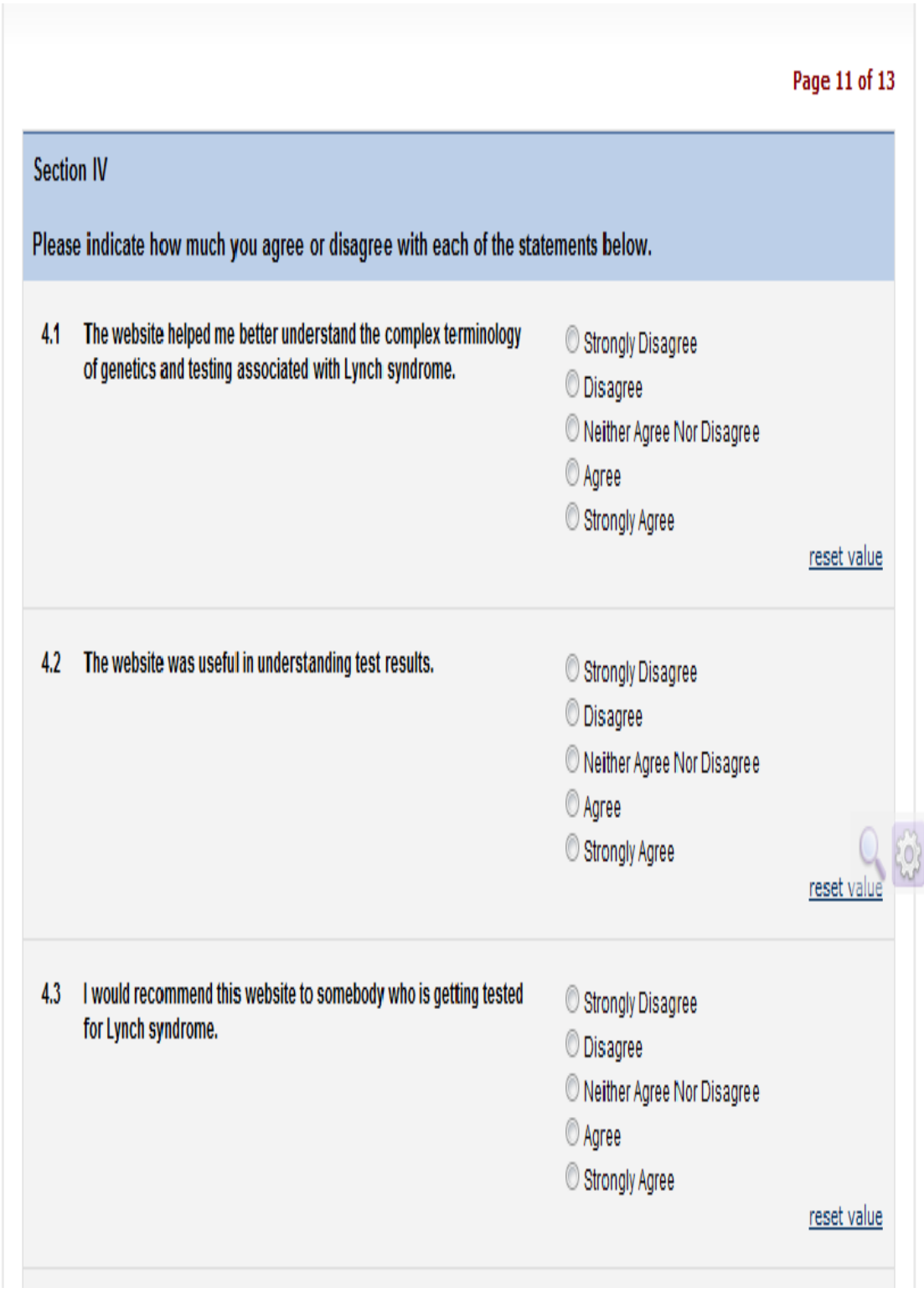



Figure 33. Screen shot of the survey displaying questions on usefulness of the website

# APPENDIX D

# USABILITY TEST SCRIPT

(Downloaded and adapted from
http://www.howto.gov/sites/default/files/usability-test-script.pdf)

| |
|---|
| Web browser should be open to Google or some other "neutral" page |

Hi, _____. My name is Mrudula, and I'm going to be walking you through this session today.

I am a Master's student in the Biomedical Informatics Department. As part of the thesis project, we have developed a website for cancer patients.

We're asking people to try using a website that we're working on so we can see whether it works as intended. The session should take about 30 minutes.

The first thing I want to make clear right away is that we're testing the *site*, not you. Do not worry about making mistakes.

As you use the site, I'm going to ask you as much as possible to try to think out loud: to say what you're looking at, what you're trying to do, and what you're thinking. This will be a big help to us.

Also, please don't worry that you're going to hurt our feelings. We're doing this to improve the site, so we need to hear your honest reactions.

If you have any questions as we go along, just ask them. I may not be able to answer them right away, since we're interested in how people do when they don't have someone sitting next to them to help. But if you still have any questions when we're done I'll try to answer them then. And if you need to take a break at any point, just let me know.

You may have noticed the camera. With your permission, we're going to videotape the computer screen and what you have to say. The video will be used only to help us figure out how to improve the site, and it won't be seen by anyone except our research team.

If you would, I'm going to ask you to sign a simple permission form for us. It just says that we have your permission to tape you, but that it will only be seen by the people working on the project.

| |
|---|
| **Give them a recording permission form and a pen** |

**While they sign it, START the SCREEN RECORDER**

Do you have any questions before we begin?

Okay. Before we look at the site, I'd like to ask you just a few quick questions.

Roughly how many hours a day would you spend using the Internet, including web browsing and email?

Less than one hour
One to three hours
More than three hours

How often do you spend time looking at online health related information?

once in a week
once in a month
once in a year

OK, great. We're done with the questions, and we can start looking at things.

Now open Google Maps and find address to the nearest airport. Please "think aloud" as you do this.

**Click on the bookmark for the site's Home page.**

First, I'm going to ask you to look at this page and tell me what you make of it: what strikes you about it, for whom this site is for, what you can do here, and what it's for. Just look around and do a little narrative.

You can scroll if you want to, but don't click on anything yet.

**Allow this to continue for two minutes, at most.**

Thanks. Now I'm going to read out a scenario and ask you to try doing some specific tasks. I'm going to read each one out loud and give you a printed copy.

And again, as much as possible, it will help us if you can try to think out loud as you go along.

**Hand the participant the scenario, and read it aloud.**

**Hand the participant the first task, and read it aloud.**

**Allow the user to proceed until you don't feel like it's producing any value or the user becomes very frustrated.**

**Repeat for each task or until time runs out.**

Thank you very much for your time, that was very helpful.

Do you have any questions for me, now that we're done?

**Stop the screen recorder and save the file.**

**Reply to previously unanswered questions.**

**Thank them and escort them out.**

**Scenario**:

Please read the following scenario:

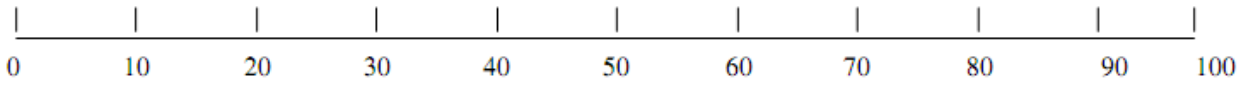
40 year old Mrs.Y was recently operated for colon cancer. The hospital that did the surgery for Mrs.Y tested her tumor tissue to see if her cancer is associated with Lynch syndrome. Lynch syndrome is a hereditary condition which increases a person's risk of getting certain cancers, including colon and endometrial (uterus) cancers. A few days later Mrs. Y received a letter from the hospital which informed her that the "**Immunohistochemistry (IHC) test performed on your colon cancer indicated that the tumor tissue is missing the DNA repair protein called MSH2 protein**". A visit with a genetic counselor was recommended.

**Task 1:**

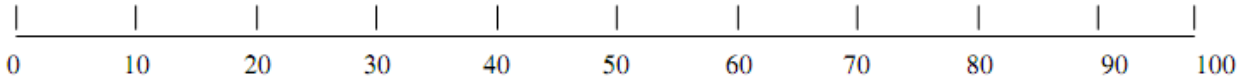
**Using the website, please help Mrs Y find out answers to the questions below.**

**Please circle the right option.**

Q1. Out of every 100 people in the general population, how many will have colon cancer at some point in their lifetime?




Q2. Among 100 people detected with Lynch syndrome, how many will have colon cancer at some point in their lifetime?




Q3. If Lynch syndrome is detected in a woman, what is the risk that her children may have Lynch syndrome?

- ☐ no risk
- ☐ 1/2
- ☐ 1/4
- ☐ will definitely have the predisposition
- ☐ I don't know

**Task 2:**

Mrs. Y meets with a genetic counselor and in the genetic counseling session, the counselor tells her that she needs to collect more information about her family history to evaluate her risk for Lynch syndrome.

**Please help Mrs.Y find answers to the questions below:**

Q1.What are the indications in her family history that might point to her risk for Lynch syndrome?

Q2. Please help Mrs.Y in finding out what information she can collect about her family members.

**Task 3:**

The genetic counselor looked at her family history and found that some of her close family relatives have also had colon cancer and that her grandmother was diagnosed with endometrial (uterus) cancer when she was 40. Considering these factors and the age of diagnosis of colon cancer of Mrs. Y and her IHC test result, the counselor has ordered a genetic test. Genetic testing detected that she has a mutation in the MSH2 gene.

**Please help Mrs. Y find answers to the questions below:**

Q1. Does Mrs.Y have Lynch syndrome?

Q2.What are the next steps to prevent a Lynch syndrome associated cancer if a person is detected with Lynch syndrome?

Q3. What can the close relatives of a person diagnosed with Lynch syndrome do to prevent a Lynch syndrome associated cancer?

# APPENDIX E

# SAMPLE R CODE FOR DATA ANALYSIS

```
#####################################################################
                          Data preparation
#####################################################################


##### Read in data set #####

setwd("C:/Users/mini/Desktop") #Set the working directory to desktop
dfdt <- read.table("C:/Users/mini/Desktop/Tailored_labels3.csv",
header = TRUE, sep=",")        #Read tailored csv datafile into R
dfdnt <- read.table("C:/Users/mini/Desktop/NonTailored_labels3.csv",
header = TRUE, sep=",")        #Read nontailored csv datafile into R
dfdcomb <-
read.table("C:/Users/mini/Desktop/CombinedData_labels3.csv", header
= TRUE, sep=",") #Read the combined data csv datafile into R
#(includes all participants data (N=90)

utils:::menuInstallPkgs()
require (car)                                          #For graphics

##### Participant Exclusion and Dataset Preparation #####

### Exclude pt_id=68 in Tailored group and pt_id=5 in the
NonTailored group.  Remove the same in the combined dataset also
dfdt<-subset(dfdt, pt_id!=68)                          #Tailored
'68' %in% dfdt$pt_id                                   #Check

dfdnt<-subset(dfdnt, pt_id!=5)                         #Nontailored
'5' %in% dfdnt$pt_id                                   #Check

dfdcomb<-subset(dfdcomb, pt_id!=5 & pt_id!=68)      #Combined data
dfdcomb$pt_id                                          #Check


#####################################################################
  Analysis of baseline characteristics of the included participants
#####################################################################

########## Demographic variables ##########

##### age #####

shapiro.test(dfdcomb$age)  #p<0.05 evidence of non-normality


### Density plot for age (to check for normality) ###
dnsA <- with(subset(dfdcomb, grp=="NonTailored"),
density(age,na.rm=T))              #Get densities of measure groups.
dnsB <- with(subset(dfdcomb, grp=="Tailored"), density(age,na.rm=T))

plot(dnsA, xlim=(range(c(dnsA$x, dnsB$x))*c(1,1.2)),
ylim=range(c(dnsA$y, dnsB$y)),
```

```
     main="Age Distribution", xlab="age", ylab="", axes=TRUE,
col="red")           #Produce density plot of NonTailored group age.
grid()                  #Place gridlines in plot.
lines(dnsB,col="blue")  #Produce density plot of Tailored group age.
txt <- c(paste("NonTailored",sep=""), paste("Tailored", sep=""))
#Build text for legend.

legend("topright", txt, lty=1, lwd=2, cex= 1.2, col=c("red","blue"))
#Use legend to place descriptive text.

### Compute median and Interquartile range for age as it is not
normal
summary(dfdnt$age)
summary(dfdt$age)

### Nonparametric point estimates of age by wilcox test ###

wilcox.test(age ~ grp, data=dfdcomb)
with(subset(dfdcomb,grp=="NonTailored"),wilcox.test(age))
with(subset(dfdcomb,grp=="Tailored"),wilcox.test(age))


##### gender #####
### Compute counts and percentages

with(dfdnt,(table(gender, exclude=NULL)))
            #To get counts of NULL values also
with(dfdnt, prop.table(table(gender, exclude=NULL))*100)
            #Compute percentages

with(dfdt,(table(gender, exclude=NULL)))

with(dfdt, prop.table(table(gender, exclude=NULL))*100)

### Fisher's exact test to compare groups ###

gendermtx <- matrix(c(9,13,35,29),ncol=2,byrow=TRUE)
      #Prepare matrix with counts of males and females in both
groups
colnames(gendermtx) <- c("NT","T")
rownames(gendermtx) <- c("Male","Female")
gendermtx <- as.table(gendermtx)
gendermtx        #Check
fisher.test (gendermtx)

##### edulevel (Highest education level) #####

### Compute counts and percentages
with(dfdnt,(table(edulevel, exclude=NULL)))
with(dfdnt, prop.table(table(edulevel, exclude=NULL))*100)

with(dfdt,(table(edulevel, exclude=NULL)))
with(dfdt, prop.table(table(edulevel, exclude=NULL))*100)
```

```
### Fisher's exact test to compare groups ###
edumtx <- matrix(c(0,0,3,9,5,5,16,14,20,15),ncol=2,byrow=TRUE)
      #Prepare matrix with counts of education levels in both groups
colnames(edumtx) <- c("NT","T")
rownames(edumtx) <- c("Less than high school", "High school graduate
or equivalent (GED)",  "Vocational / technical school degree/
certificate", "College graduate", "Postgraduate/professional
degree")
edumtx <- as.table(edumtx)
edumtx                  #Check
fisher.test (edumtx)

########## Internet usage variables ##########

### Compute counts and percentages for each Internet usage variable
with(dfdnt,(table(internet_comfort, exclude=NULL)))
with(dfdnt, prop.table(table(internet_comfort, exclude=NULL))*100)

with(dfdt,(table(internet_comfort, exclude=NULL)))
with(dfdt, prop.table(table(internet_comfort, exclude=NULL))*100)


with(dfdnt,(table(daily_internethours, exclude=NULL)))
with(dfdnt, prop.table(table(daily_internethours,
exclude=NULL))*100)

with(dfdt,(table(daily_internethours, exclude=NULL)))
with(dfdt, prop.table(table(daily_internethours, exclude=NULL))*100)


with(dfdnt,(table(frequency_internetuse, exclude=NULL)))
with(dfdnt, prop.table(table(frequency_internetuse,
exclude=NULL))*100)

with(dfdt,(table(frequency_internetuse, exclude=NULL)))
with(dfdt, prop.table(table(frequency_internetuse,
exclude=NULL))*100)


### Fisher's exact test to compare groups ###

# internet_comfort (comfort with Internet)
icomfortmtx <- matrix(c(9,7,3,1,1,2,8,6,23,27),ncol=2,byrow=TRUE)
                #Prepare matrix with counts
colnames(icomfortmtx) <- c("NT","T")
rownames(icomfortmtx) <- c("Very uncomfortable","Somewhat
uncomfortable", "Neutral","Somewhat comfortable", "Very
comfortable")
icomfortmtx <- as.table(icomfortmtx)
icomfortmtx      #Check
fisher.test (icomfortmtx)

# daily_internethours (hours spent daily using the Internet)
```

```
ihoursmtx <- matrix(c(2,3,23,19,19,21,0,0),ncol=2,byrow=TRUE)
                #Prepare matrix with counts
colnames(ihoursmtx) <- c("NT","T")
rownames(ihoursmtx) <- c("Less than one hour","One to three hours",
"More than three hours","Do not use the internet")
ihoursmtx <- as.table(ihoursmtx)
ihoursmtx #check
fisher.test (ihoursmtx)

# frequency_internetuse (frequency of Internet use for health
information)
ifreqmtx <- matrix(c(11,12,18,18,0,0,14,8,1,5),ncol=2,byrow=TRUE)
                #Prepare matrix with counts
colnames(ifreqmtx) <- c("NT","T")
rownames(ifreqmtx) <- c("Very frequently","Somewhat frequently",
"Never","Somewhat infrequently", "Very infrequently")
ifreqmtx <- as.table(ifreqmtx)
ifreqmtx          #Check
fisher.test (ifreqmtx)


#####################################################################
            Analysis of task completion data (taskvar)
#####################################################################

### Compute counts and percentages of correct responses ###

with(dfdnt, length(taskvar[taskvar=="correct"]))
with(dfdnt, length(taskvar[taskvar=="correct"])/length(taskvar)*100)

with(dfdt, length(taskvar[taskvar=="correct"]))
with(dfdt, length(taskvar[taskvar=="correct"])/length(taskvar)*100)

### chi-square test to compare groups #####
taskvarmtx <- matrix(c(35,29,9,15),ncol=2, byrow=TRUE)
                #Create matrix of correct and incorrect responses
colnames(taskvarmtx) <- c("NT","T")
rownames(taskvarmtx) <- c("Correct","Incorrect")
taskvarmtx                                                  #Check
chisq.test(taskvarmtx)

### Bar plot for task completion ###
with (dfdcomb, barplot(table(grp, taskvar), beside=T, main="Task
completion by group", ylab="No of responses", xlab= "Option",
names.arg = c("None or 0%", "1 in 4 or 25%", "All or 100%", "1 in 2
or 50% (correct)"),legend.text=T, args.legend=list (x=4.5,y=34)))

with (dfdcomb, table(grp, taskvar))                         #Check
```

```
#######################################################################
                    Analysis of knowledge data
#######################################################################

########## Analysis of total knowledge scores #########

### Compute range and interquartile range ###
with(subset(dfdcomb,grp=="NonTailored"),range(kscore))
with(subset(dfdcomb,grp=="Tailored"),range(kscore))

with(subset(dfdcomb,grp=="NonTailored"),median(kscore))
with(subset(dfdcomb,grp=="Tailored"),median(kscore))


### Check for normality of kscore (Shapiro-Wilk normality test) ###
shapiro.test(dfdcomb$kscore)      #p<0.05 evidence of non-normality


### Non-parametric point estimates  of kscore by wilcox test ###
wilcox.test(kscore ~ grp, data=dfdcomb)
with(subset(dfdcomb,grp=="Tailored"),wilcox.test(kscore,conf.int=T))
with(subset(dfdcomb,grp=="NonTailored"),
      wilcox.test(kscore,conf.int=T))


########## Analysis of individual knowledge questions #########
### Compute counts and %s of correct responses for each knowledge
question
### Compare groups by Chi-squared tests ###

#ihc_result
with(dfdnt, length(ihc_result[ihc_result=="correct"]))
with(dfdt, length(ihc_result[ihc_result=="correct"]))
with(dfdnt, length(ihc_result[ihc_result=="correct"]))*100/44
with(dfdt, length(ihc_result[ihc_result=="correct"]))*100/44

ihc_resultmtx <- matrix(c(30,39,14,5),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(ihc_resultmtx) <- c("NonTailored","Tailored")
rownames(ihc_resultmtx) <- c("Correct","Incorrect")
ihc_resultmtx           #Check matrix
chisq.test(ihc_resultmtx)


#genetictest_result
with(dfdnt,
length(genetictest_result[genetictest_result=="correct"]))
with(dfdt,
length(genetictest_result[genetictest_result=="correct"]))
with(dfdnt,
length(genetictest_result[genetictest_result=="correct"]))*100/44
with(dfdt,
length(genetictest_result[genetictest_result=="correct"]))*100/44
```

```
genetictest_resultmtx <- matrix(c(35,30,9,14),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(genetictest_resultmtx) <- c("NonTailored","Tailored")
rownames(genetictest_resultmtx) <- c("Correct","Incorrect")
genetictest_resultmtx
            #Check matrix
chisq.test(genetictest_resultmtx)


#ls_important
with(dfdnt, length(ls_important[ls_important=="correct"]))
with(dfdt, length(ls_important[ls_important=="correct"]))
with(dfdnt, length(ls_important[ls_important=="correct"]))*100/44
with(dfdt, length(ls_important[ls_important=="correct"]))*100/44

ls_importantmtx <- matrix(c(36,31,8,13),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(ls_importantmtx) <- c("NonTailored","Tailored")
rownames(ls_importantmtx) <- c("Correct","Incorrect")
ls_importantmtx
#Check matrix
chisq.test(ls_importantmtx)


#family_alert
with(dfdnt, length(family_alert[family_alert=="correct"]))
with(dfdt, length(family_alert[family_alert=="correct"]))
with(dfdnt, length(family_alert[family_alert=="correct"]))*100/44
with(dfdt, length(family_alert[family_alert=="correct"]))*100/44

family_alertmtx <- matrix(c(44,41,0,3),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(family_alertmtx) <- c("NonTailored","Tailored")
rownames(family_alertmtx) <- c("Correct","Incorrect")
family_alertmtx
#Check matrix
chisq.test(family_alertmtx)


#family_test
with(dfdnt, length(family_test[family_test=="correct"]))
with(dfdt, length(family_test[family_test=="correct"]))
with(dfdnt, length(family_test[family_test=="correct"]))*100/44
with(dfdt, length(family_test[family_test=="correct"]))*100/44

family_testmtx <- matrix(c(43,42,1,2),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(family_testmtx) <- c("NonTailored","Tailored")
rownames(family_testmtx) <- c("Correct","Incorrect")
family_testmtx
#Check matrix
chisq.test(family_testmtx)
#ihcresult_susancancer
```

```
with(dfdnt,
length(ihcresult_susancancer[ihcresult_susancancer=="correct"]))
with(dfdt,
length(ihcresult_susancancer[ihcresult_susancancer=="correct"]))
with(dfdnt,
length(ihcresult_susancancer[ihcresult_susancancer=="correct"]))*100
/44
with(dfdt,
length(ihcresult_susancancer[ihcresult_susancancer=="correct"]))*100
/44

ihcresult_susancancermtx <- matrix(c(30,34,14,10),ncol=2,
byrow=TRUE)                          #Create matrix of correct and
incorrect responses
colnames(ihcresult_susancancermtx) <- c("NonTailored","Tailored")
rownames(ihcresult_susancancermtx) <- c("Correct","Incorrect")
ihcresult_susancancermtx
       #Check matrix
chisq.test(ihcresult_susancancermtx)

#mutatedgene_inherit
with(dfdnt,
length(mutatedgene_inherit[mutatedgene_inherit=="correct"]))
with(dfdt,
length(mutatedgene_inherit[mutatedgene_inherit=="correct"]))
with(dfdnt,
length(mutatedgene_inherit[mutatedgene_inherit=="correct"]))*100/44
with(dfdt,
length(mutatedgene_inherit[mutatedgene_inherit=="correct"]))*100/44

mutatedgene_inheritmtx <- matrix(c(39,37,5,7),ncol=2, byrow=TRUE)
                   #Create matrix of correct and incorrect responses
colnames(mutatedgene_inheritmtx) <- c("NonTailored","Tailored")
rownames(mutatedgene_inheritmtx) <- c("Correct","Incorrect")
mutatedgene_inheritmtx
       #Check matrix
chisq.test(mutatedgene_inheritmtx)


#children_ls_risk
with(dfdnt, length(children_ls_risk[children_ls_risk=="correct"]))
with(dfdt, length(children_ls_risk[children_ls_risk=="correct"]))
with(dfdnt,
length(children_ls_risk[children_ls_risk=="correct"]))*100/44
with(dfdt,
length(children_ls_risk[children_ls_risk=="correct"]))*100/44

children_ls_riskmtx <- matrix(c(42,42,2,2),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(children_ls_riskmtx) <- c("NonTailored","Tailored")
rownames(children_ls_riskmtx) <- c("Correct","Incorrect")
children_ls_riskmtx                       #Check matrix
chisq.test(children_ls_riskmtx)
```

```
#susan_cancertype
with(dfdnt, length(susan_cancertype[susan_cancertype=="correct"]))
with(dfdt, length(susan_cancertype[susan_cancertype=="correct"]))
with(dfdnt,
length(susan_cancertype[susan_cancertype=="correct"]))*100/44
with(dfdt,
length(susan_cancertype[susan_cancertype=="correct"]))*100/44

susan_cancertypemtx <- matrix(c(32,29,12,15),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(susan_cancertypemtx) <- c("NonTailored","Tailored")
rownames(susan_cancertypemtx) <- c("Correct","Incorrect")
susan_cancertypemtx                   #Check matrix
chisq.test(susan_cancertypemtx)


#testing_true
with(dfdnt, length(testing_true[testing_true=="correct"]))
with(dfdt, length(testing_true[testing_true=="correct"]))
with(dfdnt, length(testing_true[testing_true=="correct"]))*100/44
with(dfdt, length(testing_true[testing_true=="correct"]))*100/44

testing_truemtx <- matrix(c(29,36,15,8),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(testing_truemtx) <- c("NonTailored","Tailored")
rownames(testing_truemtx) <- c("Correct","Incorrect")
testing_truemtx
#Check matrix
chisq.test(testing_truemtx)


#imp_siblings_test
with(dfdnt, length(imp_siblings_test[imp_siblings_test=="correct"]))
with(dfdt, length(imp_siblings_test[imp_siblings_test=="correct"]))
with(dfdnt,
length(imp_siblings_test[imp_siblings_test=="correct"]))*100/44
with(dfdt,
length(imp_siblings_test[imp_siblings_test=="correct"]))*100/44

imp_siblings_testmtx <- matrix(c(43,35,1,9),ncol=2, byrow=TRUE)
                  #Create matrix of correct and incorrect responses
colnames(imp_siblings_testmtx) <- c("NonTailored","Tailored")
rownames(imp_siblings_testmtx) <- c("Correct","Incorrect")
imp_siblings_testmtx
      #Check matrix
chisq.test(imp_siblings_testmtx)

#children_notinherit_cancer
with(dfdnt,
length(children_notinherit_cancer[children_notinherit_cancer=="corre
ct"]))
```

```
with(dfdt,
length(children_notinherit_cancer[children_notinherit_cancer=="corre
ct"]))
with(dfdnt,
length(children_notinherit_cancer[children_notinherit_cancer=="corre
ct"])) *100/44
with(dfdt,
length(children_notinherit_cancer[children_notinherit_cancer=="corre
ct"])) *100/44

children_notinherit_cancermtx <- matrix(c(35,37,9,7),ncol=2,
byrow=TRUE)                   #Create matrix of correct and
incorrect responses
colnames(children_notinherit_cancermtx) <-
c("NonTailored","Tailored")
rownames(children_notinherit_cancermtx) <- c("Correct","Incorrect")
children_notinherit_cancermtx
            #Check matrix
chisq.test(children_notinherit_cancermtx)



##### Bar plot of group performance on knowledge questions #####
### Create vectors of correct responses for knowledge questions for
each group separately ###

ntgrpcorrect<-with (dfdnt,
c(length(ihc_result[ihc_result=="correct"]),
 length(genetictest_result[genetictest_result=="correct"]),
      length(ls_important[ls_important=="correct"]),
      length(family_alert[family_alert=="correct"]),
      length(family_test[family_test=="correct"]),
      length(ihcresult_susancancer[ihcresult_susancancer=="correct"]
),
      length(mutatedgene_inherit[mutatedgene_inherit=="correct"]),
      length(children_ls_risk[children_ls_risk=="correct"]),
      length(susan_cancertype[susan_cancertype=="correct"]),
      length(testing_true[testing_true=="correct"]),
      length(imp_siblings_test[imp_siblings_test=="correct"]),
      length(children_notinherit_cancer[children_notinherit_cancer==
"correct"]))*100/44)

ntgrpcorrect<-round(ntgrpcorrect,2)

ntgrpcorrect                                          #Check


tgrpcorrect<-with (dfdt,
c(length(ihc_result[ihc_result=="correct"]),
      length(genetictest_result[genetictest_result=="correct"]),
      length(ls_important[ls_important=="correct"]),
      length(family_alert[family_alert=="correct"]),
```

```
      length(family_test[family_test=="correct"]),
      length(ihcresult_susancancer[ihcresult_susancancer=="correct"]
),
      length(mutatedgene_inherit[mutatedgene_inherit=="correct"]),
      length(children_ls_risk[children_ls_risk=="correct"]),
      length(susan_cancertype[susan_cancertype=="correct"]),
      length(testing_true[testing_true=="correct"]),
      length(imp_siblings_test[imp_siblings_test=="correct"]),
      length(children_notinherit_cancer[children_notinherit_cancer==
"correct"]))*100/44)

tgrpcorrect<-round(tgrpcorrect,2)
tgrpcorrect                                                #Check


height <- rbind(ntgrpcorrect, tgrpcorrect)    #Create a two row
matrix
 mp <- barplot(height, beside = TRUE,
 ylim = c(0, 120), names.arg =
c("Q1","Q2","Q3","Q4","Q5","Q6","Q7","Q8","Q9","Q10","Q11","Q12"),
 ylab= "% of correct responses",
 xlab = "Question",legend.text=c("Nontailored","Tailored"))
#Use height and set 'beside = TRUE' to get pairs
#Save the bar midpoints in 'mp'
#Set the bar pair labels to Q1:Q12



########## Effect of baseline characteristics on kscore #########
#Kruskal-Wallis test
#To detect the effect of baseline characteristics (except age) on
kscore

with (dfdcomb, kruskal.test(kscore ~ gender))
with (dfdcomb, kruskal.test(kscore ~ edulevel))
with (dfdcomb, kruskal.test(kscore ~ internet_comfort))
with (dfdcomb, kruskal.test(kscore ~ daily_internethours))
with (dfdcomb, kruskal.test(kscore ~ frequency_internetuse))

with (dfdcomb, summary (lm(kscore ~ age)
#Simple linear regression of age on kscore

with (dfdcomb, summary (step(lm(kscore ~ age + gender +
edulevel+internet_comfort +  daily_internethours +
frequency_internetuse+grp))))                 #Step-wise selection
with (dfdcomb, summary (lm(kscore ~ internet_comfort)))
            #Model with the best individual predictor of kscore
```

```
#####################################################################
                    Analysis of usability data
#####################################################################

### Compute means and sds for the usabilty variables ###

usability_nt <- with(dfdnt,data.frame(dialogue, users_language,
min_memoryload,consistency,  location_feedback, exits_clear,
expected_functions, easy_to_navigate))
#Create dataframe of usability data (Nontailored group)
usability_nt<-as.vector(usability_nt)         #Convert to vector
usability_nt                                  #Check the vector
apply(usability_nt,2,mean,na.rm=T)            #Compute means


usability_t <- with(dfdt,data.frame(dialogue, users_language,
min_memoryload, consistency, location_feedback, exits_clear,
expected_functions,easy_to_navigate))
#Create dataframe of usability data (Tailored group)
usability_t<-as.vector(usability_t)           #Convert to vector
usability_t                                   #Check the vector
apply(usability_t,2,mean,na.rm=T)             #Compute means


### Compare group means by Welch Two Sample t-test ###

t.test(dfdnt$dialogue,dfdt$dialogue)
t.test(dfdnt$users_language,dfdt$users_language)
t.test(dfdnt$min_memoryload,dfdt$min_memoryload)
t.test(dfdnt$consistency,dfdt$consistency)
t.test(dfdnt$location_feedback,dfdt$location_feedback)
t.test(dfdnt$exits_clear,dfdt$exits_clear)
t.test(dfdnt$expected_functions,dfdt$expected_functions)
t.test(dfdnt$easy_to_navigate,dfdt$easy_to_navigate)

t.test(usability_nt, usability_t)
             #Compare total group mean scores



#####################################################################
                    Analysis of usefulness data
#####################################################################

### Convert to numeric data ###

#understand_terminology
dfdnt$understand_terminologynumeric<-
as.numeric(factor(dfdnt$understand_terminology,
      labels=c(1,2,3,4,5), levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree", "Strongly Agree")))
```

```
dfdt$understand_terminologynumeric<-
as.numeric(factor(dfdt$understand_terminology,
      labels=c(1,2,3,4,5), levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree","Agree", "Strongly Agree")))

#understand_results
dfdnt$understand_resultsnumeric<-
as.numeric(factor(dfdnt$understand_results,
      labels=c(1,2,3,4,5), levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree","Strongly Agree")))

dfdt$understand_resultsnumeric<-
as.numeric(factor(dfdt$understand_results,
      labels=c(1,2,3,4,5), levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree","Strongly Agree")))

#recommend_website
dfdnt$recommend_websitenumeric<-
as.numeric(factor(dfdnt$recommend_website, labels=c(1,2,3,4,5),
      levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree","Strongly Agree")))

dfdt$recommend_websitenumeric<-
as.numeric(factor(dfdt$recommend_website, labels=c(1,2,3,4,5),
      levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree", "Strongly Agree")))

#adequate_reasons_screening
dfdnt$adequate_reasons_screeningnumeric<-
as.numeric(factor(dfdnt$adequate_reasons_screening,
labels=c(1,2,3,4,5),
      levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree", "Strongly Agree")))

dfdt$adequate_reasons_screeningnumeric<-
as.numeric(factor(dfdt$adequate_reasons_screening,
labels=c(1,2,3,4,5),
       levels=c("Strongly Disagree", "Disagree",
       "Neither Agree Nor Disagree", "Agree", "Strongly Agree")))

# better_communicate
dfdnt$better_communicatenumeric<-
as.numeric(factor(dfdnt$better_communicate, labels=c(1,2,3,4,5),
      levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree","Strongly Agree")))

dfdt$better_communicatenumeric<-
as.numeric(factor(dfdt$better_communicate, labels=c(1,2,3,4,5),
      levels=c("Strongly Disagree", "Disagree",
      "Neither Agree Nor Disagree", "Agree","Strongly Agree")))
```

```
### Compare groups by t-test

t.test(dfdnt$understand_terminologynumeric,dfdt$understand_terminolo
gynumeric, correct=F)
t.test(dfdnt$understand_resultsnumeric,dfdt$understand_resultsnumeri
c)
t.test(dfdnt$recommend_websitenumeric,dfdt$recommend_websitenumeric)
t.test(dfdnt$adequate_reasons_screeningnumeric,dfdt$adequate_reasons
_screeningnumeric)
t.test(dfdnt$better_communicatenumeric,dfdt$better_communicatenumeri
c)


usefulness_nt <-
with(dfdnt,data.frame(understand_terminologynumeric,understand_resul
tsnumeric,recommend_websitenumeric,
adequate_reasons_screeningnumeric, better_communicatenumeric))

#Create dataframe of usefulness data (Nontailored group)
usefulness_nt<-as.vector(usefulness_nt)       #Convert to vector
usefulness_nt #check
apply(usefulness_nt,2,mean,na.rm=T) #compute means


usefulness_t <-
with(dfdt,data.frame(understand_terminologynumeric,understand_result
snumeric,recommend_websitenumeric,
adequate_reasons_screeningnumeric, better_communicatenumeric))
#Create dataframe of usefulness data (Tailored group)
usefulness_t<-as.vector(usefulness_t) #convert to vector
usefulness_t #check
apply(usefulness_t,2,mean,na.rm=T) #compute means

t.test(usefulness_nt, usefulness_t)
# Compare total group mean scores
```

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