

Sharing Genetic Data under US Privacy Laws

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Abstract: Clinical medical practice and biomedical research utilize genetic information for specific purposes. Irrespective of the purpose of obtaining genetic material, methodologies for protecting the privacy of patients/donors in both clinical and research settings have not kept pace with rapid advances in genetics research. When the usage of genetic information is not predicated on the latest laws and policies, the result places all-important patient/donor privacy at risk. Some methodologies err on the side of overly stringent policies that may inhibit research and open-ended diagnostic activity, whereas an opposite approach advocates a high-degree of openness that can jeopardize patient privacy, inappropriately identify disease susceptibility of patients and their genetic relatives, and thereby erode the doctor-patient privilege. As a solution, we present a framework based on the premise that acceptable clinical treatment regimens are captured in workflows used by caregivers and researchers and therefore their associated purpose are inherent to and therefore can be extracted from these workflows. We combine these purposes with applicable consents that are derived from applicable laws and practice standards to ascertain the releasability of genetic information. Given that federal, state and institutional laws, rules and regulations govern the use, retention and sharing of genetic information, we create a three-level rule hierarchy to apply the laws to a request and auto-generate consents prior to releasing. Our hierarchy also identifies all pre-conditions that must be met prior to the genetic information release, any restrictions and constraints to be enforced after release, and the penalties that may be assessed for violating these terms. We prototype our system using open source tools, while ensuring that the results can be added to existing Electronic Medical Records (EMR) systems.

1 INTRODUCTION

Genetic studies match genotypic and phenotypic data to associate genetic markers with onset of diseases (Ritchie et al., 2015). Multiple studies also show that preventive care costs significantly less than treatment upon disease onset and diagnosis (Németh et al., 2013), (Pihoker et al., 2013). Furthermore, rapid advancement of genetic research continues to lengthen the list of predictable diseases. However, both research and clinical use of genetic information entail privacy challenges that differ from usage of other medical data in following ways:

* **Ethics:** Privacy of genetic data differs from traditional medical information privacy for example, as protecting patients' private information (e.g., Protected Health Information - PHI) is an ethical and legal obligation. Data for genotype-phenotype matching can be used to stigmatize or discriminate

against genetic relatives of a donor, so the dangers of its exposure must be carefully weighed against the benefits of its use (Ritchie et al., 2015), (Lowrance and Collins, 2007), (McGuire and Gibbs, 2006). There is an ongoing ethical debate between the two different schools of thought, one in which the donor gives open consent for using his/her data vs. the other that advocates explicit purpose-based consent (McGuire and Gibbs, 2006).

* **Legal Issues:** Due to the unusual situation of being able to expose relative's genetic composition, genetic privacy has been proposed as categorical privacy that differs from traditional individual-centered concepts of privacy in literature (Lunshof et al., 2008). Federal (HIPAA and GINA), state laws and institutional policies provide the legal framework for the sharing of genetic information. Furthermore, genetic privacy laws vary from state-to-state and may be inconsistent with, or more or less stringent than, federal regulations.

* **Social Implications:** Societal views are often reflected in law and/or organizational policies, so their implications are likely inextricably intertwined with laws and policies governing genetic privacy and what constitutes informed consent.

As a solution, we provide an encompassing framework consisting of workflow-enforced genetic privacy as well as biomedical consent management, consistent with state and federal genetic privacy laws such as statute, regulation and precedent.

Following this Introduction, Section 2 addresses related work; Section 3 reviews the prior work on the prototype, Section 4 describes the overall architecture and design for the implementation of our genetic services workflow that enforces appropriate informed consent based on applicable law to achieve genetic privacy; Section 5 addresses the updates made to the system as further state laws have been implemented, Section 6 provides a specific example use Arizona state laws, and, finally, Section 7 presents conclusions.

2 RELATED WORK

Many researchers have suggested adopting traditional information protection methodologies to protect patients' confidentiality. Yet, this might not be effective due to the uniqueness of being traceable to an individual or group of individuals (Mascalzoni et al., 2008), (Gostin and Hodge, 1999). Some genetic information of an individual may not only precisely identify him/her as high risk of certain hereditary disease(s), but also indicate that his/her relatives have the same risks due to heritable genes.

Prince et al. describes three practical genetic counselling cases that illustrate genetic discrimination (Prince and Roche, 2014). The fundamental covenant of protecting patient privacy is embodied in patient-doctor privilege. Conversely, many scholars believe that genetic information is essentially familial in nature and is referred to as the Genetic Information is Familial Thesis (GIFT) (Liao, 2009), because sharing such information will benefit related groups of individuals. Some countries have regulations to enforce sharing such information among family members (Lucassen and Kaye, 2006), (ASHG, 1998). However, many publications discuss and debate the familial approach, with their authors advocating the view that humans possess the rights of privacy and to protect those that do not want to know (Liao, 2009), (ASHG, 1998). Conversely, rapid innovations in genetic research require wide accessibility to many genetic databases. The idea of

open access in the field of genomic research is expressed in the Bermuda Principles and the Fort Lauderdale Agreement, which has been applied in North America and in the UK for funded research (Sherlock, 2009). Genetic research typically requires additional metadata with genetic data sets, such as demographic details family relationships, medical history, etc. These metadata elements can be exploited for tracing an individual's identity.

In general medicine, an informed consent, especially informed privacy consent, provides the proper opportunity and knowledge for patients and research participants to understand and decide how the medical community can use and share their identifiable medical information, in addition to the risks and benefits of treatment regimes. Analogously, informed consent tailored for genetic research, clinical usage and counselling constitutes a strong basis for ensuring appropriate genetic privacy. Some genetic medical practices and biomedical research are performed without obtaining appropriate informed consent such as enticing participants in a study without obtaining the proper informed consent. To address this issue, some researchers advocate different methodologies such as using highly-stringent policies to maintain patient confidentiality, but this approach potentially risks limiting scientific innovation (Kaye et al., 2012). Yet, other researchers have proposed a new, open-consent model for medical and scientific genetic research (Lunshof et al., 2008) or open-access policies for genetic data sharing (Hallinan and Friedewald, 2015).

EMRs play a vital role of sharing medical information among participating actors based on their usage scenarios. Using EMRs for genetic services present a unique set of challenges (Kaye et al., 2009). Belmont et al. highlighted the privacy, ethical and legal issues of handling genetic data in EMRs (Mascalzoni et al., 2008). The study conducted by Scheuner et al. to validate if current EMR systems meet genetic information needs (Belmont and McGuire, 2009) shows an overall lack of support for functionality, structure, and tools for clinical genetic practice. A more recent study of the state of EMRs supporting genomics for personalized medicine identifies structure of data as a challenge (Scheuner et al., 2009).

As a solution, an approach based on the premise that acceptable clinical treatment regimens are captured in workflows used by caregivers and researchers and therefore their associated purpose are inherent to and therefore can be extracted from these workflows (Reep et al., 2016).

Some researchers suggested that the legislation for generating and using genetic information properly is pivotal to improving genetic privacy (Ullman-Cullere and Mathew, 2011). In 2013, the Health Insurance Portability and Accountability Act of 1996 (HIPAA) Omnibus Rule included genetic information as PHI to be regulated under the privacy portion of HIPAA. Nonetheless, states may have different definition of genetic information. The combination of Federal privacy laws along with the various state laws form a fragmented regulatory and statutory landscape for permissible information sharing and consent management. To be valid, informed consents for genetic privacy must comply with these laws and regulations. Indeed, significant regulatory gaps create additional burdens in providing automated ways to obtain and generate information consent in EMRs.

3 PRIOR WORK

Releasing genetic medical information involves addressing a number of unique considerations not present for other types of medical records. Genetic information is a component of protected health information where the individual's identity may be embedded directly into the data structures. In addition, the genetic information provides insight into almost every aspect of an individual's health. Within the United States, the special characteristics have resulted in laws, regulations and policies targeting the criteria where genetic information can be released, the requirements (or preconditions) that must be fulfilled before information release, and obligations that must be enforced once the information has been released. We previously proposed a mechanism to address the problem space using three distinct components:

- Workflow to gather information, execute a rules engine, display the outcome, obtain acceptance from the user of the results, and enforce requirements associated with information release.
- An ontological rule-base that takes the data from the workflow, evaluates the applicable laws, determines the pre-conditions and obligations, and decides on the releasability of genetic data.
- A consent service that interacts with the workflow engine and the ontology to pass data back and forth. The service includes the Rule Hierarchy Algorithm which combines the outcomes from the three levels (Federal, State

and Organization) and provides a final result for permitting or denying access.

We have expanded the number of states that are incorporated in the prototype. In order to address the wide range of situations reflected in these laws, we have implemented a number of changes to the ontology, workflow and rules to process the actual States laws. The major changes have been in the workflow component and are addressed in the rest of this paper along with other corresponding modifications to the ontology and consent service.

4 ARCHITECTURE AND DESIGN

The process to release genetic medical information is based on two related set of processes as seen in Figure 1. In the first process for policy evaluation, each set of laws, rules and regulations at the Federal, State and medical organization levels are examined for applicability to the request being made. The request may be either to perform medical procedures used to obtain genetic test results or for the genetic information from the tests contained in the medical record. The outcome of the Policy Evaluation Service will either allow the request to continue, potentially based on enforcing specific consent requirements, or deny the request outright.

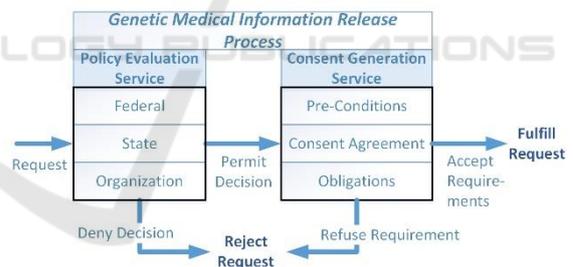


Figure 1: Release Processes.

One of the main components of the policy evaluation is to generate the requirements under which the requested access can be granted. These requirements encompass one or more activities related to verifying that any consent agreements have been signed, indicated pre-conditions are met, and that the enforcement mechanism for post-release obligations have been established. The activities are combined into a consolidated set for enforcement if there are multiple rules that meet the evaluation criteria.

4.1 System Architecture Abstraction

The system workflow to enforce consent requirements orchestrates the various components necessary to invoke genetic information protection as shown in Figure 2. After the information on the subject, request and the requester is gathered, the access decision is made by the policy evaluator. If a permit decision is returned, the consent generation service uses the workflow engine to display the individual pre-conditions for validation along with generating the text for the required consents, and enforcing the obligations associated with the data release. The information released is performed once the workflows steps for the consent generation process is completed.



Figure 2: Workflow Construct.

4.2 Policy Design

Our policies are written as a collection of rules that use three main abstract entities with their associated attributes:

- **Request:** this abstraction incorporates the subject of the request, the purpose for requesting the information, and the resource (part of the medical record) that the request addresses.
- **Requester:** the person/entity making the request to access the medical information including their role, their organization, and other auxiliary attributes of this organization.
- **Response:** the determination applying the appropriate rules to come to an access decision. The Response includes a list of any pre-conditions to be verified before the information is released, specific

consent clauses that the subject must sign, and obligations that must be enforced upon information release. A separate Response instance is created for each of the Federal, State and Organization levels that are then evaluated for a final decision.

Our policies consist of rules that codify the policy. The Purpose, Resource and State (where the request is being made) are required as the minimum data set with other components added to address specific situations. For example, a request to access data for the Law Enforcement purpose will require either the Requester's Role or Organization relationships to perform the validations. If the rule generates a Permit Access response, then any requirements (pre-conditions, consent clauses and obligations) are dictated and used to populate the Response.

The Federal and State rules include an option for an "override" capability so that the other levels can change the permission already established. For example, if the Federal rule grants access but the State laws are allowed to deny the access request, the Federal response override flag is set to true. The override flags are used in conjunction with Federal, State and Organization responses to generate a consolidated Final Access Decision.

Each rule is structured to identify the criteria under which it is applicable, the outcome of whether access is permitted or denied, and any requirements placed on an information release. The rule criteria includes:

- Purpose the information will be used for once released (Required)
- Request Target as either a specific test to be performed or genetic medical information (Required)
- State in which the request is made (Required)
- Requester attributes such as whether parent or guardian (Optional)
- Requester role such as in law enforcement (Optional)
- Requester's organization such as associated with medical facility (Optional)
- Subject attributes such as whether of consent age (Optional)

The output of the rule sets the following properties:

- Level that generated the rule (Required as Federal, State or Organization)
- Access Permission is granted (Required as Permit or Deny)
- Override Allowed for the rule at lower level (Required for Federal or State levels as true or false)
- Decision Source to trace back specific text generating the rule (Required)
- Pre-conditions that must be validated prior to

- release (Optional and may be more than one)
- Consent Clauses that must be accepted (Optional and may be more than one)
- Obligations that must be enforced upon information release (Optional and may be more than one)
- Penalties if specified pre-conditions or obligations are not met (Optional and may be more than one).

4.3 Policy Evaluator Design

The Policy Evaluator uses the rules in order to generate an access decision and, when appropriate, the associated pre-conditions, consent text and obligations that are associated with the genetic information release. The workflow gathers the information used in the rule evaluation either through querying the user or accessing external data sources such as the facility EMR. The Policy Evaluator is described in Algorithm 1.

Algorithm 1: EvaluatePolicies.

```

Input: Workflows, RuleBase
FOR EACH entity (Request, Requester) (1)
  READ data values from workflow (2)
  POPULATE current entity properties (3)
FOR EACH rule (4)
  EVALUATE rule criteria (5)
  IF rule criteria met (6)
    RETRIEVE associated Response Instance
      (Federal, State, Organization) (7)
    SET Response Decision for rule (8)
    IF Decision = "Permit" (9)
      ADD Preconditions, Consent
        Clauses, Obligations to
        Response (10)
    IF Precondition OR Obligation
      HAS Penalties (11)
      ADD Penalties to Response (12)
    END IF
  END EACH
SET Final Response = Federal Response (13)
If State Access Decision = Final Access Decision
  AND Final Access Decision =
  "Permitted" (14)
  ADD State Response Preconditions,
  Consent Clauses, Obligations and
  Penalties to Final Response (15)
IF State Access Decision <> Final Access Decision
  AND Federal Override = TRUE (16)
  SET Final Access Decision = State Access
  Decision (17)
  IF State Access Decision = "Permitted" (18)
    ADD State Response Preconditions,
    Consent Clauses, Obligations
    and Penalties to Final
    Response (19)

```

```

SET Final Override = State Override (20)
IF Organization Access Decision = Final Access Decision
  AND Final Access Decision =
  "Permitted" (21)
  ADD Organization Response Preconditions,
  Consent Clauses, Obligations and
  Penalties to Final Response (22)
IF Organization Access Decision <> Final Access
  Decision AND
  Final Override = TRUE (23)
  SET Final Access Decision = Organization Access
  Decision (24)
  IF Organization Access Decision =
  "Permitted" (25)
    ADD Organization Response,
    Preconditions, Consent Clauses,
    Obligations and Penalties to
    Final Response (26)
  RETURN Final Decision and related Preconditions,
  Consent Clauses, Obligations and Penalties (27)

```

At a high-level the Policy Evaluator process is as follows:

1. Retrieve request and requester information gathered from workflow and populate the process entities. (1-3)
2. Execute each rule that is applicable to the Request and Requester properties. (4-5)
3. If the rule is applicable, store the output to the corresponding response entity including pre-conditions, consent text, obligations for an information release and penalties for failing to enforce requirements for access decisions. (6-12)
4. Use the Rules Hierarchy Algorithm to combine the Federal, State and Organization outcomes and determine the final result (permit or deny) along with assembling the preconditions, consent clauses, obligations and penalties (13-26)
5. Return the final results components so that the Consent Generation Process can be performed (27).

4.4 Consent Generation Service Design

The Consent Generation Service processes the policy evaluator output when a Final Decision is made to potentially permit the disclosure of genetic information. First, the service enforces all requirements set by the policies prior to allowing the genetic information release. As seen below, the consent agreement signature is obtained, every pre-condition validated, and all obligations set in order for the information release to the requester. Once the algorithm is completed and the release decision is set, the information is passed back to the workflow for display to the requester. If the releases is approved,

the EMR can then provide the genetic information to the requester.

The high-level algorithm for the Consent Generation Service is described in Algorithm 2.

Algorithm 2: GenerateConsent.

```

Input: Workflows, Final Decision
SET release = TRUE
IF Final Decision includes Consent Clauses (1)
    CREATE Agreement (2)
    FOR EACH Consent Clause (3)
        ADD Consent Clause TO (4)
            Agreement (4)
        OBTAIN Signature on Agreement (5)
        IF signature NOT Obtained (6)
            SET release = FALSE (7)
    END IF (8)
IF Final Decision includes Pre-Conditions (9)
    FOR EACH Pre-condition (10)
        VALIDATE Pre-Condition Met (11)
        IF Pre-Condition NOT Met (12)
            SET release = FALSE (13)
    END EACH (14)
END IF (15)
IF Final Decision INCLUDES Obligations (16)
    FOR EACH Obligation (17)
        SET Obligation enforcement (18)
        IF Obligation NOT Enforced (19)
            SET release = FALSE (20)
    END EACH (21)
END IF (22)
RETURN release (23)
    
```

At a high-level the Consent Generation process is as follows:

1. Initialize release flag to be true (1)
2. If there are any consent clauses associated with the information release, create a new agreement and then add all the consent clauses from each rule into one document for the subject’s signature (2-5). Deny the release if no signature is obtained (6-7).
3. If there are any pre-conditions associated with the information release, validate that each one has been successfully met (9-11). Deny the release if any pre-condition is not validated (12-13).
4. If there are any obligations associated with the information release, set the enforcement mechanism for each one (16-18). Deny the release if any obligation is not set for enforcement (19-20).
5. Return the resulting release value to the workflow and EMR.

5 IMPLEMENTATION ENHANCEMENTS

This section describes how we prototyped our model

as described in our previous paper and expanded the prototype with new functionality to include refinements as we have implemented laws from additional states. These improvements are the focus of the rest of this paper.

Figure 3 shows the interactions between the workflow engine, the Consent Service and the ontology. The combination of these components implements the Policy Evaluation Service and the Consent Generation Service to provide privacy protection for genetic medical information. The workflow component is implemented using YAWL (Yet Another Workflow Language). The ontology and associated rules for policy evaluation was developed with Protégé and the DL Reasoner. The consent service was developed in Java for the interactions between the ontology and workflow. In addition, the Rules Hierarchy Algorithm was implemented using Java due to the limitation of DL addressing specific negation situations inherent in laws and policies.

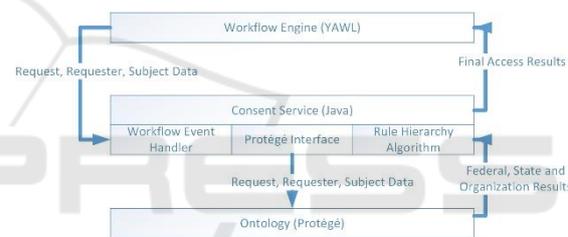


Figure 3: Prototype Components.

5.1 Workflow Map Upgrade

The primary focus on our recent research efforts has been on enhancing the workflow component to better reflect the consent process needed to obtain permission to release data by collecting all pre-conditions and then implementing the associated obligations for post-release. The updates improve the process for releasing genetic information and ensuring privacy protections by separating out the pre-condition activities prior to information release approval and the obligations enforcement required after the information release.

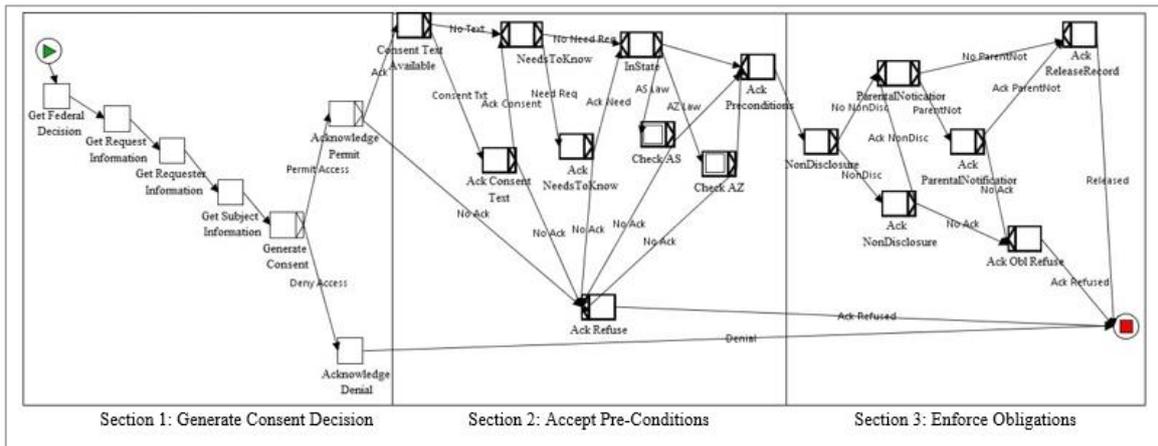


Figure 4: Genetic Privacy Workflow.

As shown in Figure 4, there are three major sections to the workflow which is implemented in YAWL. In the first section, the consent workflow performs the Information Gathering regarding the permissibility of access in relation to Federal laws along with data properties for the request, the requester and the subject. The “Generate Consent” step uses an event handler in the workflow that is tied to Java code in the Consent Service. As described below, the Consent Service makes the Access Decision on whether access will be permitted for the user along with collating all the pre-conditions, obligations and consent text from each level (Federal, State and Organization). These are used by the workflow for the user to acknowledge the results

If consent is granted, then in Section 2 the “Consent Text Available” step implements the Consent Agreement Generation to display the specific language for all consent clauses so the subject can electronically sign the consent agreement. The Pre-Condition Verification is performed and the user must acknowledge that each individual precondition is met with a separate confirmation for each one. During this section, the state-specific pre-conditions are also checked in sub workflows via the “InState” gate.

Once all the pre-conditions have been acknowledged, the workflow moves into Section 3 to establish the Obligation Enforcement mechanisms for any obligations that must be enforced with the permission. If the user fails to acknowledge any of the pre-conditions or obligations, the workflow states that situation to the user and permission is denied. At the end of the workflow, the results are returned to the associated EMR to perform the actual information release if approved.

5.2 Implementing Policies using Ontologies

The ontology changes introduced since the previous prototype encompass both additional attributes to capture specific conditions along with several structure changes as seen in Figure 5. (Changes from the previous ontology model are in italics.) The structural changes were as follows:

- Adding an Activity class to support State laws for obtaining consent prior to performing activities related to genetic privacy such as genetic testing. (As opposed to requests for Resources which is contained in the medical record generated after the activity was completed.
- Separating out requirements that must be enforced prior to information release (Precondition class) from those that must be enforced after the data is released for use (obligations).
- Adding a Penalty class to articulate the possible outcomes should the pre-condition or obligation requirements are not met.

In addition to these structural changes, additional Boolean data properties were added to Purpose, Subject, Requester, Role and Organization classes in order to support conditions associated with specific rule processing.

For example, the Subject class in Figure 5 provides selected information about the person who is the patient or client in the medical records being accessed for genetic information. A Boolean flag was added to Subject (*isDeceased*) to address a genetic information release under Arizona law (AZ 12-2802.E) for when the subject is deceased. Since other Arizona law (AZ 12-2802.A.6) permitted information release when the health care provider (physician or organization) ordered a genetic test (attribute) or if

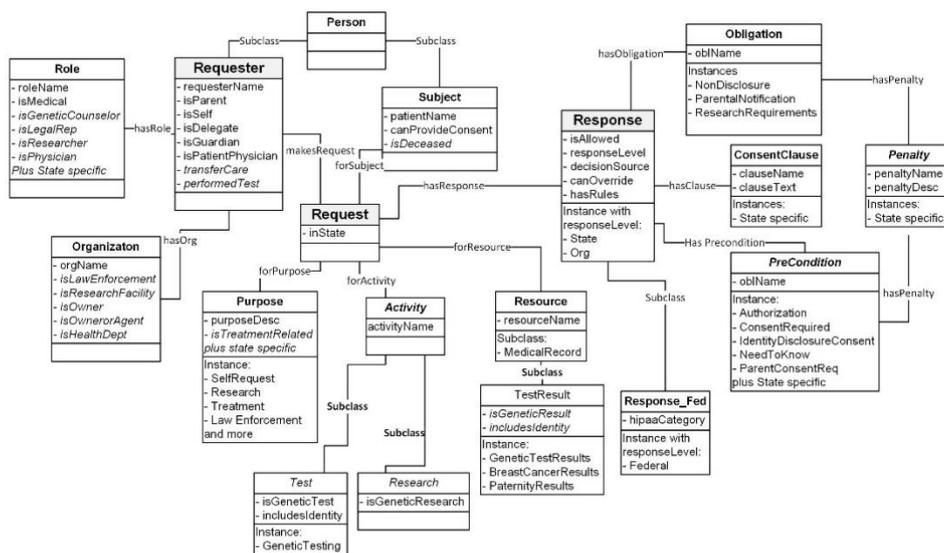


Figure 5: Genetic Privacy Ontology.

care was transferred from a provider that had access to genetic information (attribute) (AZ 12-2802.A.11), the Requester data properties now includes *performedTest* and *transferCare* flags. Similar situations required additions to the other classes. More flags are expected as additional laws, regulations and policies are added to the ontology

Another set of Boolean data properties were added to abstract out specific aspects of dealing with genetic data. In the first case, because some genetic tests only deal with specific parts of the genome that do not identify a specific individual (such as for a specific disease), an *includeIdentity* flag is used to provide additional restrictions when the test includes protected information like those used in law enforcement. In addition, Boolean data properties were added to permit enforcement of the genetic restrictions without listing individual tests or test results. The properties are *isGeneticTest* (Test subclass), *isGeneticResearch* (Research subclass) and *isGeneticResult* (TestResult subclass). The ontology contains only the information from the EMR that is necessary to implement genetic privacy rules.

5.3 Automatically Generating Consents

The Consent Service serves as the integration engine between the workflow/EMR and the ontology. Once the request, requester and subject attributes are gathered in the workflow steps (Section 1 of the workflow) and used to populate the workflow variables, the Consent Service is triggered by the workflow engine, as the next step, that is

GenerateConsent.

The service collates the data from the workflow variables for subject, request and requester, populates the ontology, invokes the rules processor, retrieves the intermediate results from the ontology, invokes the Rule Hierarchy Algorithm to reconcile the Federal, state and organization level results, and finally generates the final access permissions. The final permissions are transferred back to the workflow along with the associated pre-conditions and obligations. The outcome includes the consolidated list of conditions for all three levels. For example, the list of consent clauses required by both the Federal regulations and organizational policies.

Our initial prototype was modelled on preliminary work associated with representative state laws. As described above, we have identified specific attributes that are needed to implement new scenarios as we have implemented the full set of laws from additional states. So far the primary difference to the consent service from our initial prototype involves supporting the ontology changes for additional classes and properties in transferring data between the ontology and workflow. In addition, these class and property changes impacted the Rules Hierarchy Algorithm with the additions of the *PreCondition* and *Penalty* classes.

In the Rules Hierarchy Algorithm, the Result variables for the Answer, Pre-conditions, Obligations, Decision Source, Clauses, Penalties, and Rules are initialized to the corresponding federal variables, which were retrieved from Protégé. The Federal Override variable is then evaluated to determine if other rules are to be evaluated. If so, the

algorithm checks for existing State answers and, if found, determines if the Federal and State answer match. The system adds the State variables to the Result variables when the Federal and State match while the Results variables are set to the State results when there is no match.

For the Organization level, the algorithm determines if there is an Organization result and if there is a State result with a State Override flag set to true or there is no State answer. If the Results are the same, then the Algorithm adds the Organization variables to the Result variables otherwise the Results variables to be equal the Organization values if results are different and the override flag is set to true. At the end of processing the Results variables are passed back to the workflow engine.

6 ARIZONA CASE STUDY

As a case study, Arizona permits access to genetic information for purposes not explicitly stated in the law if consent is obtained first. (AZ 12-2802.A.2).

The first YAWL screen shown in Figure 6 is for the *Get Request Information* step in the workflow process to describe why the request is needed, what part of the medical record is to be accessed, in what state the action is being performed and an option to get permission to perform an activity (such as Genetic Testing) instead of accessing the genetic information resource. The *Get Requester Information* shows the key meta-data needed for the requester and the related entities such as organization and role. Each of the four Get steps have a similar screen. (Because Federal laws are well established and addressed in current policies, our focus at this time is on the implementation of state laws. Therefore the Federal access permission and override option is gathered using a graphical user interface.)

The ontology is populated with data from the workflow after all the information gathering steps are completed. The ontological rules engine is invoked and the rule specific for this case study are executed. The SWLR rule for this condition is:
Rule: makesRequest(?r, ?req), inState(?req, "AZ"), forResource(?req, ?resource), isGeneticResult(?resource, true), forPurpose(?req, ?pur), isAZAllowed(?pur, false), hasResponse(?req, ?resst), responseLevel(?resst, "State"), oblName(?pre, "ConsentRequired"), clauseName(?clause, "AZGeneticAuthorization")
 →

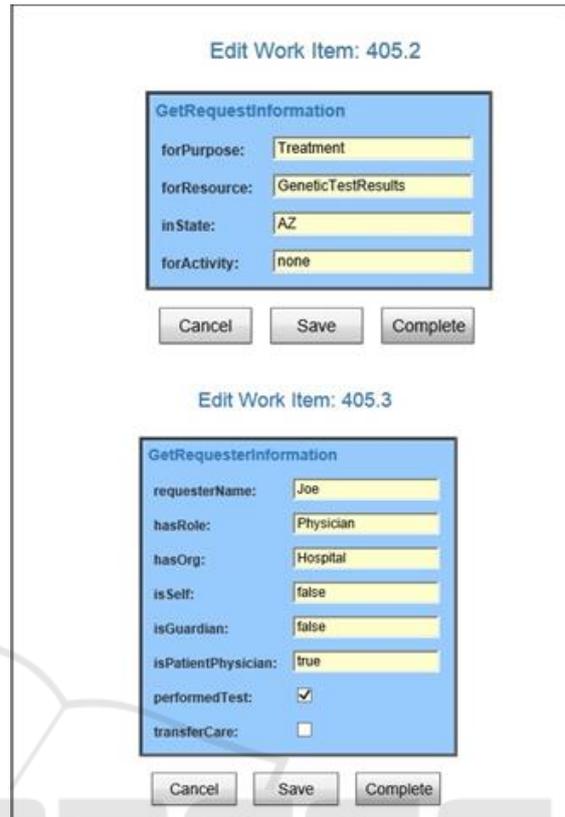


Figure 6: Workflow Entry Screen Shots.

isAllowed(?resst, true), canOverride(?resst, false), decisionSource(?resst, "AZ LAW 12-2802.A"), hasPreCondition(?resst, ?pre), hasClause(?resst, ?clause), hasRule(?resst, 57)

In this rule,

- ?r is for the Requester of the Request
- ?req is for the Request that links the various components, such as Subject, Purpose and Resource
- ?pur is the Purpose that is associated with the Request
- ?resst is the State Response object that is associated with the Request.
- ?resource is for the “GeneticTestResults” part of the medical record
- ?pre has the pre-condition that ConsentRequired must be obtained for this rule
- ?clause indicates the consent agreement for the patient must include the AZGeneticAuthorization clause

These SWRL statements are explained in Table I.

Table 1: Sample Pre-Condition Rule.

SWRL Statement	Explanation
<i>makesRequest(?r, ?req)</i>	Links Requester for the Request
<i>inState(?req, "AZ")</i>	Request is for Arizona
<i>forResource(?req, ?resource)</i>	Links Request with the Resource
<i>isGeneticResult(?resource, true)</i>	Restricts the rule to a Resource that is identified as a genetic test results
<i>forPurpose(?req, ?pur)</i>	Links Request with Purpose
<i>isAZAllowed(?pur, false)</i>	Restricts the rule to only execute when the purposes is not specifically allowed in Arizona
<i>hasResponse(?req, ?resst)</i>	Links the Request with a Response to store answer
<i>responseLevel(?resst, "State")</i>	Gets the Response for State level to store answers
<i>oblName(?pre, "ConsentRequired")</i>	Gets the Pre-Condition with the name for Consent Required
<i>clauseName(?clause, "AZGeneticAuthorization")</i>	Gets the Clause for Arizona authorization
<i>-> isAllowed(?resst, true)</i>	Sets the State response to access is allowed
<i>canOverride(?resst, false)</i>	Sets the state Response to not allow override by organization
<i>decisionSource(?resst, "AZ LAW 12-2802.A")</i>	Sets the State response to reflect the decision source as state law
<i>hasPreCondition (?resst, ?pre)</i>	Links the retrieved Pre-Condition with the State response
<i>hasClause(?resst, ?clause)</i>	Links the retrieved Clause with the State response
<i>hasRule(?resst, 57)</i>	Sets the rule number to 57 for reference

When the Pellet reasoner finds the instance for access in Arizona for a genetic test result based on a purpose not specifically addressed, the rule is executed and the ?resst data properties are populated with the indicated values. In addition, ?pre and ?clause instances are associated with the response as conditions to accessing the record. (The rule links the permission to access the genetic information with any associated pre-conditions, obligations and consent clauses.)

The reasoner output for the AZ State result is shown in Figure 7. The output also includes references to a second rule and the NonDisclosure obligation. In Arizona, genetic information releases also require the enforcement of a non-disclosure

requirements (AZ 12-2802.F) which is reflected in Rule 54. As the last steps for the Consent Service processing, the service extracts the response information from the ontology. The results are then evaluated using the Rule Hierarchy Algorithm to combine the responses for the Federal, State and Organizational rules into the final decision.



Figure 7: AZ Response.

Upon completion of the Consent Service invocation, the results are passed back to the workflow. The “AcknowPermit” screen in Fig 8 shows the results for granting access permission displayed for validation by the user. This screen shows the outcome to the user from the ontology rule processing and the Rules Hierarchy Algorithm evaluation.

Once the user acknowledges the overall results in Figure 9, the workflow then ensures that each pre-condition is completed prior to genetic information release. Each pre-condition clause is evaluated for applicability in this case and the appropriate actions taken to enforce the requirement. The individual pre-conditions are displayed and accepted separately to develop an audit trail of acceptance and to ensure all requirements are acknowledged.

In the AZ case study, the workflow first displays the consent text and requires that the clauses be accepted by the subject for the information release as seen in Figure 9. (The YAWL screen will be replaced with a digital signature implementation upon integration with an EMR system.)

Once the generic pre-conditions that are applicable to all states have been evaluated, the main workflow in Figure 4 goes to the “In State” step to determine if there are additional pre-conditions based on the state where the information request is being performed. This attribute-based determination evaluation is used to reduce unnecessary steps in the workflow.

Figure 8: AZ YAWL Results Confirmation.

Figure 9: AZ YAWL Results Confirmation.

Separate sub-workflows then enforce the requirements for that state through user validation for each specific requirement. The AZ sub-workflow is shown in Figure 10 which has separate requirements to address situations for genetic research, the state cancer registry, transferring care between providers, information release under subpoenas, and deceased subjects. Any of the conditions would generate a separate confirmation screen to ensure the applicable pre-conditions have been met.

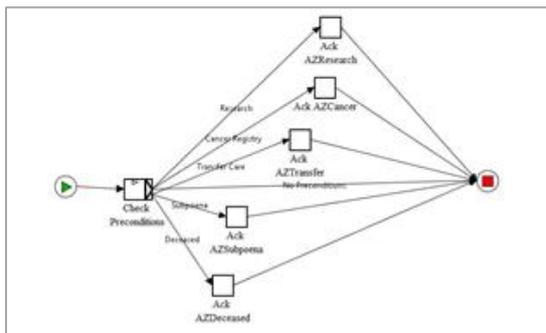


Figure 10: Arizona Sub-Workflow.

Failing to complete any pre-conditions moves the workflow to the *Ack Refuse* step as seen in Figure 4

and then to the subsequent end of the workflow without permitting information release. If all the pre-conditions are met, the workflow moves to enforcing the obligations associated with the actions as seen in Section 3 of the workflow diagram in Figure 5. Each obligation also has a separate acknowledgement to ensure the appropriate actions are taken.

For this case study, an additional confirmation screen is displayed for the NonDisclosure obligation seen in Figure 8. (The state enforces a requirement that all genetic results may not be disclosed beyond the person or organization that receives the information.) Upon completion of the obligation steps, the workflow ends and the information release of genetic information occurs with all federal, state and local laws, rules, and regulations implemented and enforced.

7 CONCLUSIONS

We provide a framework to ensure the appropriate availability of genetic medical information while enforcing the privacy protections. The expanded prototype works to bring together the applicable operational data in an EMR workflow into our framework to provide a definitive and consolidated response for access and the associated pre-conditions/obligations for information disclosure. While we continue to implement additional Federal and State rules to develop a comprehensive repository and rule base, our ongoing work focus on the interactions with representative policies and procedures for a medical organization. The pre-conditions and obligations will undergo further analysis to formalize the interactions and pro-actively identify potential conflicts within the rule set. This intersection will allow rules to be generated based on the risk of releasing protected privacy information. We expect the resulting prototype to demonstrate the overall capabilities needed to meet the medical community’s access requirements while balancing the individual rights to privacy and ownership of their genetic medical data.

REFERENCES

Ritchie, M., Holzinger, E., Li, R., Pendergrass, S. and Kim, D. (2015). "Methods of integrating data to uncover genotype-phenotype interactions." *Nature Reviews Genetics* 16.2. 85-97.

Németh, A., Kwasniewska, A., Lise, S., Schnekenberg, R., Becker, E., Bera, K. and Talbot. K. (2013) "*Next*

- generation sequencing for molecular diagnosis of neurological disorders using ataxias as a model.*" Brain. awt236.
- Pihoker, C., Gilliam, L., Ellard, S., Dabelea, D., Davis, C., Dolan, L. and Mayer-Davis, E. (2013). "Prevalence, characteristics and clinical diagnosis of maturity onset diabetes of the young due to mutations in HNF1A, HNF4A, and glucokinase: results from the SEARCH for Diabetes in Youth." *The Journal of Clinical Endocrinology & Metabolism* 98.10. 4055-4062.
- Lowrance, W. and Collins, F. (2007). "Identifiability in genomic research." *SCIENCE* 317. 600-602.
- McGuire, A. and Gibbs, R. (2006). "No longer de-identified." *SCIENCE-NEW YORK THEN WASHINGTON-* 312.5772. 2006. 370.
- D'Abramo, F., Schildmann, J. and Vollmann, J. (2015). "Research participants' perceptions and views on consent for biobank research: a review of empirical data and ethical analysis." *BMC medical ethics* 16.1. 2015. 1.
- Lunshof, J., Chadwick, R., Vorhaus, D. and Church, G. (2008). "From genetic privacy to open consent." *Nature Reviews Genetics* 9.5. 2008. 406-411.
- The Health Insurance Portability and Accountability Act of 1996 (HIPAA). *Pub. L. 104-191, 110 Stat.* 1936, codified as amended at 42 U.S.C x300gg and 29 U.S.C x1181 et seq. and 42 U.S.C x1320d et seq.
- Genetic Information Non-discrimination Act of 2008 (GINA). *Pub. L. 110-233, 122 Stat.* 883, codified as amended in scattered sections of 26, 29, and 42 U.S.C.
- Mascalzoni, D., Hicks, A., Pramstaller, P. and Wjst, M. (2008). "Informed consent in the genomics era." *PLoS Med* 5.9. e192.
- Gostin, L., and Hodge Jr., J. (1999) "Genetic privacy and the law: an end to genetics exceptionalism." *Jurimetrics.* 21-58.
- Prince, A. and Roche, M. (2014). "Genetic information, non-discrimination, and privacy protections in genetic counseling practice". *Journal of genetic counseling* 23.6. 891-902.
- Liao, S. (2009) "Is there a duty to share genetic information?". *Journal of medical ethics* 35.5. 306-309.
- Lucassen, A and Kaye, J. (2006). "Genetic testing without consent: the implications of the new Human Tissue Act 2004." *Journal of medical ethics* 32.12. 690-692.
- American Society of Human Genetics Social Issues Subcommittee on Familial Disclosure, ASHG STATEMENT *Professional Disclosure of Familial Genetic Information.* 1998) *Am. J. Hum. Genet.* 62: 474-483.
- Sherlock, E. (2009) "Disclosure of patient's genetic information without their consent- Is the "public interest" really a Sufficient Justification?". *Genomics Law Report.* 2009. Available at: <http://www.genomicslawreport.com/index.php/2009/11/10/disclosure-of-patientsgenetic-information-without-their-consent-is-the-public-interest-really-a-sufficient-justification/>. [Accessed 2 March 2015].
- Kaye, J., Gibbons, S., Heeney, C., Parker, M. and Smart, A. (2012). "Governing biobanks: Understanding the interplay between law and practice." Bloomsbury Publishing.
- [Hallinan, D. and Friedewald, M. (2015). "Open consent, biobanking and data protection law: can open consent be 'informed' under the forthcoming data protection regulation?" *Life sciences, society and policy* 11.1. 1.
- Kaye, J., Heeney, C., Hawkins, N., De Vries, J. and Boddington, P. (2009). "Data sharing in genomics—reshaping scientific practice". *Nature Reviews Genetics* 10.5. 331-335.
- Mascalzoni, D., Hicks, A., Pramstaller, P. and Wjst, M. (2008). "Informed consent in the genomics era." *PLoS Med* 5.9. e192.
- Belmont, J. and McGuire, A. (2009). "The futility of genomic counseling: essential role of electronic health records." *Genome medicine* 1.5. 1.
- Scheuner, M., de Vries, H., Kim, B., Meili, R., Olmstead, S. and Teleki, S. (2009) "Are electronic health records ready for genomic medicine?". *Genetics in Medicine* 11.7. 510-517.
- Ullman-Cullere, M. and Mathew, J. (2011) "Emerging landscape of genomics in the electronic health record for personalized medicine." *Human mutation* 32.5. 512-516.
- Gymrek, M., McGuire, A., Golan, D., Halperin, E. and Erlich, Y. (2013) "Identifying personal genomes by surname inference." *Science* 339.6117. 2013. 321-3.
- Reep, M., Yu, B., Wijesekera, D. and Costa, P. (2016), "Sharing Data under Genetic Privacy Laws". In: *Proceedings of the Eleventh Conference on Semantic Technology for Intelligence, Defense, and Security.* [online] Fairfax: CEUR Workshop Proceedings, pp. 46-54. Available at: <http://ceur-ws.org/Vol-1788/> [Accessed: 25 July 2017].