INTEGRATING R MODELS WITH WEB TECHNOLOGIES

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Abstract: We describe a software framework designed to shorten the translation of research models from theory to clinical practice. The framework integrates research and clinical practice into a single software architecture. Specifically, we present a *Survival Probability Predication Architecture* (SPPA), which is an extensible software platform allowing researchers to experiment with their statistical models and make rapid delivery of these models to clinical practice without a lengthy software development cycle.

1 INTRODUCTION

With personalized medicine, information such as a patient's genotype, molecular profiles, or clinical phenotypes is often used to make a decision on medication, provision of a therapy, or the initiation of a preventative measure. To make such a decision, health care teams need to be able to access the most current treatment plans and adjust their strategies accordingly and with confidence. One of the key challenges is to make a quick delivery for such systems at lower development costs, and allow greater interdisciplinary collaboration in treating patients (Tan et al., 2005).

A number of models for predicting cancer survival have been investigated and published, but few of them have ever been tested in clinical settings and even fewer have been used eventually in clinical practice. They are often developed in a statistical programming environment, such as R (www.r-project.org). As a statistical programming environment is intended to be used in biomedical research and not for clinical application, a final software translation is usually required to code the model into a computer system appropriate for a clinical setting. Due to costly software development processes, most of the models remain in literature and their translation never actually happens.

In this paper, we present a prototype system that integrates statistical cancer survival prediction models into web-based applications. The system is based on web technologies to allow for mobility and to achieve wide user access. Its information exchange backbone uses standard-compliant XML formats, and it is built as a set of multiple standalone Java applications.

2 USER INTERFACE

Our Lung Cancer Survival Prediction web application takes as input historical information on previous patients and specific information about a current patient. It calculates the current patient's survival probability and presents the findings as a chart and/or a table. To use this web-based tool, the end user (e.g., a clinician or a data entry person) enters patient clinical information and then submits the information. Once the request is received, the tool initiates statistical model(s) and passes the inputs to the model(s). After completing the calculation, the model(s) returns the results to the tool, and the tool formats and presents the results of the prediction model, viewable as either a chart or table. The user can change patient information, select different treatments, and examine the results in real-time.

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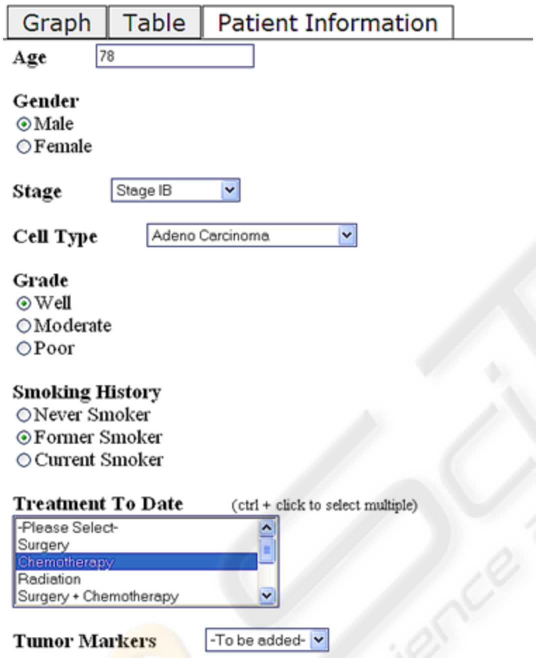
2.1 Data Input

The system allows for different model(s) for various cancer types. Even within the same type of cancer, different models may use different sets of input from the user. However, we assume all models require some core inputs from the user. For example, all models require basic information including patient's age, gender, and cancer cell type, stage and grade when predicting a cancer patient's survival probability. Additional information such as the patient's smoking status and history for lung cancer, and the treatments received by the patient could be used in a specific model to improve prediction accuracy. All of this information is gathered with the Patient Information Entry Form shown in Figure 1.



Age 78

Gender
● Male
○ Female

Stage: Stage IB

Cell Type: Adeno Carcinoma

Grade
● Well
○ Moderate
○ Poor

Smoking History
○ Never Smoker
● Former Smoker
○ Current Smoker

Treatment To Date (ctrl + click to select multiple)
-Please Select-
Surgery
Chemotherapy
Radiation
Surgery + Chemotherapy

Tumor Markers: -To be added-

Figure 1: Patient Information Entry Form.

The tool is designed to integrate multimodality data, such as genomic information, to make better predictions and to aid individual physicians in providing the best treatment for their patients. As the models being researched and developed vary from time to time, data input to the models will change accordingly. Such changes require the tool to be adjusted based on the models to be used. As designed, the researcher can make these changes directly by adjusting the user interface for his/her new model without the need to consult a computer programmer.

2.2 Presentation of the Results

The user interface presents the results of the statistical model as graphs and tables as shown in Figures 2 and 3 respectively. At the time a patient is diagnosed with lung cancer, a clinician would be able to use the tool to compare the effects of different treatment options on the patient's survival probability. Over time, as the patient receives specific treatment, more data is generated affecting his or her survival probability. In deciding further treatment for the patient, the clinician can use the tool to investigate treatment options that take this new data into account.

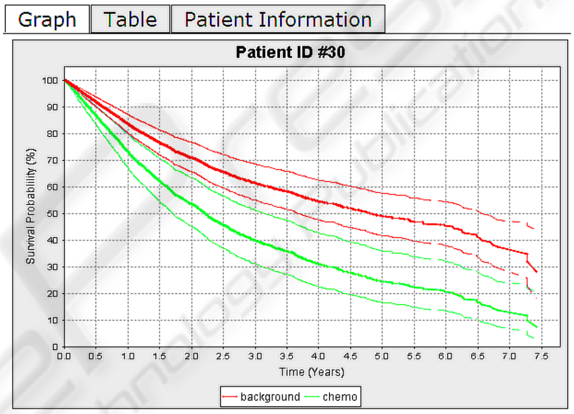
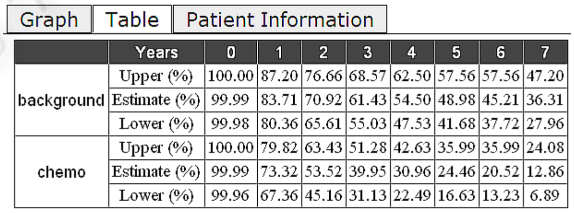


Figure 2: Graph View of Prediction Results.



	Years	0	1	2	3	4	5	6	7
background	Upper (%)	100.00	87.20	76.66	68.57	62.50	57.56	57.56	47.20
	Estimate (%)	99.99	83.71	70.92	61.43	54.50	48.98	45.21	36.31
	Lower (%)	99.98	80.36	65.61	55.03	47.53	41.68	37.72	27.96
chemo	Upper (%)	100.00	79.82	63.43	51.28	42.63	35.99	35.99	24.08
	Estimate (%)	99.99	73.32	53.52	39.95	30.96	24.46	20.52	12.86
	Lower (%)	99.96	67.36	45.16	31.13	22.49	16.63	13.23	6.89

Figure 3: Table View of Prediction Results.

3 ARCHITECTURAL DESIGN

Our platform allows researchers to add and remove statistical models and to make changes to the input area of the user interface. Table 1 summarizes the functions that can be performed by researchers, clinicians, and data entry people. In designing the architecture of our framework, the guiding principle was to create an environment that researchers and diagnosticians could use to experiment with various diagnostic models and potential treatments without having to acquire expertise in a computer program-

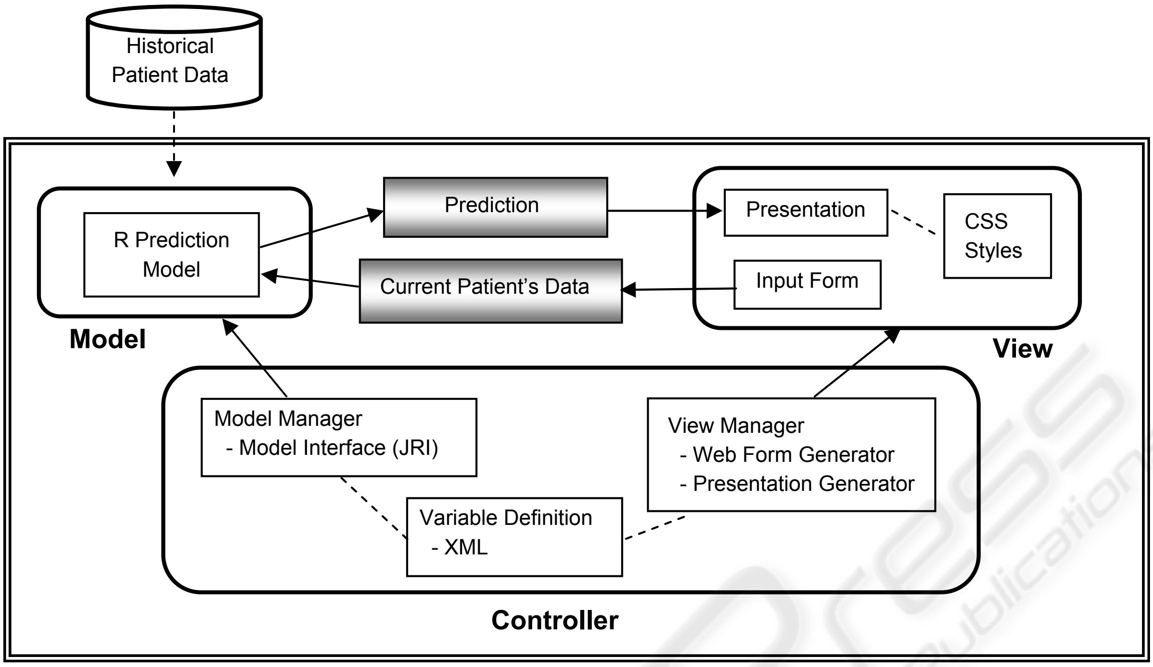


Figure 4: Survival Probability Prediction Architecture.

ming language and environment. The resulting *Survival Probability Prediction Architecture* (SPPA) is designed for experimentation with diagnostic models and survival prediction. SPPA is based on the Model-View-Controller architectural pattern, as shown in Figure 4. It provides both a mechanism for defining models and a mechanism for testing the model in a clinical setting.

Table 1: Software Functions Provided to User Groups.

User Group	Functions Supported
Researchers	Add and remove prediction models in R; Change database for the model; Modify user interface
Clinicians	Add, view, and modify a patient record; Compare and select treatments
Data entry person	Add, view, and modify a patient record

3.1 Controller

The heart of the SPPA is the Controller. The Controller was designed to be sufficiently general enough to enable quick and seamless modification of the system by non-computer specialists. Although we expect researchers to be proficient in a statistical programming language like R, we do not expect them to be proficient in Java. Likewise, diagnosticians should be able to navigate a web page, but they should not have to generate one to be able to view the results of a model.

In order to insulate the researchers and clinicians from its internals, the Controller is subdivided into three components: the Model Manager, the View Manager, and the Variable Definition component. The Model Manager uses JRI (www.rforge.net/JRI) to provide an interface between the Java methods of the Controller and the prediction model, which is currently written in R. However, the Model Manager enables researchers to build diagnostic models using any statistical programming language of their choice. At present, SPPA only supports statistical models written in R, but it can be easily modified to support any statistical modeling language by extending the Model Manager to provide an interface between Java and the new statistical modeling language.

The View Manager is responsible for providing the researcher and/or the clinician with the results of the prediction model on a given patient. It consists of two components: the Web Form Generator and the Presentation Generator. Information (e.g., age, gender, etc.) associated with new patients is gathered through a web page form that is generated by the Web Form Generator. The Web Form Generator works with the XML definitions of the Variable

Definition component to dynamically create the web form.

The glue that connects the Model with the View is the Variable Definition component. The Variable Definition component uses XML to define the type and structure of the inputs that describe the state of the patient, and defines which models use which inputs. The XML files are used by both the Model Manager and the View Manager. The View Manager uses the XML definitions within the Web Page Generator to create the Patient Information Entry Form like the one given in Figure 1. Once the clinician has completed the form, the inputs that he/she entered about the patient are passed to the prediction model via the Model Manager.

3.2 Prediction Model

There are three major components that support the prediction model. In addition to the prediction model itself, the Model Manager and Variable Definition components of the Controller work together to help researchers and clinicians work with different prediction models. SPPA was specifically designed to separate out the functionality of prediction modeling so as to minimize the type and level of modifications that are necessary to experiment with different models.

Obviously, to experiment with different models, the researcher needs to build a new prediction model. If, however, the new prediction model is written in R and uses the same input parameters as the current prediction model then no additional modifications are needed. The researcher need merely replace the current R prediction model with the new one. If, on the other hand, the researcher needs to add some additional input parameters then he/she must also modify the Variable Definition component of the Controller to define the structure and form of the new inputs in addition to replacing the current prediction model with the newly generated one.

It is also possible to build a new prediction model using a programming language other than R, but such a change also requires a change to the Model Manager. JRI serves as an interface between Java and R. Changing to a different statistical programming language would require embedding a Java method that defines an interface between Java and the new statistical programming language.

The actual prediction models we used in building the system take inputs describing a given patient (e.g., age, gender, stage) along with a suggested treatment and then predicts the survival probability of the patient. In our previous work, we analyzed over 5,000 consecutively enrolled non-small cell lung cancer patients and developed two models for predicting lung cancer patient's survival probability (Sun et. al., 2006). The first model uses patient's information available at the time of diagnosis and has been proven prognostic in our previous work. It uses age, gender, stage, cell type, and tumour grade as inputs. The second model uses additional information, including the treatment options and patient's smoking status.

3.3 User View

The user view is controlled by the View Manager as described above. It is not necessary to change the Web Form Generator when adding new inputs to the prediction model. Researchers need only change the XML definitions in the Variable Definition component of the Controller without making any changes to the Web Form Generator. SPPA allows the researcher to make changes to the inputs to his/her prediction model without having to make changes in the Java code. Furthermore, given the existence of XML editors, researchers can change XML definitions without a complete understanding of XML.

The information that is gathered via the web page form is stored in a file using the format defined by the XML tags of the Variable Definition component and then transmitted to the Prediction Model. If the clinician is dealing with an existing patient, then the web page form is initially filled in with that patient's information. The result of the Prediction Model is a collection of data that predicts the patient's survivability. The Presentation Generator allows the user to view this data using two different formats: a graph view and a table view. The graph view of the data, given in Figure 2, is created with a Java freeware JFreeChart (www.jfree.org/jfreechart). The table view, which is obtainable by selecting the Table tab, is given in Figure 3.

4 CONCLUDING REMARKS

We developed a software framework, the *Survival Probability Prediction Architecture* (SPPA), for translation of research findings into a clinical application in a timely fashion and at low cost. For investigators, SPPA helps them to plug in a developed statistical model, adapt a database, and make their models available for clinical practice. A coherent presentation of the patient's information and the prediction of a cancer patient's survival allows a physician to plan, deliver, and evaluate the most appropriate treatment for the patient.

We compared the results from the first statistical model with the results produced from SPPA. The graphs and tables in both cases were virtually identical. We have also assessed the tool's extensibility using the second model with additional inputs. Variable Definition component was modified to include the new input variables to be used in the model, and the server was restarted. SPPA requested the appropriate inputs for patients for the second model and generated the correct graphs and tables. A more comprehensive assessment of SPPA, such as evaluations on task completion efficiency (Hu et al., 2007) and the system's successfulness (DeLone and McLean, 2003), still needs to be conducted.

As a framework prototype, there are several useful features that are not yet included in SPPA. The inclusion of wireless support would allow a larger variety of mobile devices to access the tool. A database is another planned addition to the platform for storing and retrieving patient information. We would also like our platform to grant different permissions to the users with authentication.

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