

# Server and Interface for Patient Risk Assessment

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JASON (YINGTONG) ZHAO

MENTOR: DR. GIL ALTEROVITZ

# Abstract

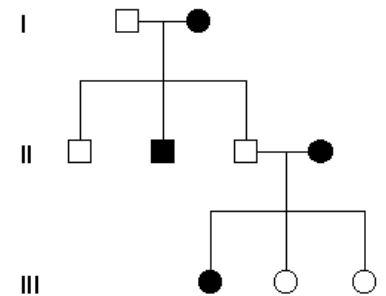
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- There is an advantage to spotting diseases early
- For hereditary diseases, we can do so by focusing on high-risk genes
- Genetic risk evaluations based on family disease history can be simple and effective
- Current solutions, however, are too technically demanding

Research topic:

- Making computer risk evaluations more accessible

**Dominant Pedigree**



# Goals

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- Builds on current software back-end
  - Incorporates and runs the software
- Compatible with industry-standard format (FHIR)
- Allows end-user interaction
- Easy to deploy



# Methods

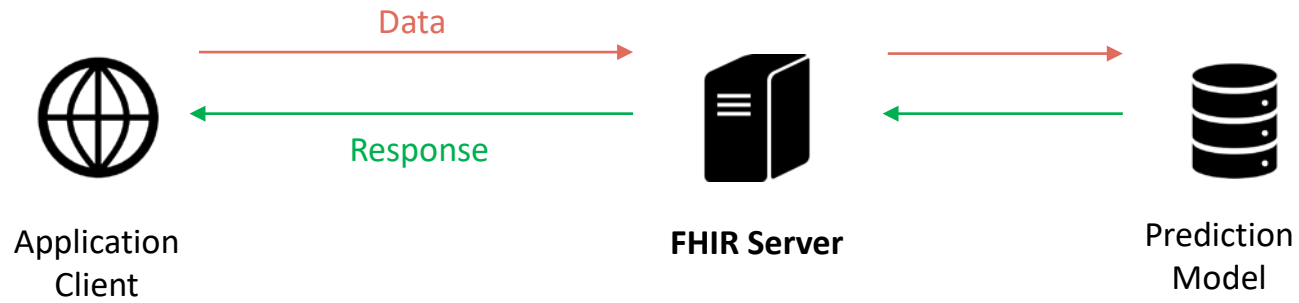
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We employ a two-part solution:

- FHIR Server
  - Communicates with existing prediction model
  - Used by applications, including the web interface
- Web Interface
  - Communicates with FHIR server
  - Used by the end user

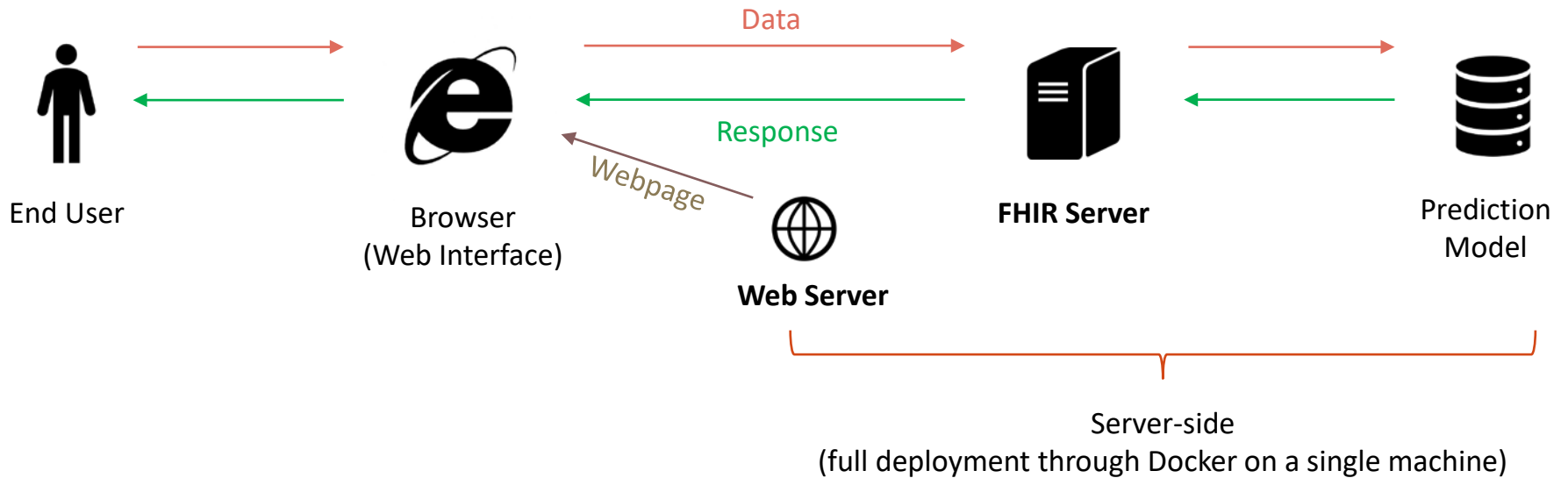
# API Function

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# End-User Function

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# FHIR Server

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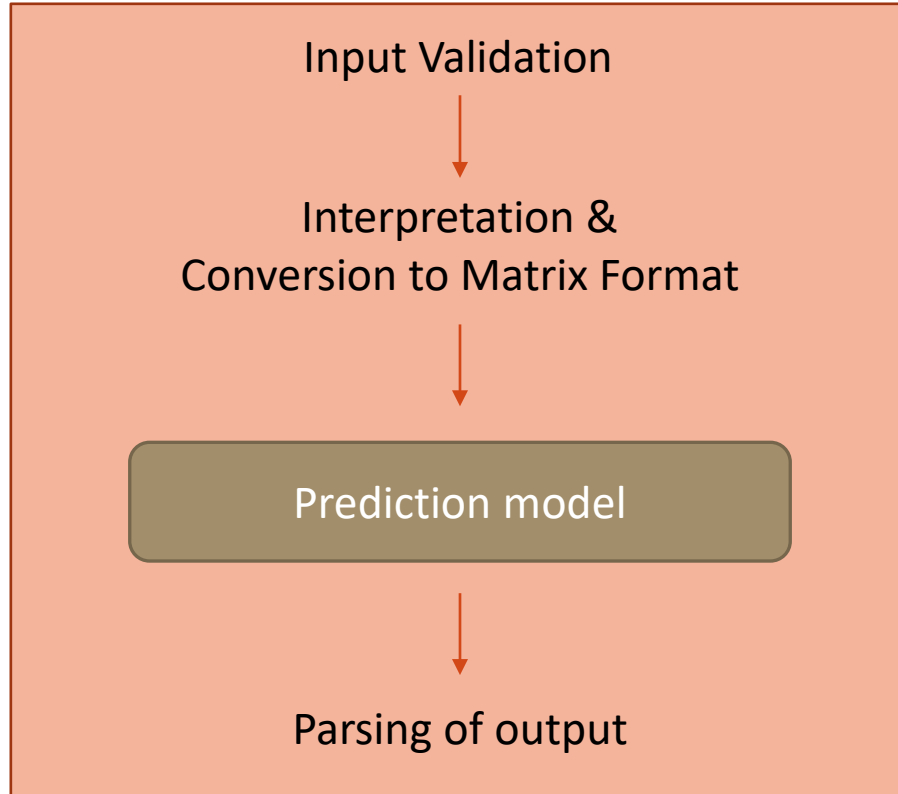
- Uses prediction model for risk assessment calculations
  - Launches software with server
  - Loads datasets
  - Converts and relays data
- Works standalone as API that allows usage of existing patient data
- Technologies:
  - Python (Flask)
  - Docker



JSON Request



FHIR Server



Input Validation



Interpretation &  
Conversion to Matrix Format



Prediction model



Parsing of output



JSON Response



# Web interface

- Browser-based, client-side
- Communicates with FHIR server on the same host as web server
- Enables end-user interaction
- Technologies:
  - JavaScript (React.js)
  - Docker
  - Web server: Nginx



Inherited Cancer Risk Evaluation App

Please enter family data below.

Patient Gender Relationship to patient Age Ethnicity  
Female Self  Deceased 67 AJ

Affected by Cancer

REMOVE ADD NEW MEMBER

Press "Evaluate" to calculate your risk:

EVALUATE RISK

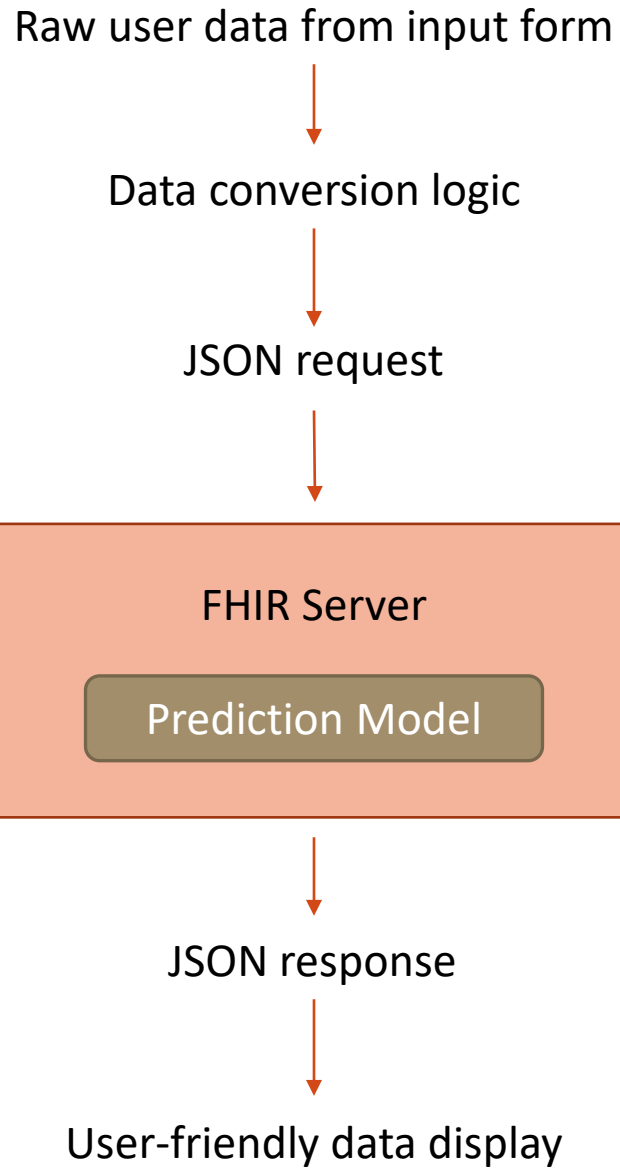
Results:

## Breast Cancer

Age	Probability
68	0.776%
70	1.554%
72	2.326%
74	3.086%
76	3.828%
78	4.541%
80	5.208%
82	5.812%
84	6.340%

## Ovarian Cancer

Age	Probability
68	0.089%
70	0.180%
72	0.273%
74	0.367%
76	0.461%
78	0.554%
80	0.643%
82	0.728%
84	0.805%



# Future

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- New backend prediction model
  - Open-source for unrestricted deployment
  - Circumvents limitations in the old program's design and formats
  - Optimized to optionally take some already available data
  - Incorporates more datasets

# Future (cont.)

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- More flexible specifications
  - Easier to use existing data as input to standalone FHIR server
- Web UI design
  - Tabs, hints, about page, etc.
- Additional supported diseases/features
- Security
- User testing and evaluation

# Acknowledgements

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