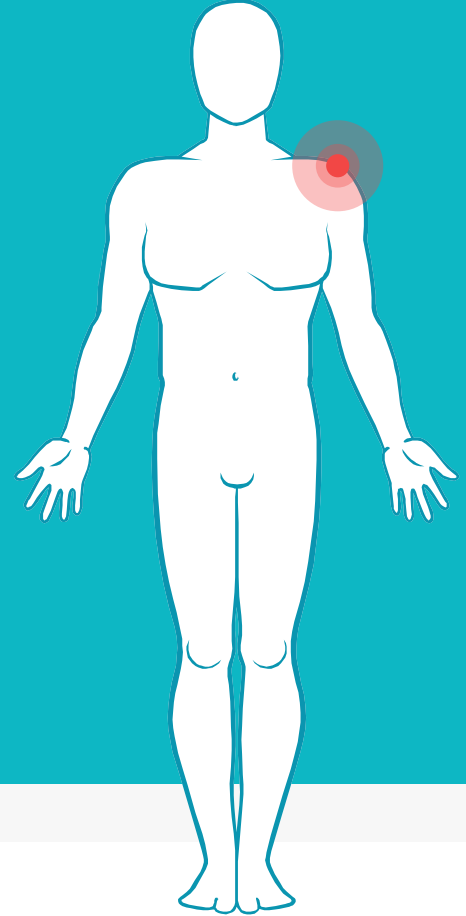# Precision Cancer Medicine:
A SMART Web App

Makiah Bennett & Jack Flahive

"I GAVE IT A HEALTHY DOSE OF DENIAL, BUT IT DIDN'T HELP."

Motivations
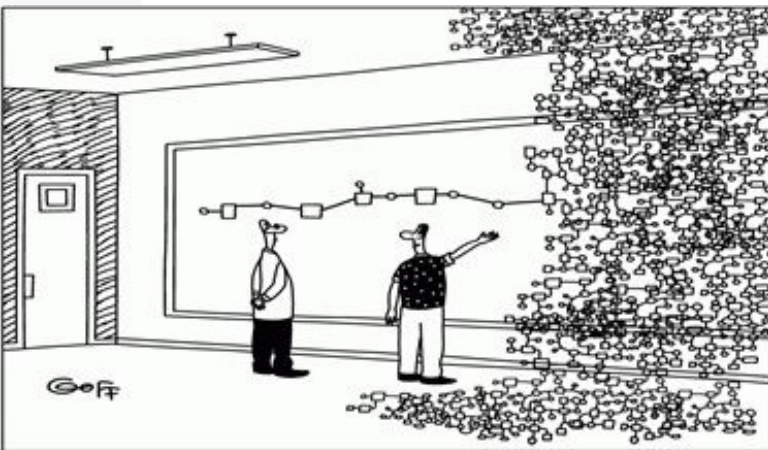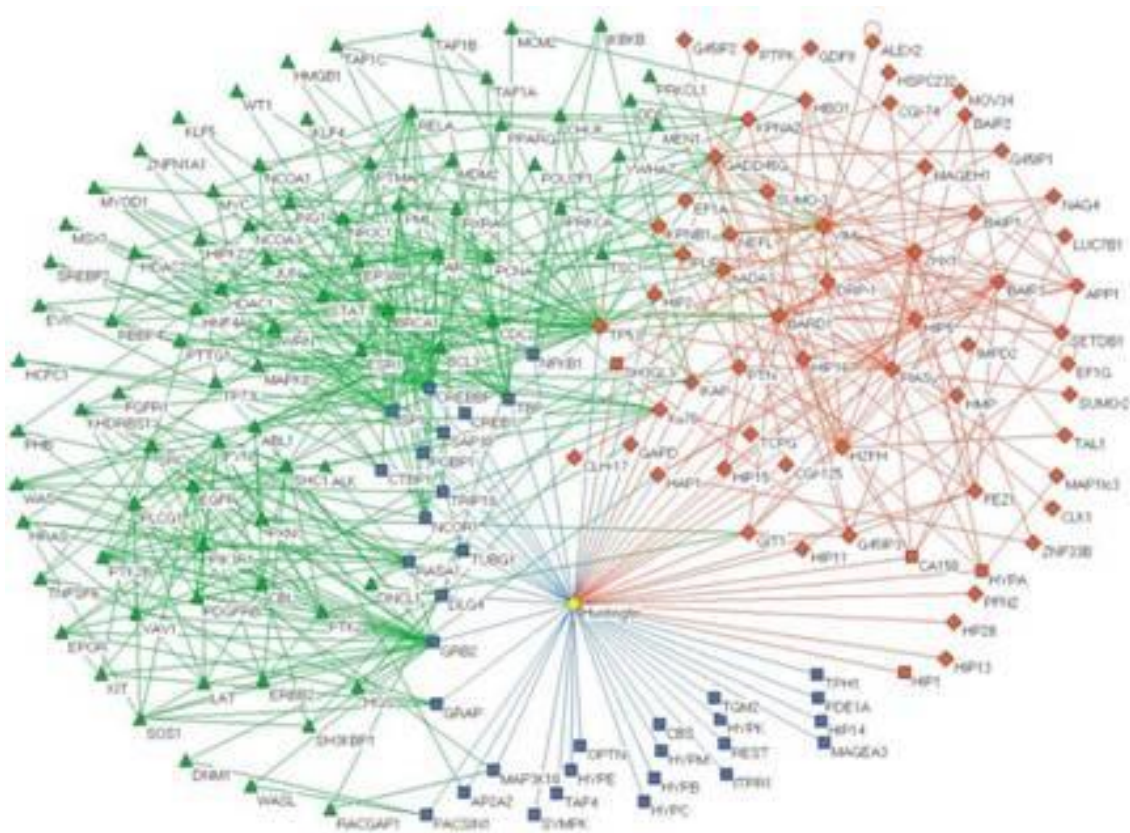
Why bother?

First Motivation: Vast Data

Second Motivation: EHRs Overly Complex

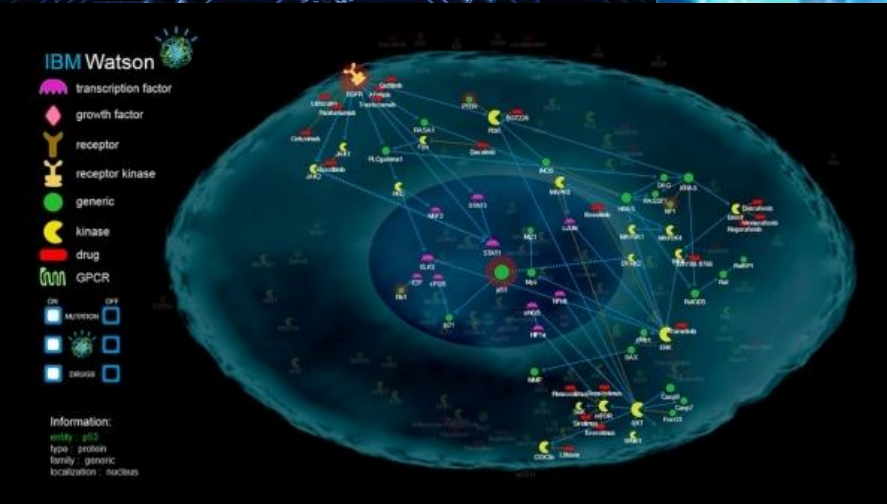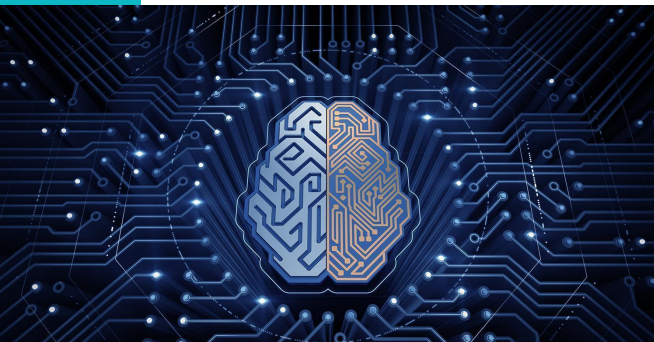"This is where the idea for the new EHR starts getting a little complicated."

Third Motivation: AI

Background

Prerequisites to understanding the app.

Precision Medicine

An emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person.

"

–NIH (National Institutes of Health)

The Precision Cancer Medicine Initiative

"Doctors have always recognized that every patient is unique, and doctors have always tried to tailor their treatments as best they can to individuals. You can match a blood transfusion to a blood type — that was an important discovery. What if matching a cancer cure to our genetic code was just as easy, just as standard? What if figuring out the right dose of medicine was as simple as taking our temperature?"

- *President Obama, 2015*

FHIR aims to simplify implementation without sacrificing information integrity. It leverages existing logical and theoretical models to provide a consistent, easy to implement, and rigorous mechanism for exchanging data between healthcare applications.

"

– *hl7.org*

*[..] a set of **open specifications** to integrate apps with Electronic Health Records, portals, Health Information Exchanges, and other Health IT systems.*

"

– *docs.smarthealthit.org*

[...] an open-source implementation of the FHIR specification in Java.

"

– *hapifhir.io*

Development

In progress!

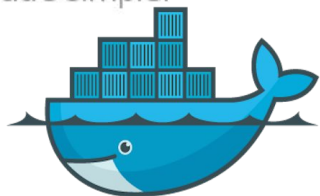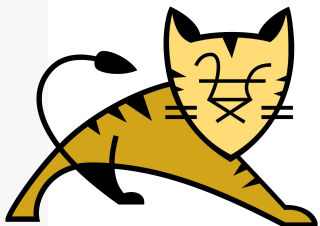# The S4G2 Server Backend

The Front-End

Mutations	
Name	**Variant**
AURKA	E4499K
CCND1	V2037F
CHEK2	R156P
EWSR1	loss
FOXP1	R1031Q
GID4	F171fs*3
TP53	Amplification
JAK2	D423E
CDKN1B	Amplification

Fitzgerald, Dean

Trump, Donald
DeVos, Betsy
Pence, Michael
Schmoe, Joe
Biden, Joe
Obama, Barack
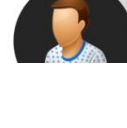
Those here are grouped in order of their similarity to their genome's mutations.

```
var server = app.listen(process.env.PORT || 8080, "0.0.0.0", function ()
{
    console.log('Server listening at http://' + server.address().address + ':' + server.address().port);
});
```

Driver Genes

John Smith

Gender: M
DOB: 24 June 1990
Height: 182 cm

Predictions

Comparisons

Wiki

Settings

SMART

Potential Driver Genes
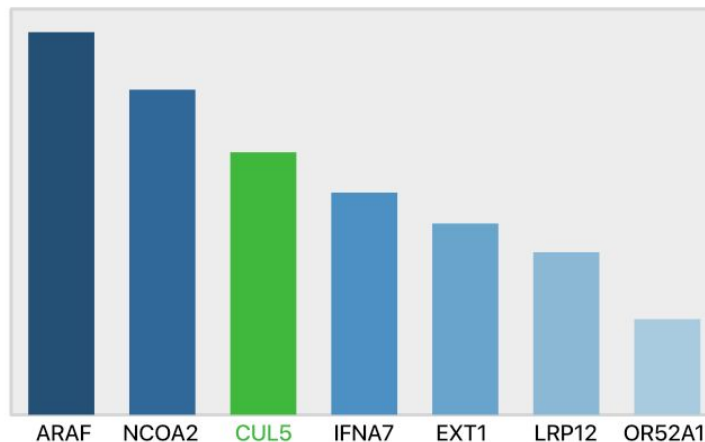
ARAF   NCOA2   CUL5   IFNA7   EXT1   LRP12   OR52A1
*Genes will be ranked by a SMART-PCM Score

Currently Viewing:

Gene	Driver	PCM Score	Mutation			Drug
			Mut. Syntax	Category	Prot. Syntax	
CUL5	Yes	0.73	c.T1630G	point coding	p.F544V	AT-406

Go To:
Full Data | Top 50 Genes | Drugs

PCM Web App   Home   About   Profile   Log Out

John Smith
Gender: M
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Mutations

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Mutations

Name	Variant
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GID4	F171fs*3
TP53	Amplification
JAK2	D423E
CDKN1B	Amplification

Mutated Genes Observed in Breast

«   1   2   3   »

SMART
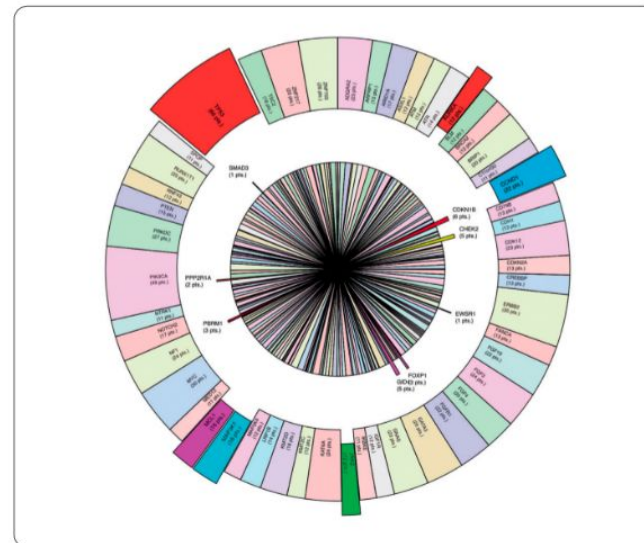
Convolution

▷ 3 Main Layers

  ▸ Layer 1: Prioritizes cancer "driver" mutations.

  ▸ Layer 2: Links mutations to genes using logistic regression.

  ▸ Layer 3: Generates a prioritized list of drugs targeting driver genes.

▷ Similar to the iCAGES pipeline.

Appendix

- ▷ Electronic Health Record (EHR)
  - ► Electronic version of a patient's medical history
- ▷ Substitutable Medical Applications and Reusable Technology (SMART) Health IT Platform
  - ► Open access API that classifies and packages genomic information for use in clinical applications
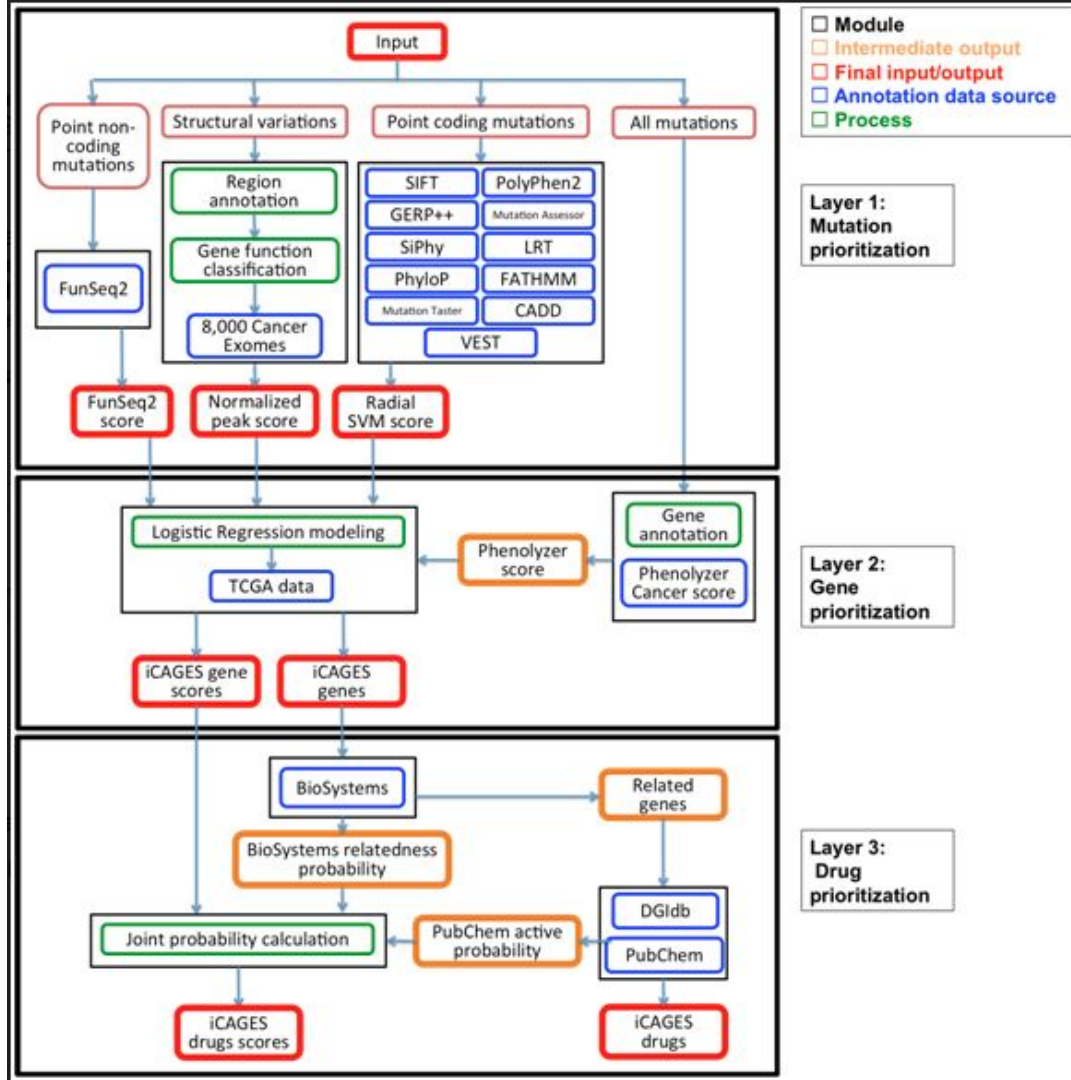 - ► Allows for the integration of different data types in one application
- ▷ Fast Healthcare Interoperability Resources (FHIR)
  - ► Standard for exchanging healthcare information electronically
- ▷ Single Nucleotide Polymorphisms (SNPs)
  - ► The variation of a single base pair in a DNA sequence
- ▷ VCF Files
  - ► "Variant Call Format": the raw file data format which our database provides for parsing. Used in the Texas patient database to which we refer for data.

Acknowledgements

▷ Thank you to Dr. Alterovitz for the much-needed help and support and the project idea!
▷ Thank you to Maksym Korablyov for answering and continuing to answer our many questions on machine learning!
▷ Thank you to MIT PRIMES for the enjoyable and interesting research opportunity!

THANKS!

Any questions?

You can find us at

- ▷ makiahtbennett@gmail.com
- ▷ jack.flahive@gmail.com