-- Standardizing genomics API to facilitate utilization of genetic data in clinics and laboratories

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Problems of Current Genomics Communication

 No standard API (Application Programming Interface)

- Lack means of communication
- Not integrated with clinical network



"Plug" doesn't work



Representation of Genetic Data

- Contents are essentially the same
 - Sequences (ATGC..) and genetic files
- Data are structured differently
- Different approaches of authentication
 Most follow OAuth but implement differently

SMART Provides a Solution

- Substitutability Medical Applications Reuseable Technology
- Generic design of API
 Developers focus on the app



• Integration with clinical data



- Approaches substitutability differently because of differences between clinical and genomic data
- Integration of genetic data among heterogeneous sources

Bridging clinics by providing CCDA Genomics

- CCDA(Consolidated Clinical Document Architecture) -- an adopted format for transferring medical documents
- Summary of a patient's genetic report



• Authentication

- OAuth2 open standard for authentication
- Two versions
 - Container Container
 - App Container

Data representation

- Structured in FHIR-style (Fast Health Interoperability Resource)
- Interlinked data models
- Grouped by records





Sequence					
+pateint: Resource(Patient) 1 +type: Code 11					
+quality: integer 01 +quantity: float 01					
+lab: Resource(Lab) 01					
01					
Coordinate					
+chromosome: string 11 +start: integer 11 +stop : integer 11					

Resource Example

Sequence



Resources are organized by 'record':

- A **record** groups all resources owned by a patient
- An account contains one or more **records**
- A record can either be internal or external
 - Both are perceived as the same by external source



Current Implementation

 Imports data from cloud services and translates to SMART Genomics' format

• Demo app

• Genomics Advisor (collaboration with Peijin Zhang)



App

<u>a</u>

Application Development



Future plans

Design more data models

• Planning to add microarray (lab for gene expression)

• Write more apps to demonstrate the API's functionalities

- A user friendly API playground for developer to understand basic aspects of the API
- Distribute the code for the community to adopt
- Deploy as a reference container
 - Developers can register their app and try it out

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4				*		
				SMART		
		Register new app				
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2			App name:	Genomics Advisor		
			App description:	Risk Calculation of Diseases		
<u> </u>			Launch uri:	localhost:8000/		
			Dedirect wit	100011051.0000/		
			Redirect un:	localhost:8000/receive_code/		
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END

Two aspect of the API

- Authentication
 - OAuth2 open standard for authentication

Data representation

- use gene coordinate as identifier -- e.g. chr13_123_124
- Implemented FHIR
- Resources grouped by **records**

Authentication

• Follows OAuth2 protocol

- access token
- refresh token
- Two versions
 - app-container -- throwaway access without refreshtoken
 - container-container -- permanent access
- Enables data sharing

