# Ontology-Based Data Interchange

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## Use Ontology to Drive:

- Creation of Alternative Data Models from i2b2
  - Desirable when supporting computation directed to various data models
- Allowing there to be Multiple Fact tables in i2b2
  - Desirable when want i2b2 on top of other data models
  - Desirable when accumulating large static fact tables
- Distribution of Queries to Multiple i2b2 Hives
  - Desirable when Query Endpoint is not SQL

# Creation of Alternative Data Models from i2b2

Jeff Klann Ph.D.

## 12b2 is a Giant Data Sponge

### **Generally Represents Patient Data**



## i2b2 Star Schema



## Concept\_dimension "look" ...

CONCEPT_PATH	CONCEPT_CD	NAME_CHAR
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.4	Toxic myopathy
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.5	Myopathy in endocrine diseases
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.6	Symptomatic inflammatory myop
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.8	Other myopathies
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.81	Critical illness myopathy
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.89	Other myopathies
\i2b2\Diagnoses\Neurologic Disorders (320-389)\Peripheral nerve disorde	ICD9:359.9	Myopathy, unspecified
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(260) Kwashiorkor\	ICD9:260	Hypoproteinosis
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(261) Nutritional maras	ICD9:261	Marasmus
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(262) Other severe pr	ICD9:262	Other severe protein-calorie mal
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(263) Other and unspe	ICD9:263	Other and unspecified protein-c
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(263) Other and unspe	ICD9:263.0	Malnutrition of moderate degree
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(263) Other and unspe	ICD9:263.1	Malnutrition of mild degree
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(263) Other and unspe	ICD9:263.2	Dwarfism, nutritional
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(263) Other and unspe	ICD9:263.8	Other protein-calorie malnutrition
\i2b2\Diagnoses\Nutritional deficiences (260-269)\(263) Other and unspe	ICD9:263.9	Protein-calorie undernutrition

## New Information Model Ontology

Consensus Ontology can live alongside other ontologies

(For example: PCORNet CDM ontology and the i2b2 demo ontology in this case) 🖻 🗖 Clinical Trials 🖻 🚾 Custom Metadata 🖻 🗖 Demographics 🖻 <u>阿</u> Diagnoses 🖻 🚾 Diagnoses (ICD10) 🗄 🛜 Expression Profiles Data 🖻 <u>ति</u> Laboratory Tests 🗄 🔂 Medications 主 🗖 PCORnet Core E Marcological PCORnet Demographics 🗄 🚾 PCORnet Diagnoses 🗄 🚾 PCORnet Encounters 🖻 🚾 PCORnet Enrollment 🗄 🚾 PCORnet Procedures 🖻 🚾 PCORnet Vital Signs 🗄 👩 Procedures 🗄 👩 Providers 🗄 👩 Reports

### Adapting i2b2 to PCORNet Data Model

1. Ontology-Driven Physical Transformation into PCORNet Common Data Model with a Generalizable approach to adapt to other Common Data Models



## Physical data transformations to non-i2b2 formats ontology driven





Bold fout indicates fields that cannot be null due to primary key definitions or record-level constraints.

## **ARCH Network Participation**



# Extending i2b2 for Multiple Fact Tables

Lori Phillips MS

## i2b2 Star Schema





#### OMOP v5



C	observation_fact
PK PK PK PK PK PK	Patient Num Encounter Num Concept CD Observer CD Start D. te Modifier <u>D</u> Instance Num
	End_Date ValType_CD TVal_Char NVal_Num ValueFlag_CD Observation_Blob

Field	Required	Туре	Description
procedure_occurrence_id	Yes	integer	A system-generated unique identifier for each procedure occurrence
person_id	Yes	integer	A foreign key identifier to the person who is subjected to the procedure. The demographic details of that person are stored in the person table.
procedure_concept_id	Yes	integer	A foreign key that refers to a standard procedure concept identifier in the Standardized Vocabularies.
procedure_date	Yes	date	The date on which the procedure was performed.
procedure_type_concept_id	Yes	integer	A foreign key to the predefined concept identifier in the Standardized Vocabularies reflecting the type of source data from which the procedure record is derived.
modifier_concept_id	No	integer	A foreign key to a standard concept identifier for a modifier to the procedure (e.g. bilateral)
quantity	No	integer	The quantity of procedures ordered or administered.
provider_id	No	integer	A foreign key to the provider in the provider table who was responsible for carrying out the procedure
visit_occurrence_id	No	integer	A foreign key to the visit in the visit table during which the procedure was carried out
procedure_source_value	No	varchar(50)	The source code for the procedure as it appears in the source data. This code is mapped to a standard procedure concept in the Standardized Vocabularies and the original code is, stored here for reference. Procedure source codes are typically ICD-9-Proc, CPT-4, HCPCS or OPCS-4 codes.
procedure_source_concept_id	No	integer	A foreign key to a procedure concept that refers to the code used in the source.
qualifier_source_value	No	varchar(50)	The source code for the qualifier as it appears in the source data.





## Ontology Tables Need to be Created -Build ontology of OMOP standard concepts









Ontologies covering the condition, procedures, drug, measurement and observation domains. All terms are mapped to standard concepts using OMOP's mapping tables

## Create views for OMOP Fact Tables

	OBSERVATION_FACT	CONDITION
PK	PATIENT_NUM	PERSON_ID
PK	ENCOUNTER_NUM	VISIT_OCCURENCE_ID
PK	CONCEPT_CD	CONDITION_CONCEPT_ID
PK	PROVIDER_NUM	PROVIDER_ID
PK	START_DATE	CONDITION_START_DATE
PK	MODIFIER_CD	
PK	INSTANCE_NUM	
	End_date	CONDITION_END_DATE
	Valtype_cd	
	Tval_char	
	Nval_num	
	Valueflag_cd	
	Observation_blob	

CREATE VIEW [dbo]. [CONDITION VIEW] (patient\_num, encounter\_num, concept\_cd, provider\_id, start\_date, modifier\_cd, instance\_num, end\_date, valtype cd, tval char, nval num, valueflag cd, observation\_blob) AS SELECT person id, visit occurrence id, cast(condition\_concept\_id as varchar), cast(provider\_id as varchar), condition start date, '@', 1, condition\_end\_date, cast(null as varchar), cast(null as varchar), cast(null as decimal), cast(null as varchar), cast(null as varchar(max) **FROM** condition

## Use Ontology Tables to direct Queries to proper Fact Table view

Prepend c\_facttablecolumn with OMOP domain view and modify CRC to parse into 'domain\_view' and 'c\_facttablecolumn'

c_name	c_facttablecolumn	c_tablename	c_columnname	c_operator	c_dimcode
Diabetes mellitus	condition_view.concept_cd	concept_dimension	concept_path	LIKE	\i2b2\Diagnoses\Endocrine disorders (240-259)\Other endocrine gland (



select patient\_num from condition\_view where concept\_cd IN

#### (select

concept\_cd from concept\_dimension where concept\_path like '\i2b2\Diagnoses\Endocrine disorders (240-259)\Other endocrine gland diseases (250-259)\(250) Diabetes mellitus\%')

## Queries can be performed in i2b2



Query across 3 domains: condition, medication, measurement.

CDM populated with OMOP's Synthetic Public Use File data (synPUF)<sup>2</sup> for 1000 patients.

## Successful OMOP Queries:

- Query types included
  - Multi-panel, multi-domain queries
  - Date constrained queries
  - Occurs > x queries
  - Value constrained queries
  - Temporal queries
- Queries not fully worked out
  - Modifier queries
  - Ancillary tables
  - Cover all OMOP Ontologies

## Same Approach to PCORNet CDM



Bold font indicates fields that cannot be null due to primary key definitions or record-level constraints.

# Demo of linking OMOP and i2b2 web services



- Medicare Claims Synthetic Public Use Files (SynPUFs) in OMOP v5 CDM is background data set
- <u>https://www.i2b2.org/webclient/</u>
  - Username: omop
  - Password: demouser



# Distribution of Queries to Multiple i2b2 Hives

Christopher Herrick MBA

## **Hives Distributed in a Network**



## **Hives Distributed in a Network**



## A Patient Information Commons from Specialized i2b2 Hives



## **The Parent Hive Distributes Queries**



## **The Child Hives Return Queries**



## **The Parent Hive Returns Results**



## **Common Sequence for Research Registries**

- 1) A researcher creates a registry of patients
- 2) Data is collected on the patients
  - Abstracted from clinical chart as summary data and imaging
  - Questionnaires are given and/or Interviews with patients are performed
- 3) Data is analyzed and published
- Opportunity is lost many researchers wish to combine with fresh clinical data and data from other registries

## **Two Approaches for Connecting Data**

#### **Enterprise Centric**

Data is shared with all researchers across the enterprise. This is similar to how the Research Patient Data Registry (RPDR) currently displays and shares data with investigators across all of Partners.

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Registries that become part of the enterprise centric view allow their data to be easily tied and queried with other enterprise wide data sources in the Big Data Commons.

This mode requires researchers to have the proper consents in place for their data to be queried from an enterprise level. Access to the identified data would still be controlled by the individual registry groups

#### **Registry Centric**

Data is imported into a registry for easier querying and analysis of patient cohorts; however, that data is not made readily available to the greater enterprise



Registries can supplement their project specific data by connecting with enterprise available datasets that are part of the Big Data Commons network. Access to the enterprise sets allow investigators to fill in important data gaps they may have with their own data

This mode is important if researchers have not collected the proper patient consents or, for other reasons, are not able to make their data available to the broader enterprise. Investigators would still be able to grant access to individual researchers who wish to collaborate.

## **An Enterprise Centered Data Network**

#### **Genomic Data**

Genomic data collected through the Biobank lives in a separate repository, but is made available for connecting with clinical data. All patients within the Biobank are accessible



#### **Research Repository**

Broad repository of clinical data made available for research is the center point for all querying. Contains the entire Partners patient population.



#### **Imaging Repository**

DICOM Metadata is extracted from images downloaded from mi2b2. This may be supplemented by a limited amount of tags on all images given to us by Radiology group. Contains references to all patients from who we have imaging data

#### **Notes & Reports**

Notes and reports on all patients are collected and put into a separate data repository that can be full text indexed. Specific security precautions are used to limit the PHI that can be queried directly



#### **Project Registry**

Individual research groups may contribute their data or findings back to the Partners enterprise for querying and use by all researchers across the organization. Data is used for the greater good.

## **A Registry Centered Data Network**

#### **Genomic Data**

Genomic data collected through the Biobank lives in a separate repository, but is made available for connecting with clinical data. Only patients contained in the project registry can be queried within this network

#### **Notes & Reports**

Notes and reports on all patients are collected and put into a separate data repository that can be full text indexed. Specific security precautions are used to limit the PHI that can be queried directly **Only patients contained in the project registry can be queried within this network** 



#### **Project Registry**

The central access point for this type of data network is the project specific registry. All queries will be limited to the patients that are part of this project.



#### **Imaging Repository**

DICOM Metadata is extracted from images downloaded from mi2b2. This may be supplemented by a limited amount of tags on all images given to us by Radiology group. Contains references to all patients from who we have imaging data. **Only patients contained in the project registry can be queried** within this network



#### **Clinical Data**

Repository that contains most clinical data from legacy systems as well as Epic for all patients across the enterprise. Only patients contained in the project registry can be queried within this network

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Brisskit Portal	
Upload XLS - New Project	File       Image: Solution of the solu
Existing Project	Paste     Image: Construction of the second se
Delete Project	A4 $\checkmark$ : X $\checkmark$ $f_x$ pr-00001 $\checkmark$
View Data	project2_1_optional 1 ID OBS_START_DATE AGE GENDER RACE DEATH MARITAL_STATUS WORK_STATUS W 2 null null Age Sex Race Death Marital Status Work Status W 3 null null age Sex Race death marital status work status w 4 null null age Sex Race death marital status work status w
Your i2b2 instance	4       pr-00001       02-06-2014       12:00:00       35 Mi       Hisparic       1 single       ruintme         5       pr-00002       02-06-2014       12:30:00       46 F       Asian       1 married       not employed         6       pr-00003       03-06-2014       13:23:00       54 M       White       1 widowed       parttime         7       pr-00004       04-06-2014       11:45:00       33 F       White       1 separated       self employed         8       pr-00005       null       65 M       Asian       0 divorced       retired
	READY SUM: 84016.8 Ⅲ
	tab Vital Status is mapped to the column Death in the 'Data' tab. This spreadsheet also contains 5 optional columns which are OBS_START_DATE, AGE, GENDER, RACE and DEATH. OBS_START_DATE is a special column which marks the start

- BRISSKit is open source Biomedical Research Software as a Service Kit
- Developed by University of Leicester
- Allows spreadsheets of data to be auto imported into an i2b2 hive

# Instantly Connected Databases in the Big Data Commons





## **Services**

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Brisskit Portal Upload XLS - New Project Upload XLS - Existing Project Ontology Mapper Delete Project View Data Your (2b2 Instance)	PC-SURE (22)     Carlow     Car

#### **Obtain Summary Tables**

99	0/	100 Selected								
	¥	ID	Gender	Age	Race	Diabetes mellitus	Family history [Contains: Diabetes]	HGB ASC (LOINC:4548-4)	HGB A1C (LODIC:4548-4)	HG8 A1C (L00xCr4548-4
	₩	100000003	Male	41	asian	12	54	43	4.1	6.9
	₩	100000008	Male	23	hispanic	3	12	54	4.2	6.7
	₩	100000011	Female	60	white	21	21	43	4.6	7.1
	₩	100000013	Female	83	black	34	9	65	4.7	5.9
	₩	100000015	Male	32	hispanic	1	10	34	4.4	6.3
	₩	100000029	Male	25	hispanic	3	25	25	5.1	6.8
	₩	100000043	Male	61	hispanic	23	14	21	4.9	6.5
	₩	100000045	Female	89	asian	37	15	54	4.9	6.6
	₩	100000054	Female	66	asian	43	6	45	4.8	6.6
	₩	100000066	Female	22	black	32	4	33	5.2	7.0
	₩	100000070	Male	38	black	43	11	38	5.5	6.5
	₩	100000077	Male	13	black	12	8	42	4.4	6.7
	₩	100000080	Male	33	indian	32	13	48	4.2	6.5
	₩	100000083	Female	65	black	33	4	39	4.7	6.6
	*	100000087	Male	55	asian	36	6	42	4.8	6.9
	*	100000096	Female	76	black	54	17	43	4.9	6.5
	*	100000099	Male	36	black	32	0	39	5.2	6.6
	₩	1000000108	Male	66	asian	43	1	25	5.3	6.7
	*	1000000109	Male	63	hispanic	31	4	29	4.9	5.9
8	¥	1000000112	Male	17	black	17	0	14	4.7	6.8
	*	1000000119	Female	72	white	43	32	45	4.4	5.9
1	ж.	100000133	Camala	16	aeian	20	,		40	66
Showing Patients 1 to 100 of total 2003									Next 10	

#### Link to Detailed Data



Atlases provide a visual guide for Radiology Decision Support, such as determining Perinatal Hypoxic Ischemic Encephalopathy

ADC map from 4 infants: Each statistically compared to age matched atlas yields visual guide to pathology

Quantitative analysis tools + large data sets = Great insights for practicing doctors



## Presentation of Baby Brains Registry in i2b2



# Sign the DUA



The Clinical Image Bank is a web-based query tool that allows Partners investigators to query and download data from curated phenotypically characterized pediatric patient cohorts. You can also view and make requests for medical images directly from the image bank.





Request images from the Clinical Image Bank

#### Registration Form

Enter Your Information			
Partners Username: *	?	E-mail address: *	2
nw096		nwattanasin@partners.org	
Full Name (e.g. Doe, John): *			
Wattanasin, Nich			
Sign Data Use Agreement		[ Print this DUA ] [ View in new	v browser window ]
Partners HealthCare Clinical Image Bank			*
Data Use Agreement - Clinical Image Bank Por	tal (S	September 11th, 2017)	
Please read the terms of this Data Use Agreemen HealthCare Clinical Image Bank Portal. The Clinic	it ("Ai al Im	greement") carefully before accessing the Partn age Bank Portal provides direct access to:	ers
(1) Limited Data Set health information, for purposi your potential research project(s) and the availability	ses o lity of	f running queries to determine the feasibility of of clinical images for the project(s); and	conducting
(2) Clinical Images and/or Limited Data Set health	infor	mation, for purposes of conducting such projec	t(s).
As used in this Agreement, "Limited Data Set" me dates and birth dates) and certain geographic info	ans i rmati	nealth information that may include dates (such	as admission 🖕
By checking this box, you agree to t	he (	Clinical Image Bank Data Use Agree	ement.
✔ Type your Full Name to Sign: *		Job Title: *	
Department: *		Institution: *	
		Complete Regi	stration

## Definition to Extract Table for Analysis



## Table Extracted



## Images Viewable



## Flow of Healthcare Innovations



## Tribute to...

- I2b2/BD2K Core Team
  - Issac Kohane
  - Paul Avillach
  - Griffin Weber
  - Christopher Herrick
  - Alyssa Goodson
  - Lori Phillips
  - Michael Mendis
  - Victor Castro
  - Janice Donahoe
  - Nich Wattanasin
  - Wayne Chan
  - David Wang
  - Mike Ollendieck
  - Jeff Klann
  - Andrew Cagan
  - Bhaswati Ghosh
  - Retta Metta

- Biobank Team
  - Natalie Boutin
  - Scott Weiss
  - Vivian Gainer
- Innovation Team
  - Randy Gollub
  - Sandy Aronson
  - Heidi Rehm
  - Calum MacRea

## Thank You

## Appendix

# Multi-Fact Table in Genomic Use Case Alyssa Goodson MS

## Use of Static Genomic Fact Table



#### Variant Call Format (VCF)

##filef ##filed ##sourc ##FORMA ##INF0=	ormat=VC ate=2016 e=PED T= <id=gt <id=rsid< th=""><th>Fv4.2 0127 ,Number=1,Type= ,Number=.,Type=</th><th>String,De</th><th>me key=va type a escriptic</th><th>tadata line alue pairs ti nd format o on="Genot on="dbSNP</th><th>s in the fc nat define of specific ype"&gt; ID in b</th><th><ul> <li>A specification maintained by the Global Alliance Data Working Group File Formats Task Team</li> <li>Used for describing genomic positions (loci)</li> </ul></th><th></th><th></th></id=rsid<></id=gt 	Fv4.2 0127 ,Number=1,Type= ,Number=.,Type=	String,De	me key=va type a escriptic	tadata line alue pairs ti nd format o on="Genot on="dbSNP	s in the fc nat define of specific ype"> ID in b	<ul> <li>A specification maintained by the Global Alliance Data Working Group File Formats Task Team</li> <li>Used for describing genomic positions (loci)</li> </ul>		
##INF0=	<id=vari< td=""><td>antEffect,Numbe</td><td>r=.,Type=</td><td>=String,</td><td>Descripti</td><td>on="Vari</td><td>iant annotation (if present) in the following format:</td><td></td><td></td></id=vari<>	antEffect,Numbe	r=.,Type=	=String,	Descripti	on="Vari	iant annotation (if present) in the following format:		
##conti	GeneSym	length-24025062	CTIDIID:0	c.Nomenc	tature	TSegProt	einiv:p.Nomenclature/variantEffect. *>		
##conti	a = < ID = 2.	length=24319937	3>				a ta bar an an air an an an ta air an ta bha tha air an ta ann an ta bha air an ta an ta bha air an ta		
##conti	g= <id=3,< td=""><td>length=19802243</td><td>0&gt;</td><td></td><td></td><td></td><td>eight mandatory tab-delimited columns with the headers:</td><td></td><td></td></id=3,<>	length=19802243	0>				eight mandatory tab-delimited columns with the headers:		
##conti	g= <id=4,< td=""><td>length=19115427</td><td>6&gt;</td><td></td><td></td><td></td><td>#CHROM, POS, ID, REF, ALT, QUAL, FILTER, and INFO</td><td></td><td></td></id=4,<>	length=19115427	6>				#CHROM, POS, ID, REF, ALT, QUAL, FILTER, and INFO		
##conti	g= <id=5,< td=""><td>length=18091526</td><td>0&gt;</td><td></td><td></td><td></td><td></td><td></td><td></td></id=5,<>	length=18091526	0>						
#CHROM	PUS	ID KEF	ALI	QUAL	FILIER	INFO	FURMAL 010061321010_N01C01-1000/854	CT	a /a
1	1/538	JHU_1.1/53/		A	•	•	RSID= <u>rs20046632;</u> VariantEffect=WASH/P NR_024540.1:n.58/+68G>1 p./ intron	GI	0/0
1	704251	JHU_1.704250	A	G	•	•			
1	737203	JHU_1.73/202	G	A	•	•	RSID= <u>FS309980014</u> GI 0/0		
1	740243	JHU_1.740242		C C	•	•			
1	740189	JHU_1./40188	A	G	•	•		1 /1	
1	752500	153094315	G	A	-	•	RSID= <u>rs3094310</u> ; VarianteTTect=rAM87b[NR_103536.1:n18365A[p.=]Upstream G	1/1	0 10
1	776394	JHU_1.//0393	G	A	•	•	RSID=rs1438/0/10;VariantEffect=LINC01128 NR_047519.1:1.288-0640G>A p./ intron	GT	0/0
1	779286	rs149978434	L T	A	•	•	RSID=rs149978434; VariantEffect=LINC01128 NR_047519.11n.288-3748C>A  p. (]Intron	GI	0/0
1	779744	JHU_1.//9/43	!	u u	•	•	RSID=rs145028227; Varianterrect=LINC01128 NR_047519.1:n.288-3290[>G[p.?]Intron	GI	0/0
1	/83318	rs6686696	A	G	•	•	RSID=rs6686696; VariantEffect=LINC01128 NR_047519.1:n.440+132A>G[p./]intron	GI	0/0
1	786796	JHU_1.786795	L	<u>+</u>	•	•	RSID=rs148833/34; Varianteffect=LINC01128 NR_047519.1:n.441-511C>1 [p.?] Intron	GI	0/0
1	786949	JHU_1 786948	G		•	•	RSID=rs140908266; VariantEffect=LINC01128 NR_04/519.1:n.441-3586>  p. / Lintron	GI	0/0
1	/8/21/	JHU_1./8/216	G	A	•	•	RSID= <u>r5369238012</u> ; Varianteffect=LINC01128 NR_047519.1:n.441=90G>A p./ intron	GI	1/1
1	/8/428	JHU_1.787427	G	A	•	•	RSID=r55/5685800; Varianterrect=LINC01128 NR_047519.1:n.56265A1[exon G]	0/0	
1	/88/13	JHU_1.788712	!	C	\ •	•	RSID=rs2980306; VariantEffect=LINC01128 NR_04/519.1:n./21-58/>C/p.//intron	GI	1/1
1	790760	JHU_1./90/59	A	G	\•	•	RSID=rs80164/48; VariantEffect=LINC01128  NR_04/519.1:n.2/10A>G  exon G	1/1	
1	791853	JHU_1.791852	G	A	•	•	RSID= <u>rs6684487;</u> VariantEffect=LINC01128[NR_047519.1:n.3803G>A  exon GT	0/0	
1	793521	JHU_1.793520	T	G	• \	•	RSID= <u>rs376882577;</u> VariantEffect=LINC01128[NR_047519.1:n.54717>G[]exon GT	0/0	
1	793750	JHU_1.793749	G	Т	• \	•	RSID= <u>rs202099173</u> ;VariantEffect=LINC01128[NR_047519.1:n.5700G>T] exon GT	0/0	
1	/93770	JHU_1.793769	G	A	• \	•	R51D=r514/3/1531;VariantEffect=LINC01128 NR_047519.1:n.5720G>A  exon GT	0/0	
1	794332	JHU_1.794331	G	A	• \	•	R51D=rs1212/425; VariantEffect=LINC01128  NR_047519.1:n.6282G>A  exon GT	0/0	
1	796775	JHU_1.796774	Т	C	• \	•	RSID= <u>rs111922608</u> ;VariantEffect=LINC01128 NR_047519.1:n.*1949T>C p.= downstream	GT	0/0
1	797549	JHU_1.797548	G	Т		\ <b>.</b>	RSID=rs200288882 GT 0/0		

- FORMAT column (optional) is used and contains the "GT" keyword to specify that genotype data exist
- The #CHROM, POS, REF and ALT fields are taken directly from the MEGA Consortium chip manifest file provided by Illumina
- ID field contains unique id for each position
- QUAL and FILTER fields are not utilized for these data
- Annotations for each position are stored in the INFO column

Final column = genotype of the individual at this genomic position



出	#CHROM	POS	ID	REF	ALT		INFO SUBJECT_1						
ž	1	752566	rs3094315	G	Α		RSID=rs3094315;VariantEffect=FAM87B NR_103536.1:n185G>A p.= upstream						
								$\rightarrow$					
⊢.													
Ú Ú	PATIENT_NU	M CON	ICEPT_CD I	NSTANC	CE_NUM	VALTYPE_CD	TVAL_CHAR	NVAL_NUM	OBSERVATION_BLOB				
4	1	SO:	0001483	338	720	В	CHROM_1	752566	rs3094315,G_to_A,FAM87B,homozygous_ref,upstream,ID_rs3094315				

## I2b2 observation\_fact table

#### CONCEPT\_CD

• Two concepts with codes from Sequence Ontology: SNP (SO:0001483) or indel (SO:1000032)

#### INSTANCE\_NUM

- The set of all SNPs for each patient will all have the same encounter number and date
- The concept codes will be the same for all SNPs (SO:0001483) and for all indels (SO:1000032).
- The set of all SNP facts will be enumerated in the instance\_num field to make the primary key unique, as will the set of all indels.

#### VALTYPE\_CD

• always equal "B" to indicate that data are stored in the observation\_blob field and to trigger the full text search already existing in the i2b2 environment

#### TVAL\_CHAR

Chromosome

#### NVAL\_NUM

Position

#### OBSERVATION\_BLOB

<RSID | "missing\_rsid">,<REF\_TO\_ALT>,<GENE\_SYMBOL | "missing\_gene">,<ZYGOSITY | "missing\_zygosity">,<CONSEQUENCE | "missing\_consequence"><CHIP\_ID>

LARGESTRING search of OBSERVATION_BLOB									
CONCEPT_CD	INSTANCE_NUM	VALTYPE_CD	OBSERVATION_BLOB						
SO:0001483	1	В	rs3094315,G_to_A,FAM87B,homozygous,upstream						
SO:0001483	2	В	rs3131972,A_to_G,FAM87B,homozygous,upstream						
SO:0001483	3	В	rs61770172,C_to_G,FAM87B,homozygous,exon						
SO:0001483	4	В	rs3115860,C_to_A,FAM87B,homozygous,exon						
SO:0001483	5	В	rs12567639,G_to_A,FAM87B,homozygous,downstream						
SO:0001483	6	В	rs377214516,C_to_T,LINC01128,homozygous,upstream						
SO:0001483	7	В	rs540936498,C_to_T,LINC00115,homozygous,exon						

## **Ontology Formulation**



</ValueMetadata>







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P	Navigate Terms       Find         Biobank Consent Information       Biobank Demographics (*)         Biobank Genomics (*)       Biobank Genomics (*)         Biobank Genomics (*)       Biobank Health Information         Biobank Sample Types (*)       Biobank Sample Types (*)         Curated Disease Population       Healthcare Data (*)         Healthy Populations (Control       Biobank Genomics (*)	Ank Portal Genomic Pill  Search by Gene Use the gene name box below, a selecti Gene Name*: Please note the zyg a particular variant ( Zygosity*: Consequence:	ot [Logout]  Cuery Tool  a box to specify the variant for which to se on list will appear after you type the first of APOA1BP  osity options in the dropdown box. See th homozygous for the reference/reference Heterozygous (reference/alternate alle Please make a selection  [Select all] [All protein-altering [Frameshift [Missense ]Nonsense ]Start loss	e <u>wiki</u> on h allele).	Overview	<pre>     Find Patients      yping in the search      for patients without      OK Cancel </pre>	Make R	roup 3 curs > 0; denthy ~	Performance		E
					l	OK Cancel					



## Query Formulation in SQL

#### dbSNP rs identifier

select count(distinct patient\_num)
from observation\_fact
where contains(observation\_blob, 'FAM148 AND (stop\_loss OR
missense)')

#### **Gene Name**

select count(distinct patient\_num)
from observation\_fact
where contains(observation\_blob, 'rs183605470 AND
heterozygous')

## Times to complete queries

