



BioHackathon 2016

Core Meeting Jun 22 2016

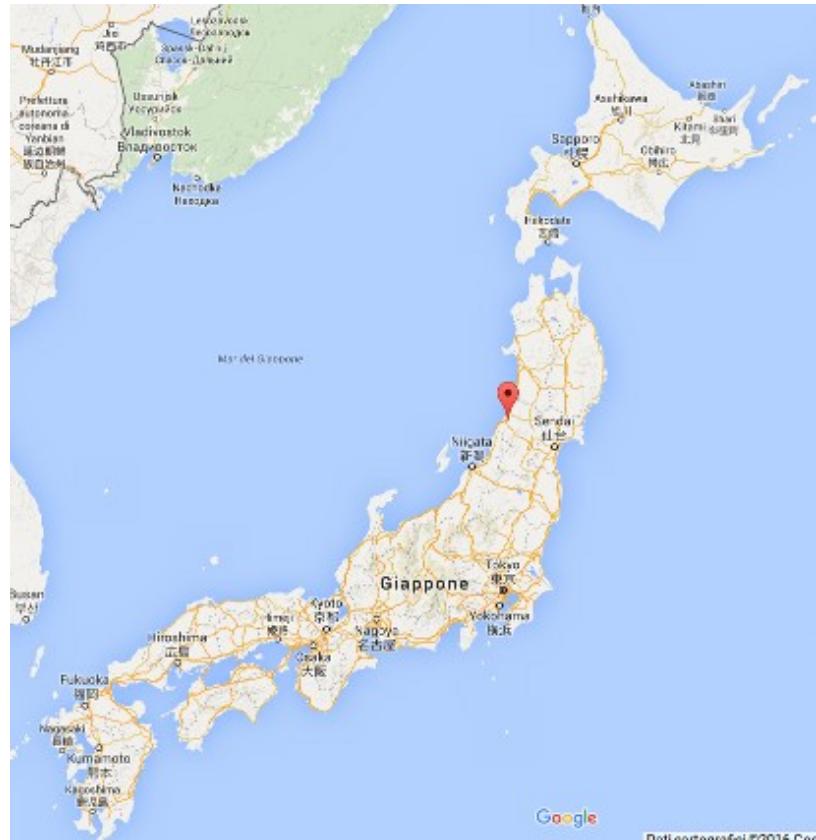


EMBL – European Bioinformatics Institute
Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SD, UK



Where

- **Tsuruoka,**
Yamagata
Prefecture Japan
- Semi-rural area
- Local food
specialties (sea
food, vegetables)
- 18 sake varieties!





Arrival and stay at Hotel Tatsunoyu





あけび花の展











大人用大浴場
大人用大浴場
大人用大浴場
大人用大浴場





おしながき

海中産ナイヤガラワイーン
金前酒

前菜

白の盛り合わせ

刺身三重盛り合わせ

だ追り

漁ざ

むきそば

海月 妻少々

台の物

タジン蒸し

牡蠣の

バジルベースト焼き

白身魚のすり身豆腐

豚の物

庄内鶏産 もずく酢

揚げ物

蟹しんじょう

金子

バジルベースト焼き

白身魚のすり身豆腐

豚の物

庄内鶏産 もずく酢

揚げ物

蟹しんじょう

金子

バジルベースト焼き

白身魚のすり身豆腐

豚の物

庄内鶏産 もずく酢

揚げ物

蟹しんじょう

鰯の味噌漬
龍の湯
調理部一回







吹き

食事

揚げ

酢の

蓋の

味







Day 1

- Symposium at Metabolome Campus,
Institute of Advanced Biosciences, Keio
University
 - Oldest university of Japan
 - Metabolomics and data driven systems
biology



Metabolomics Center

- Biormakers from CE-MS:
 - major depression
 - various types of cancer (saliva tests)
- Stool analyses from gut environment information
- Synthetic spider silk production
- Several spin-offs

Talks

- Present EpiRR

EpiRR datasets

Project	Type	Status	ID	Local name	Description
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00000940.1	roadmap-epigenomics:E071	REMC Epigenome (Class 2) for Brain Hippocampus Middle using donors/samples:149;150
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00000949.1	roadmap-epigenomics:E085	REMC Epigenome (Class 2) for Fetal Intestine Small using donors/samples:H-24595; H-23769
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00000957.1	roadmap-epigenomics:E095	REMC Epigenome (Class 2) for Left Ventricle using donors/samples:STL001;STL003
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00000983.1	roadmap-epigenomics:E109	REMC Epigenome (Class 2) for Small Intestine using donors/samples:STL001; STL003
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00000987.1	roadmap-epigenomics:E084	REMC Epigenome (Class 2) for Fetal Intestine Large using donors/samples:H-24595; H-23769
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00001027.1	roadmap-epigenomics:E100	REMC Epigenome (Class 2) for Psoas Muscle using donors/samples:STL001; STL003
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00001035.1	roadmap-epigenomics:E087	REMC Epigenome (Class 4) for Pancreatic Islets using donors/samples:pancreatic_islets_normal_0/0/00; pancreatic_islets_normal_3/27/09; ZD4_273
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00001039.1	roadmap-epigenomics:E011	REMC Epigenome (Class 2) for hESC Derived CD184+ Endoderm Cultured Cells using donors/samples:262;263
NIH Roadmap Epigenomics	Composite	Complete	IHECRE00001044.1	roadmap-epigenomics:E050	REMC Epigenome (Class 2) for Primary Hematopoietic Stem Cells G-CSF-mobilized Female using donors/samples:RO_01480; RO_01508; RO_01536;
CEEHRC (CEMT)	Pooled samples	Complete	IHECRE00000223.1	CEMT0038	Primary Cell from Normal Mammary gland-Breast from donor ID: CEMT_35-38_pool (pooled sample from multiple donors) (age Mixed, Female, cell type: gland-Breast with disease_status: NA) from Aparicio/Eaves Lab
CEEHRC (CEMT)	Pooled samples	Complete	IHECRE00000228.1	CEMT0036	Primary Cell from Normal Mammary gland-Breast from donor ID: CEMT_35-38_pool (pooled sample from multiple donors) (age Mixed, Female, cell type: gland-Breast with disease_status: NA) from Aparicio/Eaves Lab
CEEHRC (CEMT)	Pooled samples	Complete	IHECRE00000231.1	CEMT0037	Primary Cell from Normal Mammary gland-Breast from donor ID: CEMT_35-38_pool (pooled sample from multiple donors) (age Mixed, Female, cell type: Mammary gland-Breast with disease_status: NA) from Aparicio/Eaves Lab

IHECRE00000940.1

Type	Composite
Status	Complete
Project	NIH Roadmap Epigenomics
Local name	roadmap-epigenomics:E071
Description	REMC Epigenome (Class 2) for Brain Hippocampus Middle using donors/samples:149;150
Is live version?	yes

Metadata

biomaterial_type	Primary Tissue
tissue_type	Hippocampus Middle
taxon_id	9606
species	Homo sapiens
donor_ethnicity	NA
collection_method	Post-Mortem
donor_sex	Male
tissue_depot	Brain
sample common name	Brain, Hippocampus Middle
biomaterial_provider	Rush University Medical Center

Raw data

Assay type	Experiment type	Archive	Primary ID	Secondary ID	Link
ChIP-Seq	Histone H3K9me3	GEO	GSM916034		View in archive
ChIP-Seq	Histone H3K9me3	GEO	GSM773017		View in archive
ChIP-Seq	Histone H3K27ac	GEO	GSM773020		View in archive
ChIP-Seq	ChIP-Seq Input	GEO	GSM773019		View in archive
ChIP-Seq	Histone H3K27me3	GEO	GSM1112800		View in archive
ChIP-Seq	Histone H3K4me3	GEO	GSM773022		View in archive
ChIP-Seq	Histone H3K27ac	GEO	GSM916035		View in archive
ChIP-Seq	Histone H3K4me3	GEO	GSM916040		View in archive

Notes

- Talks with Eric Deutsche about track hubs
 - Develop and maintain Peptide Atlas, ProteomeXchange consortium
 - Not really into track hub technology, UCSC has proteomics tracks based on their data which UCSC has created on their behalf
- Michel Durmontier, Stanford University
 - Open API: standardise REST API descriptions
 - vendor neutral description based on Swagger
 - allows humans/computer to discover service w/o access to documentation/source code
- Meet Prof. Yutaka Suzuki, leaves that day

Stay at Hotel Tachibanaya











マッサージ MASSAGE

お早目にフロント(8番)へお申し込み下さい。

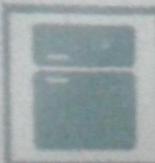
Please call the front desk (dial 8) as early as
possible.



タクシー TAXI

お早目にフロント(8番)へお申し込み下さい。

Please call the front desk (dial 8) as early as
possible.



冷蔵庫 REFRIGERATOR

お部屋の冷蔵庫は品物を出します
に料金がフロントにて明示され
なっております。どうぞご利用下さい。
エックアウトの際フロントでご精算下さい。
If you take out an article from a refrigerator
of your room, the front desk indicates a
charge. Please use it.



お会計 CHECK

お会計はチェックアウトの際、フロントにて
ご精算下さい。

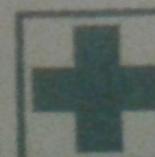
Please SETTLE the accounts at the front
desk.



芸妓・コンパニオン GEISHA GIRL

お早目にフロント(8番)へお申し込み下さい。

Please call the front desk (dial 8) as early as
possible.



病気 ILLNESS

気分が悪くなったり、病気の発作が起こりました
したら亟急フロント(8番)にご連絡下さい。

Please call the front desk (dial 8) if you get
ill, and you feel queer.

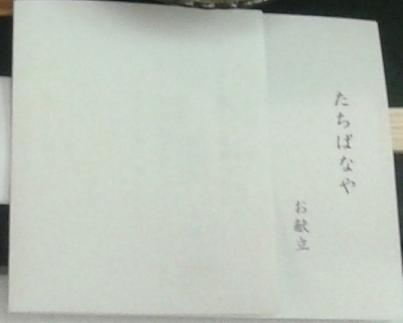
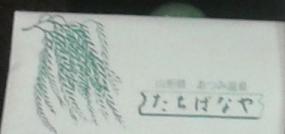
歡迎 BioHackathon 2016 様





F





たちばなや

お献立

食前酒 出羽の雪
前菜 鶏とキヤベツの
ミルフィーユ仕立て

お造り 鮮魚盛り合せ

焼き物 銀鮨たまり焼 奉書包

小鉢 庄内浜産黒バイ貝旨煮

お凌ぎ むきそば

煮物 海老真丈庄内麩巻

蒸し物 海風茶碗蒸し

鍋物 山形牛のすきやき

お食事 庄内産はえぬき

昆布炊きごはん

留椀 あさり汁

香の物 たまり漬

デザート テイラミスと苺

平成二十八年六月吉日

たちばなや

調理長

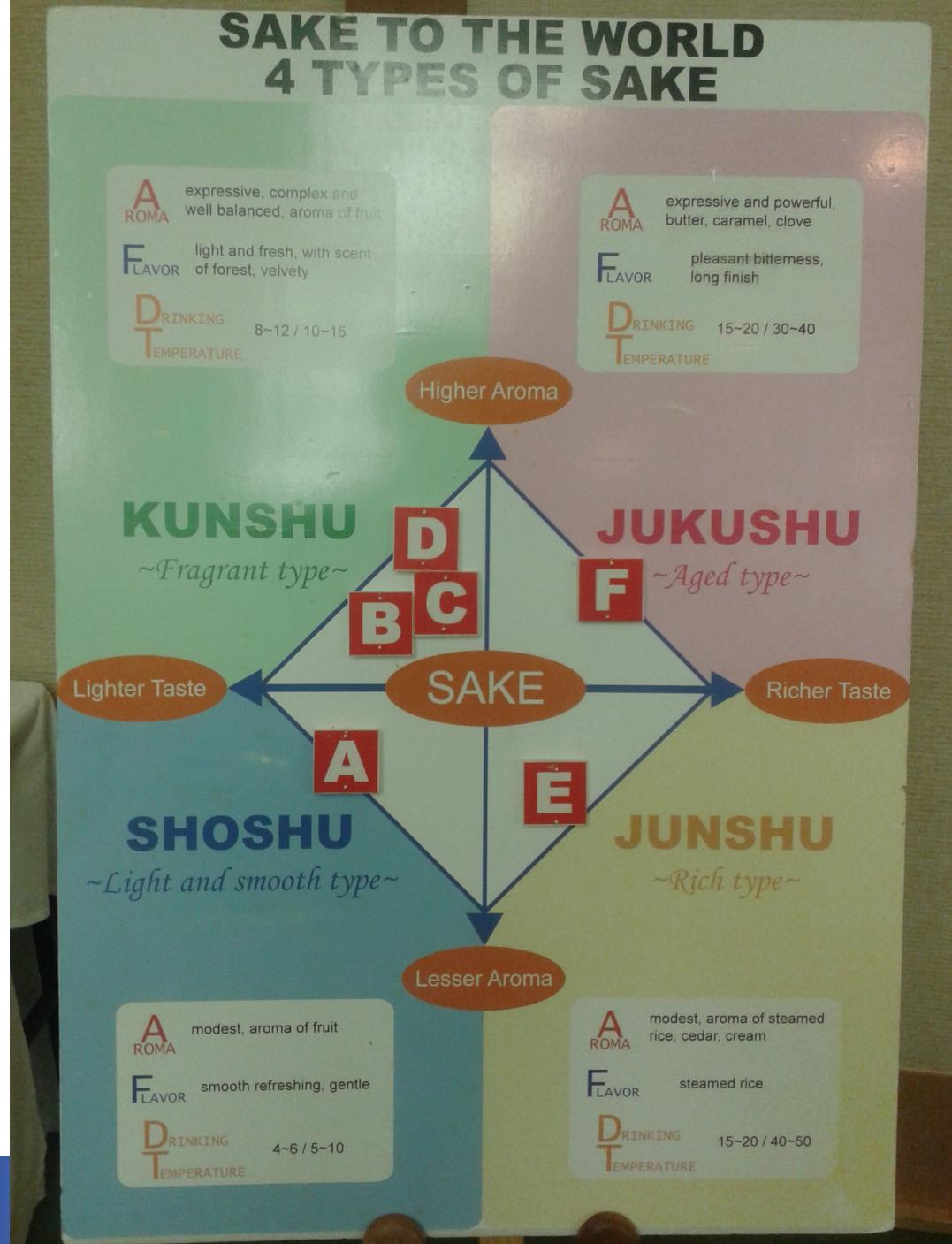
斎藤



早めにご飯をご希望の方は
係にお申し付け下さい。

SAKE TO THE WORLD

4 TYPES OF SAKE



Day 2

- Hackathon begins
- First working groups are formed
 - 100 people editing the same google doc proposing specific topics

https://docs.google.com/document/d/1_hwd9gxUgg14hY_LDyLjhauA_vMKPZOO429EjJ3tkV8/edit

Topics

- Software
- RDF/LOD
- Ontology
- **Genomics (incl.
transcriptomics/epigenomics)**
- Machine Learning, text/data mining

Genomics Work Group

- iHEC
 - chair: Shin Kawano (DBCLS), on behalf of Prof. Suzuki
 - Goal: DBTSS-iHEC integration?
 - Interested: me, Lillian Ashmore (Baylor College of Medicine)
 - Initial meeting:
 - poor communication (Shin)
 - vague references to his work (DBTSS RDF)
 - failed to understand objectives

ChIP Atlas

- Integrative DB for visualizing/use public ChIP-seq data
- Covers public ChIP-seq data submitted to SRA (ENA,NCBI,DDBJ)
- 30000 experiments

<http://chip-atlas.org>

- Prototype available at dropbox URL
- Could not talk, all interested people involved in other groups

ChIP-Atlas - Peak Browser

[Tutorial movies ▾](#)

Visualize All Peaks from Published ChIP-Seq data.

[H. sapiens](#)[M. musculus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

Antigen Class

[All antigens \(16138\)](#)

DNase-seq (1024)

Histone (3824)

RNA polymerase (629)

TFs and others (5088)

Input control (1956)

Unclassified (596)

No description (3021)

Cell type Class

[All cell types \(16138\)](#)

Adipocyte (120)

Blood (4559)

Bone (200)

Breast (1712)

Cardiovascular (498)

Digestive tract (1205)

Epidermis (431)

Threshold for Significance

50

100

200

500

[Antigen](#)[Cell type](#)[View on IGV](#)[Download BED file](#)







Evening

- Meet Hideya Kawaji, RIKEN University (FANTOM5)
 - produce track hubs for the project
 - shown him the registry, very interested!
 - leaves in the morning, but decided to work together
- Alcohol!



Day 3

- Data sharing with track hubs work group formed
- Kawaji (email)
 - wants to register FANTOM5 hub
 - interesting Idea: **embed biodalliance into registry view**
- Debugged FANTOM5 submission
 - fails, hub is not standard compliant
 - Kawaji to take action
- Raoul Bonnal (Istituto Nazionale Genetica Molecolare)
 - RNA-seq data from immune system studies, ChIP-seq data soon
 - very interested in registry, idea exchange

Day 3

- Discussion with Lillian on DBTSS-iHEC integration
 - no support from Kawano (engaged in other projects)
 - hold on until we get a clearer picture as to what their objectives are
 - helped installing/debugging virtuoso
- Email Suzuki asking clarifications

DBTSS-iHEC

- Plan is to make iHEC data searchable (via RDF) from DBTSS
- DBTSS has been made RDF compatible
 - TSS → RDF available
 - working on ChIP-seq conversion
- Ask if iHEC contemplates to do the same
- JSON search is made for some metadata in the iHEC data portal
 - plan to expand to cover data contents?
- Emailed Laura et al.
 - replied cannot help, forwarded to David Bujold (McGill, iHEC data portal)

Day 4

- Intermediate wrap-up meeting (morning)
 - report on track hub registry/iHEC work
- Work with Kawano-san on iHEC
 - adapting BS2RDF DBTSS tool (Ruby) for iHEC (sample BS-seq data from Blueprint)
- Excursion to Mt. Haguro shrine (afternoon)



羽黒山
内所

三十三間堂

内所















最島神社 (SHIMONOSHIMA)
最島町 (SHIMONOSHIMA-CHO)
奈良県 (NARA-PREFECTURE)
日本 (Japan)
The Three Islands of Shima (最島、大島、中島)
The Three Islands of Shima (最島、大島、中島)
The Three Islands of Shima (最島、大島、中島)

錢
寶







供奉申込所

土砂崩れ
通行注意

羽黒山古事修驗道行者

秋奉右五度位
新闇澤秀峯師留魂碑

出羽三山神社奉中大光達宮司高橋追書

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Day 5

- IHEC work group
 - Bed2RDF exporter too slow
 - only convert region searched?
 - batch download and farm processing
 - SPARQL-bed: query against simple bed files without loading them into a triple store
 - could not install, MAVEN broken project
 - Loaded sample RDF, run trivial sample queries
 - Use case? e.g. methylation state of enhancer/promoter regions associated to a gene
 - need to devise a data model supporting these kind of queries
 - Feedback from David Bujold (McGill)
 - No plan to distribute JSON for data content (makes sense)

#trackhub

[View in the archives](#)



Kawaji Hideya 11:32 AM, Jun 16th

I had a look at yesterday's intermediate reports, and glad to see @tazro succeeded basic test of trackHub

And it is wonderful to have @avullo , the developer of trackHub registry. When I talked this registry to my colleague, he got excited!!!

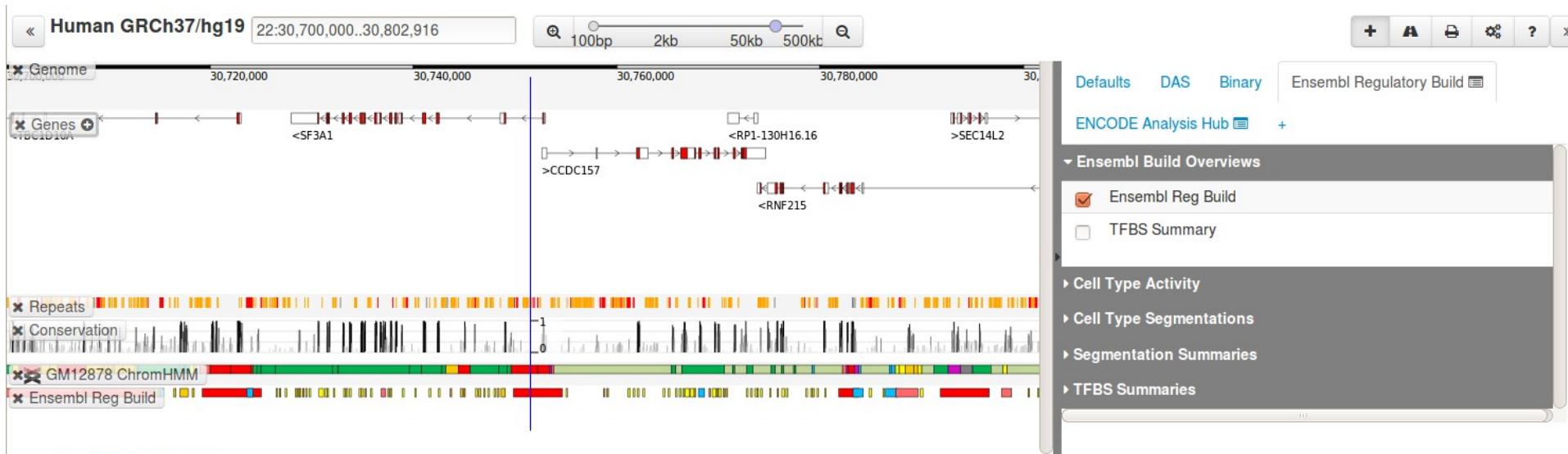
I am willing to help both of these activities.

I am also very pleased to announce that we started to host the official mirror of the UCSC Genome Browser in Japan. This should help to populate efficient sharing of genomic data via trackHub.

Day 5

- Work with Kawaji-san
 - registry website feedback (user perspective)
 - wrong links, misleading descriptions
 - glimpsing into Biodalliance
 - rudimentary support for track hubs (CORS)

```
hubs: ['http://www.biodalliance.org/datasets/testhub/hub.txt',
       'http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/hub.txt']
```



Brainstorming

- Simon, Raoul, Tazro Ohta (DBCLS)
- Registry provides valuable experimental data to biologists
- Pb: link registry content with other relevant resources, e.g. gene expression atlas

Idea

- Markup track hub with ontology terms
 - Zooma <http://www.ebi.ac.uk/spot/zooma/>
 - re-annotate track JSON with terms found
- Generate track hub RDF
 - develop JSON-LD context
- EBI RDF platform to federate query and provide information based on other resources
- Enrich registry search interface and API

Mapping Text to Ontology

ZOOMA

This is ZOOMA, an environment for discovering optimal ontology annotations based on real, manually reviewed data.

Use the box below to find possible ontology mappings for free text terms in the ZOOMA repository of curated annotation knowledge. You can add one term (e.g. 'Homo sapien') for your term (e.g. 'organism'), put this after the term, separated by a : (e.g. 'organism:Homo sapien').

What's this? *	Show me some examples... *
<input type="checkbox"/> organizing microtubule cytoskeleton <input type="checkbox"/> cytoskeleton <input type="checkbox"/> SAM <input type="checkbox"/> issue_type <input type="checkbox"/> seed <input type="checkbox"/> issue_type <input type="checkbox"/> Seed <input type="checkbox"/> issue_type <input type="checkbox"/> seed1 <input type="checkbox"/> issue_type <input type="checkbox"/> seed2 <input type="checkbox"/> issue_type <input type="checkbox"/> Seed3 <input type="checkbox"/> issue_type <input type="checkbox"/> Seed4 <input type="checkbox"/> issue_type <input type="checkbox"/> Seed5 <input type="checkbox"/> issue_type <input type="checkbox"/> seed coat <input type="checkbox"/> issue_type <input type="checkbox"/> Seed coat (100-200mg seed weight stage) <input type="checkbox"/> issue_type <input type="checkbox"/> Seed coat (400-500mg seed weight stage) <input type="checkbox"/> issue_type <input type="checkbox"/> Seed coat (50-100mg seed weight stage) <input type="checkbox"/> issue_type	Show me some examples...
<input type="checkbox"/> iso <input type="checkbox"/> cspo <input type="checkbox"/> to <input type="checkbox"/> elio <input type="checkbox"/> clsa <input checked="" type="checkbox"/> symBio <input type="checkbox"/> clsa	
Preferred datasource ranking: Unranked Datasources: <input type="checkbox"/> Ego <input type="checkbox"/> cspo <input type="checkbox"/> TGO <input type="checkbox"/> GO <input type="checkbox"/> TO	
Ranked Datasource: <input type="checkbox"/> GO <input type="checkbox"/> cspo <input type="checkbox"/> TGO <input type="checkbox"/> GO <input type="checkbox"/> TO	

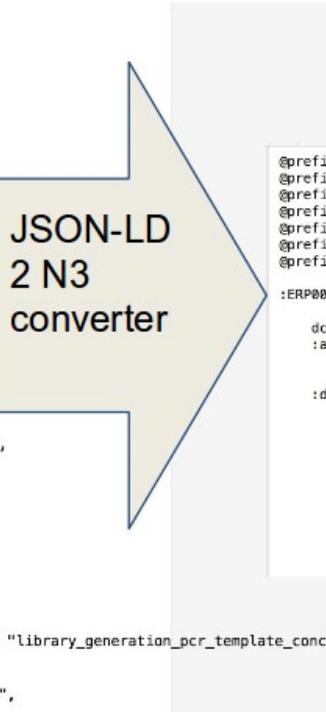
Annotations

Searches MUST include the following datasources (all searched if none selected):

cell_type	CDB Name	T cell	Good	CL_0000024	ExpressionAtlas
CEU_TYPE	erythroblast	erythroblast	High	CL_000755	ExpressionAtlas
cell_type	Fibroblast	Fibroblast	High	CL_0000037	ExpressionAtlas
cell_type	Flower bud	flower bud	Good	FO_0002056	ExpressionAtlas
				CL_0019289	ExpressionAtlas
cell_type	Hematopoietic	hematopoietic stem cell	Medium	CL_0000037	ExpressionAtlas
				EFO_0006798	ExpressionAtlas
cell_type	HN (ES H9 derived Neurons)	hahnus	Good	FO_0005958	ExpressionAtlas
cell_type	T cell	Islet of Langhans	Good	UMLS01_0030016	ExpressionAtlas
cell_type	Keratinocyte	keratinocyte	High	CL_0002012	ExpressionAtlas
cell_type	Leaf mesophyll	leaf mesophyll	High	FO_0005645	ExpressionAtlas
CELL_TYPE	macrophage	macrophage	High	CL_0002125	ExpressionAtlas
cell_type	Mammary epithelial cells	mammary epithelial cell	High	CL_0002327	ExpressionAtlas
cell_type	Melanocyte	melanocyte	High	CL_000148	ExpressionAtlas
				CL_000924	ExpressionAtlas
cell_type	Memory CD4	Memory CD4	Medium	CL_000905	ExpressionAtlas
				CL_0000031	ExpressionAtlas
T cell			Medium	CL_0000031	ExpressionAtlas
cell_type	mesophyll	mesophyll	Medium	FO_0005645	ExpressionAtlas
cell_type	monocyte	monocyte	High	CL_000576	ExpressionAtlas
cell_type	Mononuclear Cell	mononuclear cell	High	CL_0000612	ExpressionAtlas
				Orphanet_120107	Orphanet
				FO_0000100	ExpressionAtlas
cell_type			Medium	FO_0005052	ExpressionAtlas
cell_type	MT+	MT+	Medium	CL_0000024	ExpressionAtlas
cell_type	Mt-0	Mt-0	Medium	CL_0000024	ExpressionAtlas

Adding JSON-LD Context

```
{
  "@context": {
    "@vocab": "http://rdf.ebi.ac.uk/terms/trackhub/",
    "schema": "http://schema.org/",
    "type": {
      "@id": "http://www.w3.org/1999/02/22-rdf-syntax-ns#type",
      "@type": "@vocab"
    },
    "id": {
      "@type": "@vocab"
    },
    "tax_id": {
      "@type": "@vocab"
    },
    "ontology_term": {
      "@id": "http://www.w3.org/2000/01/rdf-schema#seeAlso",
      "@type": "@vocab"
    },
    "created": "http://purl.org/dc/terms/created"
  },
  "@id": "http://rdf.ebi.ac.uk/terms/trackhub/VizHub",
  "@type": "@vocab",
  "assembly": {
    "accession": "GCA_000001405.1",
    "long_name": "Genome Reference Consortium Human Build 37 (GRCh37)",
    "name": "GRCh37",
    "synonyms": "hg19"
  },
  "created": 1463561835,
  "data": [
    {
      "&gt;99%": "extraction_protocol",
      "15": "extraction_protocol_type_of_sonicator",
      "180-350": "bisulfite_conversion_percent",
      "25UM": "dna_preparation_fragment_size_range",
      "5' AATGATACGGCGACCAACCGAGATCTACACTTTCCCTACACGACGCTTCCGATCT": "library_generation_pcr_template_conc",
      "90-250": "experiment_type",
      "98.83": "GSM",
      "DNA Methylation": "library_generation_pcr_thermocycling_program",
      "GSM670059": "dateUnrestricted"
    }
  ]
}
```



```
@prefix : <http://rdf.ebi.ac.uk/terms/trackhub/> .
@prefix dcterms: <http://purl.org/dc/terms/> .
@prefix rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#> .
@prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> .
@prefix schema: <http://schema.org/> .
@prefix xml: <http://www.w3.org/XML/1998/namespace> .
@prefix xsd: <http://www.w3.org/2001/XMLSchema#> .

:ERP004388 a <http://rdf.ebi.ac.uk/terms/trackhub@vocab>,
  :scriptomatics ;
  dcterms:created 1463157536 ;
  :assembly [ :accession "GCA_000001735.1" ;
    :name "TAIR10" ;
    :synonyms "TAIR10" ] ;
  :data [ :id :ERR377676 ;
    :name "Illumina HiSeq 2500 sequencing" ; <a href='http://www.ebi.ac.uk/ena/data/view/ERR377676'>ERR377676</a> ;
    :accession "SAMEA2266655" ;
    :biosample_id "SAMEA2266655" ;
    :cell_type "all" ;
    :center_name "University of Cambridge Department of Plant Sciences" ;
    :checklist "ERC000011" ;
    :description "Arabidopsis whole leaf transcriptome replicate 3" ;
    :dev_stage "mature" ;
    :ecotype "columbia" ;
    :environmental_sample "N" ;
    :library_name "data" ;
    :library_type "DNA" ;
    :platform "Illumina HiSeq 2500" ;
    :sample_size "100" ;
    :sequencing_center "University of Cambridge Department of Plant Sciences" ;
    :sequencing_instrument "Illumina HiSeq 2500" ;
    :sequencing_technique "Illumina HiSeq 2500" ;
    :sequencing_type "Illumina HiSeq 2500" ;
    :species "Arabidopsis thaliana" ;
    :study_accession "GSE670059" ;
    :study_title "Arabidopsis whole leaf transcriptome replicate 3" ;
    :target_species "Arabidopsis thaliana" ;
    :tissue "leaf" ;
    :value "100" ] .
```

SPARQL over Track Hub

- Loaded “enriched” track hub + ontologies into RDF4J
- Example: *get tracks where metadata annotated with haemopoietic system (efo:EFO_0000798)*

SPARQL over Track Hub

```
SPARQL
1 PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
2 PREFIX efo: <http://www.ebi.ac.uk/efo/>
3 prefix trackhub:<http://rdf.ebi.ac.uk/terms/trackhub/>
4
5 # Get tracks where metadata annotated with haemopoietic system (efo:EFO_0000798)
6
7 SELECT ?s ?id ?name WHERE {
8   ?s trackhub:data ?data .
9   ?data trackhub:id ?id .
10  ?data trackhub:name ?name .
11  ?data rdfs:seeAlso ?o .
12  ?o rdfs:subClassOf* efo:EFO_0000798 .
13 }
```

SPARQL over Track Hub

S	Id	Name
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35894:rpkm_pos>	"A35894:CEMTo032:Hematopoietic:mRNA:rpkm_pos:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34725:sig>	"A34725:CEMTo032:Hematopoietic:H3K27ac:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a49963:rpkm_neg>	"A49963:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:mRNA:rpkm_neg:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35995:peak>	"A35995:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K36me3:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35995:sig>	"A35995:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K36me3:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35992:peak>	"A35992:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K4me3:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34722:sig>	"A34722:CEMTo032:Hematopoietic:H3K9me3:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34720:sig>	"A34720:CEMTo032:Hematopoietic:H3K4me1:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35993:peak>	"A35993:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K9me3:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34726:sig>	"A34726:CEMTo032:Hematopoietic:Input:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35996:peak>	"A35996:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K27ac:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<m13589:rpmmm>	"m13589:CEMTo032:Hematopoietic:smRNA:rpmmm:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34042:frc_mth>	"A34042:CEMTo032:Hematopoietic:WGBS:frc_mth:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34725:peak>	"A34725:CEMTo032:Hematopoietic:H3K27ac:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<m13589:isofrm>	"m13589:CEMTo032:Hematopoietic:smRNA:isofrm:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35993:sig>	"A35993:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K9me3:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34726:peak>	"A34726:CEMTo032:Hematopoietic:Input:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35997:sig>	"A35997:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:Input:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35991:sig>	"A35991:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K4me1:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35994:peak>	"A35994:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K27me3:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a34723:peak>	"A34723:CEMTo032:Hematopoietic:H3K27me3:peak:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35994:sig>	"A35994:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K27me3:sig:CEMT"
<http://rdf.ebi.ac.uk/terms/trackhub/EDCC_BCGSC>	<a35992:sig>	"A35992:CEMTo031:Hematopoietic:Blood-Peripheral_Leukemia - Chronic_Myeloid:H3K4me3:sig:CEMT"

ChIP-Atlas track hub

- Discussion with Tazro Ohta
- Developed prototype hub for all ChIP-seq data
 - works with UCSC browser
 - not strictly standard compliant, Ensembl would complain
- Want to extend with metadata (iHEC standards)
- Submit as it is then update

Day 6

- Final Wrap up
 - TrackHub Registry work
 - Interlinking trackhub via ontology mappings
 - IHEC
- Panel discussion
- Liquorthon!

歡迎 BioHackathon 2016 様

全国豊かな海づくり大会

Day 7

- Writeathon (Metabolome Campus, morning)
 - participant contribute to sections of BH16 paper
 - initial skeleton about TrackHubRDF work
- Cherry-picking! (afternoon)







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One night in Tsuruoka and leave



メダル

消火器
FIRE EXTINGUISHER

namco

非常口



Tokyo International Airport



Lessons learned

No matter what, keep on bowing