

Collaboration of ELIXIR and Japan BioHackathons

Toshiaki Katayama

- Database Center for Life Science

Project links

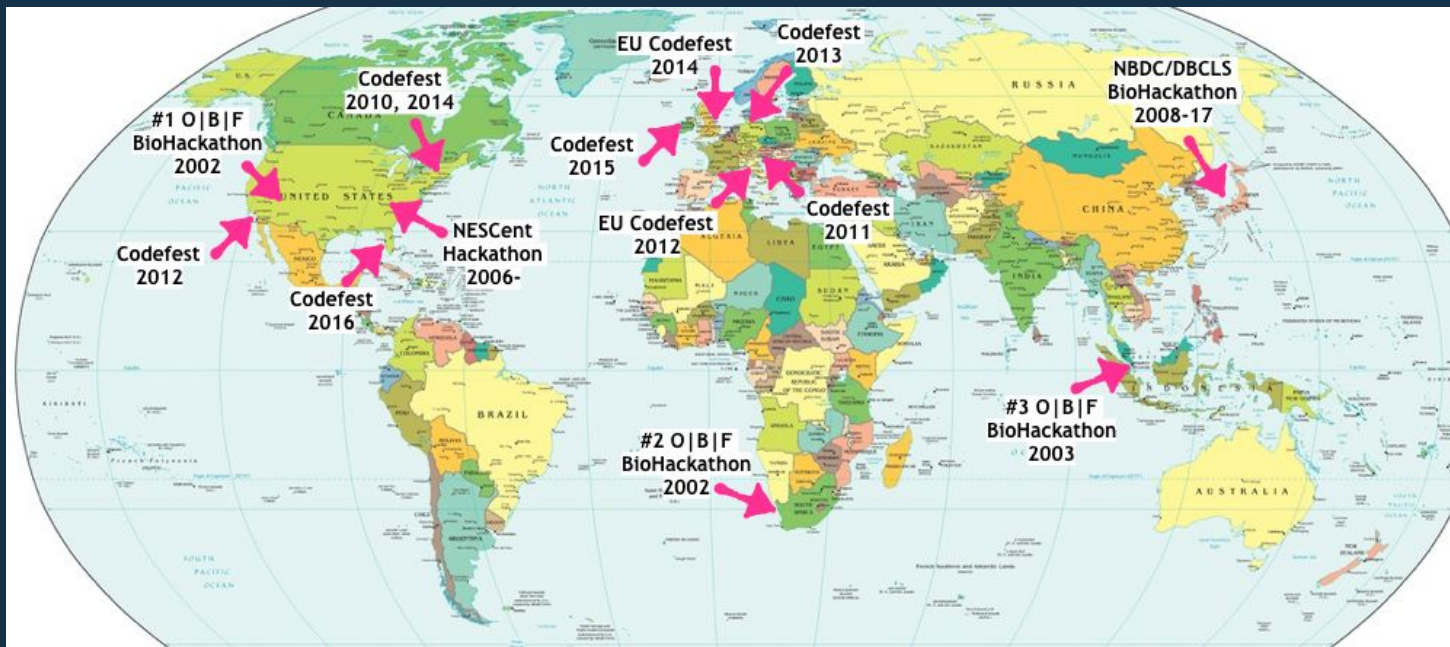
- <http://biohackathon.org/>
- <http://github.com/dbcls/bh18/>

Background information

How we get started the BioHackathon?

- BioHackathon was originally introduced by the O|B|F in 2002

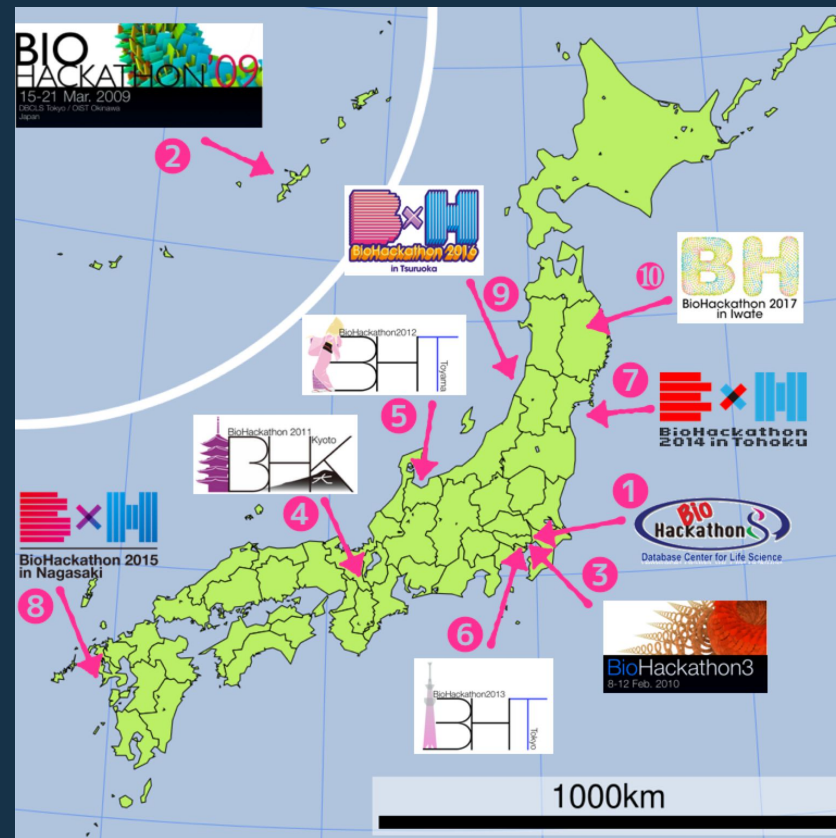
- BioPerl
- BioRuby
- Biopython
- BioJava
- :



- Interoperability of Open Bio* libraries for accessing DBs

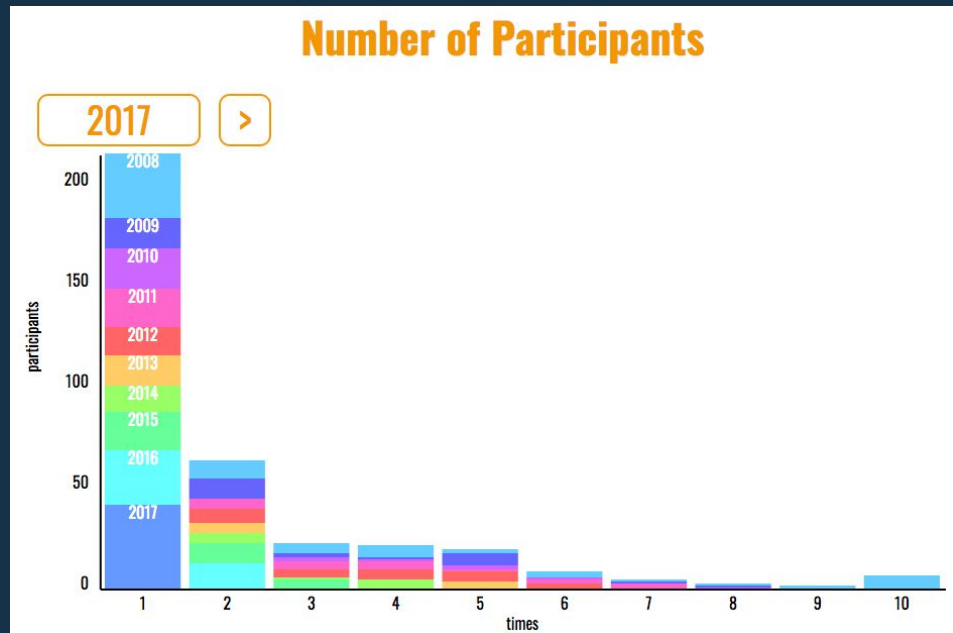
History of the NBDC/DBCLS BioHackathon

- BioHackathon 2008-2010
 - Integration of distributed bioinformatics resources with Web Services
- BioHackathon 2011-2017
 - Integration of distributed bioinformatics database contents with Semantic Web
- As we were not secured to organize the next BioHackathon after 10th, I explored possibility to organize it with ELIXIR (especially with Rafael Jimenez, thanks!)
 - → This ELIXIR BioHackathon 2018
 - + NBDC/DBCLS BioHackathon 2018



The 11th NBDC/DBCLS BioHackathon

- NBDC/DBCLS BioHackathon 2018
 - Application of integrated semantic resources including (but not limited to)
 - 1. Biomedical
 - 2. Useful substance production
 - 3. Breeding
- Register today (already over due!)
 - December 9-15 in Matsue, Japan
 - <http://2018.biohackathon.org/registration>
 - We'll welcome Matz (the Ruby's father)



Each year, we had 68 (2008) ~ 108 (2017) participants, in total, 803 participants (371 uniq) from 21 countries.

<http://biohackathon.org/10years/>

Hack organisation

Organisation of the NBDC/DBCLS BioHackathon

- Attendees
 - Call for proposals to be nominated as an invitee
 - 20~30 foreign experts and invitees + 50~80 Japanese domestic researchers (incl. organizers)
 - Can form working groups and switch to other group freely
- Schedule
 - Sunday: Public symposium
 - Monday-Friday: Hackathon
 - Monday morning: Open space discussion to define objectives and working groups
 - Wednesday: Mid-term wrap up (Excursion sometimes)
 - Friday afternoon: Wrap up
 - Saturday: Writethon
- Venue
 - 1Gb (x2 for backup) fibre optical Internet connection
 - (24hrs open) hacking room + accommodation
 - Isolated place hopefully equipped with Onsen (hot spring) and Karaoke
 - Fine food and Sake (Liquorthon at night)

Powered by
BioHackathon



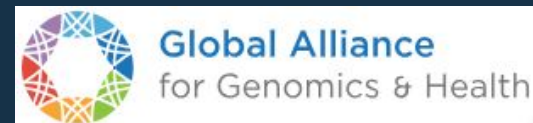
Previous publications

1. Katayama, T., Arakawa, K., Nakao, M., et al. (2010) **The DBCLS BioHackathon**: standardization and interoperability for bioinformatics web services and workflows., J. Biomed. Semantics, 1, 8.
2. Katayama, T., Wilkinson, M. D., Vos, R., et al. (2011) **The 2nd DBCLS BioHackathon**: interoperable bioinformatics Web services for integrated applications., J. Biomed. Semantics, 2, 4.
3. Katayama, T., Wilkinson, M. D., Micklem, G., et al. (2013) **The 3rd DBCLS BioHackathon**: improving life science data integration with semantic Web technologies., J. Biomed. Semantics, 4, 6.
4. Bolleman, J. T., Mungall, C. J., Strozzi, F., et al. (2016) **FALDO**: a semantic standard for describing the location of nucleotide and protein feature annotation., J. Biomed. Semantics, 7, 39.
5. Katayama, T., Wilkinson, M. D., Aoki-Kinoshita, K. F., et al. (2014) **BioHackathon series in 2011 and 2012**: penetration of ontology and linked data in life science domains., J. Biomed. Semantics, 5, 5.
6. Wimalaratne, S. M., Bolleman, J., Juty, N., et al. (2015) SPARQL-enabled identifier conversion with **Identifiers.org**., Bioinformatics, 31, 1875–7.
7. Wilkinson, M. D., Dumontier, M., Aalbersberg, Ij. J., et al. (2016) **The FAIR Guiding Principles** for scientific data management and stewardship, Sci. Data, 3, 160018.
8. ...
9. BioHackathon 2013-2014 (submitted)
10. BioHackathon 2015 (revise submitted)
11. BioHackathon 2016 (in preparation)
12. BioHackathon 2017 (in preparation)



Future works

- Continuous community efforts on standardization and interoperability of databases in life sciences
 - Genomics and Multi-omics
 - Biomedical applications
 - Bioinformatics algorithms and analysis
 - Reproducible science and workflows
- Collaboration with biomedical domains
 - GA4GH (Global Alliance for Genomics and Health)
 - Bring algorithms to data: WES, CWL, ...
 - Sharing and standard models for genotypes and variations
 - Graph genome: vg
 - AMED (Japan agency for medical research and development)
 - Japanese gnomAD and ClinVar: TogoVar, MGeND
 - and ELIXIR, of course!

















Some photos from BioHackathon 2017
















Standardization matters

- NIH strategic plan for data science
 - <https://datascience.nih.gov/strategicplanrelease>
 - According to a 2016 survey, data scientists across a wide array of fields said they spend most of their work time (about 80 percent) doing what they least like to do: collecting existing datasets and organizing data. That leaves less than 20 percent of their time for creative tasks like mining data for patterns that lead to new research discoveries.
- Imagine if
 - Data you need is already stored in an uniformed format
 - All these heterogeneous data are interconnected with globally unique identifiers
 - And semantically annotated!
 - Linked Open Data (see UniProt as one of successful examples)
 - You can just start data science and develop applications

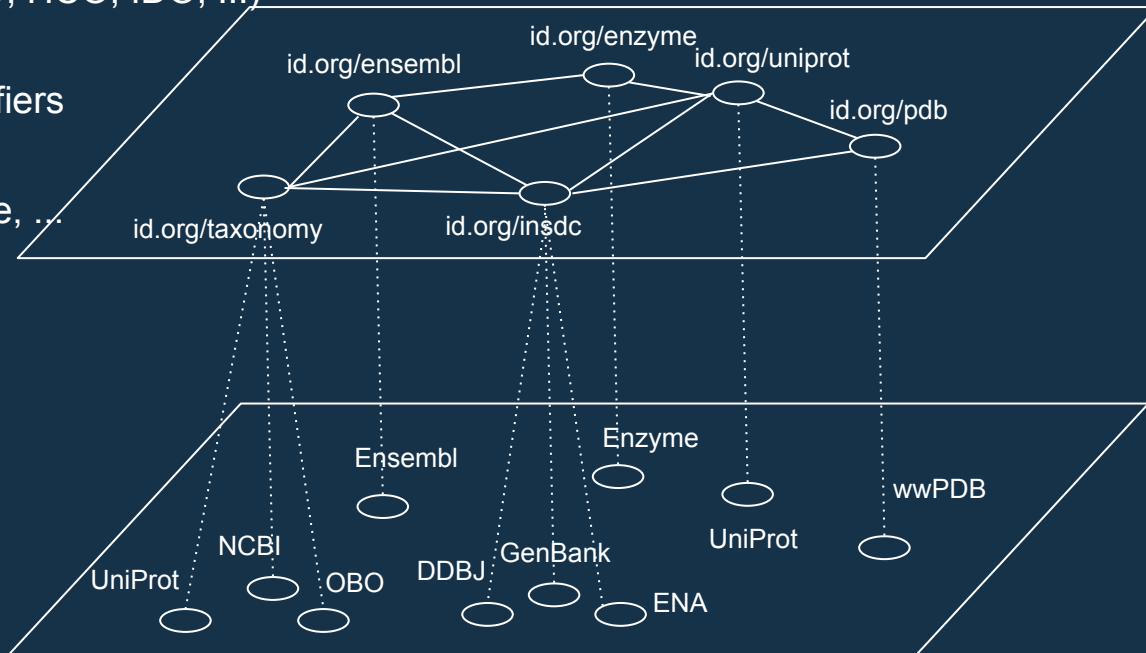
RDF resources currently available

- Nucleotide seq & annot
 - INSDC (DDBJ/DBCLS) 
- Genome
 - Ensembl (EBI) 
 - RefSeq (TogoGenome) 
- Protein seq & annot
 - UniProt (SIB) 
- Protein structure
 - PDB (PDBj) 
 - BMRB (PDBj) 
 - FAMSBASE (Chuo U) 
- Compounds
 - PubChem (NCBI) 
 - ChEMBL (EBI) 
 - NIKKaji (JST) 
- Gene expression
 - RefEx (DBCLS) 
 - ExpressionAtlas (EBI) 
- Samples
 - BioSamples (EBI/DDBJ) 
 - JCM (RIKEN) 

- Biomedical (Med2RDF)
 - ICGC, COSMIC, CIViC 
 - DGIdb, OpenTG-Gates 
 - ClinVar, dbSNP, dbVar 
 - ExAC, gnomAD 
 - HiNT, INstruct 
- Glycome
 - GlyTouCan, GlycoEpitope, WURCS, GGDonto, PAConto 
- Proteome
 - jPOST 
 - The Human Protein Atlas 
- Pathway
 - Reactome (EBI) 
- Others
 - MeSH (NCBI) 
 - BioModels (EBI) 
 - MBGD (NIBB/DBCLS) 
 - Quanto (DBCLS) 
 - :

Standardization requires community effort

- Data models
 - Organism - Genome - Gene - Variation - Phenotype - Disease - Drug - Multi-omics - ...
- Ontology
 - BioPortal and others (incl. FALDO, HCO, IDO, ...)
- Identifiers
 - Identifiers.org and compact identifiers
- Metrics
 - FAIR, YummyData, RDF guideline, ...
- Workflows
 - WES, CWL, Galaxy, ...
- Reusable Web Components
 - BioJS, TogoStanza, ...



Thank you and join us!

- Organizing a hackathon is a demanding task but should be fruitful for the future
 - Many thanks and congratulations to the ELIXIR BioHackathon organizers especially to Rafa, Dana, Layla and local organizers
 - Let's get started and have fun!
- And hopefully see you next month at the NBDC/DBCLS BioHackathon 2018
 - Register NOW! <http://2018.biohackathon.org/>



P.S. Liquorthon at night

We brought some fine Japanese Sake & Whisky. Hope you enjoy :)

