

SSBD: a database of quantitative data and microscopy images of biological dynamics

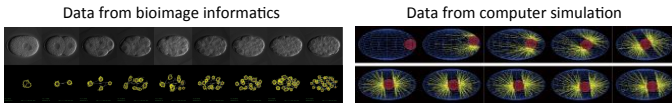
<http://ssbd.qbic.riken.jp/>

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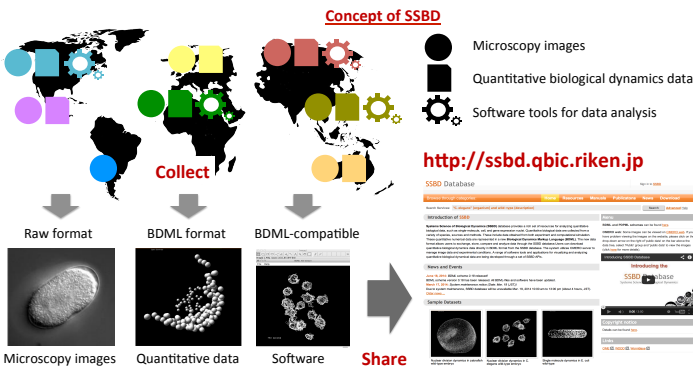
Motivation

Recent progress in bioimage informatics and mathematical modeling produced a large amount of quantitative data on spatiotemporal dynamics of various kinds of biological objects.

Example of quantitative biological dynamics data

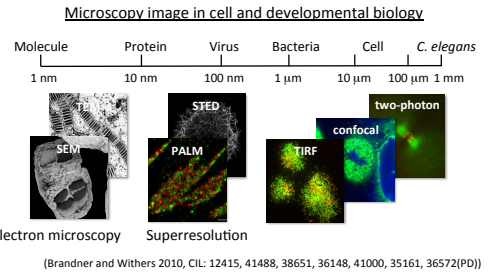


There is a need to bring these data centrally in an open and unified data format. We developed **BDML (Biological Dynamics Markup Language; Kyoda et al., Bioinformatics, 2015)** and **SSBD (Systems Science of Biological Dynamics database)**, with the support from National Bioscience Database Center of Japan. SSBD collects and shares quantitative data and microscopy images. It also includes software tools for visualization and analysis.



SSBD 2.0: collect/share microscopy images

Microscopy images are managed by using OMERO platform internally in SSBD. SSBD2.0 begins to store and share microscopy images that have not been image processed. We focus on, but not limited to, time-lapse image data that are obtained by using state-of-the-arts imaging systems. These images provide vital biological resources and allow others to reuse and to extract interesting features.



We develop SSBD to provide

- an invaluable resource for phenotype data-driven analysis, and
- a novel opportunity to develop new computational methods.

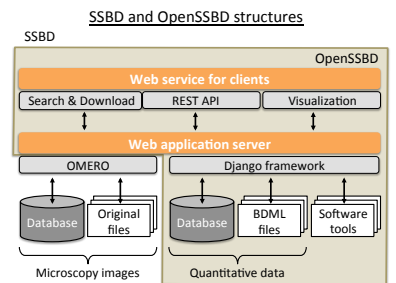
OpenSSBD: Open-source software platform

We provide OpenSSBD, open-source version of SSBD for managing quantitative data, in GitHub and Docker websites. It enables each individual scientist or research group to set up their own database on their own server to independently store and share their quantitative data.

<https://github.com/openssbd/>

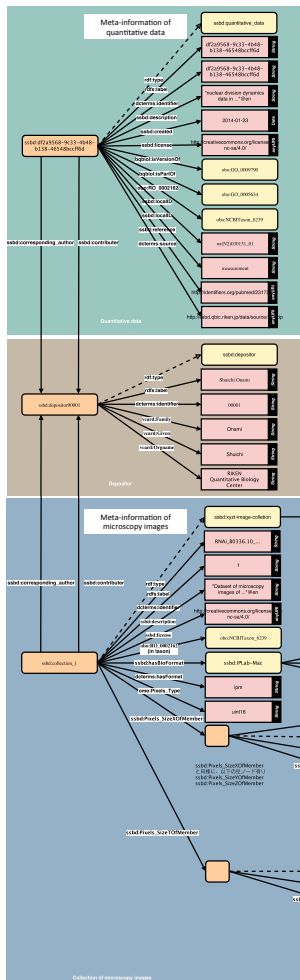
OpenSSBD includes all the essential functions of SSBD, e.g., a simple keyword search function, REST API direct access to quantitative data, and a simple browser-based viewer for data visualization. Users will need to install OMERO separately.

Examples of visualization of quantitative data



RDF formatted metadata

We provide RDF (Resource Description Framework) formatted metadata of quantitative data and microscopy images stored in SSBD.



<http://metadb.riken.jp/db/SSBD>
<http://integbio.jp/rdf/>

List of namespaces

Namespaces

rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
rdfs: <http://www.w3.org/2000/01/rdf-schema#>
owl: <http://www.w3.org/2002/07/owl#>
xsd: <http://www.w3.org/2001/XMLSchema#>
dc: <http://purl.org/dc/elements/1.1/>
foaf: <http://purl.org/foaf/terms/>
foaf: <http://xmlns.com/foaf/0.1/>
vcard: <http://www.w3.org/2006/vcard/ns#>
mia-ent: <http://www.w3.org/ns/mia-ent#>
biolink: <http://biomodels.net/biology-qualifiers/>
sio: <http://semanticscience.org/resource/>
dcterms: <http://purl.org/dc/terms/>
obo: <http://purl.obolibrary.org/obo/>
ome: <https://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2015-01/ome_xsd.html#>
ssbd: <http://metadb.riken.jp/db/SSBD/>

Examples of SPARQL query

```
PREFIX ssbd: <http://metadb.riken.jp/db/SSBD/>
PREFIX obo: <http://purl.obolibrary.org/obo/>
PREFIX biolink: <http://biomodels.net/biology-qualifiers/>

# Searching for resources related with mouse
SELECT ? rdesc FROM <http://metadb.riken.jp/db/SSBD/> WHERE {
  ? rdesc obo:RO_0002162 obo:NCBITaxon_10090 . # mouse
  ? rdesc ssbd:description ?desc .
}

# Searching for experimental resources related with pronuclear migration in C. elegans
SELECT ? rdesc FROM <http://metadb.riken.jp/db/SSBD/> WHERE {
  ? rdesc obo:RO_0002162 obo:NCBITaxon_6239 . # C. elegans
  ? biolink:isVersionOf obo:GO_0035046 . # pronuclear migration
  ? rdesc basedOn ?text FILTER Regexp(?text, "measurement", "I")
  ? rdesc ssbd:description ?desc .
}
```

Data resource update

SSBD stores quantitative data and microscopy images ranging from molecules to cells to organisms.

List of available data resources in SSBD

Species	Type	BasedOn	Reference	#BDML	#entries	#images
<i>E. coli</i>	single molecule	Simulation	Arjunan & Tomita 2010	1	721	0
<i>D. discoideum</i>	single molecule	Experiment	Komatsuzaki et al. 2014	1	987	1,800
<i>D. discoideum</i>	single molecule	Experiment/Simulation	Watabe et al. 2015	0	0	20
<i>C. elegans</i>	nucleus	Experiment	Bao et al. 2006	2	24,747	0
<i>C. elegans</i>	nucleus	Experiment	Kyoda et al. 2013	186	75,955	180x66x186
<i>C. elegans</i>	nucleus	Experiment	Toyoshima et al.	14	125,426	14
<i>C. elegans</i>	pronucleus/nucleus	Experiment	Tohsato et al.	1,582	2,430,536	4,512
<i>C. elegans</i>	nucleus	Experiment	Kyoda et al.	1,147		360x66x1147
<i>C. elegans</i>	pronucleus/microtubule	Simulation	Kimura & Onami 2005	100	2,400,100	0
<i>C. elegans</i>	locomotion	Experiment	Cronin et al. 2005	11	15,822	0
<i>D. melanogaster</i>	nucleus	Experiment	Keller et al. 2010	2	5,111,828	0
<i>D. rerio</i>	nucleus	Experiment	Keller et al. 2008	7	56,584,840	0
<i>R. norvegicus</i>	single molecule	Experiment/Simulation	Watabe et al. 2015	0	0	75
<i>M. musculus</i>	nucleus	Experiment	Bashar et al. 2012	1	2,054	2,800
<i>M. musculus</i>	gene expression	Experiment	Harima et al. 2013	2	146	2
<i>M. musculus</i>	gene expression	Experiment	Masumoto et al. 2010	8	48	0

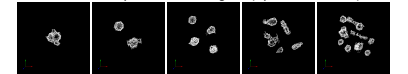
■ new data, □ currently available, ▣ planned release

Examples of quantitative data and their visualization

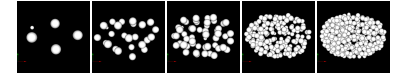
Single molecule dynamics in *E. coli* (Arjunan & Tomita 2010)



Nuclear division dynamics in *C. elegans* (Kyoda et al. 2013)



Nuclear division dynamics in *C. elegans* (Bao et al. 2006)



Nuclear division dynamics in *D. melanogaster* (Keller et al. 2010)



Ref.: Koji Kyoda, Yukako Tohsato, Kenneth H. L. Ho, Shuichi Onami (2015) Biological Dynamics Markup Language (BDML): an open format for representing quantitative biological dynamics data. *Bioinformatics* 31(7): 1044-1052.