

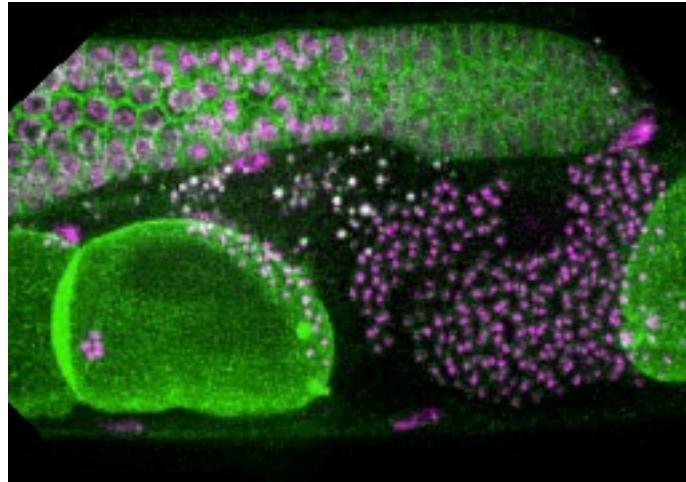
イメージングデータベースに 画像を登録し、画像を活用する

糸賀 裕弥¹⁾、京田 耕司¹⁾、大浪 修一^{1,2)}

- 1) 理化学研究所生命機能科学研究センター
- 2) 理化学研究所情報統合本部



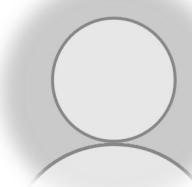
生命科学におけるイメージングの意義



細胞内外の構造や生命分子の空間分布、そしてそれらの動態を詳細に
ありのままにとらえること

||

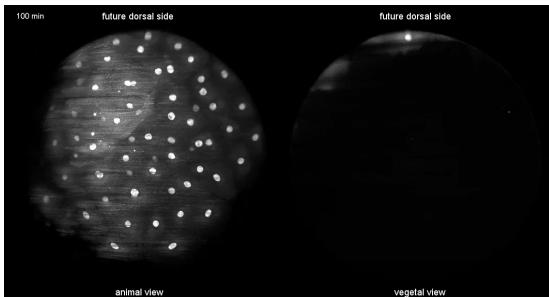
生命現象の背景にあるメカニズムを理解するために最も重要な研究手
法のひとつ



バイオイメージングの近年の状況

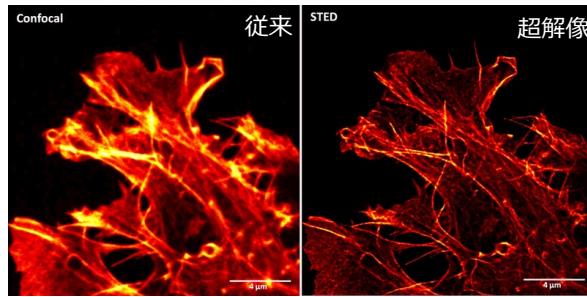
近年の生命科学分野では、最先端のイメージング技術の開発が加速している

光シート顕微鏡



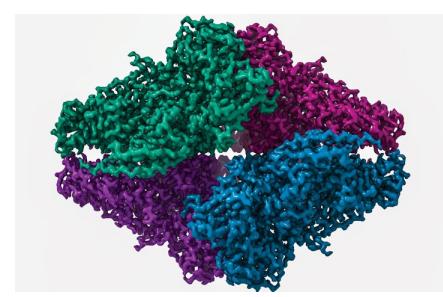
Keller et al., Science, 2008

超解像度顕微鏡



Nobel prize 2014
Betzig, Hell, Moerner

クライオ電子顕微鏡



Sarkans et al., Nat Methods, 2021

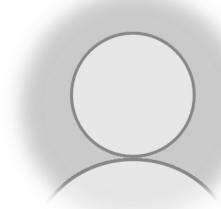
Nobel prize 2017
Dubochet, Henderson, Frank



従来の技術では観ることができなかった細胞内外の構造や生命分子の空間分布、あるいはそれらの挙動の科学的な観察や計測が可能になる



最先端のイメージング技術が研究の競争力を決定づける



バイオイメージングの近年の問題

- 最先端のイメージング装置は、高度な技術と知識を持つイメージング分野の研究者により手作りで開発される。
 - 高度な技術と知識を持つイメージング研究者は生命科学者全体の人口に比べて極めて少数
- 市販品は極めて高額



大多数の生命科学者は最先端イメージング技術を自らの研究に活用できていない

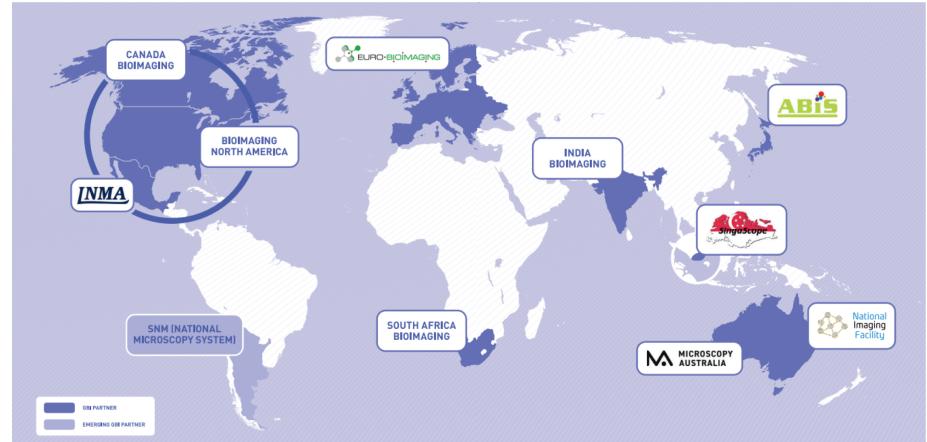


【解決策】

- 最先端のイメージング技術のオープンアクセス化
- 最先端のイメージングデータのオープンアクセス化



- 生命科学の最先端イメージング技術とデータのオープンアクセスに関する諸問題を解決する国際連携組織
- 欧州のEuro-BioImagingが全世界のコミュニティに声をかけてボトムアップ的に組織化
- 2015年に欧州の国際共同研究資金(Horizon 2020)の支援で設立
- 2020年よりChan Zuckerberg Initiativeにより助成を受ける



<https://www.globalbioimaging.org>

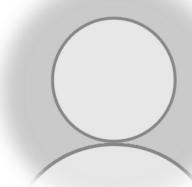
主な活動

- 国際的なリーダーからバイオイメージング施設の運営や研究政策、技術トレンドを学ぶ**年1回の国際ワークショップ (Exchange of Experience)** の開催
- 特定のテーマに関する議論や国際的な協力関係を構築するための**テーマを絞った会議や作業部会**の開催
- バイオイメージング施設の管理職や技術職のスタッフの専門的な能力開発を支援する**研修**の開催
- バイオイメージング施設のスタッフが、海外の先進的な施設から学ぶことを可能にする**スタッフ シャドーイング** プログラムの実施



Advanced Bioimaging Support

先端バイオイメージング支援プラットフォーム



支援内容について



総括支援活動 GENERAL SUPPORT

4つの支援活動の運営と、各支援活動間における緊密な連携を図るための活動を行います。ホームページなどを利用した情報発信、及び情報の共有化を図り、本プラットフォームの周知を行います。また、技術講習会やワークショップ、シンポジウムを開催して、イメージング技術の普及と先端イメージング技術の情報の共有化を図っています。他の支援プラットフォームと連携して、分野融合と国際連携も行ってまいります。

[View details »](#)

ABiS支援の概要を動画で紹介しています→ ([Youtube/2分](#))



光学顕微鏡支援 LIGHT MICROSCOPY

分子や細胞、組織の時空間的な動態を高速、かつ高分解能で捉るために、先端光学顕微鏡を用いた観察や、特殊観察技術に加えて、適切なプローブの選択・適用や、植物・海洋生物など特殊な試料調製、観察環境を要する対象について観察を支援いたします。

[View details »](#)



電子顕微鏡支援 ELECTRON MICROSCOPY

先端電子顕微鏡による生体高分子複合体の立体構造観察、組織・細胞の三次元微細構造の観察、蛍光顕微鏡観察と同一の視野の微細構造観察等を支援するとともに、必要な試料調製から観察までの技術指導を行います。

[View details »](#)



MRI支援 MR IMAGING

生体の構造と機能を、MRIを用いて可視化し定量解析する技術を標準化して提供することにより、脳画像等の研究を手がけている研究を支援するとともに、個々の研究への最適化を支援いたします。

[View details »](#)



画像解析支援 IMAGE ANALYSIS

光学顕微鏡、電子顕微鏡、磁気共鳴装置などによって取得された画像から形態や動態に関する情報を抽出し、定量的分析、可視化する技術を利用者の目的や要望に応じて支援いたします。

[View details »](#)



トレーニング TRAINING

先端バイオイメージング支援プラットフォームでは、最先端技術や特殊観察技術を必要とする課題に対する各支援活動と、一般技術に対する技術トレーニングを実施します。

[View details »](#)

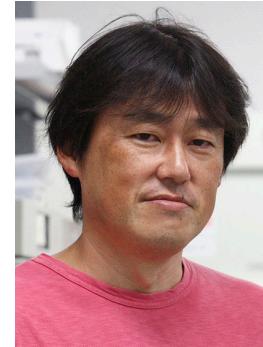
- 全国の研究者に先端バイオイメージングの技術の共用とデータ解析を支援する組織
- 2016年に文科省により生理学研究所・基礎生物学研究所を中核機関として設置
- バイオイメージングデータのオープンアクセスは含まれていない
- 日本では、生命科学データのオープンアクセスはNBDCが担当

- ABiS運営委員でもあり、NBDCでSSBDデータベースを運営する大浪がバイオイメージングデータの担当者としてGBIに参加
- 2022年度以降は、ABiSのデータ共有に大浪が関与する予定



イメージデータ作業部会

共同座長



Jason Swedlow
Univ. of Dundee
OME, IDR
-2021

Josh Moore
Univ. of Dundee
OME, IDR
2021-

Shuichi Onami
RIKEN BDR
SSBD

- 11カ国、17名の委員。南極を除くすべての大洲より委員が参加。
- バイオイメージデータのオープンサイエンスに関する諸問題について包括的に議論
 - データフォーマットの標準化
 - 國際的な公共データレポジトリの整備
 - 取得から公開までのデータの管理
 - データ解析情報の管理



Exchange of Experience IV @Singapore 2019

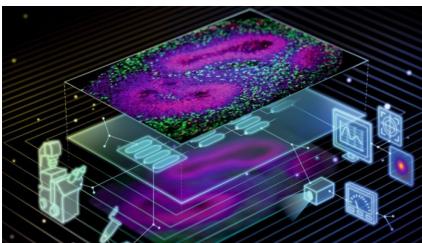


Exchange of Experience VI @Online 2021

FOCUS | 03 DECEMBER 2021

Reporting and reproducibility in microscopy

This Focus issue features a series of papers offering guidelines and tools for improving the tracking and reporting of microscopy metadata with an emphasis on reproducibility and data re-use.



Editorial and News

EDITORIAL
3 DEC 2021
Nature Methods

Minding microscopy metadata

Guidelines for improving reporting and reproducibility in microscopy take center stage in this month's Focus issue.

THIS MONTH
3 DEC 2021
Nature Methods

Caterina Strambio-De-Castillia

Sharing, teaching and singing to bring people together on microscopy standards.

Vivien Marx



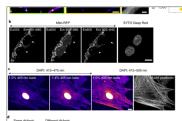
Perspective and Comment

PERSPECTIVE
7 JUN 2021
Nature Methods

Best practices and tools for reporting reproducible fluorescence microscopy methods

Comprehensive guidelines and resources to enable accurate reporting for the most common fluorescence light microscopy modalities are reported with the goal of improving microscopy reporting, rigor and reproducibility.

Paula Montero Llopis, Rebecca A. Senft ... Michelle S. Itano



COMMENT
21 MAY 2021
Nature Methods

REMBI: Recommended Metadata for Biological Images—enabling reuse of microscopy data in biology

Bioimaging data have significant potential for reuse, but unlocking this potential requires systematic archiving of data and metadata in public databases. We propose draft metadata guidelines to begin addressing the needs of diverse communities within light and... [show more](#)

Ugis Sarkans, Wah Chiu ... Alvis Brazma



COMMENT
21 MAY 2021
Nature Methods

QUAREP-LiMi: a community endeavor to advance quality assessment and reproducibility in light microscopy

The community-driven initiative Quality Assessment and Reproducibility for Instruments & Images in Light Microscopy (QUAREP-LiMi) wants to improve reproducibility for light microscopy image data through quality control (QC) management of instruments and images. It... [show more](#)

Ulrike Boehm, Glyn Nelson ... Roland Nitschke



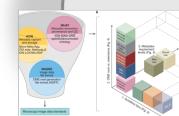
2022/2025

COMMENT
3 DEC 2021
Nature Methods

Towards community-driven metadata standards for light microscopy: tiered specifications extending the OME model

Rigorous record-keeping and quality control are required to ensure the quality, reproducibility and value of imaging data. The 4DN Initiative and BINA here propose light Microscopy Metadata Specifications that extend the OME Data Model, scale with experimental... [show more](#)

Mathias Hammer, Maximilian Huisman ... Caterina Strambio-De-Castillia



COMMENT
4 MAY 2021
Nature Methods

A global view of standards for open image data formats and repositories

Imaging technologies are used throughout the life and biomedical sciences to understand mechanisms in biology and diagnosis and therapy in animal and human medicine. We present criteria for globally applicable guidelines for open image data tools and resources for... [show more](#)

Jason R. Swedlow, Pasi Kankaanpää ... Shuichi Onami

Correspondence

CORRESPONDENCE
15 OCT 2021
Nature Methods

MethodsJ2: a software tool to capture metadata and generate comprehensive microscopy methods text

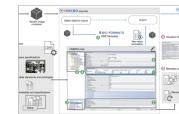
Joel Ryan, Thomas Pengo ... Claire M. Brown



CORRESPONDENCE
11 OCT 2021
Nature Methods

MDEmic: a metadata annotation tool to facilitate management of FAIR image data in the bioimaging community

Susanne Kunis, Sebastian Hänsch ... Stefanie Weidtkamp-Peters



Research Papers

BRIEF COMMUNICATION
OPEN ACCESS
3 DEC 2021
Nature Methods

Micro-Meta App: an interactive tool for collecting microscopy metadata based on community specifications

Micro-Meta App is an intuitive, highly interoperable, open-source software tool designed to facilitate the extraction and collection of relevant microscopy metadata as specified by recent community guidelines.

Alessandro Rigano, Shannon Ehmsen ... Caterina Strambio-De-Castillia

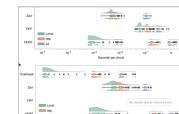


BRIEF COMMUNICATION
OPEN ACCESS
29 NOV 2021
Nature Methods

OME-NGFF: a next-generation file format for expanding bioimaging data-access strategies

OME's next-generation file format (OME-NGFF) provides a cloud-native complement to OME-TIFF and HDF5 for storing and accessing bioimaging data at scale and works toward the goal of findable, accessible, interoperable and reusable bioimaging data.

Josh Moore, Chris Allan ... Jason R. Swedlow



Comment | Published: 04 May 2021

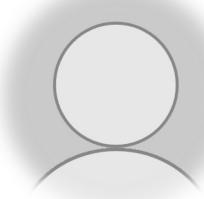
A global view of standards for open image data formats and repositories

Jason R. Swedlow , Pasi Kankaanpää, Ugis Sarkans, Wojtek Goscinski, Graham Galloway, Leonel Malacrida, Ryan P. Sullivan, Steffen Härtel, Claire M. Brown, Christopher Wood, Antje Keppler, Federica Paina, Ben Loos, Sara Zullino, Dario Livio Longo, Silvio Aime & Shuichi Onami 

Nature Methods (2021) | Cite this article

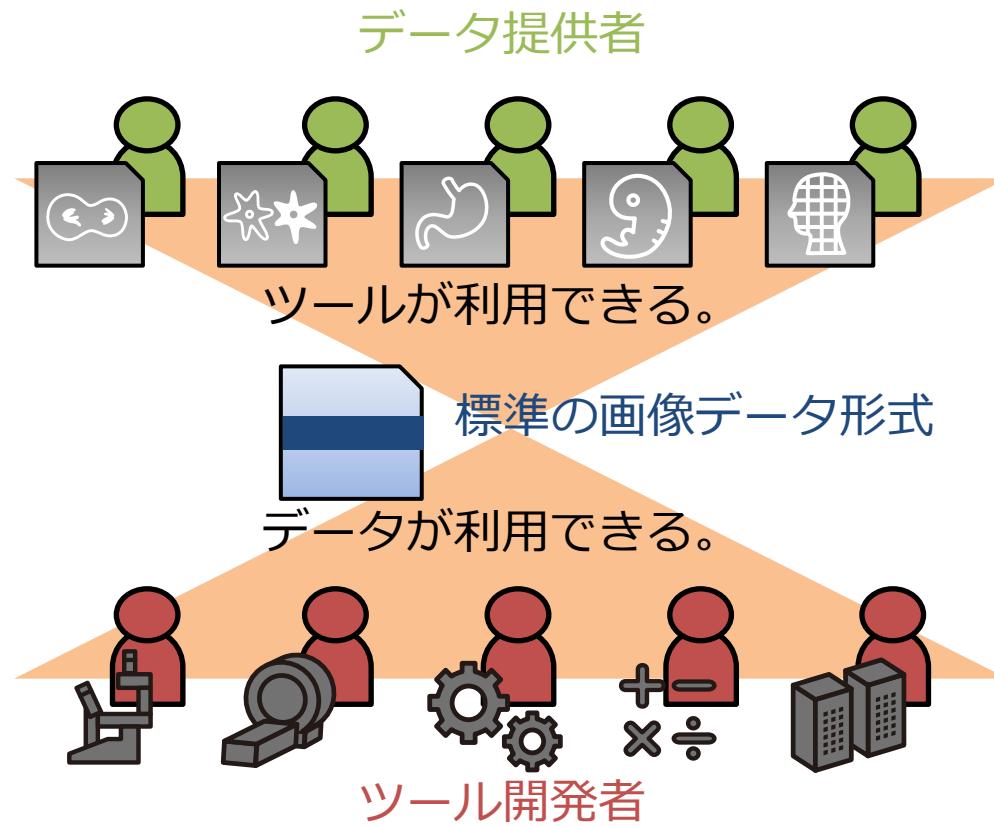
1954 Accesses | 1 Citations | 66 Altmetric | Metrics

Imaging technologies are used throughout the life and biomedical sciences to understand mechanisms in biology and diagnosis and therapy in animal and human medicine. We present criteria for globally applicable guidelines for open image data tools and resources for the rapidly developing fields of biological and biomedical imaging.



標準データ形式がなぜ必要なのか？

有用なツール開発を加速



標準データ形式がなぜ必要なのか？



バイオイメージングデータ解析のワークフローの変化

- バイオイメージングデータの利活用の多様化
- 個々の画像情報処理ツールの高性能化、専門化
 - 深層学習、セグメンテーション、物体追跡、可視化、ユーザーインターフェース
- 複数の会社/開発グループのツールをとり入れた作業が一般化
- 複数の会社/開発グループのツールを使う作業工程に適応したシステムに対する需要の増加

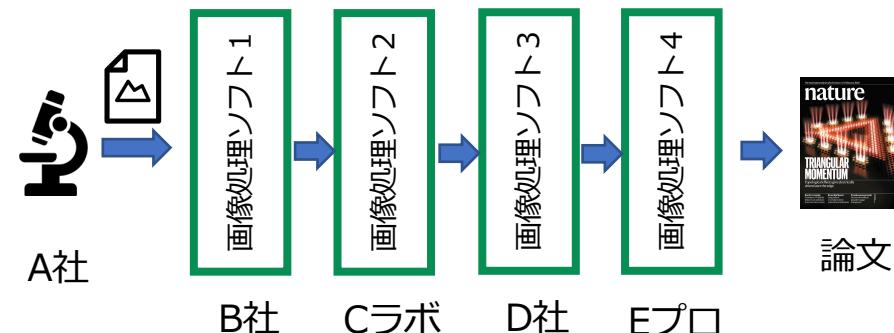


従来のワークフロー



各社は非公開の独自のデータ形式を使用

現在/これからのワークフロー

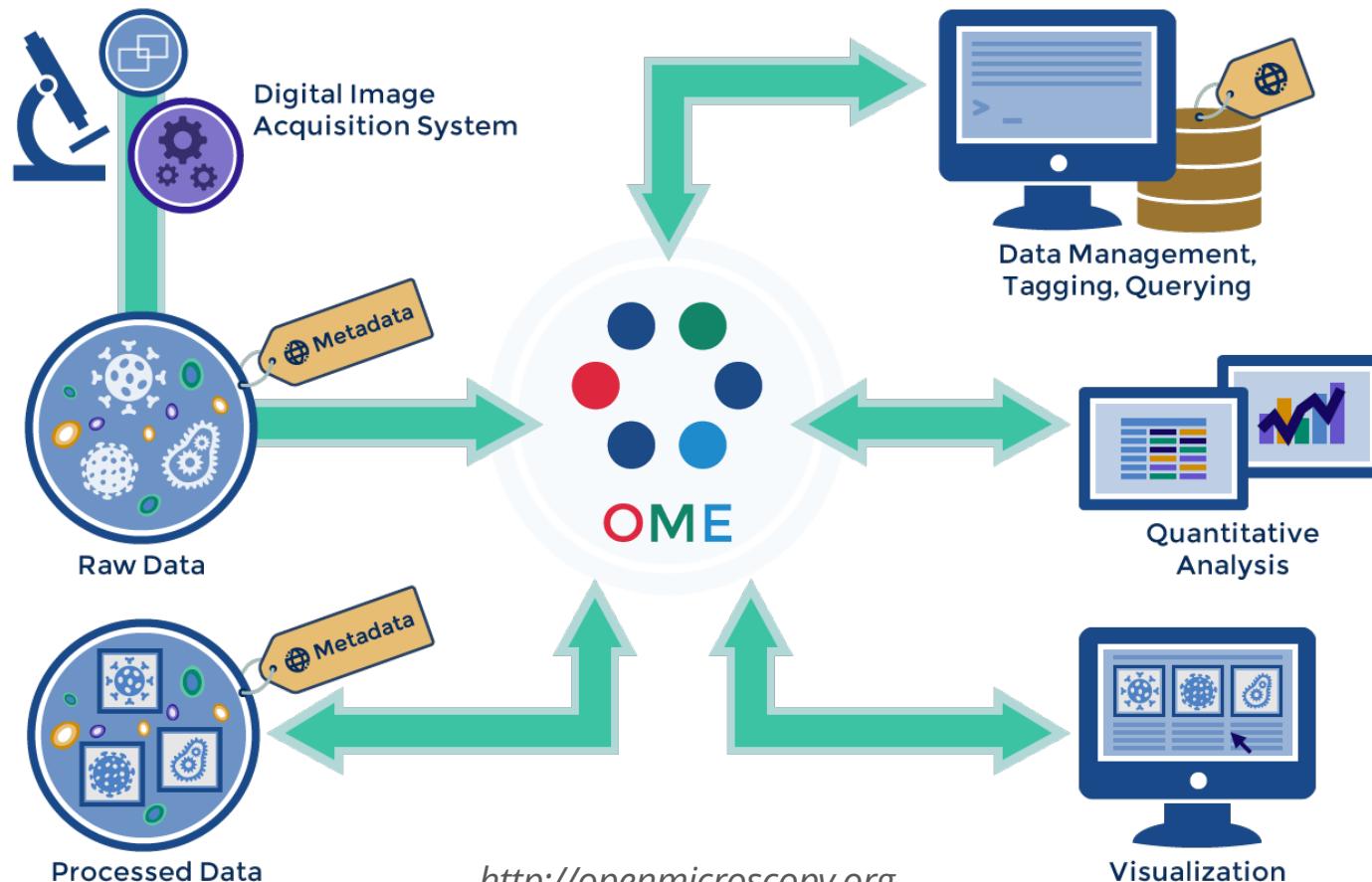


オープンな標準データ形式を使用

OMEROを介したバイオイメージングデータ解析のエコシステム

OMERO : 顕微鏡画像管理のフリー・プラットフォーム

- デファクトスタンダード
- テラバイト単位の画像、>135種類の画像フォーマットに対応

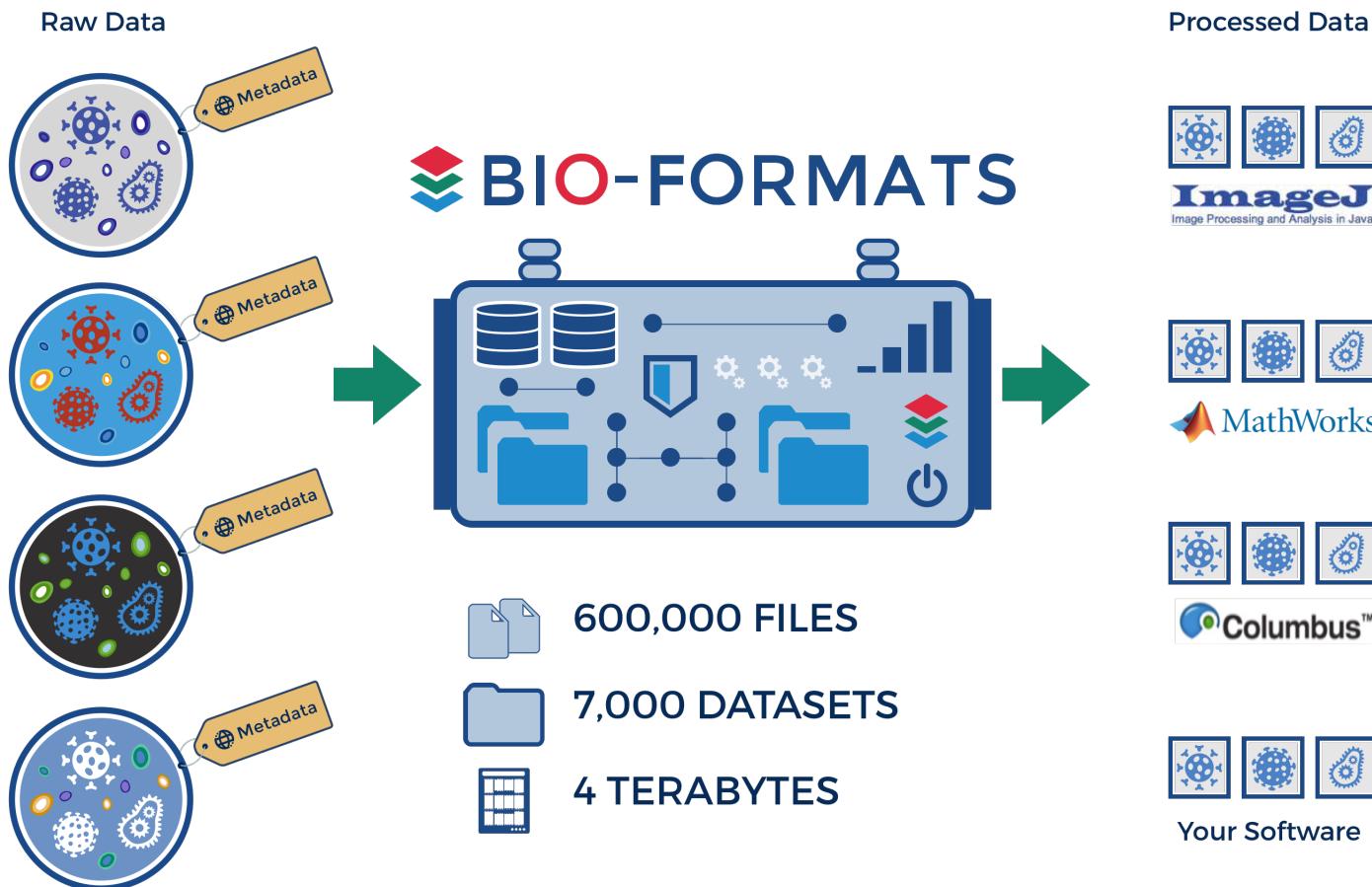




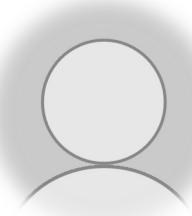
BIO-FORMATS:

各社のフォーマットをOME-TIFFに変換

- テラバイト単位の画像、>135種類の画像フォーマットに対応
- >135種類の画像フォーマットに対応



2022/8/25 Apps using Bio-Formats were started >100,000 times per day in 2015, 2016, 2017, 2018, & 2019



標準データ形式が満たすべき要件

公開性 (Openness) :

データ形式の仕様が公開されていること。

実装 (Implementation) :

データ形式の読み書きをサポートするオープンソフトウェアが提供されること。

実例 (Example) :

当該データ形式で保存された実データが供給されること。

使用許諾 (Licensing) :

データ形式に関連して提供される全てのリソースは適切なライセンスで使用許諾されること。

データ種別 (Data types) :

データ形式がサポートするデータの種別を明記すること。

管理 (Governance or change management) :

データ形式に関する意思決定と更新管理の仕組みを有すること。

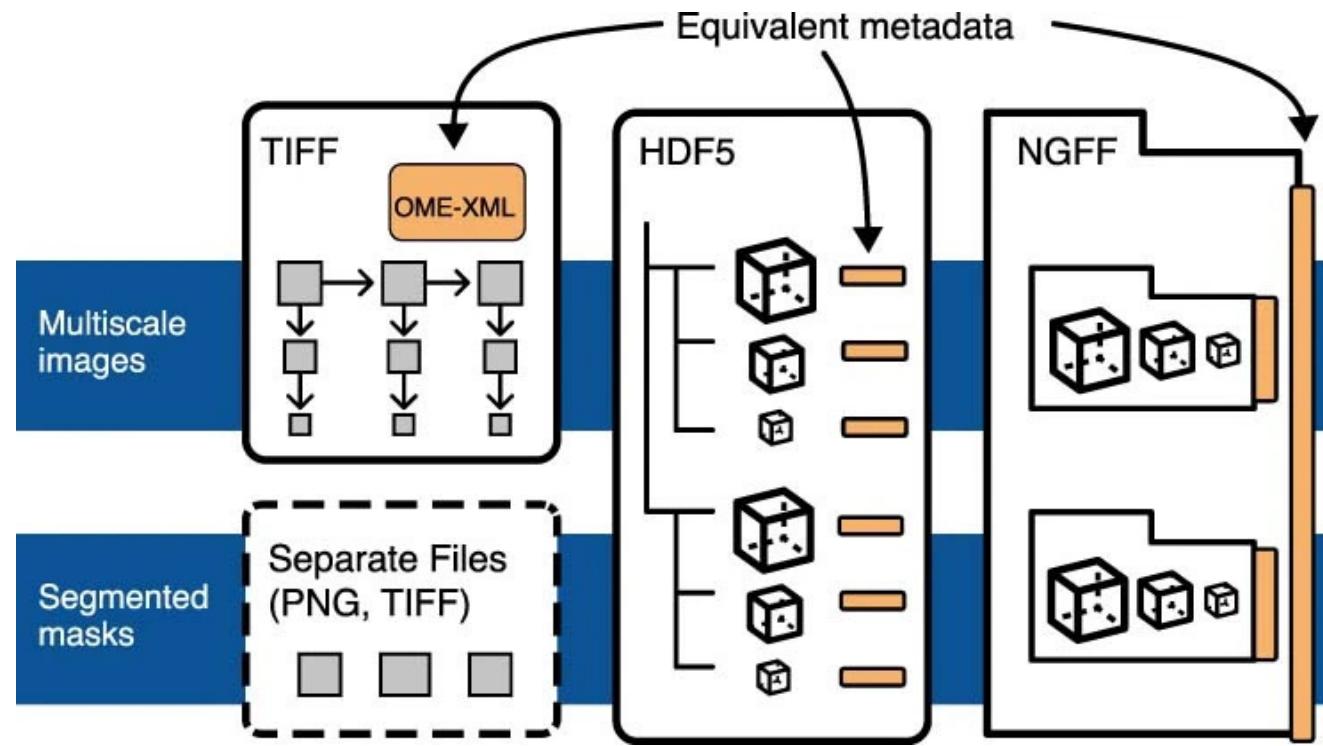
採用 (Adoption) :

データ形式が世界中で幅広く採用されること。

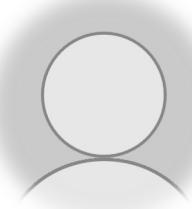


OME-NGFFフォーマット

クラウドで使用されるオブジェクトストレージのためのフォーマット



データ共有システムに関する提言



メタデータの仕様 (Metadata specifications for submission) :

データ共有システムの間で共通のメタデータの仕様をコミュニティと協力して定義すること。

バイオイメージング・データのエコシステムの構成要素 (Components of the bioimage data ecosystem) :

全ての発表論文に関連するデータを最小限のメタデータとともに格納するリポジトリ（アーカイブ）と、豊富なメタデータを付与した高付加価値データベース (AVDB: Added-value database) の2種類のデータリソースに分けること。

AIに応用可能な高付加価値データベースが満たすべき要件 (Requirement for AVDB for AI applications) :

高付加価値データベースについては、AIの学習に適したデータセットの定義づけを行うこと。

データ投稿、データ編集の認証システム (Authentication for submission and data access) :

データの投稿や編集の際の認証には、よく検証された標準的な認証システムを採用すること。

信頼できるデータリソース (Trustworthy research data resources) :

公共データの質を評価する国際的なイニシアティブからの評価を受けること。

個人識別が可能なデータの扱い (Human identifiable data) :

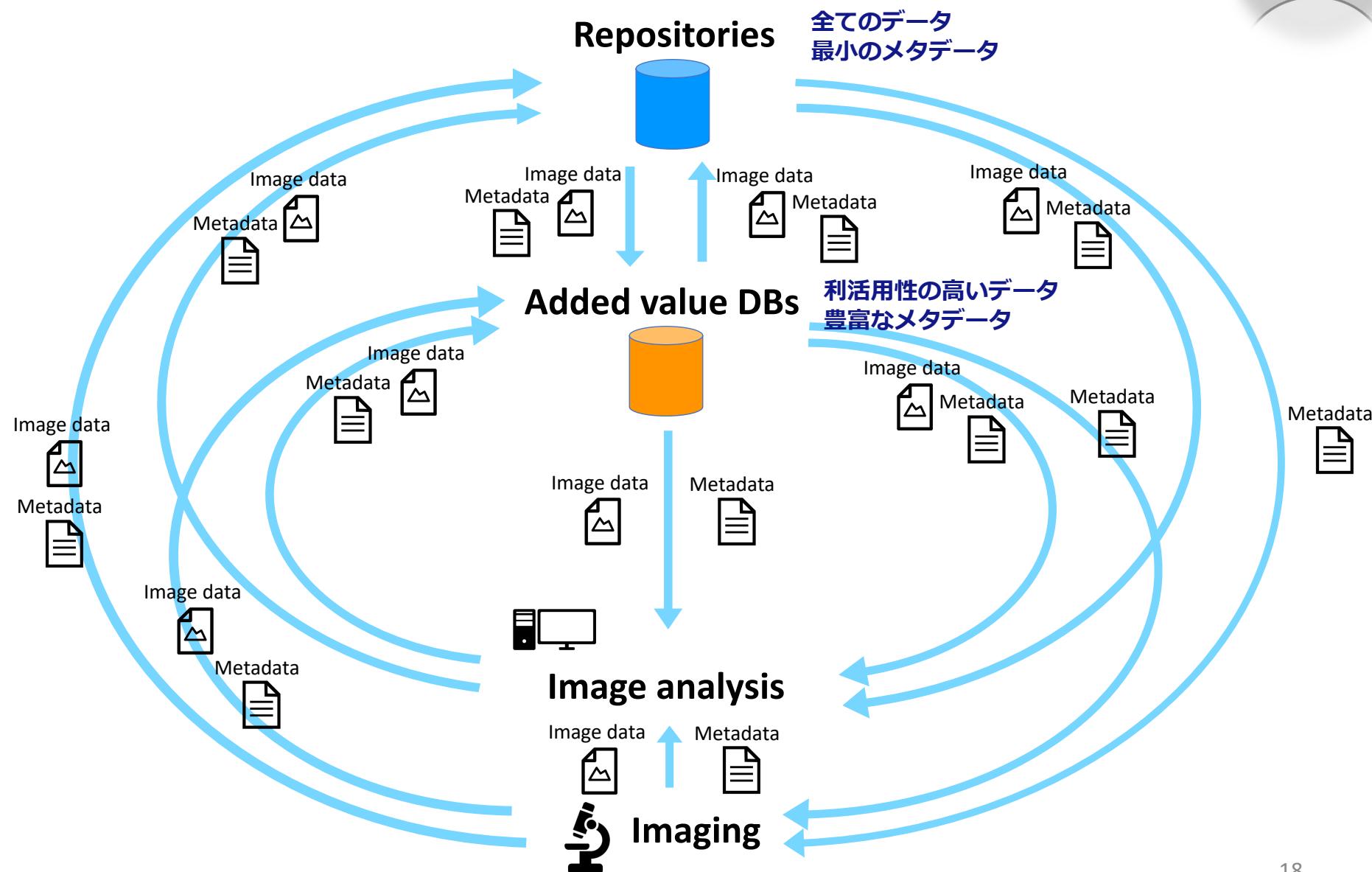
個人を特定し得るデータ等の利用について、倫理的かつ実用的な観点からの指針を策定すること。



データ共有の要件

- FAIR原則 (Wilkinson et al., 2016)
 - **F**indability, **A**ccessibility, **I**nteroperability, **R**eusability
(見つけられる。アクセスできる。相互運用できる。再利用できる。)
- FAIR原則と要求の対立
 - データは作成後、**できるだけ直ぐに**登録され、見つけられ、アクセスできるようにしたい。
 - データは適切にキュレーションされ、相互運用可能で再利用可能な形式で保存され、さらなる研究のために利用されるべきである。
 - キュレーション、データ変換には**時間が必要**

バイオイメージングデータのデータ共有システムのデザイン



欧洲のバイオイメージングデータ共有システム

EMPIAR

The screenshot shows the EMPIAR homepage. At the top, there's a navigation bar with links for EMBL-EBI Services, Research, Training, About us, and EMBL-EBI. Below the header, there's a large green electron microscopy image. The main content area has a search bar and a table listing datasets. The first dataset listed is "EMPIAR-10333 Single-Particle Cryo-EM Reconstructions of Human FACT in Complex with Partially Assembled Sub-nucleosomes [multiple data sets in TIFF, MRC and MRCS formats]". Other datasets shown include "EMPIAR-10335 Aoo-state Streptavidin [multiple data sets in MRCS format]" and "EMPIAR-10275 Structure of a synthetic beta-hairpin".

IDR

The screenshot shows the IDR homepage. It features a search bar at the top with placeholder text "Welcome to IDR" and "Search by: Name (IDR number) Type to filter values...". Below the search bar are two thumbnail images labeled "Cell-IDR" and "Tissue-IDR". The main content area is divided into sections: "Most Recent (10)" and "Time-lapse imaging (11)". Each section contains four thumbnail images with corresponding titles: "Most cellular resolution is coupled to nuclear remodelling in budding yeast", "Time-resolved imaging based on CLEM", "Time-resolved imaging-based CLEM screening", and "Mapping the perturbed new cellular perturbations".

BioImage Archive

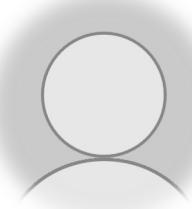
The screenshot shows the BioImage Archive homepage. It features a search bar at the top with placeholder text "Search BioImage Archive". Below the search bar are links for Home, Browse, Submit, Help, and About us. The main content area has a large banner image of a cell with various colored labels. To the right, there's a section titled "Further information" with a call for public archives for biological image data. At the bottom, there's a section titled "Examples of bioimages shared and reused" with a "Read more" link.

- 2014年設立の電子顕微鏡データの**Added Value DB**
- EMBL-EBIとOMEが企画したworkshopでの議論を元に設立
- MRC, BBSRC, Wellcome Trust等からの資金でEMBL-EBIが運営

- 2017年設立の生命科学画像データの**Added Value DB**
- OME ConsortiumとEMBL-EBIの共同プロジェクトとしてBBSRCの資金で開設
- BBSRC, Wellcome Trust, Horizon 2020 (Euro-BioImaging, Global BioImaging, CORBEL) 等からの資金で運営

- 2019年7月にEMBL-EBIが設立した生命科学の画像データの**リポジトリ**
- Euro-BioImagingとELIXIRとの共同研究により開発が進められる

日本のバイオイメージングデータ共有システム



SSBD:database

SSBD:database

Organism: ex. C. elegans

Search Clear

Introduction

System Science of Biological Dynamics database (SSBD:database) provides a rich set of open resources for analyzing quantitative data and microscopy images of biological objects, such as single-molecule, cell, gene expression nuclei, etc. Quantitative biological data and microscopy images are collected from a variety of species, sources and methods. These include data obtained from both experiment and computational simulation.

Samples

Microscopy Images

Calcium response and shape changes in oocyte of C. elegans

DIC image of nuclear division dynamics in C. elegans embryo

TEM image of retinal tissue from human embryonic stem cells

News

2020-12-24, SSBD 2020 Update
SSBD 2020 update, the metadata database fully renewed, and 77 image datasets (7GB) and 4 quantitative datasets are added. We are planning next database update in a half year for COVID-19 situation.

2020-08-12, A new paper on BD5 is published in PLOS ONE
A new paper "BD5: an open HDF5-based data format to represent quantitative biological dynamics data" is now published in PLOS ONE.
<https://doi.org/10.1371/journal.pone.0237468>

[Older news...](#)

Funding

SSBD:repository

SSBD:repository

Organism: ex. C. elegans

Search Clear

Introduction

System Science of Biological Dynamics repository (SSBD:repository) is an open data archive that stores and publishes bioimaging and biological quantitative datasets that are associated with published or to be published studies. It allows other researchers to access and download those datasets for reference or for further investigations.

Find the dataset from search box above, or see the dataset list in [Resources](#).

SSBD:repository has started operation in 2016, under the life science database integration promotion project of the Japan Science and Technology (JST), National Bioscience Database Center (NBDC). Currently it is funded from RIKEN, JST and Grant-in-Aid for Scientific Research from the Ministry of Education, Culture, Sports, Science and Technology of Japan (MEXT).

For an overview of the SSBD:database/repository, please refer to the paper,
Tohsato, Y., Ho, K. H. L., Kyoda, K., and Onami S. (2016) "SSBD: a dataset of quantitative data of spatiotemporal dynamics of biological phenomena." *Bioinformatics*, 32(22): 3471-3479
<https://doi.org/10.1093/bioinformatics/btw417>

News

2021-02-09, System maintenance on Feb 9
Due to system maintenance, the 4D visualizer and APIs will not be available on Feb 9, 9:00-16:00. Sorry for the inconvenience.

2020-12-24, SSBD 2020 Update
SSBD 2020 update, the metadata database fully renewed, and 77 image datasets (7GB) and 4 quantitative datasets are added. We are planning next database update in a half year for COVID-19 situation.

2020-08-12, A new paper on BD5 is published in PLOS ONE
A new paper "BD5: an open HDF5-based data format to represent quantitative biological dynamics data" is now published in PLOS ONE.
<https://doi.org/10.1371/journal.pone.0237468>

[Older news...](#)

Funding

バイオイメージングデータと生命動態定量
データの**Added-Value DB**

バイオイメージングデータと生命動態定量
データの**リポジトリ**

SSBD :バイオイメージングデータと生命動態情報の統合データベース

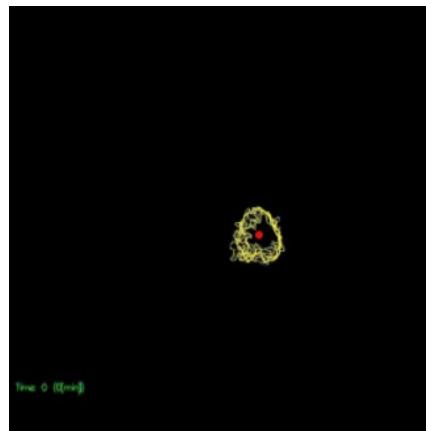
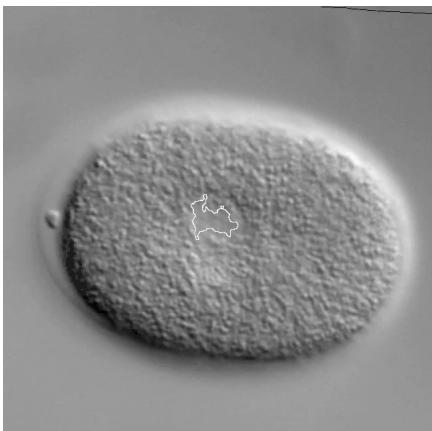


- ・ 生命動態システム科学の統合データベースとしてJST-NBDCの資金で設立(2013年)
- ・ 当初は、時空間情報を数値として含む新しい様式の生命科学の研究データとそれを取得するために用いた画像データの共有を行うDB

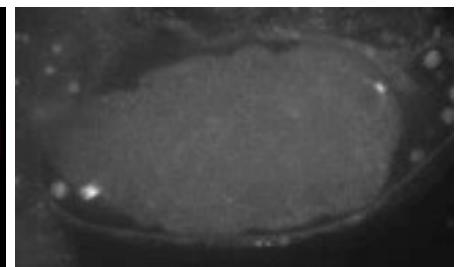
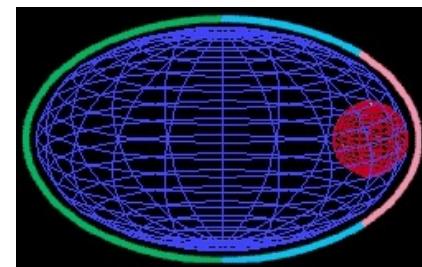
具体例

- ・ 様々な摂動条件下の生命動態の**時空間定量計測**データ
- ・ 様々なパラメータ下の生命現象の**時空間動態シミュレーション**結果

線虫胚の細胞核分裂動態計測データ



細胞核動態のシミュレーション結果



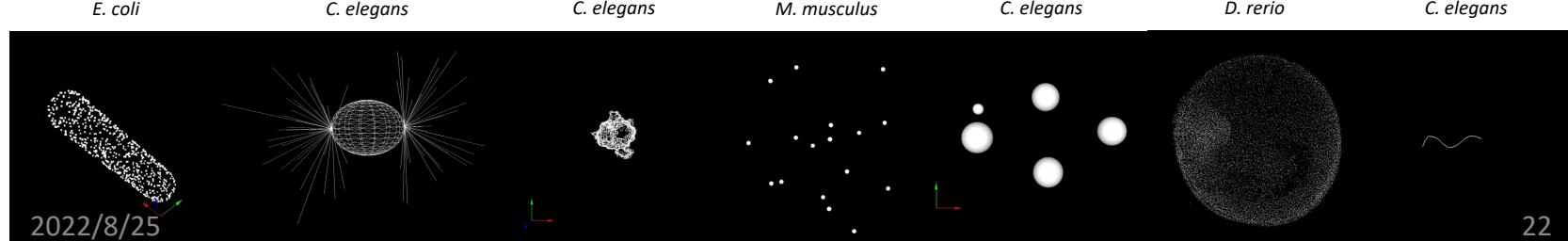
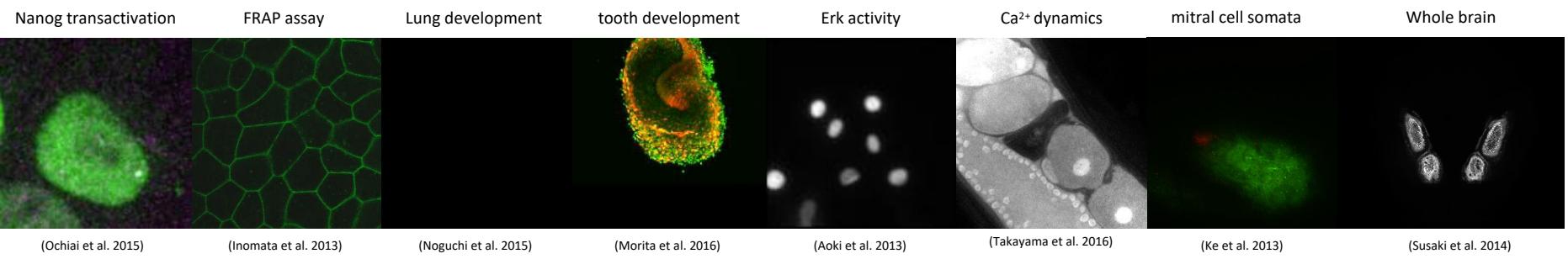
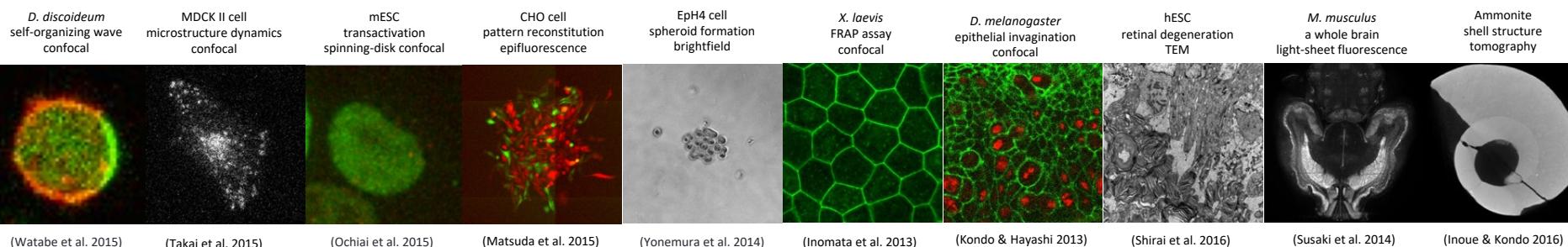
Kimura & Onami Dev. Cell 2005

Hamahashi et al. BMC Bioinformatics 2005

SSBD :バイオイメージングデータと生命動態情報の統合データベース

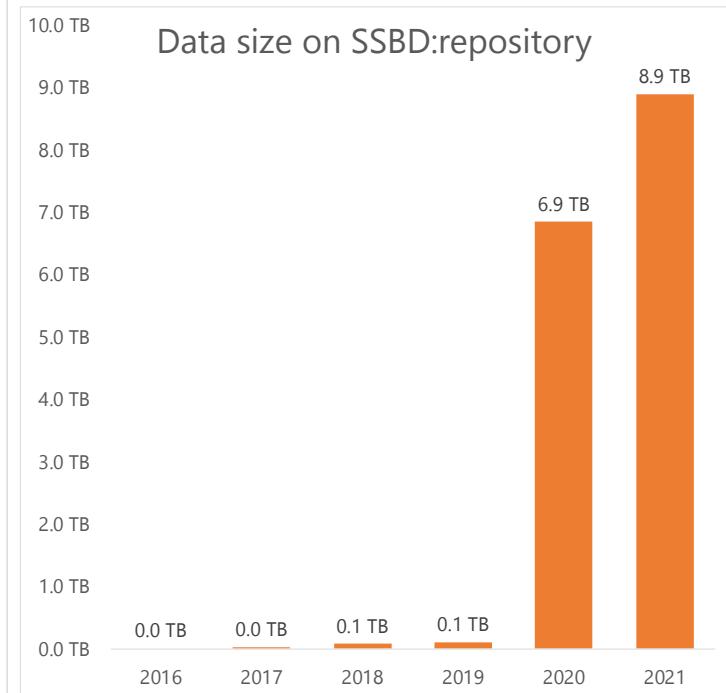
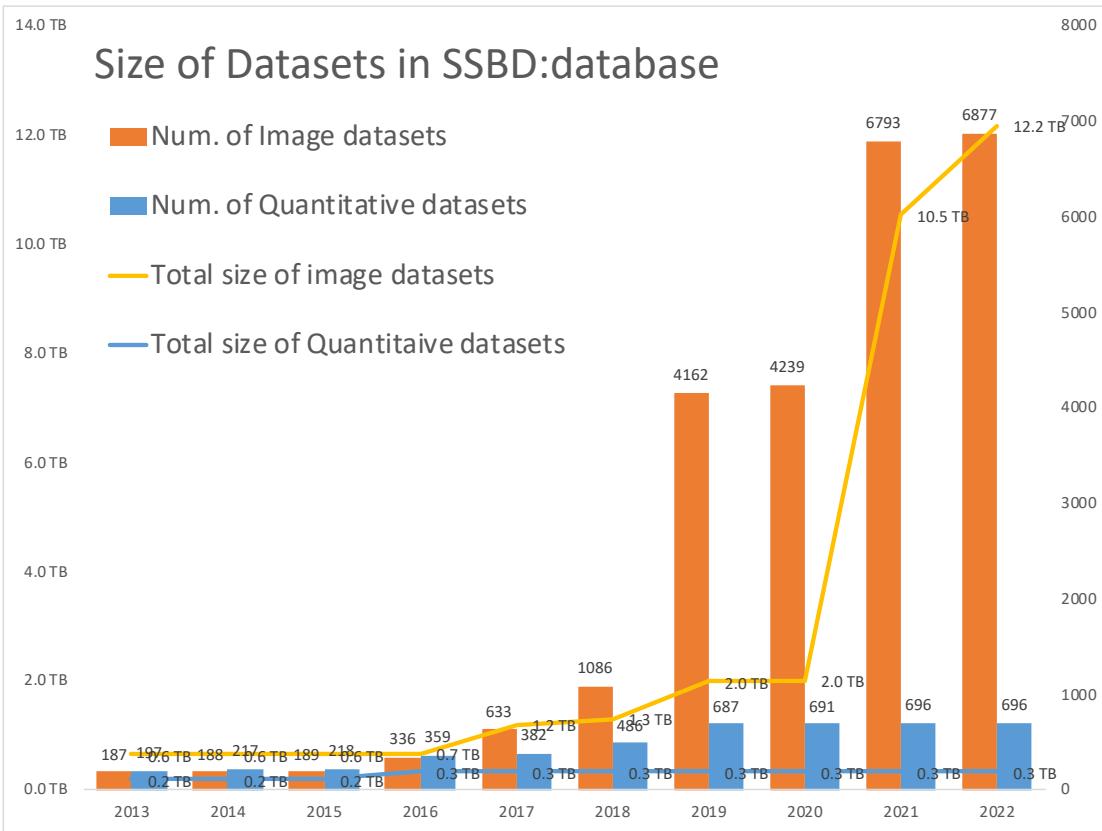


- 最先端技術で取得した生命科学画像データ、網羅的実験の生命科学画像データの共有を開始（2016年）
- 生命科学画像データのリポジトリサービスを開始（2016年）
- Added-Value DB (SSBD:database) とリポジトリ (SSBD:repository) を分離（2019年）



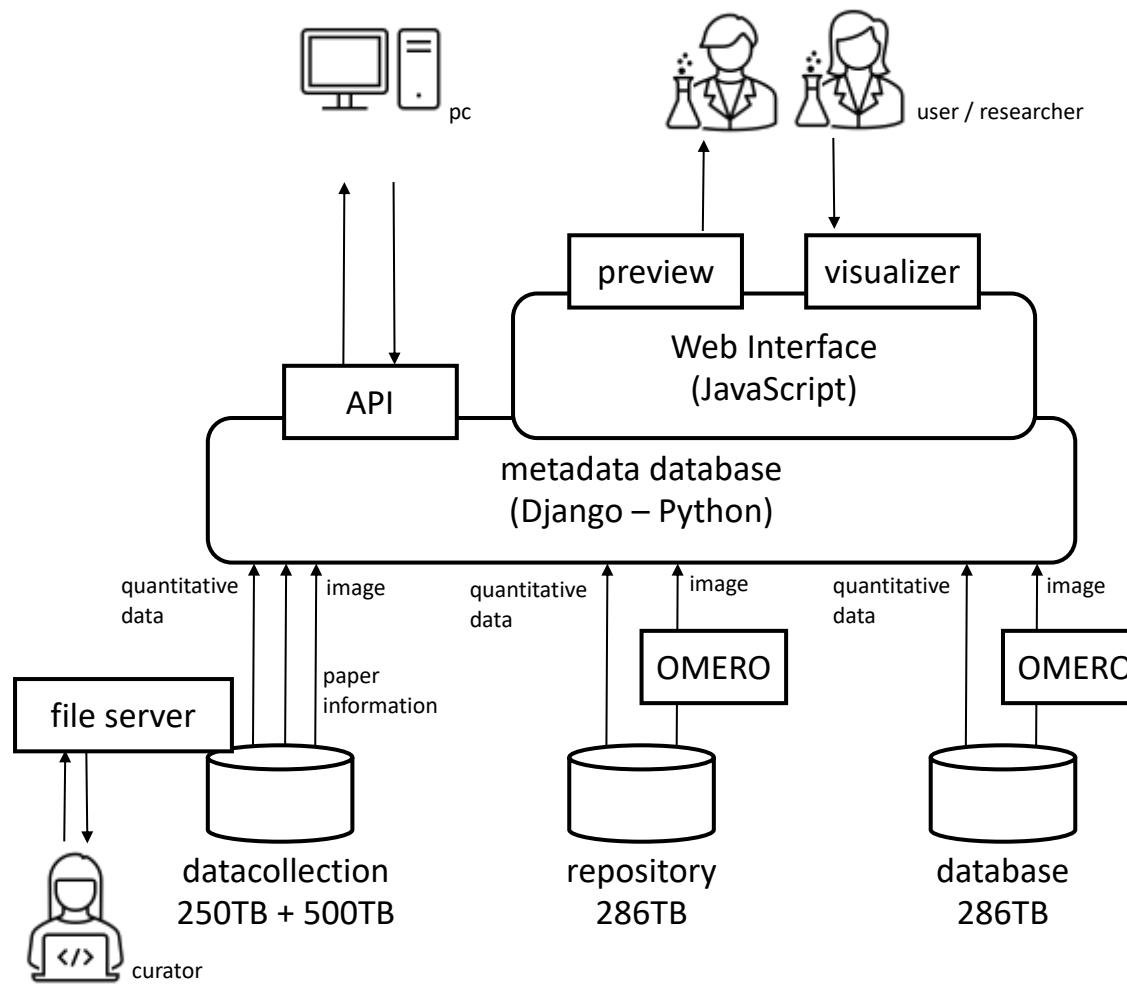


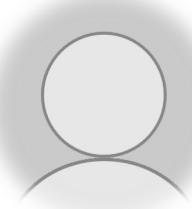
SSBD:database および SSBD:repository の統計情報





SSBDのシステム概略図





SSBD:repositoryへのデータの登録方法

- まずは、メールでお問い合わせ下さい
ssbd-repos@ml.riken.jp
- オンラインストレージRIKEN Boxによる方法
 - 数100GB程度のデータの場合
- HDDの送付による方法
 - 数TB程度のデータの場合
- SSBDデータアップロードサイトによる方法
- 登録者のオンラインストレージ経由による方法

SSBD:database へのデータ登録手順



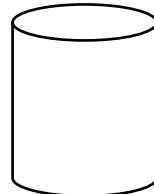
データ生産者



論文公開時/
前に登録

メタデータ
の登録

SSBD:repository



オリジナルデータの提供依頼

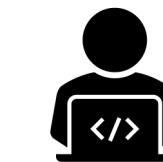
オリジナルデータの提供



詳細なメタデータの確認依頼

詳細なメタデータの確認・修正

SSBDチーム



Pubmed 等のデータベースから
論文情報を収集



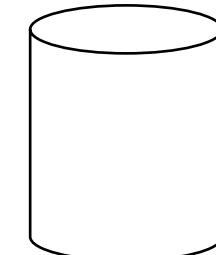
データの選別



詳細なメタデータの付与

データベース登録

SSBD:database



公開

SSBD:database における十分なメタデータ

SSBD:repository における必要最小限のメタデータ



- 十分なメタデータ
- 必須: 33 (データセットごと)
 - Title, Description, Contact, License, Data format, Paper information, Organism, Strain, Cell Line, XYZT scales, Gene Ontology, ...

- 任意: 14

Three screenshots of the 'metadata_template.v2.6.2' application interface showing different types of datasets:

- Screenshot 1:** Shows a dataset for 'SID_FirstAuthor_object'. It includes fields for Project name, Project URL, Project DOI, Project title, Project description, Version, Contact name, Contact e-mail, Contact organization, Contact department, Contact laboratory, Contact address, and Quantitative data contributors.
- Screenshot 2:** Shows a dataset for 'Image Dataset'. It includes fields for Full name, first name, middle name, last name, ORCID, E-mail, Method Summary, Paper DOI, Paper URL, Paper (Sheet), Paper (Long), Dataset ID, Strain, Cell Line, Molecular Function (MF), Biological Process (BP), Cellular Component (CC), X-scale, Y-scale, Z-scale, T-scale, and Time-lapse (Quantitative Dataset).
- Screenshot 3:** Shows a dataset for 'BDML'. It includes fields for Dataset ID, File or Folder (Quantitative Dataset) method, Title (Quantitative Dataset), Description (Quantitative Dataset), and Notes.

- 必要最小限のメタデータ
- 必須: 11 (プロジェクトで1つ)
 - Title, Description, Contact, License, Data format, Organism
- 推奨: 3
 - DOI, Paper information

- 任意: 15

Screenshot of the 'minimal_metadata_template.v2.7.sample' application interface, showing a simplified version of the metadata template with the following fields:

	A	B	C	D
1	Item	Class	Description	
2	Project name	Required	ssbd:repository:0000	
3	Project URL	Optional	http://ssbd.sdb.kenj.ac.jp/ssbd/jspedit/2020xxv/	
4	DOI	Recommended	https://doi.org/10.14631/ssbd-repos-2020.xx.x	
5	Title	Required	(Title of the project)	
6	Project Information	Required	(Description of the project)	
7	Publication Date	Required	2020xx/xx	
8	Version	Optional	1.0.0	
9	Contact Person	Required	Systems Science of Biological Dynamics repository (SSBD:repository), Kinki University	
10	First Name	Required	(Family name)	
11	Last Name	Required	(Family name)	
12	Contact E-mail	Required	mail-address@example.com	
13	Organization	Optional	Laboratory for xxx	
14	Address	Optional	x-x-x street, city, country xxxx-xxxx	
15	J-GLOBAL ID	Optional	researchmap ID	
16	ORCID	Optional	xxxx-xxxx-xxxx-xxxx	
17	Method Information	Optional	Recommended: Details in xxxx Journal, Vol. x, No. x, 2020, pp. xxxx-xxxx	
18	Method Summary	Optional	https://example.com/xxxxjournal/v/x/n/xxxx	
19	Paper DOI	Optional	Required	
20	Paper URL	Optional	Required	
21	Paper (Sheet)	Optional	Required	
22	Paper (Long)	Required	See details in Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737.	
23	Dataset ID	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
24	Organism	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
25	Strain	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
26	Cell Line	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
27	Molecular Function (MF)	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
28	Biological Process (BP)	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
29	Cellular Component (CC)	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
30	X-scale	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
31	Y-scale	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
32	Z-scale	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
33	T-scale	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
34	Time-lapse (Quantitative Dataset)	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
35	Description (Quantitative Dataset)	Optional	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
36	File or Folder (Quantitative Dataset)	Optional	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
37	File separation method	Optional	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
38	locID	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
39	Experiment	Optional	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
40	external link	Optional	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
41	extref(BDS)	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
42	Source	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
43	Workflow	Required	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
44	Notes	Optional	Kyoda K, et al. (2013) Nuclear Acids Res, 41(Database issue):D732-D737	
45	Creators	Optional	Priority 1	
46	First Name	Required	(Family name)	
47	Last Name	Required	(Family name)	
48	Contact E-mail	Optional	mail-address@example.com	
49	Laboratory	Optional	Laboratory for xxx	
50	Organization	Optional	Kyoto University	
51	Address	Optional	Kyoto, Japan	
52	J-GLOBAL ID	Optional	researchmap ID	
53	researchmap ID	Optional	researchmap ID	
54	ORCID	Optional	ORCID	
55	Creators	Optional	Priority 2	
56	First Name	Required	(Family name)	
57	Last Name	Required	(Family name)	
58	Contact E-mail	Optional	mail-address@example.com	
59	Laboratory	Optional	Lab for xxx	
60	Organization	Optional	Kyoto University	
61	Address	Optional	Kyoto, Japan	
62	J-GLOBAL ID	Optional	researchmap ID	
63	researchmap ID	Optional	researchmap ID	
64	ORCID	Optional	ORCID	



メタデータの登録方法

- MS Excelファイルへの記入による方法
- Webフォームへの入力による方法
(準備中)

	A	B	C	D
1	Item	Class	Description	
2	Project name	Required	ssbd-repos-000000	
3	Project URL	Required	http://ssbd.gbc.riken.jp/set/2020xxx/	
4	DOI	Required	ssbd-repos-000000 (Title of the project)	
5	Title	Required	(Title of the project)	
6	Description	Required	(Description of the project)	
7	Publication Date	Required	2020/xx/xx	
8	Publisher	Required	Systems Science of Biological Dynamics repository (SSBD-repository), RIKEN	
9	Resource Type	Required	JPN	
10	Dataset	Required	Dataset	
11	License / Rights	Required	CC-BY	
12	Version	Optional	1.0.0	
13	Contact Information	Required	(First name)	
14	Last Name	Required	(Family name)	
15	Contact E-mail	Required	mail-address@example.com	
16	Laboratory	Optional	Laboratory for xxx	
17	Department	Optional	Department of xxx	
18	Organization	Required	xxx University	
19	Address	Optional	x-x street, city, country xxx-xxxx	
20	J-GLOBAL ID	Optional		
21	researchmap ID	Optional		
22	ORCID	Optional	xxxx-xxxx-xxxx-xxxx	
23	Method Information	Recommended	Details in xxx Journal, Vol. x, No. x, 2020, pp. xxxx-xxxx	
24	Paper DOI	Recommended	https://example.com/xxxjournal/v/x/xxxx	
25	Paper URL	Recommended		
26	Data / File Formats	Required	GIF, GIB	
27	Data Size	Required	50 GB	
28	Organism	Required	C. elegans	
29	Strain	Optional		
30	Dataset Information	Cell Line	Optional	
31	Biological Function (BF)	Optional		
32	Biological Process (BP)	Optional		
33	Cellular Component (CC)	Optional		
34	Study Type	Optional		
35	Imaging Methods	Optional		
36	Notes	Optional		
37	Templated version	Required	2.7	
38	Creators	Priority 1		
39	First Name	Required	(First name)	
40	Last Name	Required	(Family name)	
41	Contact E-mail	Optional	mail-address@example.com	
42	Laboratory	Optional		
43	Department	Optional		
44	Organization	Required	xxx University	
45	Address	Optional		
46	J-GLOBAL ID	Optional		
47	researchmap ID	Optional		
48	ORCID	Optional		
49	Creators	Priority 2		
50	First Name	Required	(First name)	
51	Last Name	Required	(Family name)	
52	Contact E-mail	Optional		
53	Laboratory	Optional	Lab for xxx	
54	Department	Optional		
55	Organization	Required	yyy Institute of bioscience	
56	Address	Optional		
57	J-GLOBAL ID	Optional		
58	researchmap ID	Optional		
59	ORCID	Optional		

Repository name:

Database url:

Repository url:

Omero url:

Repository doi:

Repository title:

Repository description:

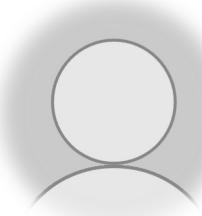
Repository license: CC BY license

Contact names:

Contact email:

Contact organization:

Contact department:



DOIの発行

DOI (Digital Object Identifier)

- <https://doi.org/> から始まるURLで
永続的にデータへのリンクを提供
 - データの実体の場所が変わった場合でも
doiを変更することなく、リンク先を変更可能
 - 変更されないリンク先として、論文中に記述可能
- SSBD:repository では
<https://doi.org/10.24631/ssbd.repos>. から始まる
URLを提供



画像データ共有時のガイドライン (1/2)

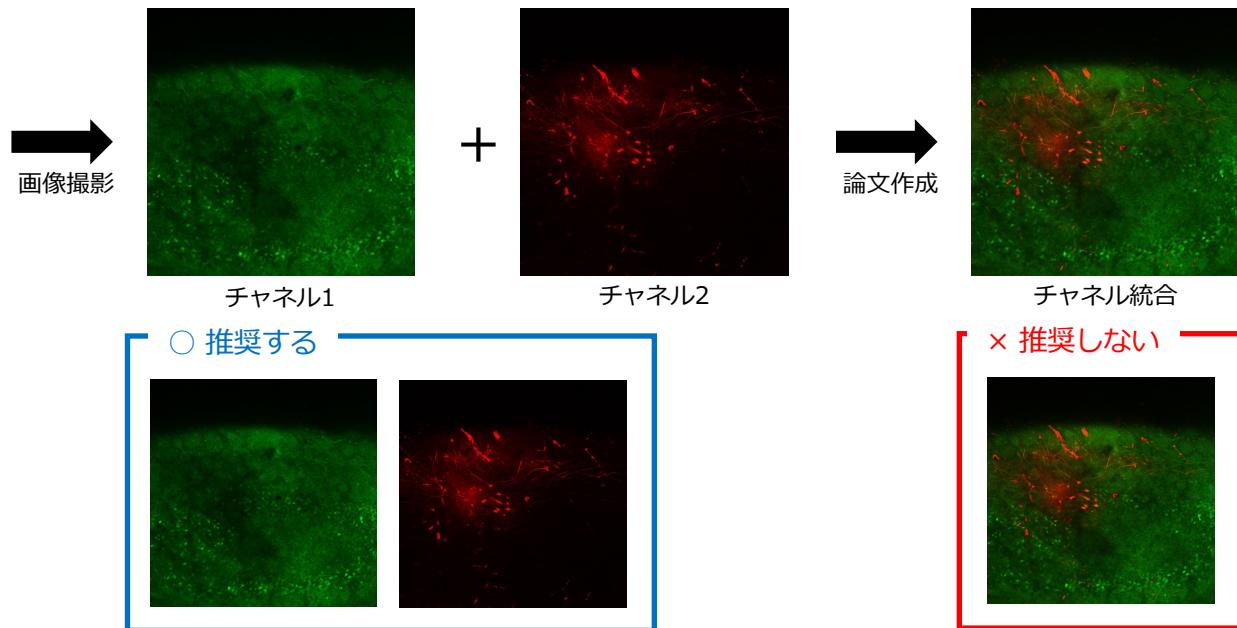
登録を推奨する画像データ

- ・オリジナルデータ（加工されていないデータ）
- ・顕微鏡メーカーのソフトウェアが出力する
オリジナル形式
- ・複数チャネルを統合していない形式
- ・深さ方向(z軸)や時間方向(t軸)の全体の画像、
可能ならばグループ化した形式
- ・刻印・加工などをしていない形式
- ・動画像ではなくタイムラプス顕微鏡画像形式



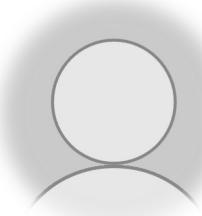
複数チャネルを統合していない形式

例1：複数チャネルで撮影した場合



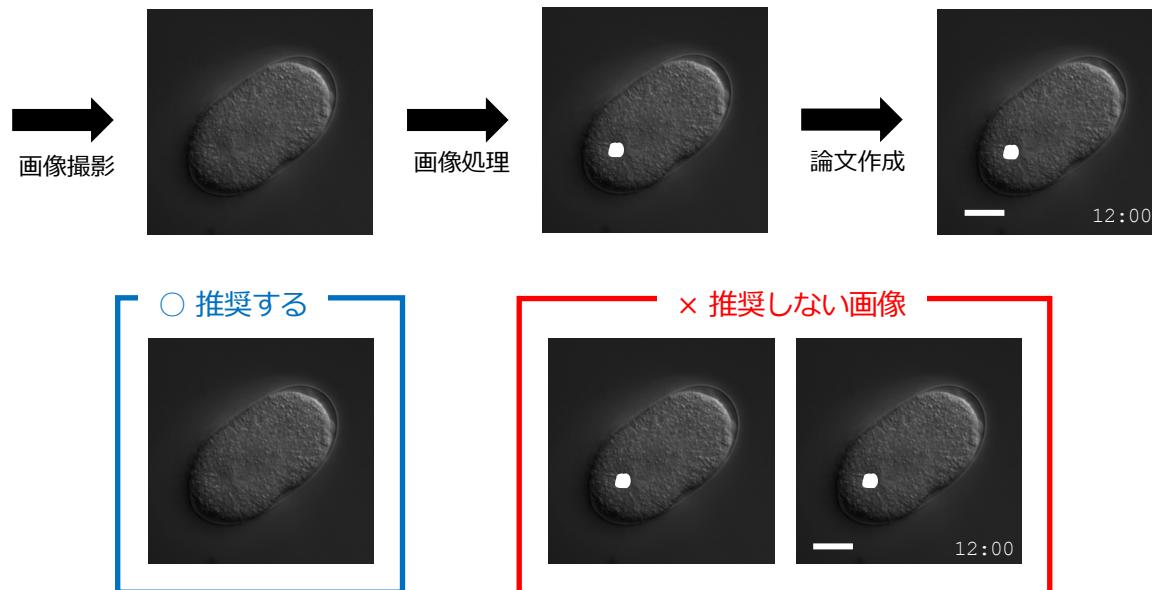
* 両チャネルの画像がまとめてひとつのファイルで保存されている場合にはそちらをお送りください。

"Confocal microscopy images of neurons associated with glomerulus stained with Alexa 647 and EYFP expression in young Thy1-YFP-H mouse hemi-brain cleared with SeeDB" by Ke et al. is licensed under CC-BY



刻印・加工などをしていない形式

例2: 画像処理・刻印をした場合



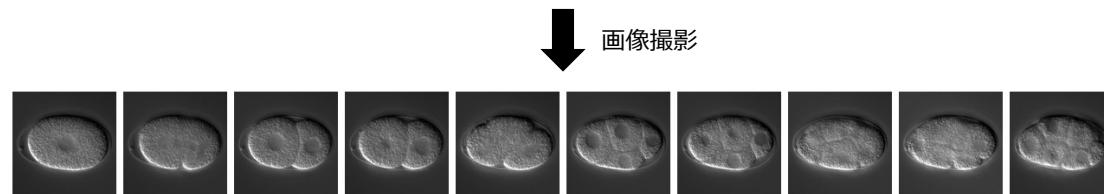
* スケールバー、タイムスタンプが自動で付加される設定で撮影した場合にはそのまま登録します。

“DIC microscopy images of wild-type *C. elegans* embryo” by Kyoda et al. is licensed under CC-BY



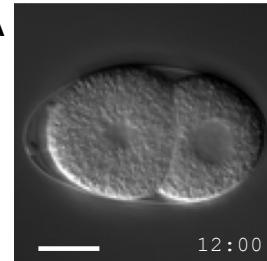
タイムラプス顕微鏡画像の全体

例3: タイムラプス画像からある時点のみを論文の図として使った場合

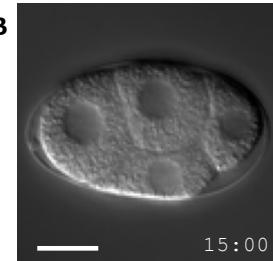


↓ 論文作成

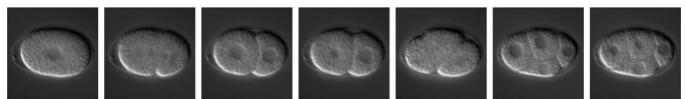
Figure 1 A



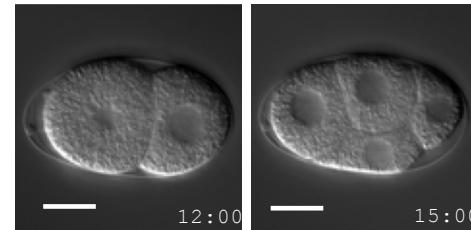
B



○ 推奨する

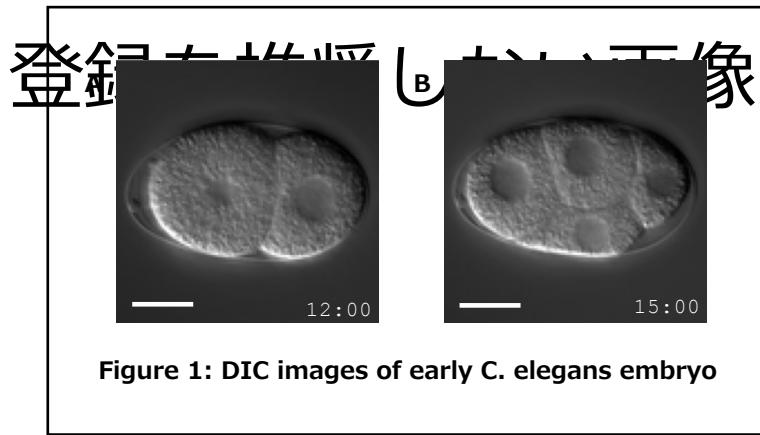


✗ 推奨しない

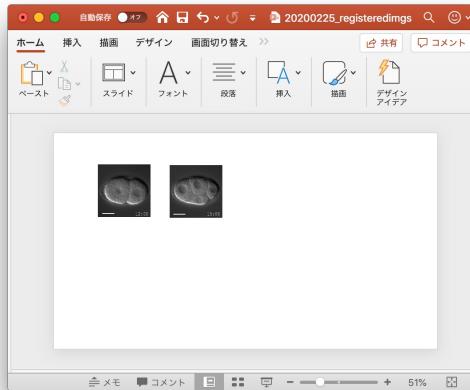




画像データ共有時のガイドライン (2/2)

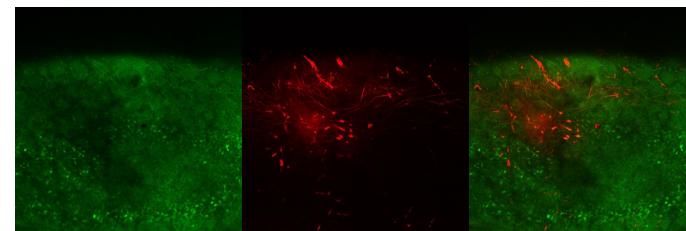


論文誌の図そのもの

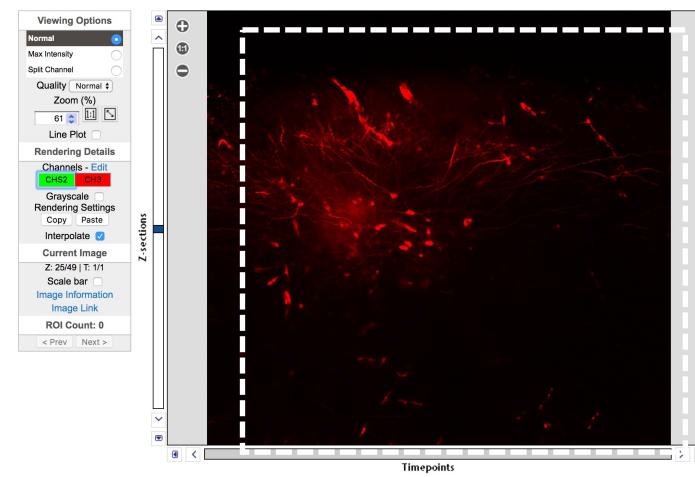


画質を低下させるソフトウェア (PowerPoint, Photoshopなど) に貼り付けたもの

"DIC microscopy images of wild-type *C. elegans* embryo" by Kyoda et al. is licensed under CC-BY



複数画像をレイアウトして結合した画像



画面からキャプチャしたもの（スクリーンショット）

"Confocal microscopy images of neurons associated with glomerulus stained with Alexa 647 and EYFP expression in young Thy1-YFP-H mouse hemi-brain cleared with SeeDB" by Ke et al. is licensed under CC-BY



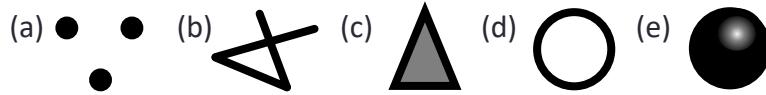
定量データ共有時のガイドライン

- 生命動態における時空間座標情報の統一フォーマット
BDML/BD5形式での登録を推奨
 - <http://ssbd.qbic.riken.jp/bdml/>
 - 4D可視化ツール、API経由でのデータアクセスが可能
- 汎用のデータフォーマットでも登録可能
 - 例) MS Excel, CSV, プレーンテキストなどの形式
 - データが解釈可能となるような注釈を付けて下さい
- 商用ソフトウェアのオリジナル形式でも登録可能
 - 例) Imarisなど
 - オリジナル形式とともに、
汎用データフォーマットに出力したファイルも登録ください

BDML/BD5: 生命動態データのための統合フォーマット

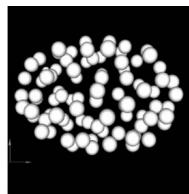


- 時空間情報を統合的に記述



- XMLを基盤

- 高い拡張性
- 高い可読性

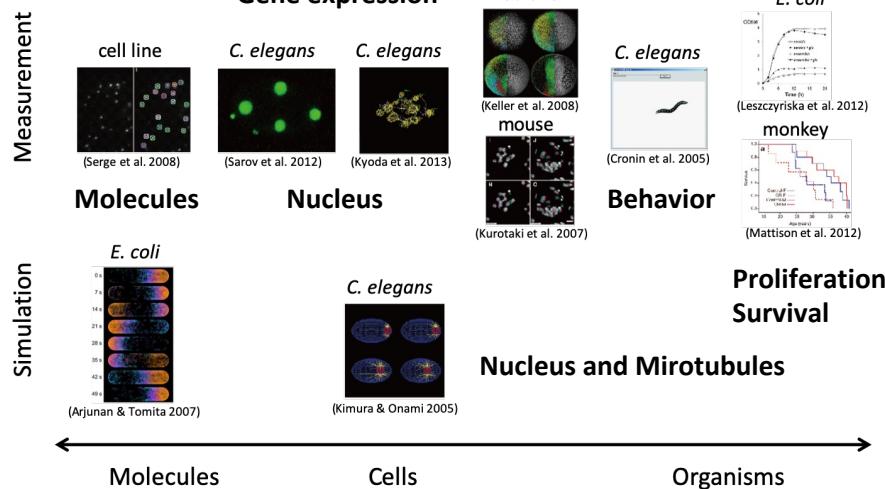


```

<data>
<component>
  <componentID>100</componentID>
  <time>1</time>
  <measurement>
    <objectRef>nucleus</objectRef>
    <point>
      <xyz>
        <x>10</x>
        <y>30</y>
        <z>18</z>
      </xyz>
    </point>
  </measurement>
</component>

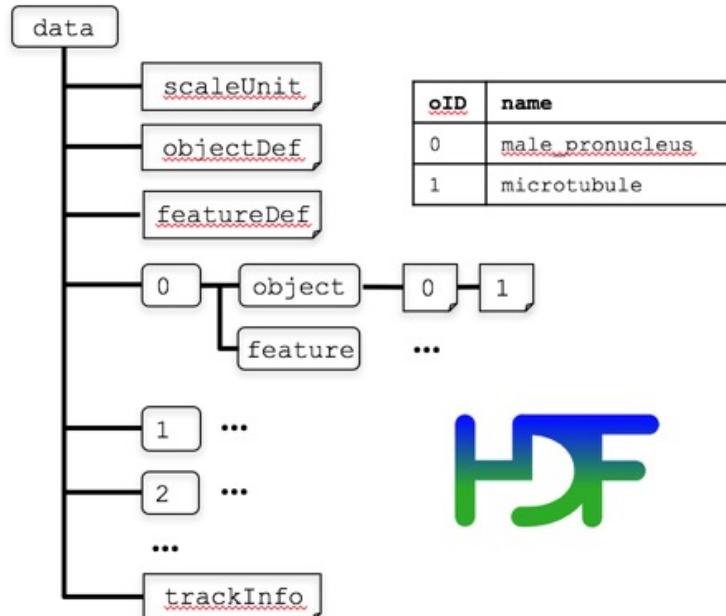
```

- 分子動態から個体の動態まで記述可能



- HDF5を基盤

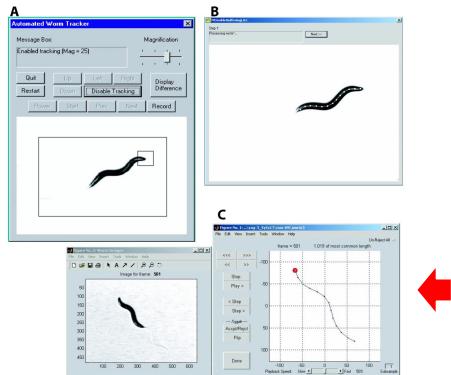
- 大規模データの効率的な取り扱いが可能



ID	t	entity	sID	x	y	z
1	0	line	0	387	153	16.6
	0	line	0	388	154	16.7
	0	line	1	365	245	15.0
	0	line	1	364	246	15.3
...						

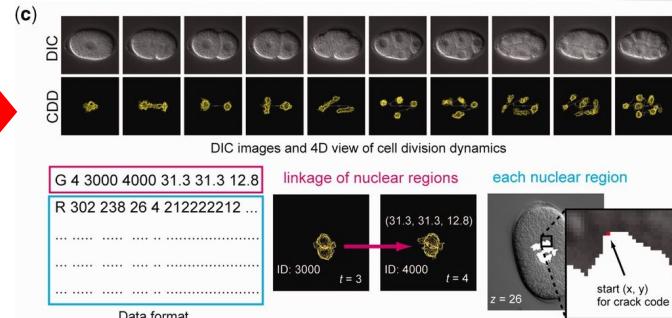
登録可能な定量データの例

例1: 個体の動態 (形状情報)



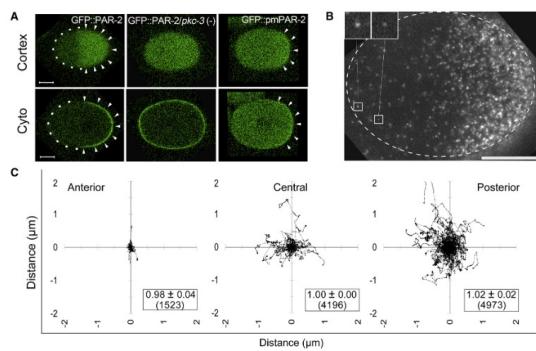
"Figure 2" by Cronin CJ et. al. (2005) BMC Genet, 6: 5 is licensed under CC-BY

例2: 細胞核分裂の動態 (輪郭情報)



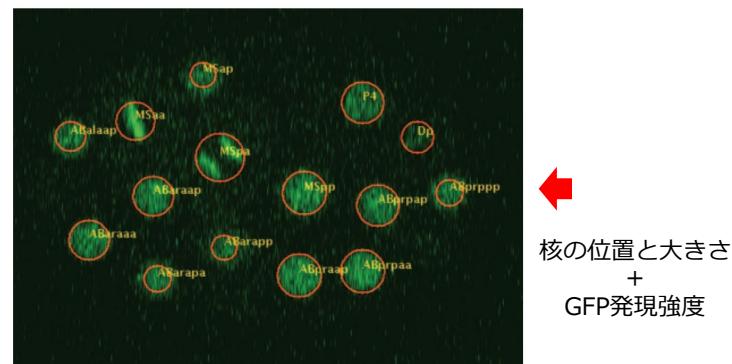
"Figure 1" by Kyoda K et. al. (2013) Nucleic Acids Res, 41(Database issue): D732-7 is licensed under CC-BY-NC

例3: 1分子の動態 (位置情報)

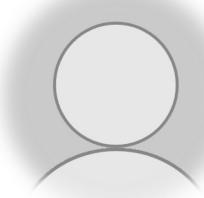


"Figure 1" by Arata Y et. al. (2016) Cell Rep, 16(8): 2156-2168 is licensed under CC-BY

例4: 細胞核分裂の動態と付加情報 (形状情報、蛍光強度)

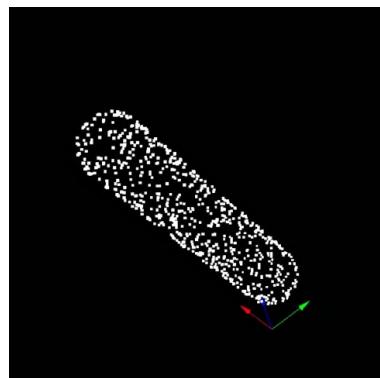


"Figure 2" by Bao Z et. al. (2006) Proc Natl Acad Sci U S A, 103(8): 2707-12, "Copyright (2006) National Academy of Sciences."



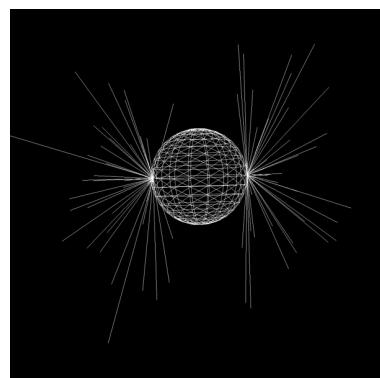
生命動態の可視化の例

E. coli



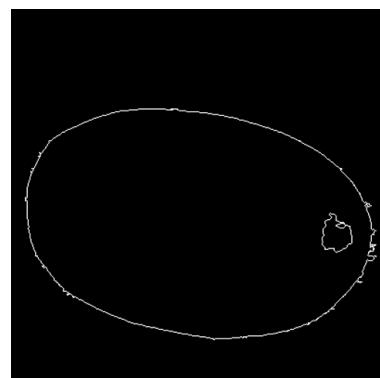
(Arjunan & Tomita 2007)

C. elegans



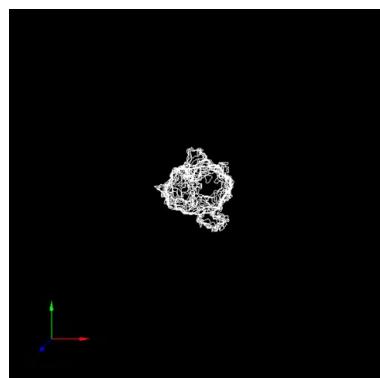
(Kimura & Onami 2005)

C. elegans



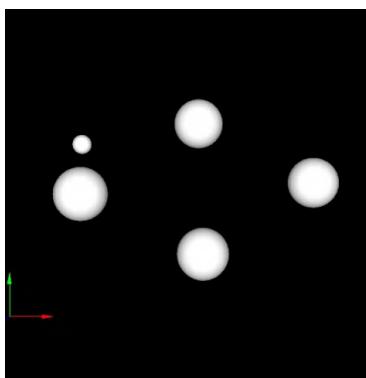
(Tohsato et al., submitted)

C. elegans



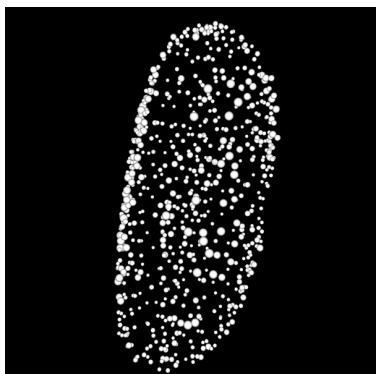
(Kyoda et al. 2013)

C. elegans



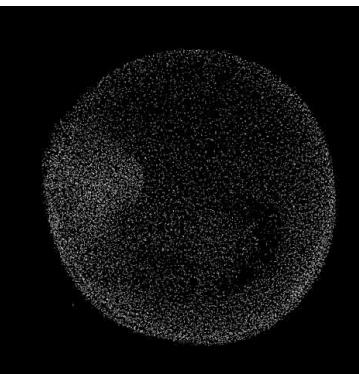
(Bao et al. 2006)

D. melanogaster



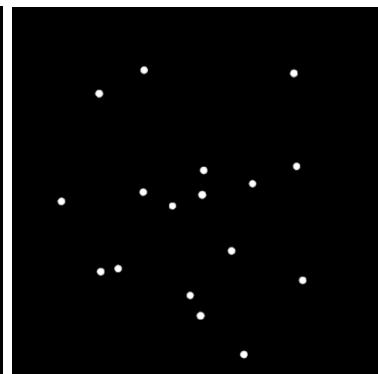
(Keller et al. 2010)

Zebrafish



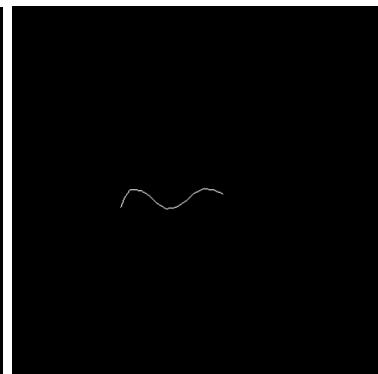
(Keller et al. 2008)

mouse



(Bashar et al. 2012)

C. elegans



(Cronin et al. 2005)

データの利活用

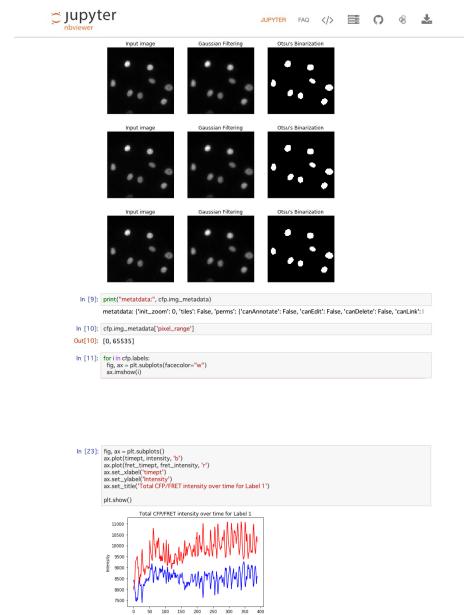
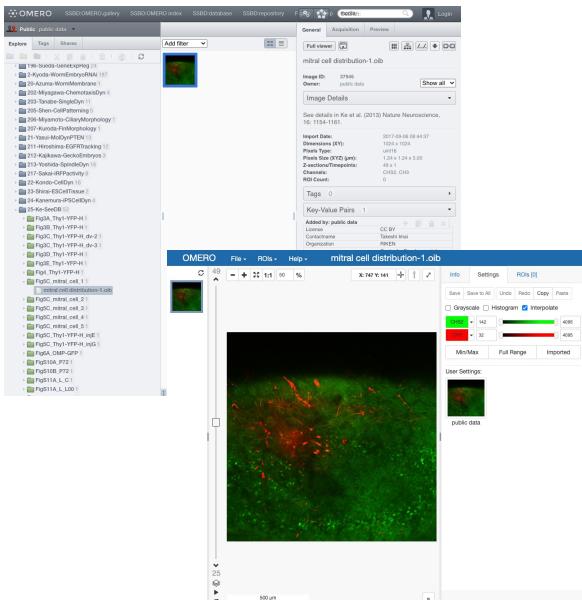


探す

見る

測る

#	Project	Release	Updated	Organism(s)	Datatype	BasedOn	# of image datasets	# of quantitative datasets	Paper
177	177-Knpp-cAMPRegulatingDyn	2022-03-31		Cani lupus familiaris; Mus musculus; Homo sapiens	cAMP-mediated signaling	Experiment	112	0	ACS Chem Biol 5(11):2848-2853
178	178-Konagaya-CellMigration	2022-03-31		Mus musculus	extracellular signal mediated kinase activity	Experiment	160	0	Cell Cycle 19(22):3167-3181
179	179-Kobayashi-BLV-Reactivity	2022-03-31		Mus musculus; Homo sapiens	bilirubin reductase	Experiment	89	0	Cell Struct Funct 45(2):131-141
180	180-Makrilia-Blossomactivity	2022-03-31		Cani lupus familiaris; Mus musculus; Homo sapiens	extracellular signal-regulated kinase activity	Experiment	115	0	ACS Sens 5(3):719-730
192	192-Kimura-SignalingDyn	2022-03-31		Chlorobacillus	equilibrium growth factor receptor binding	Experiment	60	0	Microbiome 9(1):69-78
196	196-Sueda-GeneticExpieg	2022-03-31		Mus musculus	regulation of gene expression gene expression	Experiment	24	0	Genes Dev 33(9-10):511-523
72	72-Kogure-CytoskeletonDyn	2021-11-30		Mar musculus	mitotic cell cycle, organization, nuclear envelope breakdown	Experiment	453	0	Dev Cel 41(3):287-298.e4
70	70-Yoshida-KMT-Dyn	2021-09-30		Mus musculus	mitotic cell cycle	Experiment	265	0	Dev Cel 43(5):589-602
120	120-Ding-CentromereDyn	2021-09-30		M. musculus	centromeric sister chromatid cohesion, meiotic cell cycle	Experiment	351	0	Curr Biol 31(10):1681-1689.e4
127	127-Konishi-ERKdyn	2021-09-30		Mus musculus	cell motility, activation of MAPK kinase	Experiment	143	0	Science 10/90-113



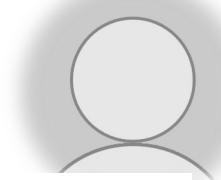
- キーワードによる探索
- ファイルのダウンロード

- ブラウザ上の可視化
- ツールを利用した可視化

- 画像データの解析
- 定量データの解析

データの検索

SSBD:databaseでデータを検索する。



SSBD:database

[SSBD:database](#) [SSBD:repository](#)

キーワードによる検索

Search
Clear

#	Project	Released	Organism	Datatype	BasedOn	# of image datasets	# of quantitative datasets	Paper
37	37-Arata-MolDynPar2	2017-10-03	Medical Subject Headline Biological Imaging Method	single molecule dynamics	Experiment	3	3	Cell Rep16(8):2156-2168
20	20-Azuma-WormMembrane	2017-03-07	Paper Microscope	cellular dynamics	Experiment	1	1	BMC Bioinformatics18(1):307
12	12-Takayama-Oocyte	2016-10-03	2020-02-03	C. elegans	oocyte shape dynamics	Experiment	119	Cell Rep15(3):625-637
11	11-Toyoshima-NeuAct	2016-05-20	2018-11-15	C. elegans	neuronal nuclear dynamics	Experiment	14	PloS Comput Biol12(6):e1004970
7	7-Cronin-WormLocomotion	2014-10-03	2018-11-15	C. elegans	behavior	Experiment	0	BMC Genet6:5
1	1-Bao-WormEmbryo	2013-10-03	2018-11-15	C. elegans	nuclear division dynamics	Experiment	0	Proc Natl Acad Sci U S A103(8):2707-12
2	2-Kyoda-WormEmbryoRNAi	2013-09-02	2020-02-03	C. elegans	nuclear division dynamics	Experiment	187	Nucleic Acids Res34 (Database issue):D732-7

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■ キーワードによる検索

- 生物種
- MeSH term
- イメージング手法
- 著者、など

■ 論文ごとにデータを分類

- データの概要表示
- データの可視化
- データファイルのダウンロード

SSBD:database

[SSBD:database](#) [SSBD:repository](#) [SSBD:OMERO](#) [Resources](#) [Tools](#) [Publications](#) [About](#) [News](#)

Summary of 2-Kyoda-WormEmbryoRNAi

Repository	-
Title	-
Description	-
Release Date	2013-09-02
Updated Date	2020-02-03
License	CC BY-SA
Number of Datasets	373 (Image datasets: 187, Quantitative datasets: 186)
Organism(s)	C. elegans
Kind	Quantitative data, Image data based on Experiment
Datatype	nuclear division dynamics
Molecular Function (MF)	
Biological Process (BP)	embryo development
Cellular Component (CC)	nucleus
Medical Subject Headline	
Biological Imaging Method	
Paper	Kyoda K, Adachi E, Masuda E, Nagai Y, Suzuki Y, Oguro T, Urai M, Arai R, Furukawa M, Shimada K, Kuramochi J, Nagai E, and Onami S, (2013), WDD: Worm Developmental Dynamics Database., Nucleic acids research, Volume 41, Issue Database issue, pages D732-7, DOI: 10.1093/nar/gks1107
Contact	Shuichi Onami , RIKEN , Quantitative Biology Center , Laboratory for Developmental Dynamics
Contributors	Eru Adachi, Eriko Masuda, Yoko Nagai, Yoko Suzuki, Taeko Oguro, Koji Kyoda, Shuichi Onami

データについての説明

- メタデータ
- データセット数
- 論文情報

		SSBD:OMERO.gallery	SSBD:OMERO index	可視化	ダウンロード
#	Dataset ID	Dataset Kind	4D View	SSBD:OMERO	Download BDML
2	RNAI_B0336.10_040518_01	Image data	4D View	gallery index	DL. Image
3	RNAI_B0336.10_040518_01	Quantitative data	4D View		DL. BDML DL. Image
4	RNAI_B0336.10_040518_02	Image data	4D View	gallery index	DL. Image
5	RNAI_B0336.10_040518_02	Quantitative data	4D View		DL. BDML DL. Image

画像データの可視化

OMEROによる画像データの観察



The image shows the OMERO software interface. On the left, the 'Explore' panel displays a list of projects and image files. A red box highlights the 'mitral cell distribution-1.oib' file. An orange arrow points from this file to the main viewer window on the right. The viewer window shows a fluorescence microscopy image of mitral cells with green and red channels. A blue box labeled 'スライダーによるz焦点面変更' (Slider for changing the z-focus plane) points to the vertical slider on the left side of the viewer. Another blue box labeled '可視化パラメータの設定' (Visualization parameter settings) points to the right-hand panel where visualization parameters like grayscale, histogram, and interpolation are set. A red box labeled '画像データのメタデータ' (Image data metadata) points to the 'Image Details' section in the central viewer area. A final red box labeled 'ファイルに含まれるメタデータ' (Metadata included in the file) points to the 'Key-Value Pairs' section below it.

■ 3つのパネル

- プロジェクト
- 画像データファイルの一覧表示
- 画像データのメタデータ表示

■ OMEROビューアー

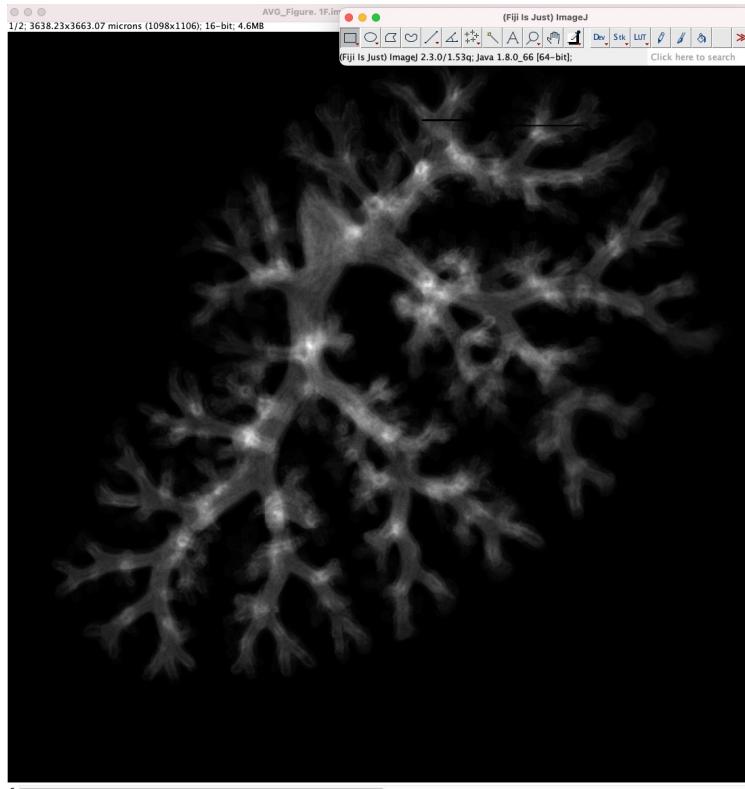
- スライダーによるz面・時点tの変更
- 可視化パラメータの設定
- ヒストグラムなどの簡単な解析

画像データの可視化

ファイルダウンロードとFiji、napariによるデータ観察



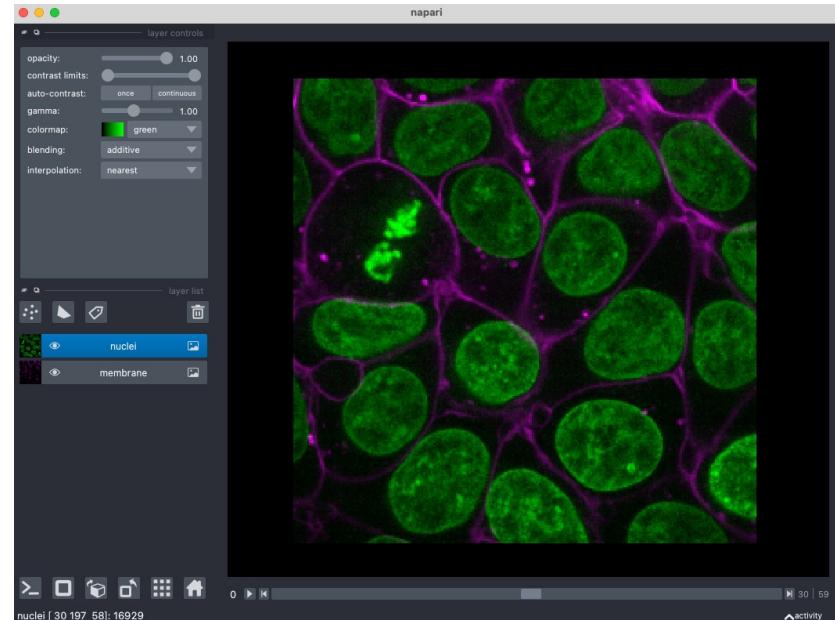
<https://fiji.sc/>



File → Import → Bio-Formats で画像データを読み込む

Fiji

<https://napari.org/stable/>



napari

定量データの可視化

SSBD-4DViewer による定量データの観察



SSBD:database

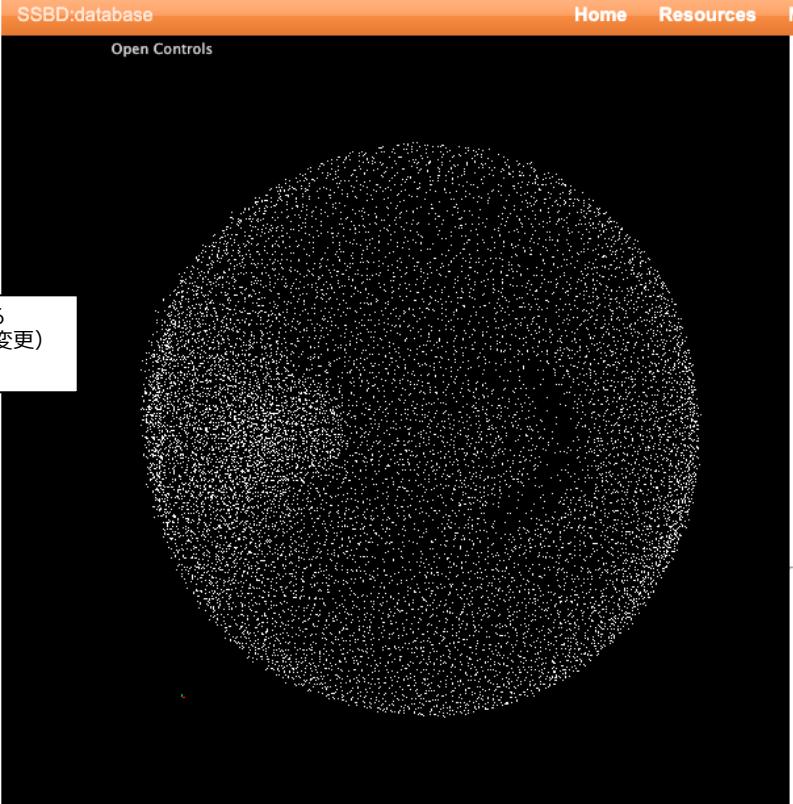
English/日本語 ▾

SSBD:database

Home Resources Manuals Publications News Software

Open Controls

マウス操作による
■ 回転（視点の変更）
■ ズームIn/Out



スライダーによる時点変更

Time series index (tsi): 437 Time (second): 39420.1

LOADING 100% Complete

データ読み込み状況の表示

データのメタデータ

BDML ID: f076c9ea-1bf2-475a-9ec2-4fcfbfe3a3ac

Title: BDML file for *in toto* reconstruction of zebrafish wild-type development

License: CC BY-NC-SA license

Description: *in toto* reconstruction of zebrafish wild-type development

Organism: D. rerio

Datatype: nuclear positions

Identifier: zebrafish_in_toto_wt.mat

Basedon: Experiment

Contributors: Philipp Keller, Annette Schmidt, Joachim Wittbrodt, Ernst Stelzer

PubMed ID: [18845710](#)

Summary of methods: See details in Keller et al. (2008) Science 322, 1065-1069.

Data Scale (XYZ, T): 1.0 x 1.0 x 1.0 (micrometer), 90.0 (second)

This 4D rendering is only an approximation of the actual data.
For more details please download the BDML file
or access it through the [RESTful API](#).

* 簡易的な可視化であることに注意
(データが間引きされている場合がある)

定量データの可視化

ファイルダウンロードとHDFViewによるデータの中身の閲覧



<https://www.hdfgroup.org/downloads/hdfview/>

The screenshot shows the main navigation bar of The HDF Group website. Under the 'Downloads' section, 'HDFView' is highlighted. Below it, there is a brief description of what HDFView is and how to download it.

Download the Latest Version

Current Release: HDFView 3.1.4

- HDFView License Info
- HDFView and Java Object Package Support Page

HDFView Software

HDFView software consists of the HDFView utility and the Java HDF Object Package.

HDFView is a visual tool written in Java for browsing and editing HDF (HDF5 and HDF4) files. Using HDFView, you can:

- View a file hierarchy in a tree structure
- Create new files, add or delete groups and datasets
- View and modify the content of a dataset
- Add, delete and modify attributes

HDFView uses the Java HDF Object Package, which implements HDF4 and HDF5 data objects in an object-oriented form.



The screenshot shows the HDFView 3.1.3 interface. It displays a tree view of an HDF5 file structure on the left, with several expanded nodes. Three specific nodes are highlighted with callouts and labeled:

- 計測したオブジェクトの定義**: A table for defining measured objects, showing columns for oid and name, with a single entry for 'nucleus'.
- 次元、スケールとユニットの定義**: A table for defining dimensions, scales, and units, showing columns for dimension, xScale, yScale, zScale, sUnit, tScale, and tUnit, with entries for '3D+T' and 'microm... minute'.
- (x, y, z, t) 座標情報と付随する情報**: A table for coordinate information, showing columns for ID, t, entity, x, y, z, radius, and label, with multiple entries for spheres.

At the bottom, there is a terminal-like window showing the command line used to run HDFView and the path to the file being viewed.

(Kyoda et al. (2020) PLoS One)

画像データの解析



ツールの利用

Fiji

ilastik

CellProfiler
CellPose

ノートブックの利用



A simple SSBD wrapper API to access images

```
In [0]: source = "ssbd"
class ssbd_image_api(object):
    BASE_URL = "http://ssbd.qbic.riken.jp/image/"
    if source == "idr":
        BASE_URL = "https://idr.openmicroscopy.org/"
    imageApi = BASE_URL+"webgateway/render_image/"
    metadataApi = BASE_URL+"webclient/imgData/"
    fmt = "?format=json;"
```

```
# getting an image from SSBD given a image id, z and t
```

```
def get_image(self, id, z, t):
    parameters = self.imageApi+str(id)+"/"+str(z)+"."+str(t)
```

```
print(parameters)
```

```
resp = requests.get(parameters)
```

```
if resp.status_code != 200:
```

```
    # This means something went wrong
```

```
    sys.exit()
```

```
imgdata = cv2.cvtColor(np.array(Image.open(BytesIO(resp.content))), cv2.COLOR_RGB2GRAY)
```

```
return imgdata
```

```
def get_metadata(self, id):
    parameters = self.metadataApi+str(id)
```

```
print(parameters)
```

```
resp = requests.get(parameters)
```

```
if resp.status_code != 200:
```

```
    # This means something went wrong
```

```
    sys.exit()
```

```
metadata = resp.json()
```

```
return metadata
```

```
In [3]: imageid = 33724
```

```
if source == "idr":
```

```
    imageid = 1884821
```

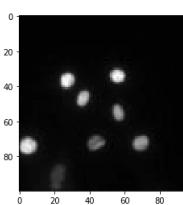
```
ssbdimg = ssbd_image_api()
```

```
example_img = ssbdimg.get_image(imageid, 0, 0)
```

```
http://ssbd.qbic.riken.jp/image/webgateway/render_image/33724/0/0
```

```
In [4]: plt.imshow(example_img, 'gray')
```

```
Out[4]: <matplotlib.image.AxesImage at 0x7f25dbe63f60>
```



プログラミングで画像解析をする

画像データの解析

Jupyter Notebookを使った画像解析



Jupyter nbviewer

JUPYTER FAQ </> ⌂ ⌄ ⌅ ⌆

A simple SSBD wrapper API to access images

```
In [0]: source = "ssbd"
class ssbd_image_api(object):
    BASE_URL = "http://ssbd.qbic.riken.jp/image/"
    if source == "idr":
        BASE_URL = "https://idr.openmicroscopy.org/"
    imageApi = BASE_URL+"webgateway/render_image/"
    metadataApi = BASE_URL+"webclient/imgData/"
    fmt = "?format=json"

    # getting an image from SSBD given a image id, z and t
    def get_image(self, id, z, t):
        parameters = self.imageApi+str(id)+"/"+str(z)+"/"+str(t)
        print(parameters)
        resp = requests.get(parameters)
        if resp.status_code != 200:
            # This means something went wrong
            sys.exit()
        imgdata = cv2.cvtColor(np.array(Image.open(BytesIO(resp.content))), cv2.COLOR_RGB2GRAY)
        return imgdata

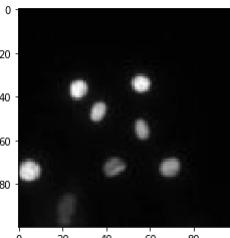
    def get_metadata(self, id):
        parameters = self.metadataApi+str(id)
        print(parameters)
        resp = requests.get(parameters)
        if resp.status_code != 200:
            # This means something went wrong
            sys.exit()
        metadata = resp.json()
        return metadata
```

```
In [3]: imageid = 33724
if source == "idr":
    imageid = 1884821
ssbdimg = ssbd_image_api()
example_img = ssbdimg.get_image(imageid, 0, 0)

http://ssbd.qbic.riken.jp/image/webgateway/render_image/33724/0/0
```

```
In [4]: plt.imshow(example_img, 'gray')
```

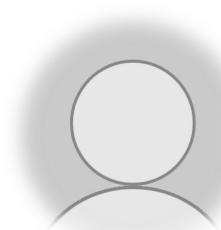
```
Out[4]: <matplotlib.image.AxesImage at 0x7f25dbe63f60>
```



- Webブラウザ上でプログラム開発・実行
 - Pythonを含む複数の言語に対応
 - インタラクティブにプログラムを実行
 - ノートブックとして保存、再実行が可能
 - ノートブックの共有

画像データ解析の例

Google Colabでのプログラムの実行



FRETの画像データを読み込んで
ERKの活性を計測するデモンストレーション

<https://nbviewer.org/github/openssbd/hikarijuku/blob/master/ImageSeries.ipynb>

Jupyter nbviewer

HikariJuku 2019

See details in Aoki et al. (2013) Molecular Cell, 52(4): 529-540 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3647000/>

In [1]:

```
import sys
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline

# HTTP library
import requests

# Stream of in-memory bytes
from io import BytesIO
# PIL library
from PIL import Image
# OpenCV library
import cv2
# math library
import math

from skimage.segmentation import active_contour
print(cv2.__version__)
# tested Python 2 or 3 + OpenCV v 3.2.0
3.4.3
```

A simple SSBD wrapper API to access images

In [2]:

```
source = "ssbd"
class ssbd_image_api(object):
    BASE_URL = "http://ssbd.qbic.riken.jp/image/"
    if source == "idr":
        BASE_URL = "https://idr.openmicroscopy.org/"
    imgDataApi = BASE_URL+"webgateway/render_image/"
    metaDataApi = BASE_URL+"webclient/imgData/"
    fmt = "?format=json"

    # getting an image from SSBD given a image id, z, and t
    def get_image(self, id, z, t):
        parameters = self.imageApi+str(id)+"/"+str(z)+"/"+str(t)
        print(parameters)
        resp = requests.get(parameters)
        if resp.status_code != 200:
            # This means something went wrong
            sys.exit()
        imgdata = cv2.cvtColor(np.array(Image.open(BytesIO(resp.content))), cv2.COLOR_RGB2GRAY)
        return imgdata

    def get_metadata(self, id):
        parameters = self.metadataApi+str(id)
        print(parameters)
        resp = requests.get(parameters)
        if resp.status_code != 200:
            # This means something went wrong
            sys.exit()
        metadata = resp.json()
        return metadata
```

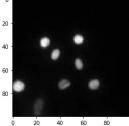
In [3]:

```
imageid = 33724
if source == "idr":
    imageid = 1884821
ssbdimg = ssbd_image_api()
example_img = ssbdimg.get_image(imageid, 0, 0)
http://ssbd.qbic.riken.jp/image/webgateway/render_image/33724/0/0
```

In [4]:

```
plt.imshow(example_img, 'gray')
```

Out[4]:



File Edit View Insert Runtime Tools Help Cannot save changes

+ Code + Text Copy to Drive

See details in Aoki et al. (2013) Molecular Cell, 52(4): 529-540 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3647000/>

[1]

```
import sys
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline

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import requests

# Stream of in-memory bytes
from io import BytesIO
# Pillow library
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# OpenCV library
import cv2
# math library
import math

from skimage.segmentation import active_contour

print(cv2.__version__)
# tested Python 2 or 3 + OpenCV v 3.2.0
4.6.0
```

順番にセル内のプログラムを実行

- A simple SSBD wrapper API to access images

[2]

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source = "ssbd"
class ssbd_image_api(object):
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        BASE_URL = "https://idr.openmicroscopy.org/"
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            sys.exit()
        imgdata = cv2.cvtColor(np.array(Image.open(BytesIO(resp.content))), cv2.COLOR_RGB2GRAY)
        return imgdata

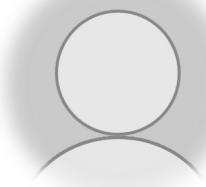
    def get_metadata(self, id):
        parameters = self.metadataApi+str(id)
        print(parameters)
        resp = requests.get(parameters)
        if resp.status_code != 200:
            # This means something went wrong
            sys.exit()
        metadata = resp.json()
        return metadata
```

imageid = 33724
if source == "idr":
 imageid = 1884821
ssbdimg = ssbd_image_api()
example_img = ssbdimg.get_image(imageid, 0, 0)
http://ssbd.qbic.riken.jp/image/webgateway/render_image/33724/0/0

[] plt.imshow(example_img, 'gray')

定量データの解析

BD5 ファイルの読み書きを行うサンプルコード



Python

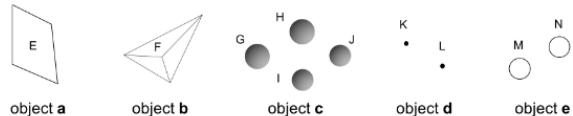
https://github.com/openssbd/BD5_samples/

Sample codes and tools for reading and writing BD5 file format

- This repository contains the sample source codes for reading and writing BD5 file formats using Python in Jupyter notebook.
- The samples include codes using either the h5py or pytables packages.

Sample codes in Jupyter notebook:

Sample codes for writing BD5 object entities:



- Writing out object entities, line, point, circle, sphere and face.

- BD5write_numpy** (uses h5py) with explanation
 - Writing line, face, sphere, point and circle objects as numpy array to BD5 files.
- BD5write_circle_details** (uses pytables) with explanation
- BD5write_circle** (uses pytables)
 - Reading in an image segmentation data stored in a TIFF image file, and write it as a circle in BD5 format.
- BD5write_point** (uses pytables)
 - Reading in an image segmentation data stored in a TIFF image file, and write it as a point in BD5 format.
- BD5write_line** (uses pytables)
 - Reading in an image segmentation data stored in a TIFF image file, and write it as a line in BD5 format.

各object entityのデータに対するファイル出力

Sample codes for writing BD5 files using h5py

- CSVread_BD5write** (uses h5py) with explanation
 - Reading in a BD5 file and writing out a CSV file/Reading in CSV file and writing out a BD5 file
- BD5write_numpy** (uses h5py)
 - Writing line, face, sphere, point and circle numpy arrays to BD5 files
- BD5Append_trackinfo_point** (uses h5py) with explanation
 - Reading in a BD5 file with time series points and then append the trackinfo points and then append the trackinfo
- BD5read_count** (uses h5py)
 - Reading in an existing BD5 file and do some simple analysis by counting the number of nuclei vs time point and plotting out a proliferation curve of *C.elegans*.
- BD5read_displacement** (uses h5py)
 - Reading in an existing BD5 file and do some simple analysis by calculating the displacement of ABal nucleus of *C.elegans*

h5pyを利用したBD5ファイルの入出力

Sample codes for writing BD5 files using pytables

- BD5write_circle_details** (uses pytables) with explanation
- BD5write_circle** (uses pytables)
 - Reading in an image segmentation data stored in a TIFF image file, and write it as a circle in BD5 format.
- BD5write_point** (uses pytables)
 - Reading in an image segmentation data stored in a TIFF image file, and write it as a point in BD5 format.
- BD5write_line** (uses pytables)
 - Reading in an image segmentation data stored in a TIFF image file, and write it as a line in BD5 format.
- BD5write_timesteries_point** (uses pytables) with explanation
 - Reading in two time series ROIs data stored in TIFF image files, and track the objects over the two time points and write that to a BD5 file.

pytablesを利用したBD5ファイルの出力

C++

<https://github.com/openssbd/BDML2BD5>

DrKenHo Update README.md		
LICENSE	Create LICENSE	2 years ago
README.md	Update README.md	2 years ago
bdml0.18.xsd	Add files via upload	2 years ago
bdml2bd5.cxx	bug fixed	2 years ago
feature.h	Add files via upload	2 years ago
fromto.h	Add files via upload	2 years ago
makefile	Add files via upload	2 years ago
object.h	Add files via upload	2 years ago
objectentity.h	Add files via upload	2 years ago
pelement.h	Add files via upload	2 years ago
property.h	Add files via upload	2 years ago
series.h	bug fixed	2 years ago
sunit.h	Add files via upload	2 years ago
trackinfo.h	Add files via upload	2 years ago
xyz.t	Add files via upload	2 years ago

README.md

BDML2BD5

BDML2BD5 is a converter from BDML file to BD5 file

- A docker container for BDML2BD5 is available at <https://github.com/openssbd/bdml2bd5-docker>
- BDML2BD5 is built on a Debian based linux distribution. For details in building it, please consult the Dockerfile here: <https://github.com/openssbd/bdml2bd5-docker/blob/master/Dockerfile>

XMLを基盤としたBDMLファイルをBD5ファイルに変換するプログラム

定量データ解析の例



BD5 ファイルの読み書きと簡単な解析プログラム

https://github.com/openssb/BD5_samples/blob/master/BD5read_count.ipynb

BD5read_count - reading in an existing BD5 file and analyse the data.

BD5read_count is a sample code to demonstrate how to read in an existing BD5 file and do some simple analysis by counting the number of nuclei vs time point and plotting out a proliferation curve of *C.elegans*.

We choose an existing BD5 file from the SSBD:database.

Ref: Bao et al. (2006) Proc Natl Acad Sci USA 103, 2707-2712.

SSBD:database ref: <http://ssbd.qbic.riken.jp/search3/800faa21-c28c-4b72-bd12-d41f2eed02e8/>

```
In [1]: # Author: Koji Kyoda
# sample code for reading an existing BD5 file perform some analysis.

import h5py

In [2]: file = "081505_L1_bd5.h5"
f = h5py.File(file, "r")
groups = f["data"]
```

BD5の読み込み

```
In [3]: import time
import matplotlib.pyplot as plt
import warnings
import matplotlib.cbook
warnings.filterwarnings("ignore",category=matplotlib.cbook.mplDeprecation)

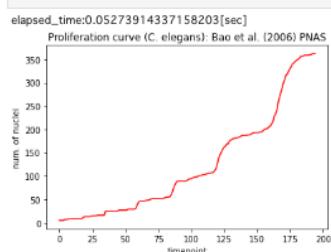
if __name__ == "__main__":
    start = time.time()
    no_of_nucleus = []
    timept = []
    count = 0
    while str(count) in groups.keys():
        name = "/data/" + str(count) + "/object/0"
        dset = f[name]
        timept.append(count)
        no_of_nucleus.append(dset.len())
        count += 1

    fig=plt.figure()
    plt.plot(timept, no_of_nucleus, 'r')
    ax = fig.add_subplot(1,1,1)
    ax.set_ylabel('num. of nuclei')
    ax.set_xlabel('timepoint')
    plottitle = 'Proliferation curve (C. elegans): Bao et al. (2006) PNAS'
    plt.title(plottitle);

    elapsed_time = time.time() - start
    print ("elapsed_time:{0}" .format(elapsed_time) + "[sec]")

elapsed_time:0.05273914337158203[sec]
```

検出したオブジェクトの数の時間変化をグラフ化



線虫の胚発生における細胞（核）数の増加曲線

日本のバイオイメージングデータ共有システム



SSBD:database

SSBD:database

Organism: ex. C. elegans

Search Clear

Introduction

System Science of Biological Dynamics database (SSBD:database) provides a rich set of open resources for analyzing quantitative data and microscopy images of biological objects, such as single-molecule, cell, gene expression nuclei, etc. Quantitative biological data and microscopy images are collected from a variety of species, sources and methods. These include data obtained from both experiment and computational simulation.

Samples

Microscopy Images

Calcium response and shape changes in oocyte of C. elegans

DIC image of nuclear division dynamics in C. elegans embryo

TEM image of retinal tissue from human embryonic stem cells

News

2020-12-24, SSBD 2020 Update
SSBD 2020 update, the metadata database fully renewed, and 77 image datasets (7GB) and 4 quantitative datasets are added. We are planning next database update in a half year for COVID-19 situation.

2020-08-12, A new paper on BD5 is published in PLOS ONE
A new paper "BD5: an open HDF5-based data format to represent quantitative biological dynamics data" is now published in PLOS ONE.
<https://doi.org/10.1371/journal.pone.0237468>

Older news...

Funding

OLSP, 科研費, JST, NBDC, 理研

SSBD:repository

Organism: ex. C. elegans

Search Clear

Introduction

System Science of Biological Dynamics repository (SSBD:repository) is an open data archive that stores and publishes bioimaging and biological quantitative datasets that are associated with published or to be published studies. It allow other researchers to access and download those datasets for reference or for further investigations.

Find the dataset from search box above, or see the dataset list in [Resources](#).

SSBD:repository has started operation in 2016, under the life science database integration promotion project of the Japan Science and Technology (JST), National Bioscience Database Center (NBDC). Currently it is funded from RIKEN, JST and Grant-in-Aid for Scientific Research from the Ministry of Education, Culture, Sports, Science and Technology of Japan (MEXT).

For an overview of the SSBD:database/repository, please refer to the paper,
Tohsato, Y., Ho, K. H. L., Kyoda, K., and Onami S. (2016) "SSBD: a dataset of quantitative data of spatiotemporal dynamics of biological phenomena." *Bioinformatics*, 32(22): 3471-3479
<https://doi.org/10.1093/bioinformatics/btw417>

Share your data in SSBD:repository

SSBD:repository covers a wide range of biological phenomena, from single molecules to cells / individuals. DOI (Digital Object Identifier) can be assigned to each dataset. Datasets in SSBD:repository are licensed under CC BY, CC BY-NC-SA, etc, upon request of the data contributors.

If you would like to share your image data or quantitative data of biological phenomena, or any

SSBD:repository

SSBD:repository

Organism: ex. C. elegans

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<https://doi.org/10.1093/bioinformatics/btw417>

News

2021-02-09, System maintenance on Feb 9
Due to system maintenance, the 4D visualizer and APIs will not be available on Feb 9, 9:00-16:00. Sorry for the inconvenience.

2020-12-24, SSBD 2020 Update
SSBD 2020 update, the metadata database fully renewed, and 77 image datasets (7GB) and 4 quantitative datasets are added. We are planning next database update in a half year for COVID-19 situation.

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Older news...

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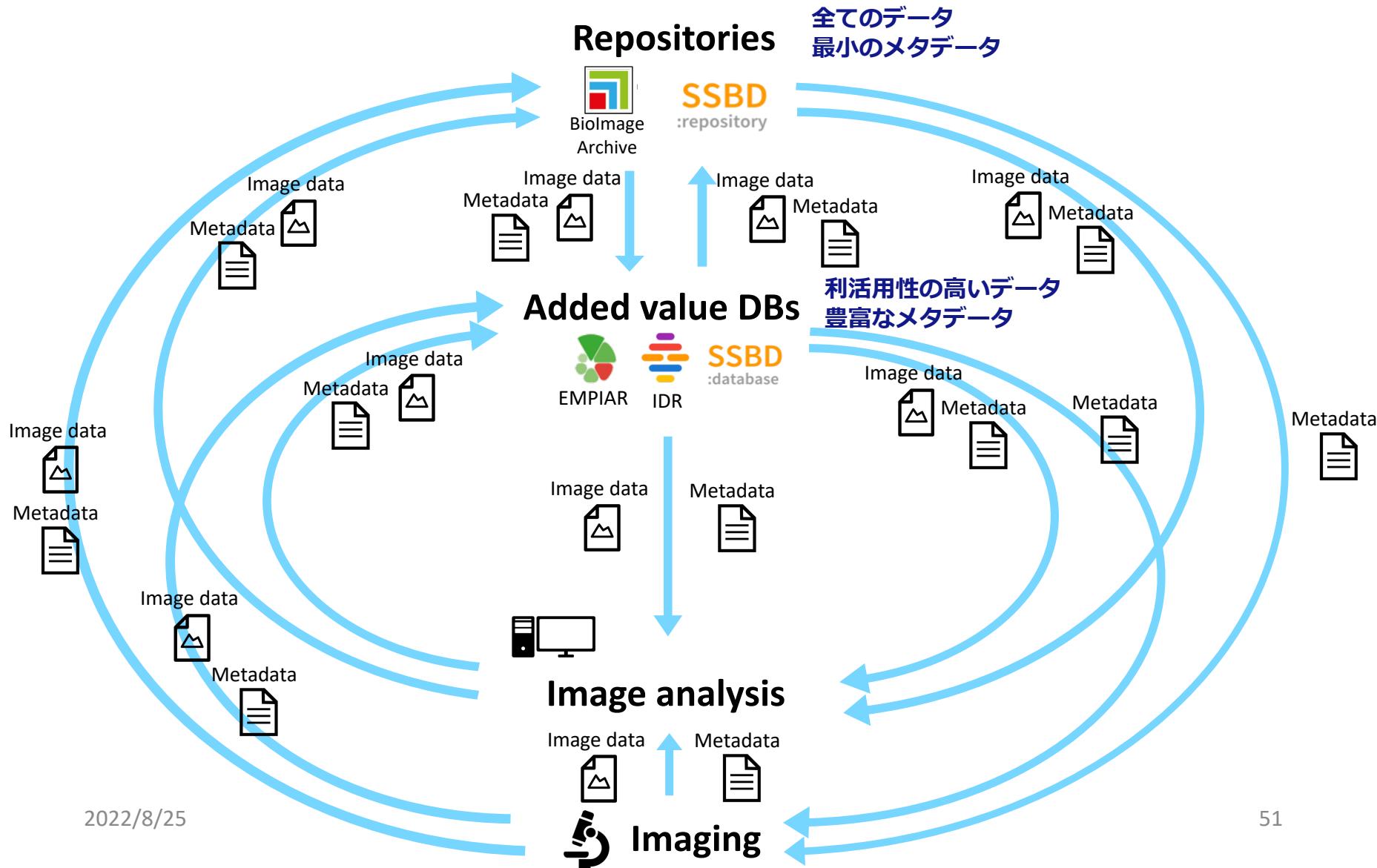
OLSP, 科研費, RIKEN

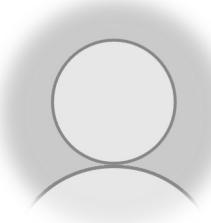
- 生命科学画像データと生命動態定量データの**Added-Value DB**
 - 2013年9月、JST-NBDCの資金で開設
 - 理研、JST、KAKENHI等からの資金で運営
 - 研究機関、研究プロジェクト、学会等と連携して、全国の最先端バイオイメージングデータを集積、公開
- 2021/8/25

- 2016年5月にSSBDデータベースに付属した生命科学画像データと生命動態定量データの**リポジトリサービス**として開始
- 2019年9月にSSBD:repositoryとしてSSBD:databaseより分離
- 現在は、理研、JST、KAKENHI等からの資金で運営



日欧のバイオイメージングデータのエコシステム





SSBD:repository をご活用下さい

- まずは、メールでお問い合わせ下さい
ssbd-repos@ml.riken.jp



Acknowledgement

SSBD Team/RIKEN BDR

Shuichi Onami
Koji Kyoda
Yukako Tohsato
Yukiko Yamagata
Fanfan Wang

ex-member

Kenneth Ho
Yasue Nakano

RIKEN OLSP

Masanori Arita
Takeya Kasukawa
Norio Kobayashi
Hiroshi Masuya
Tomomi Shimogori
Hideo Yokota

ABiS/NIBB

Naoto Ueno

OME/IDR/U Dundee

Jason Swedlow
Josh Moore
Sebastien Besson
Jean-Marie Burel
Petr Walczysko

Global BioImaging/EMBL-EBI

Antje Keppler
Federica Paina

BioImage Archive/EMBL-EBI

Matthew Hartley

BINA/Umass Chan Med School

Caterina Strambio-De-Castillia

QUAREP-LiMi/Albert-Ludwigs U

Roland Nitschke

Community

ABiS
BINA
Euro-BioImaging
Global BioImaging
OME
RIKEN Open Life Science Platform
QUAREP-LiMi

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CREST, JST
NBDC, JST
MEXT
KAKENHI
RIKEN BDR DECODE Project
RIKEN RCSTI Project



科技ハブ
産連本部

