Al for automated data collection & analysis - an ESRF perspective



The European Synchrotron

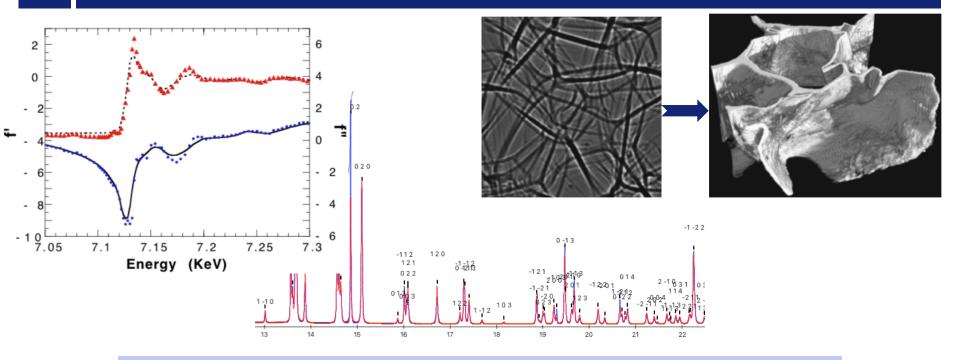
Vincent Favre-Nicolin

Algorithms & scientific Data Analysis ESRF / Experiments division



STREAMLINE has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No. 870313

SYNCHROTRON DATA ANALYSIS, CIRCA 2000

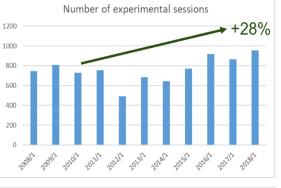


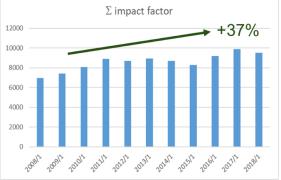
20 years ago analysing data was simpler:

- 1. Collect data (absorption spectrum, powder pattern, image..)
- 2. Fit data & determine sample structure, reconstruct 3d image (explicit modelling, local or global optimisation)
- 3. Publish !



FROM DATA COLLECTION TO DATA EXPLOITATION





Beamtime usage and data exploitation over the 2008-2018 period

2/3 of the beamline portfolio are offering "expert" emerging techniques: (ptychography, coherent diffraction imaging, serial crystallography, diffraction-contrast tomography, etc.)

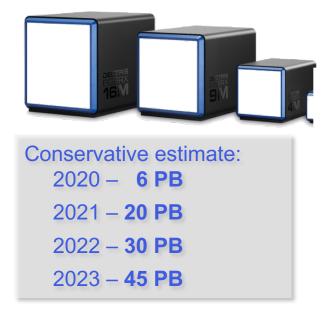


Dramatic increase of raw data produced by most beamlines

- #publications is stalling despite the increase in the #experiments !
- Delay experiment-publication=3years?
- Too much data ?
- No time to analyse ?
- Lack of good decisions during experiments ?

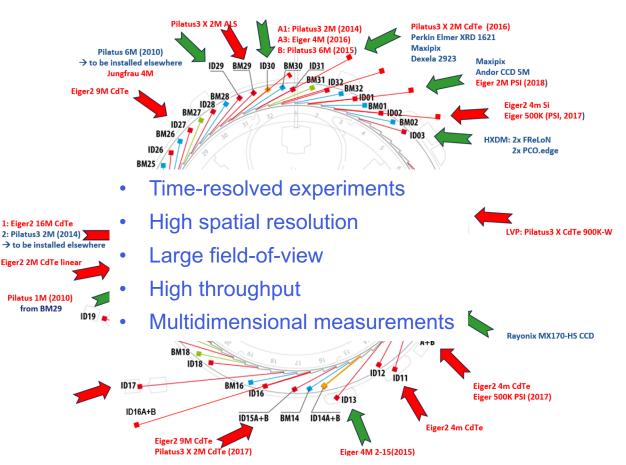


TOWARDS BIG DATA

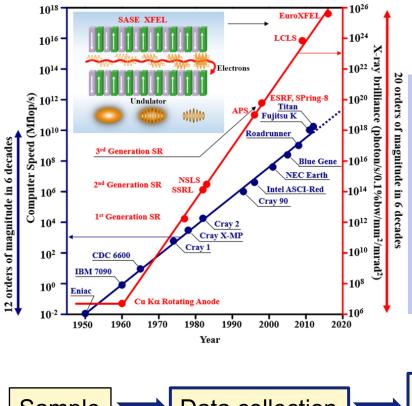


Beyond imaging: Ability to measure thousands, millions of spectra, powder patterns,...

Detector portfolio for the scattering beamlines



CHALLENGES FOR MODERN SYNCHROTRON DATA ANALYSIS



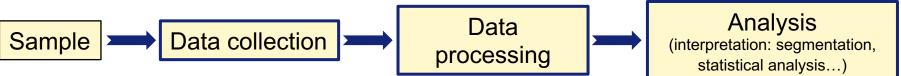
- nb neurons in human brain: 10¹²
- nb synapses10¹⁴-10¹⁵

More photons:

10¹² photons/s (10¹⁷-10¹⁸ photons/experiment)

Need to:

- Process data
- Manage radiation damage
- Interpret individual datasets
- Explore encyclopaedia of data



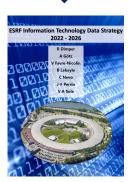


THE DATA CHALLENGE REQUIRES A HOLISTIC APPROACH

- Explosion of the data volume
- Significant increase of complexity of the data sets
- limited dedicated resources

DATA reduction, pre-processing and on-line analysis activities, in collaboration with other synchrotron centres

Establishing pipelines enabling ESRF user to benefit from National and European High Power Computing Centres for DATA analysis and modelling



DATA access and handling in collaboration with many other partners.

ESRF IT Data Strategy

DATA

EXPLOITATION

DATA POLICY

Hardware infrastructure providing DATA storage Capacity, and CPU and GPU power

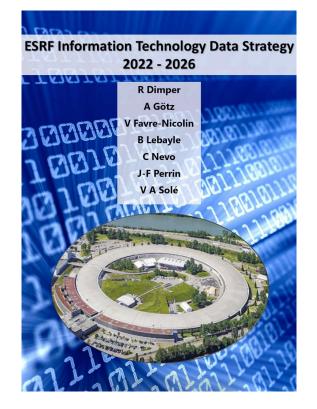
Beamline and experiment control and automation. Online data analysis



BEAMTIME

USAGE

ESRF IT DATA STRATEGY



Agenda Item # 13

https://www.esrf.fr/cms/live/live/en/sites/www/home/about/documentation.html



EXPD: ALGORITHMS & SCIENTIFIC DATA ANALYSIS (ADA)

- Provide software for data analysis, during or after experiments, on ESRF or external hardware
- 2) Develop & improve algorithms to handle high-throughput and big data using High Performance Computing techniques
- 3) Coordinate software development with the relevant beamlines, the ISDD software group and TID systems & communication, notably for Online Data Analysis solutions

Personnel: 6 permanent + 3 time-limited

(+7 FTE to be opened)





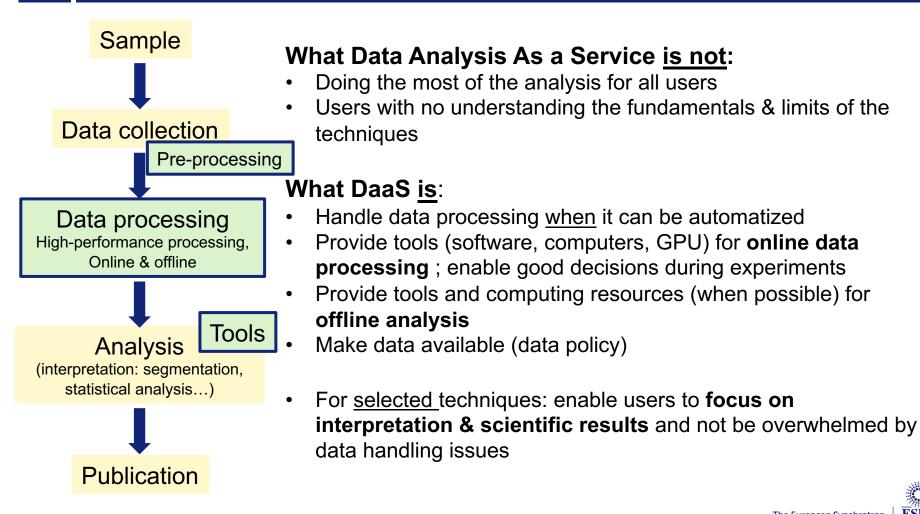
Key applications (priority given to high-throughput and flagship beamlines):

- Tomography tools (full field, XRD-CT, XRF-CT..)
- Scattering: fast azimuthal integration for powder diffraction / SAXS / WAXS
- Serial Crystallography (ID29)
- Coherent Imaging techniques
- **Spectroscopy**: scanning and core spectroscopies, including machine learning

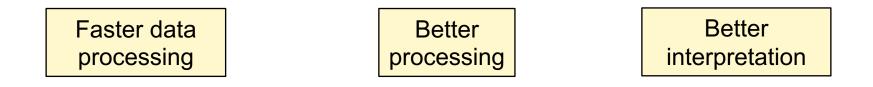


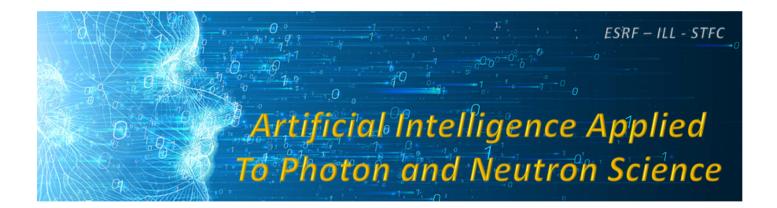
STREAMLINE

DATA ANALYSIS AS A 'SERVICE' ?



MACHINE LEARNING FOR SYNCHROTRON ?





Design better experiments Automated data collection



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1. Faster data processing

- 2. Better processing
- 3. Data Analysis
- **4. Instrument configuration**
- 5. Automated data collection
- 6. Framework for Online Data Analysis
- 7. Open Data



Example of ESRF / ID16B

Fast holo-tomography:

In-situ experiments can be done at lower resolution every 7s for up to two hours, i.e. 2000 scans, and this can be repeated three to five times a day, possibly up to eight times with improved alignment procedures.

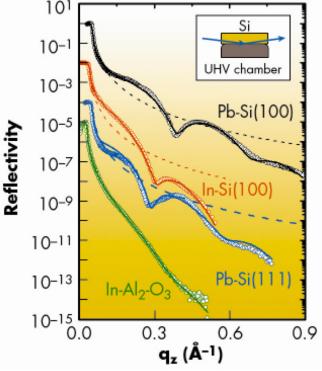
1 scan currently needs ~360 CPU cores.day

Assuming 3 000 scans per day, this would require a peak demand of 250 000 CPU cores

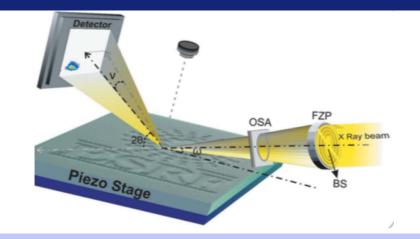




X-RAY REFLECTIVITY



Phys. Rev. Lett. 98, 116101 (2007) J. Appl. Cryst. **47**, 762–769 (2014) Page 13 I GdR IAMat I 2022-05-30 I Vincent Favre-Nicolin



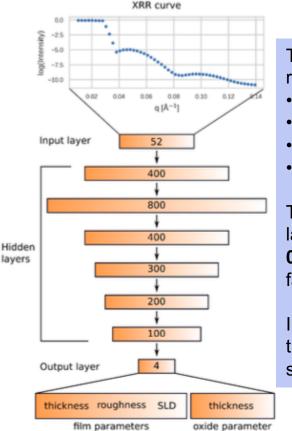
X-ray reflectivity: measure the (specular) reflected intensity allows retrieving the electronic density $\rho(z)$ as a function of depth.

This can be **fitted** (Monte-Carlo, least squares, genetic algorithms) to retrieve the thickness and roughness of layers.

Fast (continuous) scanning allows with a bright beam allows to scan surfaces up to 10³-10⁴ positions/s, allowing to acquire reflectivity curves for thousands-millions of points.



X-RAY REFLECTIVITY FITTING WITH NEURAL NETWORK

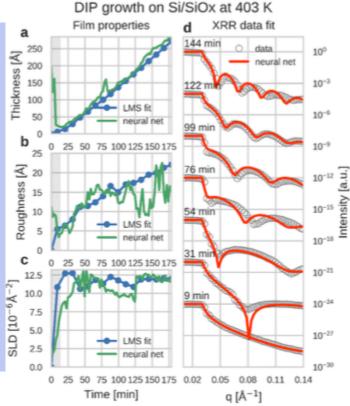


Training a neural network with a range of film parameters:

- Thickness
- Roughness
- Scattering length density
- Substrate thickness

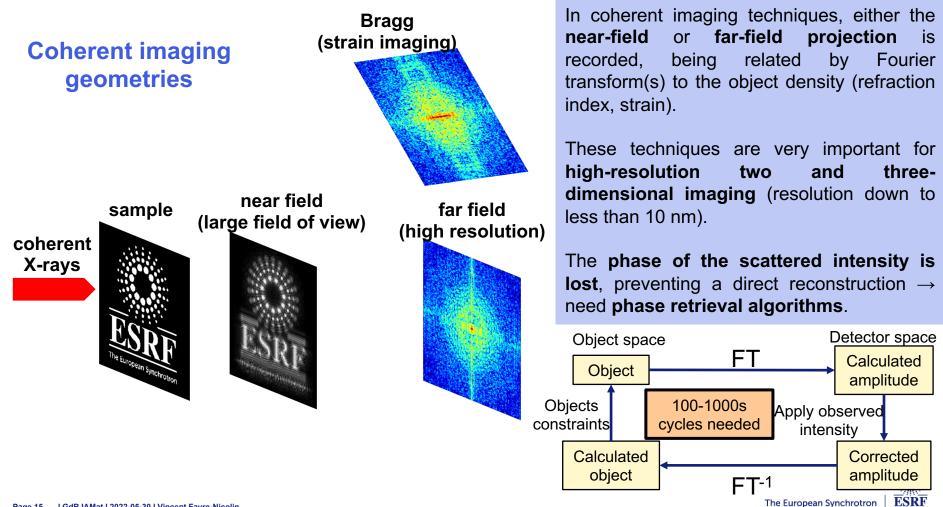
The resulting NN allows to predict the layers parameters with a **speed of 0.03-77 milliseconds per curve** – fast enough for live analysis.

Important: predictions are limited to the range of the simulated training set.

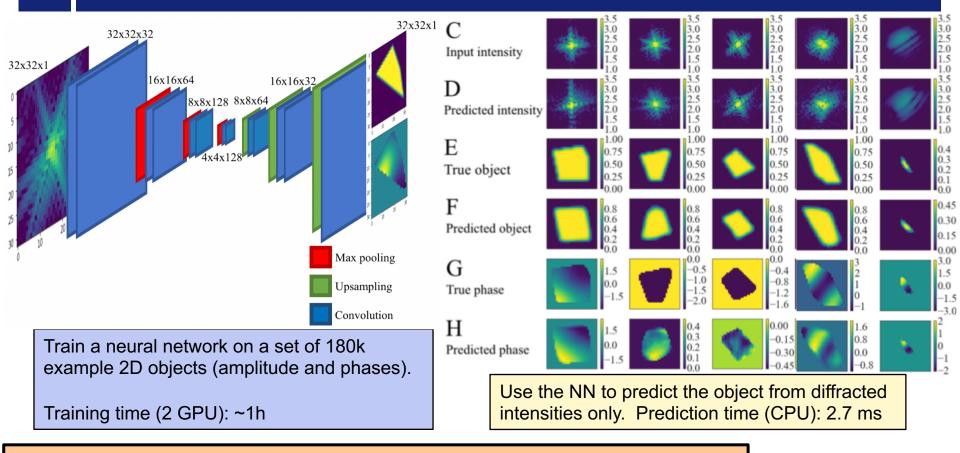




COHERENT IMAGING



COHERENT DIFFRACTION IMAGING



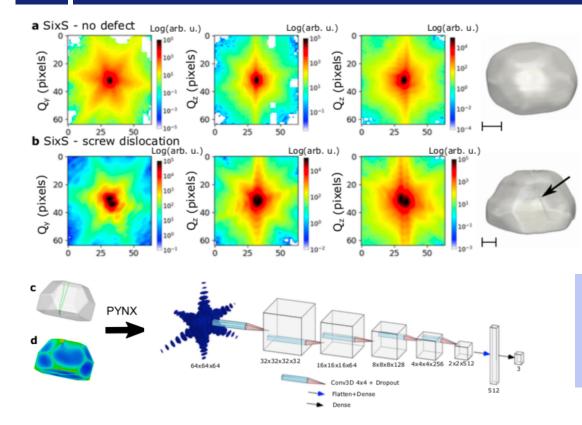
Caveats:

- Real data sets often 3D, usually 200³ to 500³ pixels large
- Fine tuning of object density and phase can take longer than initial assessment

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Sci. Rep. 8 (2018), 16520

CDI– NN DEFECTS IDENTIFICATION



In CDI, dislocations can be identified by a split-peak in the diffraction pattern

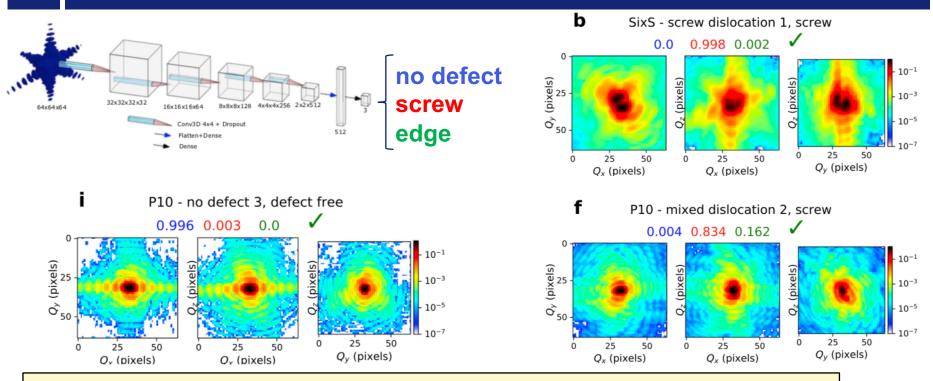
Train a NN on a variety of nanoobjects shapes and for different types of dislocations (none, screw, edge).



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Npj Comput. Mater. 7 (2021), 115

CDI– NN DEFECTS IDENTIFICATION



The NN allows to quickly identify the presence and type of dislocation.

This could be used for quick/automated identification when scanning many particles



Npj Comput. Mater. 7 (2021), 115

ML-BASED DATA ANALYSIS LIMITS ?

Benefits of Machine Learning for data analysis are clear:

- Fast results
- Nonlinear modelling

However:

- Results may not be better than traditional fitting..
- So a double approach may be required, with a fast ML step followed by a standard refinement
- The resources needed (human and computing) are increased (unless the approximate solution is enough)



1. Faster data processing

2. Better processing

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5. Automated data collection

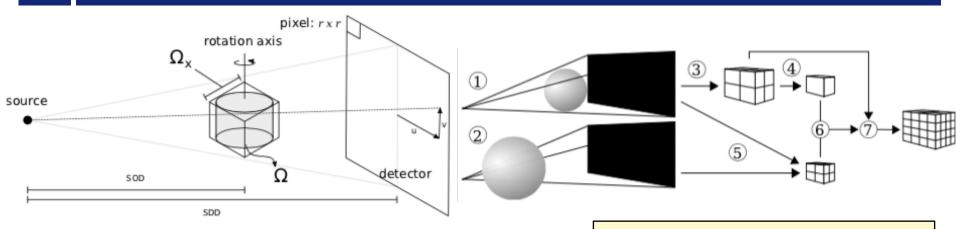
6. Framework for Online Data Analysis

7. Open Data

Key idea: try to get **more information** from the same datasets (**higher signal/noise**) compared to traditional algorithms



PHASE CONTRAST IMAGING: IMPROVE RESOLUTION



In phase contrast imaging, valuable improvements include:

- High resolution object from low resolution image
- Exploiting low signal/noise data

This would allow:

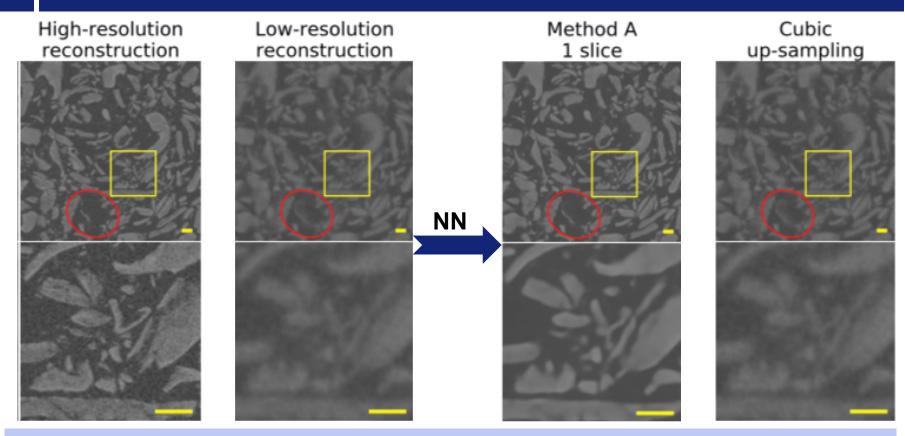
- Faster data acquisition (fewer projections)
- Less radiation damage

Method: create a neural network by acquiring a dataset at high resolution, and train it against the same data with a reduced resolution.

The NN is then tested against a different part of the same object.



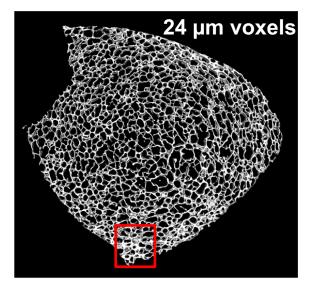
PHASE CONTRAST IMAGING: IMPROVE RESOLUTION



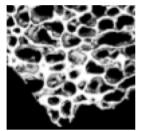
Example NN reconstruction on an oatmeal sample, training from a high resolution sub-dataset (17µm voxels) to reconstruct low-resolution ones (68µm voxels)

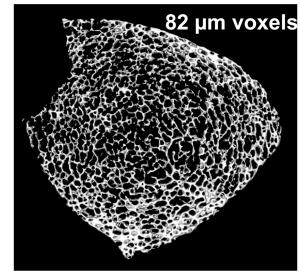


PHASE CONTRAST: IMPROVE RESOLUTION IN VIVO

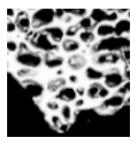


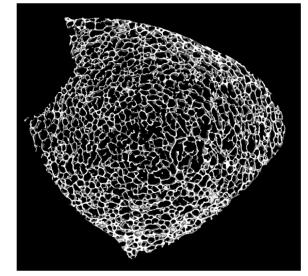
High Resolution (from μ CT)





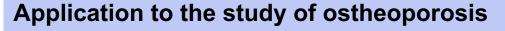
Low Resolution





Super Resolved image

The European Synchrotron



Creatis Slide courtesy of F. Peyrin PhD Y Li, 2019 ; B. Sixou, F. Peyrin (unpublished) ESRF

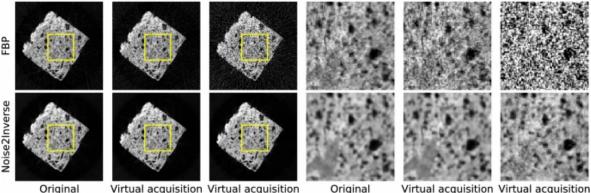
NN

NOISE2INVERSE: HIGH RESOLUTION W/O REFERENCE DATA

Deep denoising for multi-dimensional synchrotron X-ray tomography Allard A. Hendriksen¹²⁷, Minna Bührer², Laura Leone³, Marco Merlini³, Nicola Vigano⁴, Daniël M. Pelt^{1,5}, Federica Marone², Marco di Michiel⁴ & K. Joost Batenburg^{1,5}

Sci. Rep. 11 (2021), 11895

Noise2Inverse: IEEE Transactions on Computational Imaging 6 (2020), 1320



XRD-CT reconstructions

Original

Virtual acquisition Virtual acquisition time: ~70%

time: ~20%

Virtual acquisition Virtual acquisition time: ~70% time: ~20%

X-ray diffraction tomography reconstructions of a single channel of a single slice of a ceramic fragment. The leftmost column shows the reconstruction of the originally acquired data, and the next two columns show reconstructions with synthetic noise. The rightmost three columns show magnifications of the yellow region of interest.

Al-enhanced resolution of tomography reconstructions allows:

- Faster data collection for the same final quality
- Less radiation damage



IMPROVING IMAGE RECONSTRUCTION: CHALLENGES

- Variety of imaging configurations (near field, far field)
- Large datasets (2048³ to 4096³, and much more on BM18)
- Requires **training datasets** (not always..)
- **Transferability** of neural networks for different type of materials ?
- Would users need GPUs before their experiments for training ?
- Examples work well on samples with relatively simple density distributions (binary). What about more diverse samples ?



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The European Synchrotron Slide courtesy of A. Pacureanu

SEGMENTATION: MAPPING THE BRAIN CONNECTIONS

- Understand how neurons work together to interpret sensory information and to generate behavior
- Decipher the logic of neural circuits underlying learning and cognition
- Find ways to cope with neurological diseases
- Get inspired to design next generation computing architectures and improve artificial intelligence

How we go about it today

- MRI probabilistic connections between brain regions (1 voxels contains tens of thousands of neurons)
- Visible light microscopy sparse information (~ 1 in 500 000 neurons)
- EM comprehensive mapping but we only have one Drosophila brain so far which took a few years of data collection

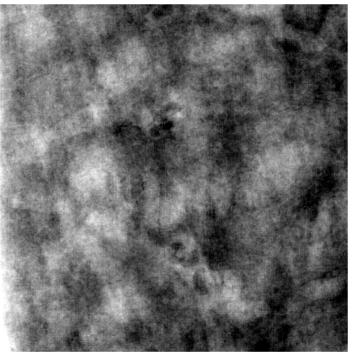




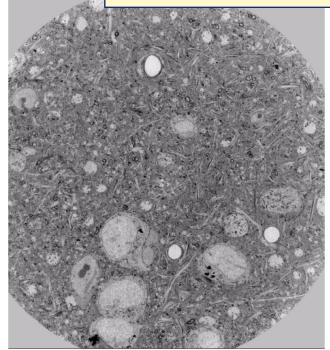
HOLO-TOMOGRAPHY: RESOLVING NEURAL NETWORKS

Connectomics in mouse cortex – complementarity with FIB-SEM & TEM Data collection ~4h (id16A)

2K or 4K pixels



See Alexandra Joita-Pacureanu ESRF webinar



Pixel size 40 nm

Phase maps (object rotation)

Holo-tomography reconstruction

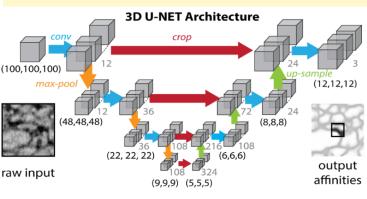
Nat. Neuroscience (2020) & bioRxiv 653188, A Pacureanu W Lee, A Kuan, J Maniates-Selvin, Harvard Medical School

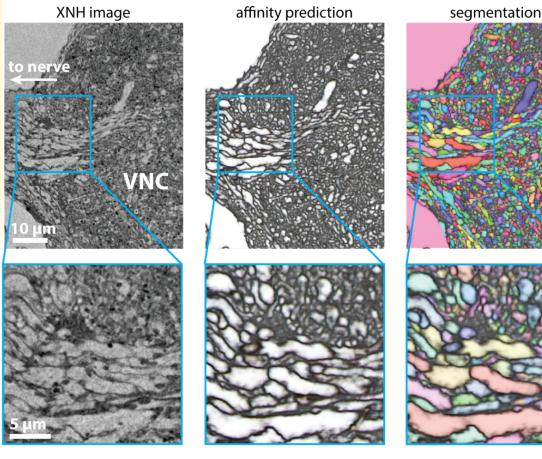




SEGMENTATION: MAPPING THE BRAIN CONNECTIONS

- Neuronal circuits are very complex and densely packed
- TB sized images
- Manual annotation takes tremendous resources – it took 60 human years to annotate 30% of a fruit fly brain
- Recent developments in deep learning give hope that automatic analysis is feasible





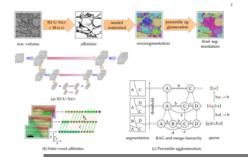
3D U-NET architecture adapted from Funke et al., TPAMI, 2018

Pacureanu et al. bioRxiv 2019



Slide courtesy of A. Pacureanu

AUTOMATIC SEGMENTATION USING DEEP LEARNING

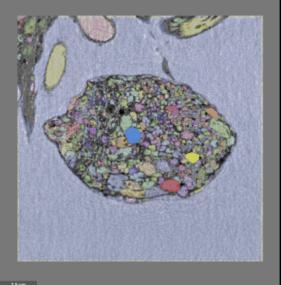


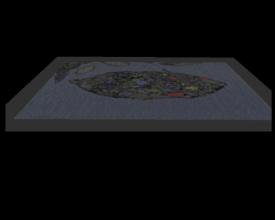
Funke et al. 2018

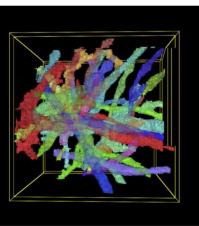
Deep Learning Automatic segmentation through convolutional neural networks

VNC: ventral nerve cord

Automated segmentation of a portion of the adult *Drosophila* VNC. Right, volumetric view of selected large-diameter neurons







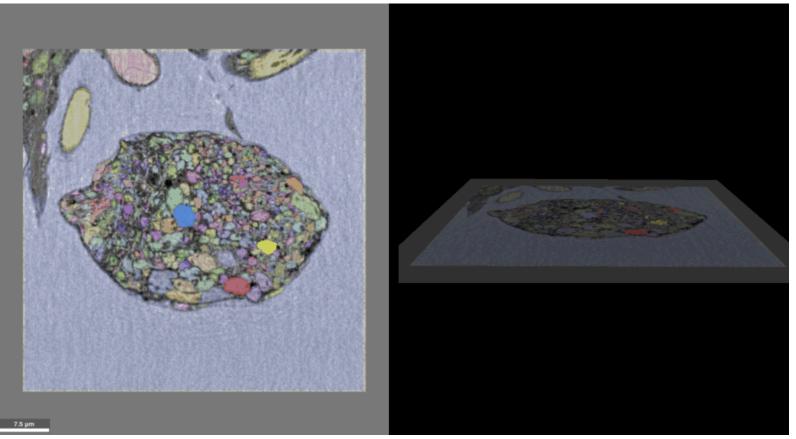
Automatic segmentation in drosophila VNC and mouse cortex

Nat. Neuroscience (2020) & bioRxiv 653188, A Pacureanu W Lee, A Kuan, J Maniates-Selvin, Harvard Medical School I GdR IAMat I 2022-05-30 I Vincent Favre-Nicolin





SEGMENTATON IN DROSOPHILIA VENTRAL NERVE CORD

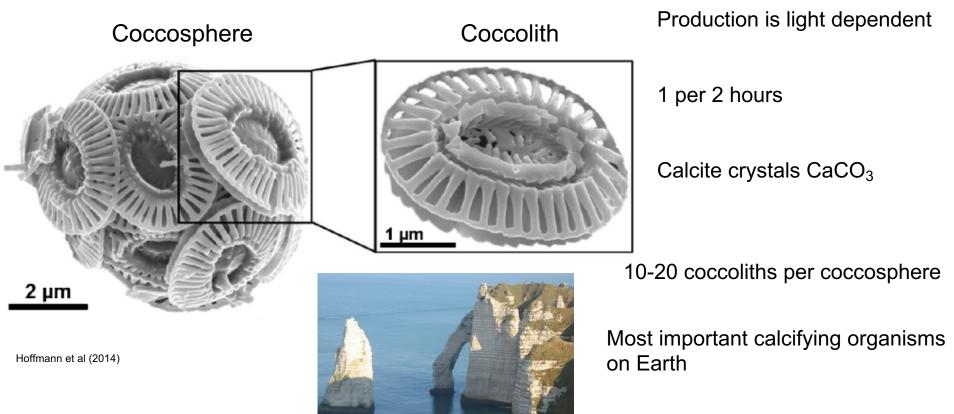


3D visualization of automatically segmented neurons in the Drosophila Ventral nerve cord (VNC)



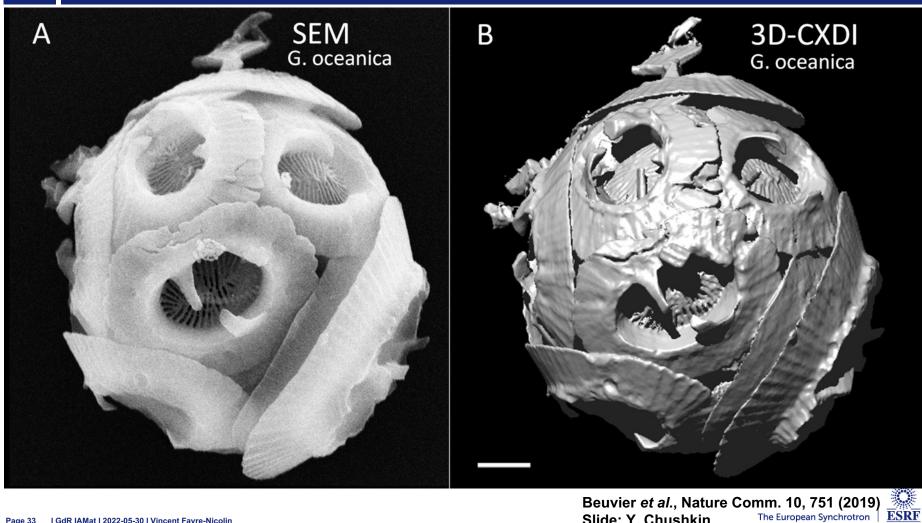
MARINE ALGAE - COCCOLITHOPHORES

Emiliania huxleyi





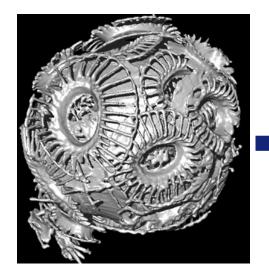
3D-CXDI



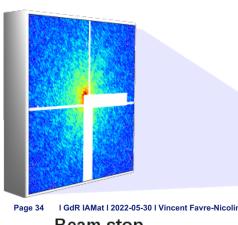
Beuvier et al., Nature Comm. 10, 751 (2019) The European Synchrotron Slide: Y. Chushkin



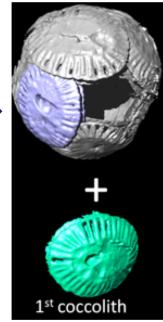
3D COHERENT DIFFRACTION IMAGING (ID10)



3D CaCO₃ Coccosphere



Segmentation

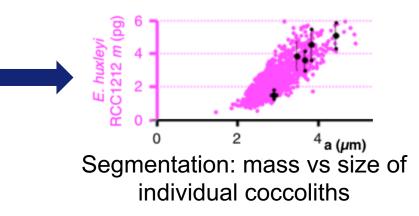


Sample

Coherent X-rays

Dataset: 512^3 pixels

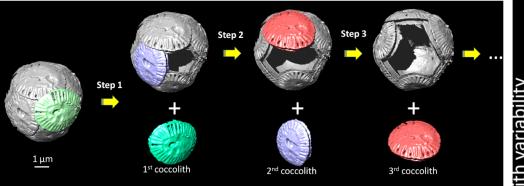
- Pixel size: 5-20 nm
- GPU reconstruction: 32s/run
- Processing (1 GPU): 15 min
- Data collection: 1~3h
- Post-EBS: 10-100x more data



Beuvier, Nature Comm. 10 (2019), 751



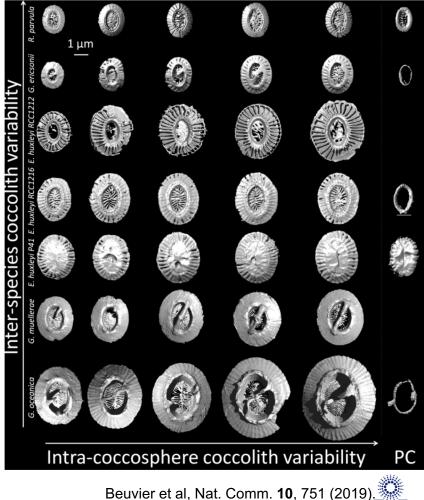
MULTIPLE DATASETS, DATABASES...



3D coherent imaging of $CaCO_3$ coccospheres (produced by phytoplankton and a large contributor to CO_2 storage) => extraction of a large collection of coccoliths

How do we process and make sense of large collections of reconstructed objects ?

Similarities, multivariate analysis, principal component analysis... Can we go **beyond model-based statistics**?



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ESRF

1. Faster data processing

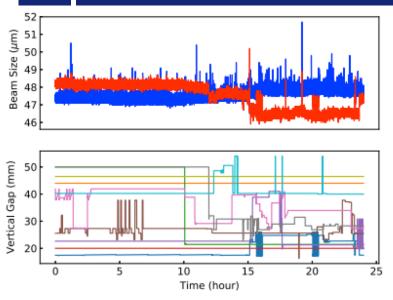
- 2. Better processing
- 3. Data Analysis

4. Instrument configuration

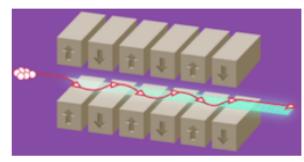
- 5. Automated data collection
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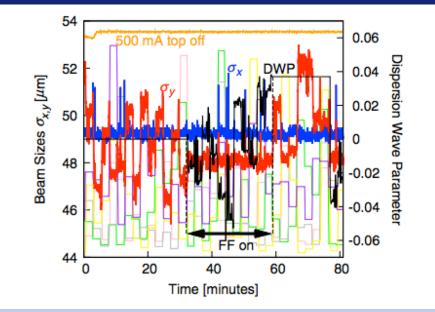


SYNCHROTRON BEAM STABILISATION



Synchrotron beam size vs time, influenced by the undulator gaps (ALS)

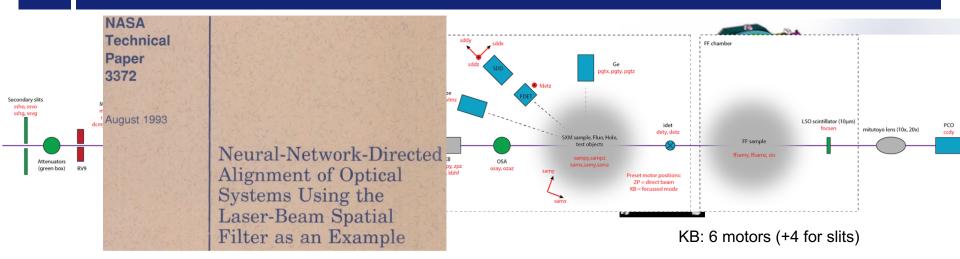




A stable beam size is essential notably for nano-focusing experiments. This is usually done using both feedback and feed-forward (FF: prediction, model based) corrections. A machine learning FF algorithm allows to improve the beam tuning.



BEAMLINE OPTICS ALIGNMENT



From source to detector, there can be >10 optical elements, each with 2-10 motors:

- Undulators
- Mirrors
- Slits
- Monochromator
- Nano-focusing optics
- Sample alignment

All alignment usually done progressively from the source, but some elements with >=4 motors (actuators), and/or non-perfect optical properties are difficult to parametrise.

• Detectors (distance, orientation, energy thresholds, analyser)



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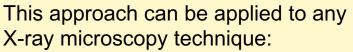


MACHINE LEARNING: AUTOMATED ACQUISITION

Accelerating Scanning X-ray microscopy

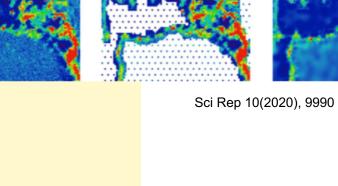
- Perform fast map (STXM)
- Identify (mask) relevant regions •
- Perform high-resolution maps in the relevant areas (XRF)

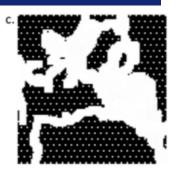
Could be extended by identifying on-the-fly the relevant areas (one line to the next)?

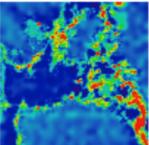


- Transmission
- SAXS/WAXS
- Powder diffraction ٠
- Fluorescence
- XAFS/XANES (dispersive)

=> Ongoing project at ESRF, financed by STREAMLINE







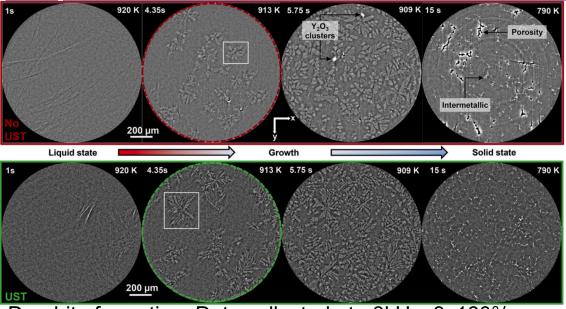
Sci Rep 10(2020), 9990 (Elettra)



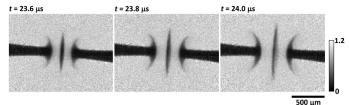
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EVENT-BASED DATA ACQUISITION



t = 23.0 μs t = 23.2 μs t = 23.4 μs



MHz radiographs of electric arc ignition Optics Express 25 (2017),13857

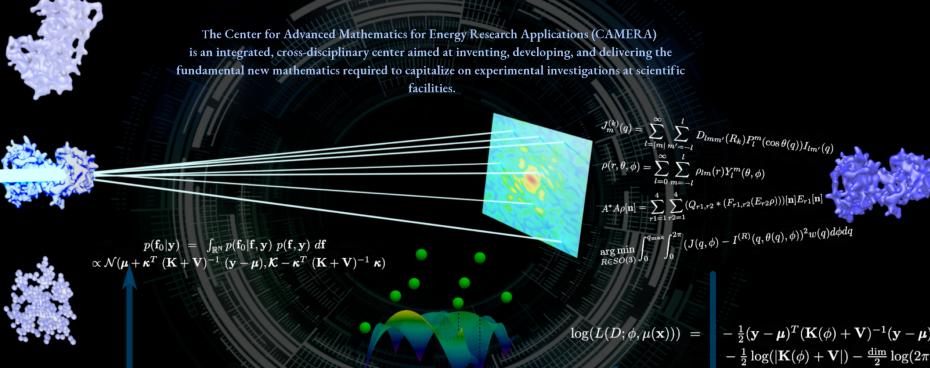
Dendrite formation. Data collected at ~3kHz, 3x180°/s during 16s (limited by 32 GB camera memory). Acta Materialia 129 (2017), 194

https://simap.grenoble-inp.fr/fr/equipes/high-performance-imaging Data collected on ID19

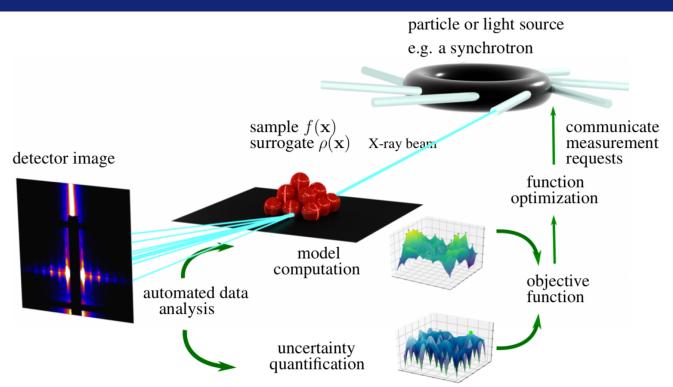
- Fast, time-resolved experiments often feature narrow relevant time frames. Fast (on-the-fly ML) analysis would allow:
- Recording only relevant parts, or varying framerates
- Automated tuning of experimental parameters (temperature)





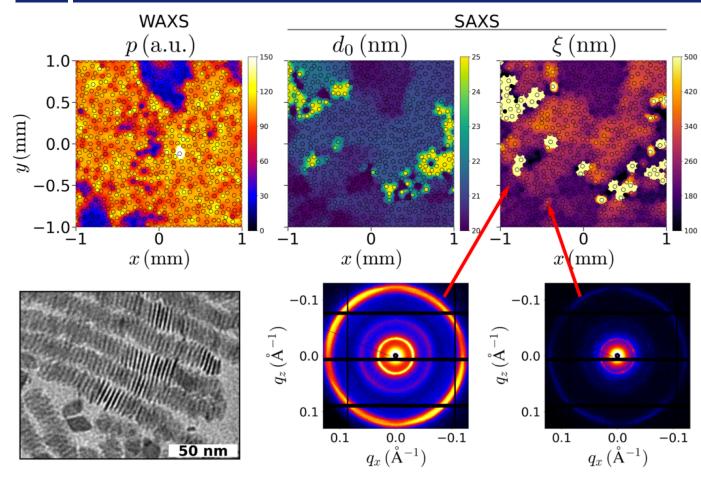






The Gaussian process uses a Bayesian approach to evaluate the parameter space which needs to be explored. First measure a few data points, then use a model (physics-aware) to evaluate the optimal points to measure to maximise the information collected

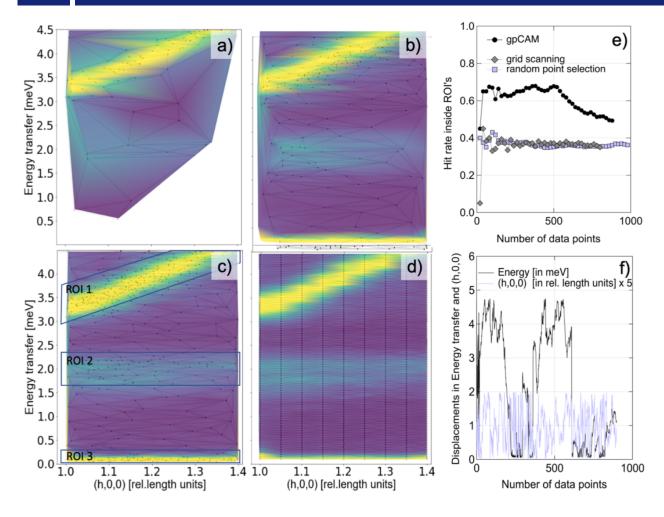
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Example automated acquisition with SAXS.

The sampling points look random but are not (overlap is minimised)





Another example at ILL using a triple-axis spectrometer.

The gpCAM data acquisition automatically maximises the number of points measured in the relevant areas



gpCAM

```
In []:
```

```
from gpcam.autonomous_experimenter import AutonomousExperimenterGP
import numpy as np

def instrument(data):
    for entry in data:
        entry["value"] = np.sin(np.linalg.norm(entry["position"]))
    return data

##set up your parameter space
parameters = np.array([[3.0,45.8],
```

[4.0, 47.011)

```
##set up some hyperparameters, if you have no idea, set them to 1 and make the training bounds large
init_hyperparameters = np.array([1,1,1])
hyperparameter_bounds = np.array([[0.01,100],[0.01,100.0],[0.01,100]])
```

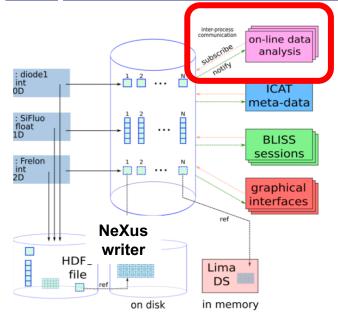


1. Faster data processing

- **2. Better processing**
- 3. Data Analysis
- 4. Instrument configuration
- 5. Automated data collection
- Framework for Online Data Analysis
 Open Data



ONLINE DATA ANALYSIS

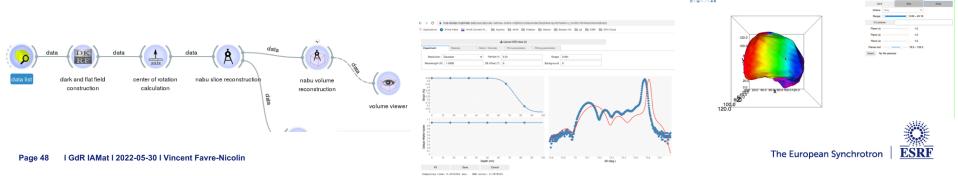


Before:

- **'one-way pipeline**': acquisition, measure, display, store, analyse Now:
 - Need (more) online analysis for user decision
- Automated analysis-driven acquisition
- Analysis procedures are not pre-defined except in a few cases (MX): need to have algorithm-development friendly interfaces
- Scientist community python-educated: provide standard access so all scientists can easily access & work on data

Development axes:

- **On-the-fly (in-memory) data access** (up to 16 GB/s) for analysis/triage/compression... (see: Memcached, ASAP:O, Bluesky's DataBroker)
- Workflows
- User interfaces (web,..)



LIVE DATA ACCESS ?

- Detectors (example: Eiger 4M @ 2kHz) allow data collection > 100 Gb/s
- Default 'fast' network data access operates at 25 Gb/s (GPFS)
- Data access can currently be done:
 - From a REDIS database

From LIMA (2D data)

- Fast (in-memory) but not standardised
- From hdf5 files, once written/flushed to disk => slow: (de)compression + disk

For 'live' data processing we are working on a new standardised in-memory data access to enable fast analysis and AI-driven automated data collection

=> enable online data analysis for computational scientists



BLISS: PYTHON INTERFACE TO THE DATA ACQUISITON

rom bliss.scanning.scan import Scan

from bliss.scanning.chain import AcquisitionChain
from bliss.scanning.acquisition.motor import SoftwarePositionTriggerMaster
from bliss.scanning.acquisition.counter import SamplingCounterAcquisitionDevice

chain = AcquisitionChain()
chain.add(SoftwarePositionTriggerMaster(m0, 5, 10, 10),
 SamplingCounterAcquisitionDevice(i0, 0.01, npoints=10))
scan = Scan(chain)

Associate them in the chain chain.add(monitor_timer, diode_device) # Now the fast acquisition

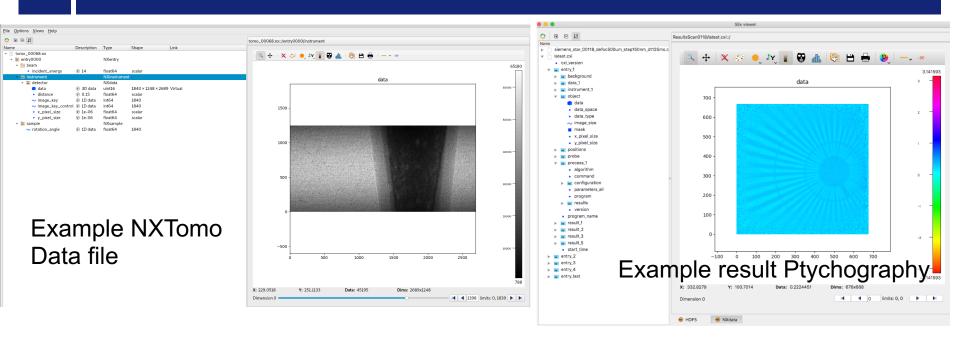
create a motor master for a position trigger



- BLISS: the ESRF's new data acquisition system
- Progressively replacing SPEC on all beamlines
- Python-based
- More friendly to interface with data analysis programs



HDF5+NEXUS: STANDARD DATA FORMAT



Use of the HDF5 data format allows to store all raw data and experimental parameters for processing.

The NeXus format provides a standard organisation for the different fields. NB: not *all* data is yet collected as hdf5, but the % is increasing





ESRF

FAIR RECOMMENDATIONS

27 recommendations !

Define		Implement		Embed ar	nd sustain				
Concepts for FAIR implementation	FAIR culture	FAIR ecosystem	Skills for FAIR	Incentives and metrics for FAIR data and services	Investment in FAIR				
Rec. 1: Define FAIR for implementation	Rec. 4: Develop Interoperability frameworks	Rec. 7: Support semantic technologies	Rec. 10: Professionalise data science & stewardship roles	Rec. 12: Develop metrics for FAIR Digital Objects	Rec. 14: Provide strategic and coordinated funding				
Rec. 2: Implement a Model for FAIR Digital Objects	Rec. 5: Ensure data management via DMPs	Rec. 8: Facilitate automated processing	Rec. 11: Implement curriculum frameworks and training	Rec. 13: Develop metrics to certify FAIR services	Rec. 15: Provide sustainable funding				
Rec. 3: Develop components of a FAIR ecosystem	Rec. 6: Recognise & reward FAIR data & stewardship	Rec. 9: Certify FAIR services	Above line = priority recommendations						
Rec. 16: Apply FAIR broadly	Rec. 18: Cost data management	Rec. 22: Use information held in DMPs	Below line = supporting recommendations	Rec. 25: Implement and monitor metrics	Rec. 27: Open EOSC to all providers but ensure services are FAIR				
Rec. 17: Align and harmonise FAIR and Open data policy	Rec. 19: Select and prioritise FAIR digital objects	Rec. 23: Develop components to meet research needs		Rec. 26: Support data citation and next generation metrics					
	Rec. 20: Deposit in Trusted Digital Repositories	Rec. 24: Incentivise research infrastructures to support FAIR data							
	Rec. 21: Incentivise reuse of FAIR outputs		 https://doi.org/10.2777/1524						

- **1. Faster data processing**
- 2. Better processing
- 3. Data Analysis
- **4. Instrument configuration**
- 5. Automated data collection
- 6. Framework for Online Data Analysis

7. Open Data



MULTIPLE DATASETS, DATABASES...

Many open databases available:

Experimental structures and properties

ChEMBL	Bioactive molecules with drug-like properties	https://www.ebi.ac.uk/chembl
ChemSpider	Royal Society of Chemistry's structure database, featuring calculated and experimental properties from a range of sources	https://chemspider.com
Citrination	Computed and experimental properties of materials	https://citrination.com
Crystallography Open Database	Structures of organic, inorganic, metal-organic compounds and minerals	http://crystallography.net
CSD	Repository for small-molecule organic and metal-organic crystal structures	https://www.ccdc.cam.ac.uk
ICSD	Inorganic Crystal Structure Database	https://icsd.fiz-karlsruhe.de
MatNavi	Multiple databases targeting properties such as superconductivity and thermal conductance	http://mits.nims.go.jp
MatWeb	Datasheets for various engineering materials, including thermoplastics, semi- conductors and fibres	http://matweb.com
NIST Chemistry WebBook	High-accuracy gas-phase thermochemistry and spectroscopic data	https://webbook.nist.gov/chemistry
NIST Materials Data Repository	Repository to upload materials data associated with specific publications	https://materialsdata.nist.gov
PubChem	Biological activities of small molecules	https://pubchem.ncbi.nlm.nih.gov

Solid Spectroscopy Hosting Architecture of Databases and Expertise

https://www.sshade.eu

Can we make more use of open databases ?

- Cross-validation / categorisation
- Open data policy (e.g. <u>https://www.esrf.eu/datapolicy</u>) will provide tons of raw data
- ... can this be combined in a more digestible, explorable form ?



https://www.esrf.fr/datapolicy

ESRF EUROPEAN SYNCHROTRON RADIATION FACILITY

30 November 2015

The ESRF Data Policy

The ESRF aims to implement a Data Policy starting as soon as possible in 2016. The main elements of this policy comprise:

- Data ownership
- Data curation
- Data archiving
- Open access to data

This policy follows largely the recommendations of the PaN-data Europe Strategic Working Group laying out a common framework for scientific data management at photon and neutron facilities (Deliverable D2.1, PaN-data Europe, co-funded by the European Commission under the 7th Framework Programme)



MAIN ELEMENTS OF ESRF DATA POLICY

Data are under embargo for 3 years but can be released earlier by the experimental team

- All data have a DOI assigned automatically at the session level with appropriate high-level metadata from proposal
- Experimental team can register a DOI for a subset or superset of the data on provision of high-level metadata e.g. abstract
- PI can request an extension to the embargo period
- **DOI must be cited when data are re-used**
- Processed data can be uploaded to data portal
- Data can be downloaded from https://data.esrf.fr
- After embargo period and/or on creation of bespoke DOI Data are available under CC-BY-4.0 licence as Open Data

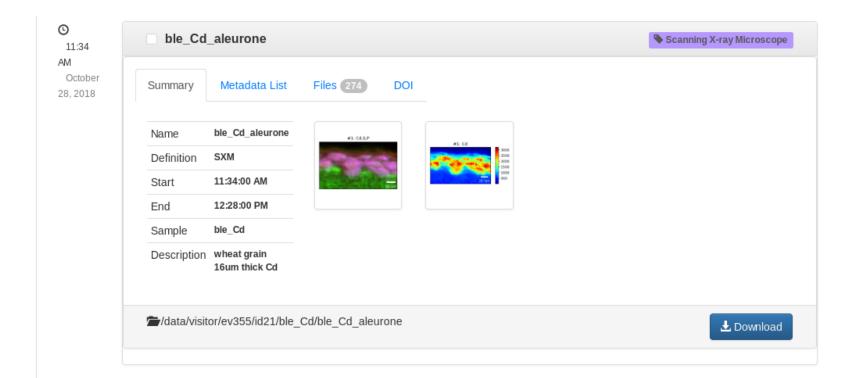


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• MX-2076	BM29	BAG for the Structural Biology Group	6	2	237 MB	186	 	DOI 10.15151/ESRF-ES-142840456
• SC-4855	ID16A	Quantitative Localization of Dendrime	1	1	91 KB	1	 	DOI 10.15151/ESRF-ES-142840375
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IH-EV-5	ID21	Estudy of Cr speciation in soils	4	2	23 MB	15	 	DOI 10.15151/ESRF-ES-142481073
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 IM-17 	BM05	imaging of 25 samples bouillon cube						
• IH-LS-3	ID16B	Continuation of LS2780, radiography					 	DOI 10.15151/ESRF-ES-141963373
O IM-11	ID16B	Rock samples	40	10	1 TB	130720		
O IN-1102	ID19	On site industrial experiment						
• BLC-11821	ID16B	Sample stage alignment for holotomo	8	1				
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IX-62	ID30B	Pharma studies	19	19	452 MB	114		
• MX-2073	ID30A3	London Cancer BAG comprising the I	33	24	82 GB	1506	 	DOI 10.15151/ESRF-ES-140506618

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Structural Evidence for a Role of the Multi-functional Human Glycoprotein Afamin in Wnt Transport

Abstract *

Afamin, a human plasma <u>dycoprotein</u> and putative transporter of hydrophobic molecules, has been shown to act as extracellular chaperone for poorly soluble, <u>acvtated Wnt</u> proteins, forming a stable, soluble complex with functioning <u>Wnt</u> proteins. The 2.1-Å crystal structure of <u>glycosylated</u> human <u>dfamin</u> reveals an almost exclusively hydrophobic binding cleft capable of harboring large hydrophobic molecules, has been shown to act as extracellular chaperone for poorly soluble, binding pocket of <u>afamin</u> was modeled as <u>paintolesic</u> acid, presenting the native O-<u>acvtation</u> on serine 209 in human <u>Wnt3a</u>. The modeled complex between the experimental <u>afamin</u> structure and a <u>Wnt3a</u> <u>homology</u> model based on the <u>XWnt8-F2aCPED</u> fragment complex crystal structure is compelling, with favorable interactions comparable with the crystal structure complex. <u>Afamin</u> readily accommodates the conserved <u>palmitoyiated</u> serine 209 of <u>Wnt3a</u>, providing a structural basis how <u>afamin</u> solublizes hydrophobic and poorly soluble <u>Wnt</u> proteins.

Name	Proposal	Technique
mesh-AFAMIN-revi-B5-1_1_1719726	OPID-1	
mesh-AFAMIN-revi-B5-1_1_1719728	OPID-1	
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line-AFAMIN-revi-B5-1_2_1719742	OPID-1	
line-AFAMIN-revi-B5-1_3_1719744	OPID-1	
line-AFAMIN-revi-B5-1_4_1719745	OPID-1	
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†∎ D	elete	
	Name	Surname
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	Matthew W.	Bowler
	Bernhard	Rupp

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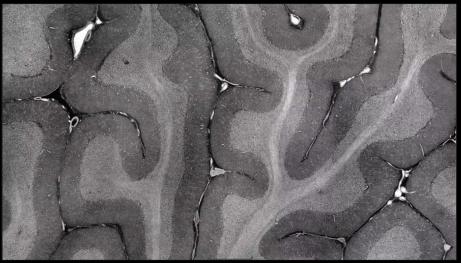
Welcome to the Human Organ Atlas

EXPLORE

The Human Organ Atlas uses **Hierarchical Phase-Contrast Tomography** to span a previously poorly explored scale in our understanding of human anatomy, the micron to whole intact organ scale.

Histology using optical and electron microscopy images cells and other structures with sub-micron accuracy but only on small biopsies of tissue from an organ, while clinical CT and MRI scans can image whole organs, but with a resolution only down to just below a millimetre. HiP.CT bridges these scales in 3D, imaging intact organs with ca. 20 micron voxels, and locally down to microns.

We hope this open access Atlas, enabled by the ESRF-EBS, will act as a reference to provide new insights into our biological makeup in health and disease. To stay up to date, follow @HiP-CT \$



HiP-CT imaging and 3D reconstruction of a complete brain from the body donor LADAF-2020-31. More videos can be viewed on the HiP-CT YouTube channel

Collaborators

- UCL, London, England: Peter D Lee, Claire Walsh, Simon Walker-Samuel, Rebecca Shipley, Sebastian Marussi, Joseph Jacob, David Long, Daniyal Jafree, Ryo Torii, Charlotte Hagen
- ESRE, Grenoble, France: Paul Tafforeau, Elodie Boller
- Medizinische Hochschule Hannover, Germany: Danny D Jonigk, Christopher Werlein, Mark Kuehnel
- Universitätsmedizin der Johannes Gutenberg-Universität Mainz, Germany: M Ackermann
- University Hospital of Heidelberg, Germany: Willi Wagner
- Grenoble Alpes University, Department of Anatomy, French National Center for Scientific Research: A Bellier
- Diamond Light Source, Harwell, UK: Andy Bodey, Robert C Atwood
- Imperial College London, UK: JL Robertus



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The UK Medical Research Council

The Wellcome Trust



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The German Registry of COVID-19 Autopsies (DeRegCOVID), supported by the German Federal Ministry of Health

https://human-organ-atlas.esrf.eu/

Reference

Funding

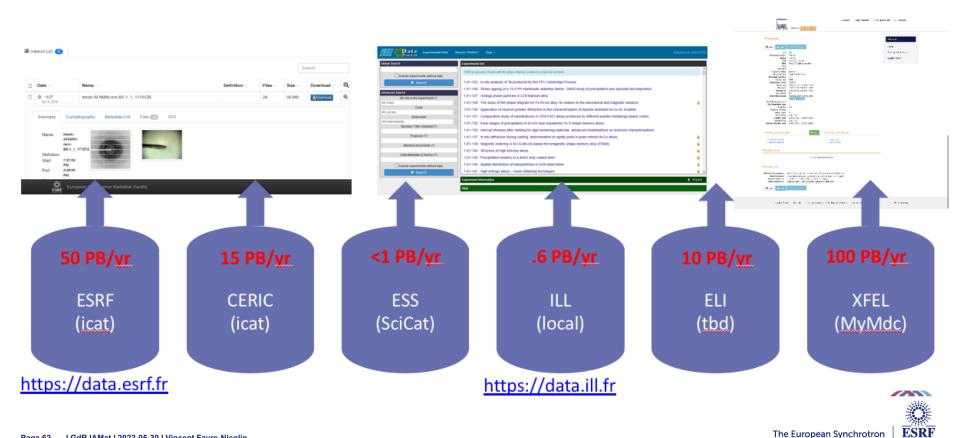
Walsh, C.L., Tafforeau, P., Wagner, W.L. et al. Imaging intact human organs with local resolution of cellular structures using hierarchical phase-contrast tomography. Nat Methods (2021). https://doi.org/10.1038/s41592-021-01317-x

Aknowledgements

École de ADAF

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OPEN DATA SEARCH

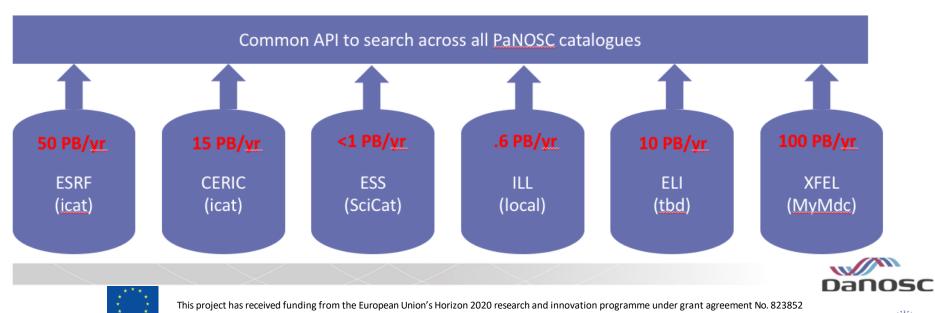




PANOSC DATASET SEARCH



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Large field of view scanning, ESRF holographic nano-tomography f... doi.esrf.fr

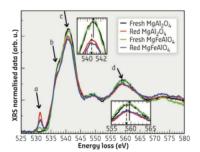
Dernière mise à jour : 2021

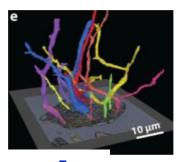
Un résultat que vous attendiez ne s'affiche pas? Découvrez comment ajouter de nouveaux ensembles de données à notre index

Large field of view scanning, holographic nano-tomography for connectomics and Li batteries Linger Linger Linger Lingsynchrotron Radiation Facility Auteurs Mexandra JOITA PACUREANU; Yang Yang; Peter CLOETENS; Julio Cegat, Da Silyoogle, hitric seat chinnes Settategal of Linger characterization



PROJECTS @ ESRF & CONCLUSION









- Automated segmentation (BM18, ID16A), Connectomics
- Classification in spectroscopy
- Open data available for training
- API for fast data access & instrument control in development
- Ongoing EU projects:
 - STREAMLINE: Al-driven X-ray Microscopy
 - ENGAGE COFUND: 5 PhD @ESRF:
 - <u>https://engage.cyi.ac.cy/?page_id=43</u>
 - X-ray diffraction mapping applied to cultural heritage
 - Coherent X-ray imaging (near field)
 - Real-time analysis of spectroscopic data
 - Al for protein Xtallography
 - Bragg (strain) coherent diffraction imaging
- Future ? Infratech EU AI4SI project, BMBF...
- Long-Term Projects with user groups are highly encouraged and would be a great tool to collaborate on AI applications !



THANK YOU for listening !

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