



ISPYB

A web-based laboratory information system
for crystal analysis with X-rays

S. Monaco



SUMMARY

- What is it?
- Main features
- A little tour through some features
- Different levels of usage
- What's next?



What is ISPYB?

- ISPYB is a Laboratory Information Management System (LIMS) linking single **crystal samples** to their corresponding **X-ray data**. It is a web dynamic application using a MySQL database.

- **Access to ISPYB?**

Through a web browser at <http://ispyb.esrf.fr>

To log-in: an ESRF Experiment number and password are required.

- **History:**

2 years old

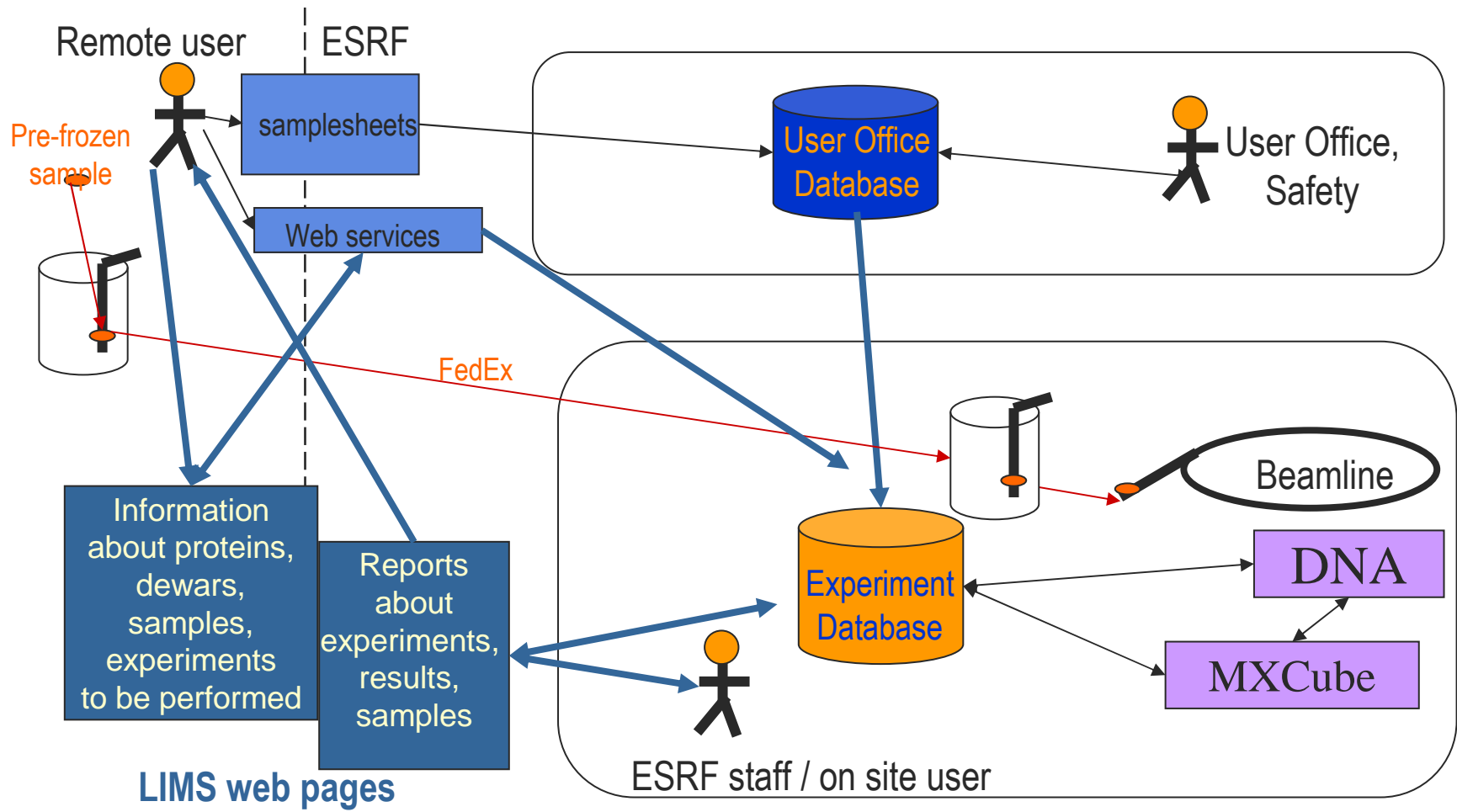
Replaces Pxweb our former LIMS (zope+python/ MySQL database) developed initially thanks to SPINE and BIOXHIT grants

Written in Java technology in order to be compatible with other synchrotrons and inhouse databases

Co-development between ESRF and BM14 ehtpx



Information flow around an MX experiment

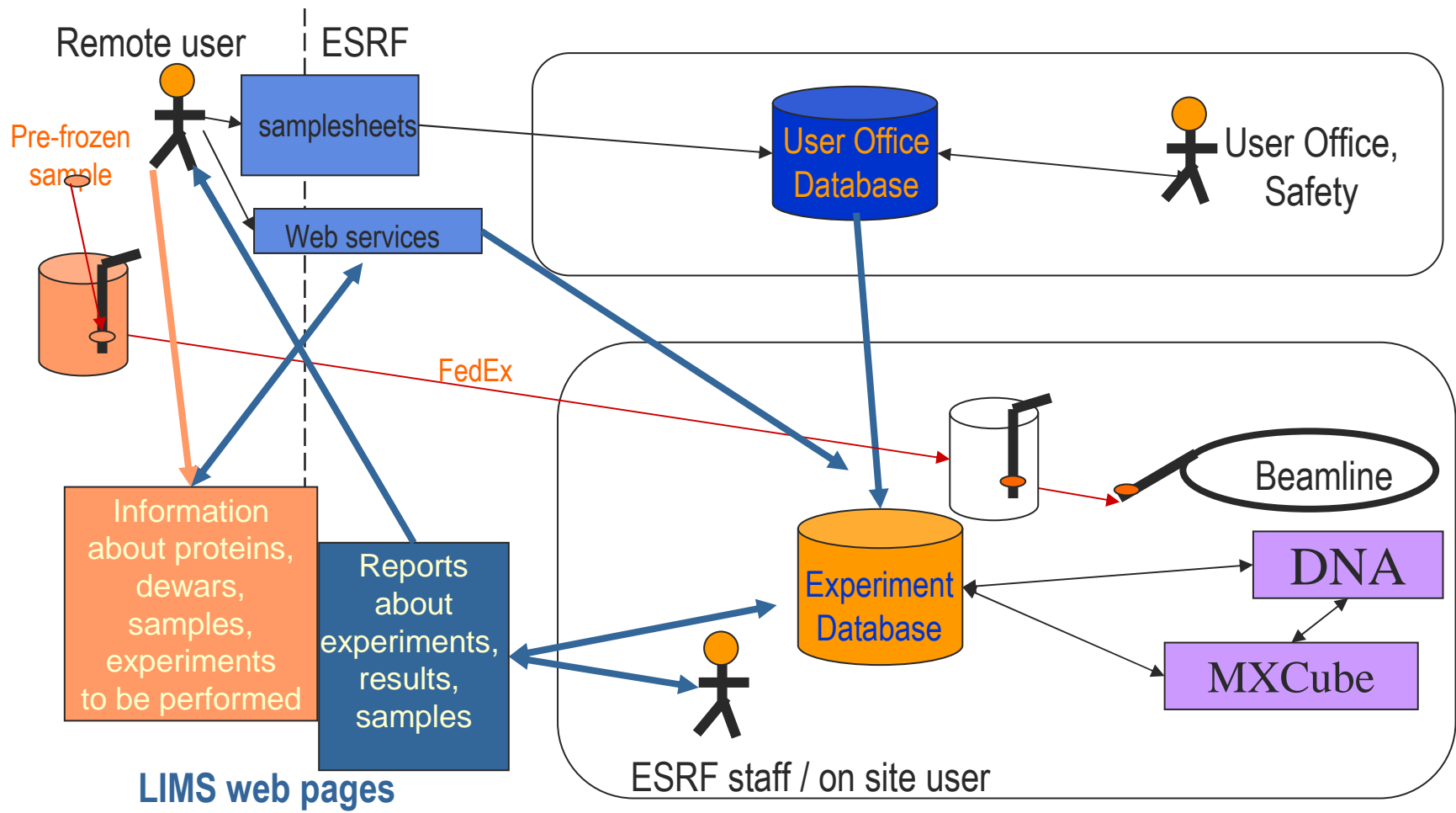




Available features

- Management of crystal samples and their relative protein information
- Description of samples sent to the synchrotron, including 'diffraction plan'
- Real time monitoring of data collections: diffraction images, crystal snapshots, harvesting of output from data analysis softwares
- Search engines for data mining
- Creation and editing of experiment reports (i.e. for MxPress© clients)

Information flow around an MX experiment





ISPYB Tour – I shipment description

- Shipment : pool of samples within containers, themselves within dewars & send to the synchrotron.
- ‘Manual description’ : create and describe each crystal sample individually in ISPYB
- ‘Semi-automatic description’: prepare an excel sheet (pre-filled with the projects) and upload it to ISPYB.



ISPYB Tour - I



Reply with Changes... Epd Review...

File Edit View Insert Format Tools Data Window Help

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85%

Sample position	Protein Name	Protein Acronym	Space Group	Sample Name	Pin Barcode	Pre-observed Resolution	Needed Resolution	Oscillation Range	Experiment Type	Anomalous Scatterer	Unit Cell	alpha	beta	gamma	Loop Type	Holder Length	Comments
1									OSC						Nylon	22	
2		A-TIM - P21							OSC						Nylon	22	
3		A-TIM - Undefined							OSC						Nylon	22	
4		A-TIM - P23							OSC						Nylon	22	
5		A315S - Undefined							OSC						Nylon	22	
6		A315S - Undefined							OSC						Nylon	22	
7		bthA315S - Undefined							OSC						Nylon	22	
8		cbl - Undefined							OSC						Nylon	22	
9		CMY-10 - Undefined							OSC						Nylon	22	
10									OSC						Nylon	22	

Template version 5

Puck Dewar CA431A Dewar1

Required information

Optional but highly recommended

Optional

Image Name on the beamline = <Protein Acronym>_<Sample Name>_<Run Number>_<Image Number>

Tips :
Worksheet name (tab name) is not used during the upload process. Feel free to rename it to anything making sense to you ...
Make sure no drop-down list is selected before saving and submitting the file to ISPyB

projects) and upload it to ISPyB.

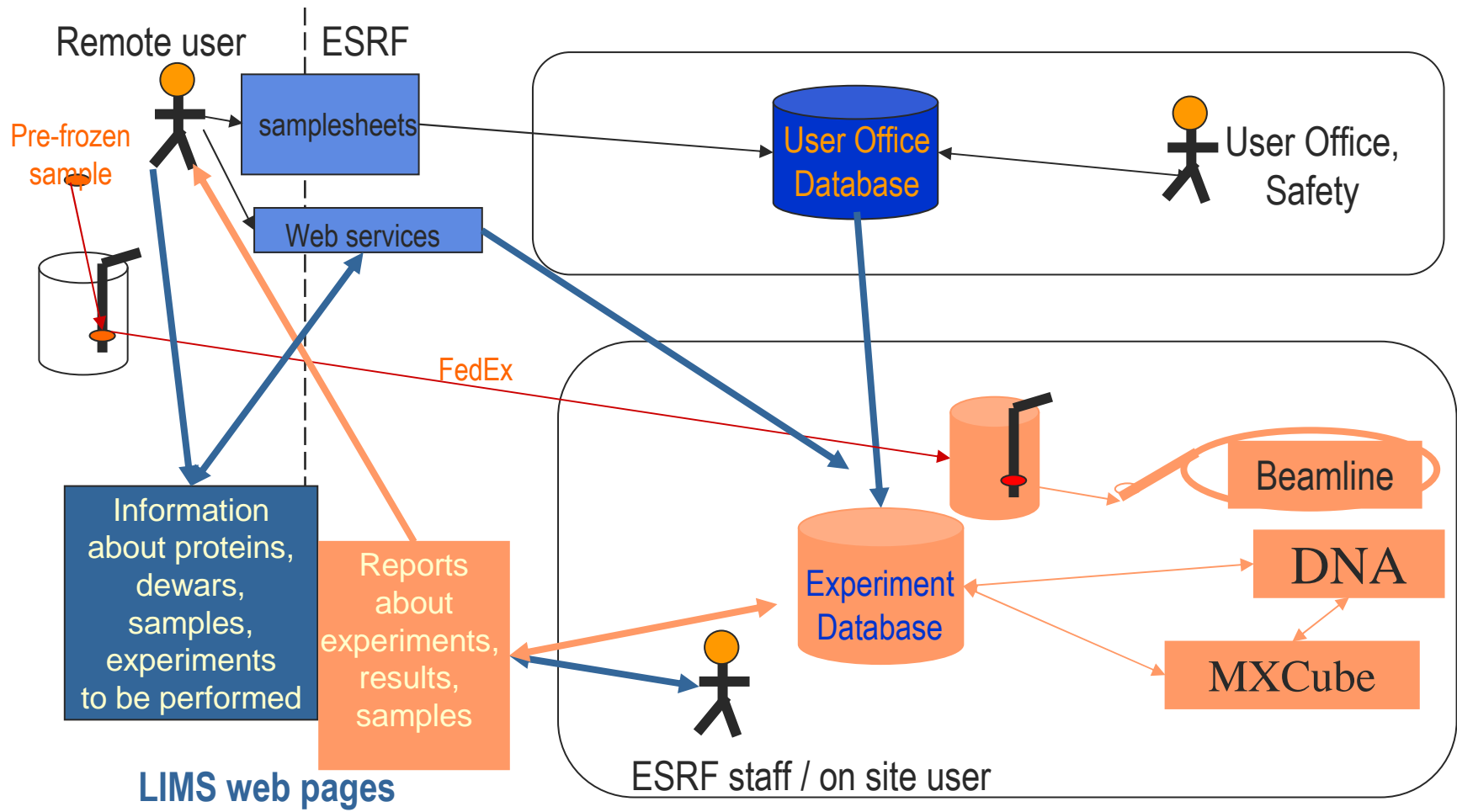


Interest of describing my shipment in ISPYB?

- Provide information between crystal producers and crystallographers at the beamline
- Provide beamline softwares with exact data directly usable in the experiment (loading sample X instead of loading sample 3 of basket 5, directory path updated)
- Mandatory for automatic screening



Information flow around an MX experiment





ISPYB Tour –II

Experimental session viewing

Wink video



Interest of the experimental session viewing

- On the D-day: follow an experiment in real time (facilitate discussion between experimentators and colleagues in their labs)
- Get exact beamline parameters
- Keep track of what crystal shape for what diffraction pattern & analysis
- Crystal ranking results
= Experiment electronic logbook

Interest of the search engine

- Follow the X-ray history of a project (acronym search)
- Follow the the X-ray history of a sample
- Allows to refer to already done experiments on that particular crystal type (help in designing a new X-ray experiment)

ISPYB 'à la carte'

- 1st level: no action by the user.

Log on the beamline control software as proposal number X: all parameters of that session will be stored in ISPYB (snapshots...no data analysis) – updated electronic logbook accessible from anywhere in the world

- 2nd level: use of DNA in parallel to the beamline control software
Same as above plus data analysis from DNA

- 3rd level: use of shipment description without pin barcodes
Same as in level 2. + experiment facilitated on the beamline + link crystal description and X-ray data

- 4th level: use of shipment description with pin barcodes
Same as in level 3. + crystal ranking possible from DNA – storage of results in ISPYB

What's next for the user interface?

- Improve existing tools: search tool..
- Expand database with other useful parameters: anomalous spectrum – Flux at sample position...
- Facilitate data export from ISPYB to user's LIMS
- Expand database to sample analysis: Data integration/scaling in tables...
- Dewar tracking

Not an exhaustive list!...



Thanks to...

- **Joint development (ESRF, eHTPX)**
- **Collaborations**
 - EBI, BioXHit
 - DNA
 - ESRF information system group (MIS) : to be compatible with other dynamic web applications of ESRF
- **Team**
 - D. Spruce (ESRF), J. Gabadinho (ESRF): BLISS
 - R. Leal (ESRF), **L. Launer (Ehtpx)**, **S. Delageniere (ESRF)**, S.Veyrier (ESRF): developers
 - S. Monaco (ESRF), M. Walsh (BM14): Scientific direction and system requirements
- **With the help from Users (feedback at ispyb@esrf.fr), and ESRF MX group**
- **And support from S. Larsen, G. Leonard, S. McSweeney, V. Rey**