Use of the Cell Accelerator Platform for Synchrotron Data Analysis*

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Motivation

- Synchrotron-based Polychromatic X-ray Micro-diffraction (PXM) data has been used to understand elastic and plastic strains

- Data from PXM experiments can consist of a large number of images

- PXM data analysis using existing software is a very time consuming process

- Synchrotron time is valuable, faster data analysis is needed
  - ideally, data can be processed at a same speed level as it is collected

- FOXMAS is developed and introduced here
  - Fast Online X-ray Micro-diffraction Analysis Software
  - It is developed on a Cell accelerator platform at SHARCNET

Outline

- PXM data analysis

- Cell accelerator platform

- Development approach

- Performance evaluation

- Conclusion and future work
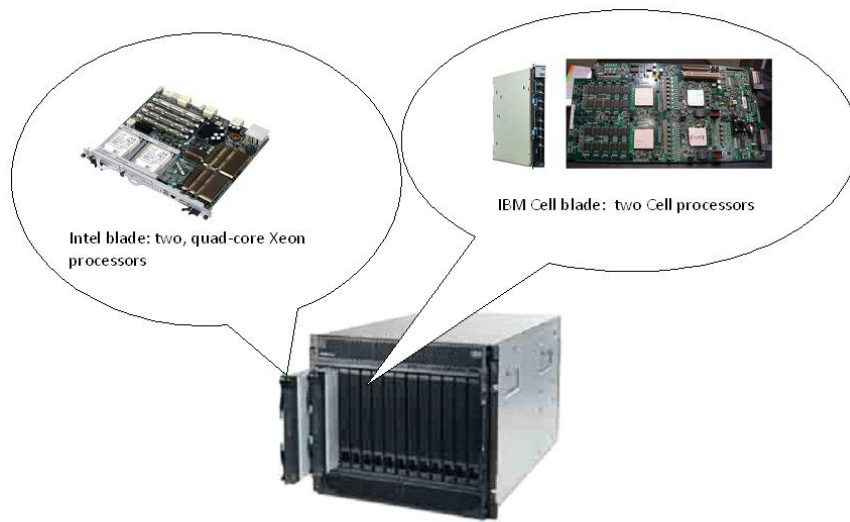
PXM data analysis

- Deals with large amount of image data
- Several procedures to analyze each of the images
- Existing software was mainly written in IDL with some backend procedures in Fortran

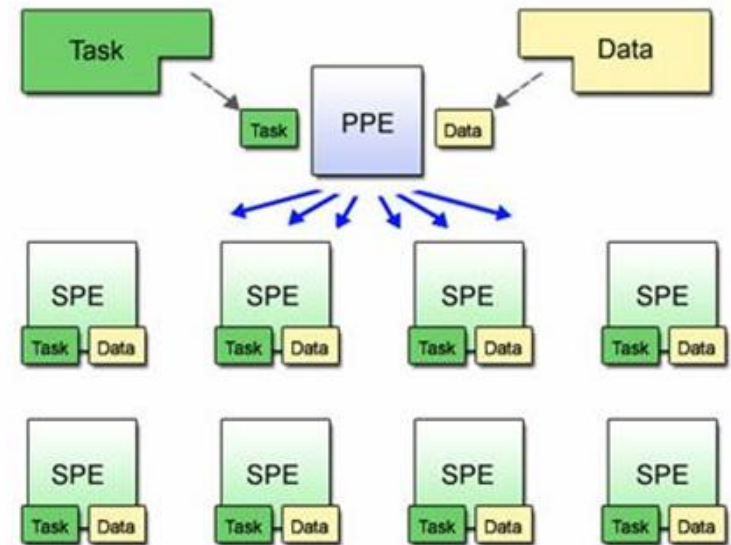PXM images

Orientation map

Strain map
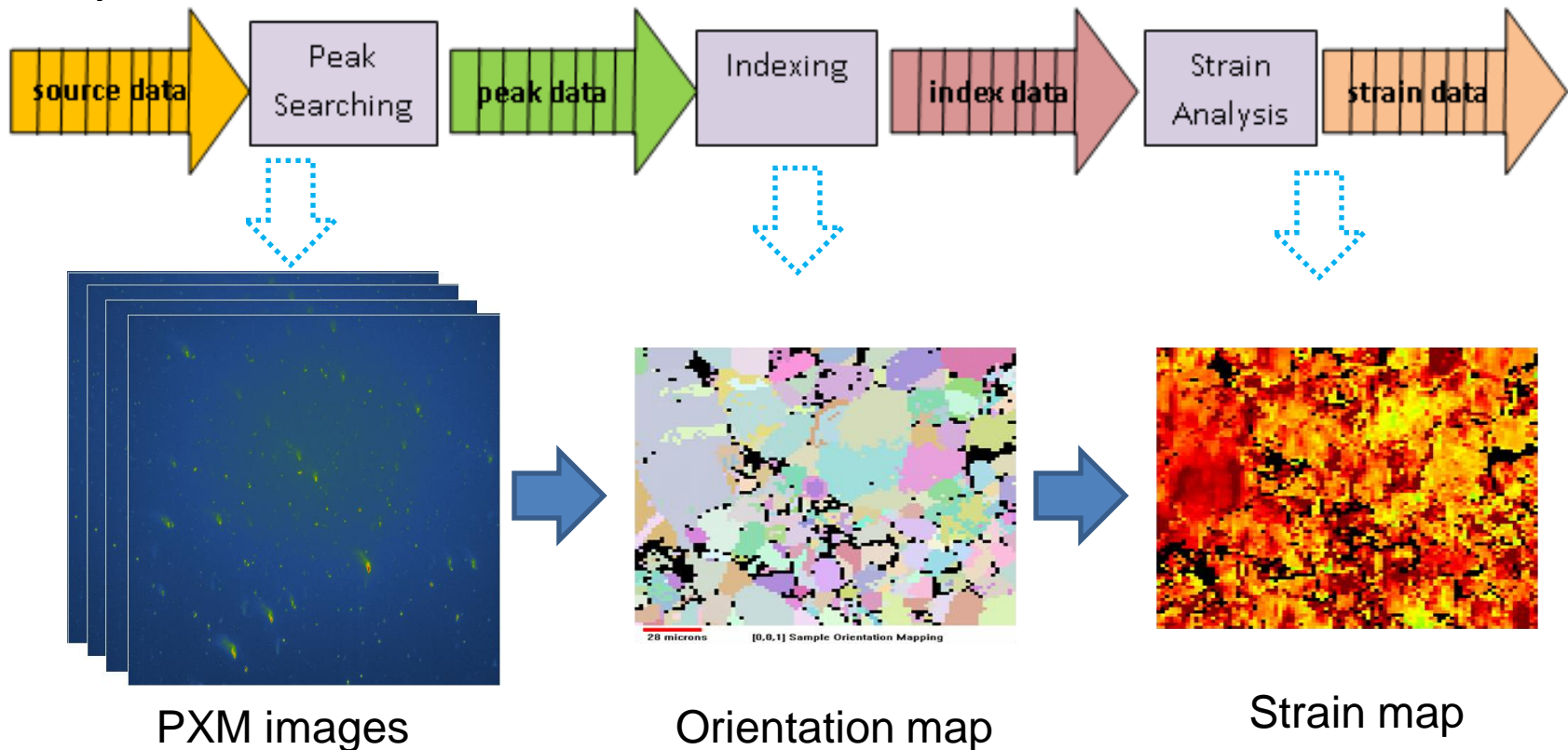
To accelerate processing speed

Target system – SHARCNET's Cell accelerator platform, called *Prickly*

Basic Cell programming model

Prickly – a BladeCenter Chassis in SHARCNET

Redesign the software

- Rewrite code in C for each procedure
  - For porting to parallel system
- Identify the performance bottleneck and target that part
  - e.g. peak searching
- Modularize the code at a finer scale
  - E.g. Peak searching involves:
    - Threshold finding
    - Blob searching
    - Curve fitting on each blob
- Identify the dependency between two modules
  - E.g. To identify what can be processed in parallel and what can be pipelined

For processing a large set of images

- Identify what only needed to be done once, and the result can be shared by all images
  - e.g. threshold finding for peak searching , loading a crystalline structure for indexing, etc.
- Efficiently allocate computation resources to maximize the throughput
  - less images processed in parallel, each image gets more resources
  - more images processed in parallel, each image gets less resources
  - what kind of resources for each task, e.g. Cell's cores or Intel's cores
- Parallel programming concerns
  - multi-thread vs. multi-process

Design of FOXMAS on *Prickly*
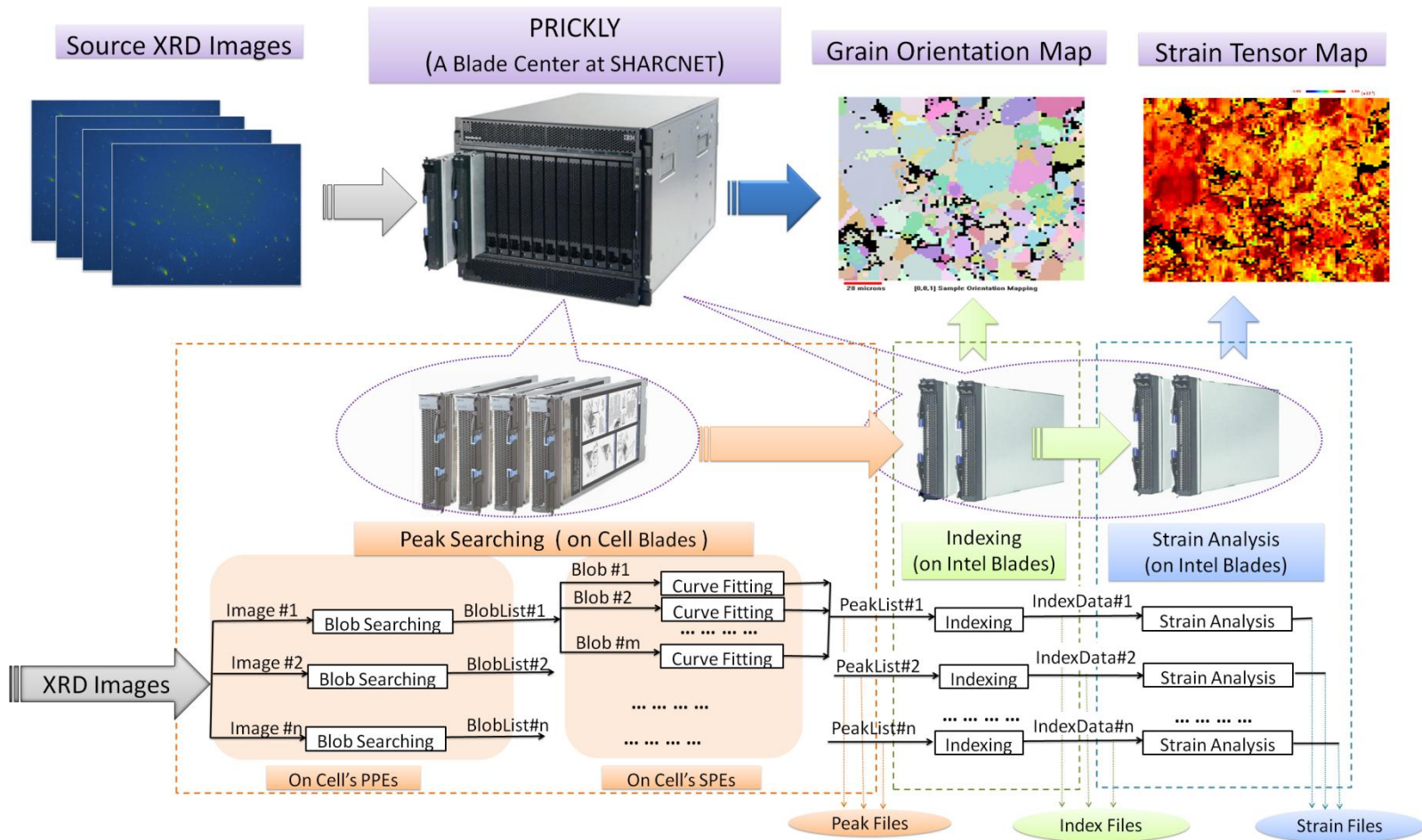
Some performance measurements

Image size: 1042X1042, 2MB/image

Sequential Speed of using IDL: 4.31sec./image

On one pair of nodes (Cell – Intel)

Parallel images	#SPE /image	Speed (sec./image)	Speedup (vs. IDL)
1	16	0.63	6.84
2	8	0.43	10.02
4	4	0.35	12.31
8	2	0.26	16.58
16	1	0.22	19.59

On multi-pair of nodes (Cell – Intel)

Pairs of nodes	Parallel image	Speed (sec./image)	Speedup (vs. IDL)
1	16	0.22	19.59
2	32	0.14	30.78
3	48	0.07	61.57
4	64	0.07	61.57

Image size: 2084X2084, 8MB/image

Sequential Speed of using IDL: 14.36 sec./image

On one pair of nodes (Cell – Intel)

Parallel images	#SPE /image	Speed (sec./image)	Speedup (vs. IDL)
1	16	2.84	5.06
2	8	1.81	7.93
4	4	1.55	9.26
8	2	1.67	8.60
16	1	1.68	8.55

On multi-pair of nodes (Cell – Intel)

Pairs of nodes	Parallel image	Speed (sec./image)	Speedup (vs. IDL)
1	4	1.55	9.26
2	8	0.96	14.96
3	12	0.70	20.51
4	16	0.59	24.34

Additional report

- The goal of this project is to achieve a real time PXM experiment and data analysis
  - data collected at CLS needs to be transferred to UWO in an ultra high speed, i.e. through CANARIE's cross country lightpath,   then processed on Prickly at UWO
- A preliminary functional test has been measured for such a scenario, including
  - sending a set of 100 PXM images (about 8MB/image) from CLS to UWO,
  - then getting processed on Prickly at UWO and presenting final results at an FTP site for users to download
  - It only took around 4 min. to complete the entire procedure.
    - about 2 min. for data transmission from CLS server to UWO server through the lightpath,
    - less than 1 min. for data transmission from UWO server to Prickly through UWO's intro-network
    - only about 1 min. to finish the data analysis on Prickly

Conclusion and Future work

- The current implementation has achieved the functionality for a high performance data analysis of PXM data

- Next step: to implement to enable the data transmission/analysis at the same time as it has been collected *during* a synchrotron experiment at CLS.
  - currently underway using the VESPERS beamline at CLS.

Acknowledgments

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- Thanks to Dong Liu at CLS for his collaborated work in the measurement of data transportation from CLS to UWO through the dedicated lightpath.

Thank you!

Online data analysis using FOXMAS