

PILATUS 500k Single Photon Counting Pixel Detector at X33

Introduction

Small angle X-ray scattering (SAXS) on biological macromolecules in solution imposes special requirements on the detector system. Due to a low scattering contrast of biological molecules and dilute solutions used, scattering signals from the solutes may be of less than one percent above the solvent scattering in the SAXS studies. Thus, the X-ray detectors such as CCD cameras or image plates (widely used e.g. in crystallography) exhibiting intrinsic electronic background are less suitable for solution SAXS experiments requiring ideally a photon-counting detection. Further, due to the high flux of photons provided by synchrotrons and the necessity of measurements close to the primary beam a high dynamic range of the detector is desired. For time resolved SAXS experiments, fast readout times are essential. These requirements are fulfilled by recently developed PILATUS pixel detectors Broennimann et al. (2006) based on a direct X-ray detection on a silicon sensor bump-bonded by indium balls to the readout electronics. A PILATUS detector configuration specifically designed for isotropic SAXS studies was recently purchased by the EMBL and installed at the X33 SAXS beamline.

Hardware

The PILATUS 500K (Fig. 1) consists of five basic modules of 487×195 pixels of 0.172 mm each. The unique strip-configuration of the modules within the 500k results in image-sizes of 2463×195 pixels and a physical size of 33×420 mm². This setup allows for a wide angular range – especially suitable for SAXS experiments as carried out at the X33 beamline. After testing the detector was set up for the users and is in operation since 22nd of November 2007. The PILATUS detector provides a much faster readout time than the MAR345 image plate used at the beamline before (3 milliseconds compared to 60 seconds). Its high dynamic range (10^6) and the absence of intrinsic noise yields a better signal-to-noise ratio and much improved stability of the background measurements compared to MAR345.

Software

Data acquisition and transfer is implemented via the DESY control system TINE Bartkiewicz and Duval (2007). Hence, the necessary server applications had to be implemented not only for the detector hardware, but also for the CanBUS-controlled beamline monitors and digital I/O ports. The I/O ports provide means to synchronize the experimental shutter protecting the samples from radiation damage with the exposure signal from the detector. During the data acquisition, beamline statistics used for data normalization are recorded (see Fig. 2).

The data reduction and processing of the detector images stored in Crystallographic Binary Format (CBF, Bernstein and Hammersley, 2005) is done without user intervention by a chain of on-site developed applications. For isotropic scattering the first step involves radial averaging of the two-dimensional scattering image with respect to the beam center, rebinning and generation of one dimensional curves. The latter are normalized by the transmitted beam intensity and collection time. Associated errors are computed using Poisson statistics from the numbers of counts in the raw data Bevington (1969). Individual time frames are compared to monitor for the radiation damage following by their appropriate averaging. The processed data are then transferred to subsequent data analysis and interpretation analysis packages.

Results

Fig. 3 displays a comparison of the radially averaged scattering from bovine serum albumin (BSA) at concentration 3.7 mg/ml after background subtraction collected by PILATUS 500k with that obtained by the MAR345 Image Plate in similar conditions. Note that the PILATUS data results in a comparable statistic, despite the much larger active area of MAR345. During November-December 2007 PILATUS 500K detector was used for data collection by more than 20 external users groups at X33 and for in-house measurements. These first results are very encouraging and demonstrate high potential of this detector in solution SAXS applications.

Acknowledgements

This work was supported by EU FP6 Design study SAXIER, grant number RIDS 011934. The authors thank P.Duval and U.Ristau for the help with TINE integration.



Figure 1: PILATUS 500k detector mounted at X33.

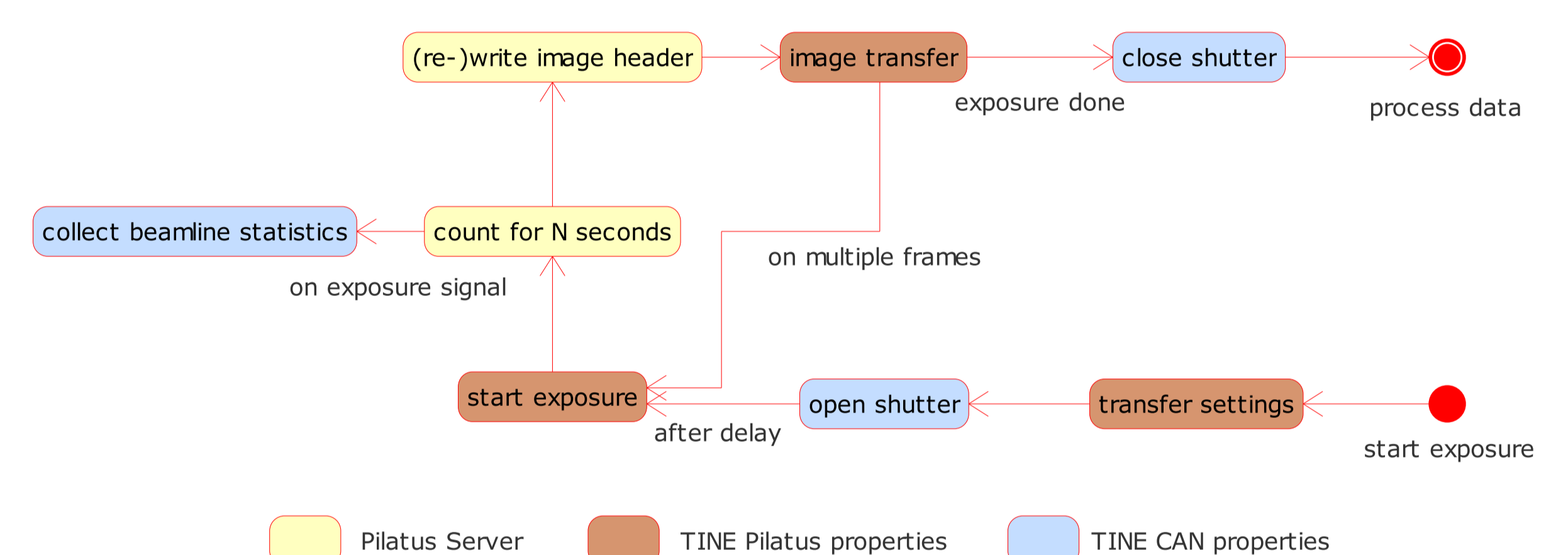


Figure 2: Acquiring data using PILATUS 500k, controlled by TINE.

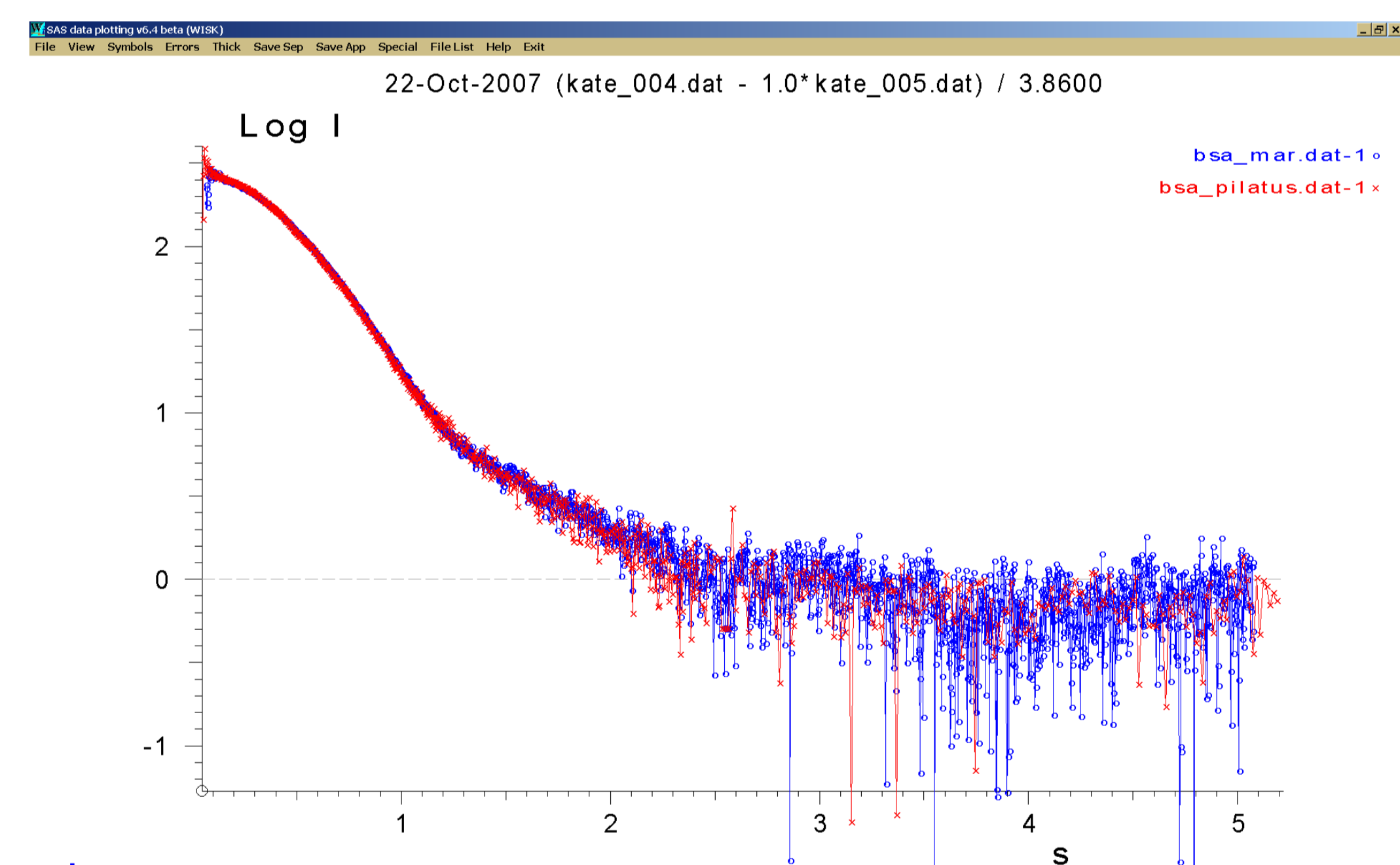


Figure 3: Comparison of scattering curves as acquired by different detectors.

References

- P. Bartkiewicz and P. Duval. TINE as an accelerator control system at DESY. *Meas Sci Technol*, 18:2379–2386, 2007.
- H. J. Bernstein and A. P. Hammersley. *Definition and exchange of crystallographic data*, volume G of *International Tables For Crystallography*, chapter 2, pages 37–43. Springer Netherlands, 2005.
- P. B. Bevington. *Data Reduction and Error Analysis for the Physical Sciences*. New York: McGraw-Hill, 1969.
- C. Broennimann, E. F. Eikenberry, B. Henrich, R. Horisberger, G. Huelsen, E. Pohl, B. Schmitt, C. Schulze-Briese, M. Suzuki, T. Tomizaki, H. Toyokawa, and A. Wagner. The pilatus 1M detector. *J Synchrotron Rad*, 13:120–130, 2006.