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#### **Authors**

Li, Xueming Zheng, Shawn Agard, David A <u>et al.</u>

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# Asynchronous data acquisition and on-the-fly analysis of dose fractionated cryoEM images by UCSFImage

Xueming Li<sup>1,\*</sup>, Shawn Zheng<sup>2</sup>, David A. Agard<sup>1,2</sup>, and Yifan Cheng<sup>1,2</sup>

<sup>1</sup>The Keck Advanced Microscopy Laboratory, Department of Biochemistry and Biophysics, University of California San Francisco, 600 16th Street, San Francisco, CA 94143

<sup>2</sup>The Howard Hughes Medical Institute, University of California San Francisco, 600 16th Street, San Francisco, CA 94143

#### Abstract

Newly developed direct electron detection cameras have a high image output frame rate that enables recording dose fractionated image stacks of frozen hydrated biological samples by electron cryomicroscopy (cryoEM). Such novel image acquisition schemes provide opportunities to analyze cryoEM data in ways that were previously impossible. The file size of a dose fractionated image stack is 20 ~ 60 times larger than that of a single image. Thus, efficient data acquisition and on-the-fly analysis of a large number of dose-fractionated image stacks become a serious challenge to any cryoEM data acquisition system. We have developed a computer-assisted system, named UCSFImage4, for semi-automated cryo-EM image acquisition that implements an asynchronous data acquisition scheme. This facilitates efficient acquisition, on-the-fly motion correction, and CTF analysis of dose fractionated image stacks with a total time of ~60 seconds/ exposure. Here we report the technical details and configuration of this system.

#### 1. Introduction

In addition to the significantly improved detective quantum efficiency (DQE), all commercially available direct electron detection cameras have high output frame rates, up to 40 frames/sec. This feature enables a novel data acquisition approach, termed dose fractionation or movie mode, where an image is readout as a stack of individual subframes recorded during the exposure. This approach enables correction of image blurring caused either by beam-induced motion or thermal and mechanical instability of the specimen holder (Bai et al., 2013; Campbell et al., 2012; Li et al., 2013a), as well as greatly increasing the total electron dose that can be used for imaging frozen hydrated biological samples (Grant and Grigorieff, 2015; Li et al., 2013a; Scheres, 2014).

Correspondence: agard@msg.ucsf.edu and ycheng@ucsf.edu.

<sup>\*</sup>Current address: School of Life Sciences, Tsinghua University, Beijing 100084, China

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We previously characterized the K2 Summit<sup>™</sup> from Gatan Inc. (Pleasanton, CA) (Li et al., 2013b) and developed a robust motion correction algorithm to correct motion-induced image blurring (Li et al., 2013a). Distinct from the two other commercially available direct detection cameras (from either Direct Electron, LP, San Diego, CA or FEI Company) (Bammes et al., 2012; Milazzo et al., 2011), the K2 Summit was developed specifically to count individual primary electrons striking the camera sensor (Li et al., 2013a; Li et al., 2013b). Moreover, it can analyze the signal cluster created by each primary electron and centroid the entry point with sub-pixel accuracy, similar to super-resolution methods in light microscopy (Shroff et al., 2007). Thus, the total effective number of pixels is quadrupled to ~58 million.

A standard procedure for collecting low-dose images of frozen hydrated protein samples sequentially steps through three low-dose modes, i.e. Search, Focus and Exposure, to record and save an image to a file system, either mounted on local computer or over the network. After an image is saved, this procedure is repeated. One of the advantages of using a digital camera is the capability of performing on-the-fly image analysis during data acquisition. Thus, some image analysis procedures can also be incorporated into the sequential low-dose image acquisition process once an image is saved. The overall acquisition procedure is well established and efficient (Suloway et al., 2005) when individual images of  $4K \times 4K$  or even  $8K \times 8K$  pixels are recorded. However, this simple sequential procedure can become tedious and inefficient when acquiring a large dataset of dose fractionated image stacks, because of the time required to save the very large image stack, especially in super-resolution mode. For example, a dose-fractionated image stack containing 32 gain corrected super-resolution subframes has a file size of ~ 7.2 gigabytes (GB). It is thus highly desirable to implement procedures that can efficiently coordinate image recording, saving, transferring and on-the-fly analysis and also provide a more compact means for storing the raw subframe data.

#### 2. UCSFImage4

We developed a simple to use computer program, named UCSFImage4, to facilitate semiautomated cryo-EM image acquisition. It mimics the manual low-dose data acquisition procedure implemented in the FEI microscope user interface and accepts full intervention from users during data acquisition. It has a simple interface and can work with different types of cameras, including scintillator-based cameras and direct detection cameras, such as K2 Summit and DE cameras.

Figure 1A shows the user interface of the program. The main interface of UCSFImage4 runs on a Microsoft Windows computer (XP or newer). It controls an FEI microscope through its TEM server (running on the FEI computer) and FEI scripting interface, and controls the camera through a camera server (Fig. 1B) that is specific for the type of camera being used. It runs on the camera computer and communicates with cameras through plug-ins. For lowdose imaging, it utilizes the Low-Dose module of Tecnai user interface. Alignment of electron optics and setup of low-dose are all performed on the microscope independent from UCSFImage4. The only calibration that UCSFImage4 requires is to correlate positional information from mouse clicks in Search mode with the stage movement. After such calibration, the user can move the specimen by mouse, pointing and clicking the new

position. The User can also use two vectors to define the positions of two neighboring holes of a holey grid with regularly spaced holes (green circles in Fig. 1A), and the program will control the CompuStage to step through each hole collecting low dose images with a predefined defocus series. In Focus mode, objective lens current is set to the value corresponding to zero defocus value set in the Tecnai interface. A real time FFT is used for manual or automated focus adjustment. In Exposure mode, an image is recorded with a predefined defocus value and saved to a pre-defined location.

UCSFImage4 has an extensible, modular design supporting a user-defined flow control, which imitates the manual three-mode low-dose data acquisition procedure. All operations of the microscope and camera during a low-dose cycle are grouped and abstracted as substeps, such as moving stage, reseting defocus, etc., and named with ID numbers. A user can customize the data acquisition procedure by selecting the sub-steps.

Among all commercial direct detection cameras, the K2 Summit is unique that it is optimized for operation in a single electron counting mode. Despite the very high internal frame rate, minimizing coincidence losses during electron counting requires that K2 images be recorded with a relative low electron dose rate (< 10e<sup>-</sup>/pixel/sec) and long exposure time (Li et al., 2013b). To use UCSFImage4 with the K2 camera, we developed a procedure of asynchronous data handling to improve the overall efficiency of data acquisition and on-thefly image analysis. Together with a number of modules, UCSFImage4 coordinates acquisition of low-dose image stacks and on-the-fly analysis for motion-correction, defocus determination, image quality assessment, and communications between camera, microscope and computers. We also configured and optimized computer hardware to facilitate such asynchronous acquisition and analysis of K2 dose fractionated image stacks from a FEI Tecnai microscope. A typical image stack of  $30 \sim 50$  subframes can be acquired every 60 seconds. This, coupled with the careful inspection of each hole with some manual intervention leads to the efficient and routine collection of very high quality data sets (Li et al., 2013a; Liang et al., 2015; Liao et al., 2013; Paulsen et al., 2015; Yan et al., 2015). Here we describe its technical details and related hardware and software configurations. While descriptions and discussions of the procedures implemented in UCSFImage4 are based upon using a K2 Summit camera with an FEI microscope, the underlying concepts are quite general and could be applied to other cameras.

#### 3. Asynchronous acquisition of dose-fractionated datasets

As discussed above, recording an image by the K2 Summit with an appropriate dose on specimen, ranging from 30 to  $100 \text{ e}^-/\text{Å}^2$ , requires a longer exposure time than typical for a non-counting camera. An image recorded at a lower magnification would require even longer exposure times. For example, using our FEI Tecnai TF30 Polara to reach a total dose of ~34 e^-/\text{Å}^2 with dose rate of ~10e^-/pixel/sec on camera, requires ~5 seconds exposure time to record an image at a magnification of 31kX, and ~13 seconds at 20kX. With such a long exposure, motion correction is an absolute necessity(Li et al., 2013a). At the maximum output rate of 40 subframes/sec, the total number of subframes for an exposure of 5 ~ 13 seconds could be 200~500 or more, although it is more typical to use between 5–10 subframes/sec resulting in 25–130 subframes in order to balance the number of subframes in

a stack with the needs for successful motion correction (Li et al., 2013a). A single K2 superresolution subframe has  $7420 \times 7676$  pixels and 8-bit pixel depth prior to gain correction, which converts each pixel to a 32-bit floating-point value. At this precision, each subframe corresponds to a size of ~230 megabyte (MB). In our current configuration, we typically target the recording of 25 ~ 60 subframes per image stack, which corresponds to 6 ~ 13 GB of raw data in one exposure.

In order to save both disk I/O time and the disk space, we now save the subframe images prior to gain correction as 8-bit integers and include the gain reference as part of the MRC extended header. This allows the gain corrected floating-point image data to be easily recreated with no loss in precision, while simultaneously increasing transfer speed four-fold and reducing file size 4-fold to 1.6 ~ 3.6 GB. The standard MRC format has six modes, 0,1,2,3,4 and 6, but does not have a mode for 8-bit unsigned integer data type (Crowther et al., 1996). To save the not-gain-corrected sub-frame images, we added a new mode, 5, for the 8-bit unsigned integer. The binary file structure of MRC file is unchanged. The gain reference is stored as 32-bit float in the extended header of the standard MRC format. Considering that other programs, such as UCSFTomo (Zheng et al., 2007), also use the extended header to store image acquisition information and until the end of the extended header. Therefore, the size of the extended header will be the total size of the image acquisition information plus that of the gain map. Multiplying the gain reference with the sub-frames converts it to standard MRC format with mode 2, 32-bit real.

To the standard K2 Summit computer configuration we added either an nVidia Tesla C2070 or K10 graphic card to carry out on-the-fly image analysis (see below). Under this basic configuration, when DigitalMicrograph (DM, Gatan Inc.) is used to record a dose-fractionated image stack, subframes are first processed on the K2 Summit processor, followed by being sequentially transferred to RAM on the K2 computer through the 10 Gb network. All data, including all subframes and their summation, are then written to the SSD. Since the entire image stack is transferred first to RAM on the K2 computer before being written to SSD, the time needed to save such an image stack is a major time block that requires optimized coordination with other steps of low-dose image recording cycle. Even with its high I/O bandwidth, it still takes 20 ~ 40 seconds to write an image stack from the K2 processor to the computer, the total time used to transfer and save an image stack is 30~50 seconds, which is much longer than a single frame acquisition.

In a strict low-dose image acquisition cycle, the microscope setting is switched sequentially between Search, Focus and Exposure modes, followed by recording and saving an image. Prolonged image transferring and saving extends the total time needed to complete a data acquisition cycle. We thus established an asynchronous data acquisition procedure to accelerate this process, that is to overlap the low-dose procedure with transferring data between the K2 processor and the SSD drive in the K2 computer and processing data on the fly (Fig. 2).

Typically in Search and Focus modes, a TV rate camera would provide a live-view of the sample, while in Exposure mode a single exposure of the camera records an image. Because direct detection cameras have a high output frame rate, they can be used for all three modes, greatly simplifying operation and eliminating unnecessary delays. After Exposure, which is usually 5~15 seconds, the K2 camera returns to the ready state and is immediately switched to live imaging mode. At the same time, the microscope is switched from Exposure to Search mode to start another low-dose imaging cycle, as show in the yellow branch in Figure 2. Locating the next sample area (Search) and adjusting focus (Focus) takes about 10~20 seconds. Together with the exposure, the time needed to complete a three-mode low-dose cycle is usually less than 30 seconds.

In a conventional, serial implementation of transferring, saving and processing the image stacks takes a significantly longer time to complete. Therefore, our main effort is to make this process more efficient. To accomplish this, we save individual subframes to SSD as they become available instead of waiting for the complete stack and overlap saving data to the network with the on-the-fly image analysis (motion correction and CTF analysis), as indicated by the green path in Figure 2. This significantly shortens the time needed for saving the image stack to SSD, but as the K2 computer no longer calculates the sum of all subframes, this must be calculated separately. However, as data saving is independent from the data acquisition, it can lag behind to an extent limited by the capacity of the SSD (1TB in our configuration). Even with the overlaps, the total saving and processing time is longer than that strictly required for the three-mode low-dose cycle (usually less than 30 seconds). To keep the two branches synchronized, we usually set a 10~20 second delay between focus and exposure modes, which also helps to stabilize the mechanical motion of the microscope stage. With such an asynchronous acquisition, a low-dose acquisition cycle can be limited to within one minute, corresponding to at least 60 stacks per hour. This is actually significantly faster than many fully automated acquisition systems.

#### 4. Coordinating data acquisition and on-the-fly image analysis

UCSFImage4 implements the asynchronous data acquisition flow of Figure 2 and uses three external modules (image binning, motion correction and CTF determination) for on-the-fly processing of dose-fractionated data (Figure 3 and Supplementary Figure 1). All modules run as individual programs and communicate through internet-sockets used by most computers so that the modules can be easily distributed to different computers with different operating systems. All the data on different computers are shared between different operating systems, either by SAMBA between Microsoft Windows and Linux or by NFS for Linux computers.

On-the-fly image analysis must be fast enough to maintain synchronization with the data acquisition with the minimal added delay. To speedup this process, we often use  $2 \times 2$  binned images instead of full size super-resolution images, although all image registration is applied to the super-resolution images. While image binning can be calculated by averaging adjacent pixels, such averaging causes signal attenuation at high frequency by a sinc function and aliasing of higher-frequency signals into the lower frequency binned images. We instead crop the central  $m/b \times n/b$  pixels from the fast Fourier transform (FFT) of the full

sized raw image of  $m \times n$  pixels (b = binning ratio), followed by an inverse Fourier transform. Such a b-fold binned image keeps exactly the same Fourier components in the Fourier space within the cropped region (resolution) as the original raw image. A potential problem is that the cropping in Fourier space is equivalent to convolving a *sinc* function with every pixel in real space. Thus, any bad pixels with very large or small intensity values will influence a large adjacent area. To minimize the influences of bad pixels, flat fielding references must be prepared carefully previous to image acquisition, and the bad pixels must be corrected before the binning.

We also carry out all image analysis using general-purpose graphic processing units (GPUs). In both the Fourier-space image binning and motion correction, the Fourier transform is the major computation that is calculated several hundred times per image stack and occupies ~90% computing time. However, on a typical CPU using the fastest FFTW3 library, a single direction FFT on a super-resolution frame ( $7420 \times 7676$  pixels) will take ~3–6 seconds. The total processing time for one stack would then be at least 20 minutes, which is too slow not only for on-the-fly but even for practical offline processing. In our configuration, we used nVidia GPUs and CUDA (nVidia) to accelerate the FFT and all other computations. GPUs have previously been used to accelerate many aspects of cryoEM image processing (Li et al., 2010; Zhang et al., 2010). They are particularly powerful for calculating FFTs; with a  $7420 \times 7676$  pixel FFT taking only ~0.05 seconds on a GTX680 GPU with 1536 cores. Image binning and motion correction are usually more than 60 fold faster on a GPU than with a comparable CPU version. For this purpose, we installed a Tesla C2070 graphic processor on the K2 computer, so that image binning and motion correction can be immediately carried out once the frame stack is ready. Both procedures can be completed in 20~30 seconds for a stack with 30~40 frames. This is sufficiently fast to give immediate feedback to user before the next image is recorded. The on-the-fly motion correction can also be done on a separated Linux workstation with one or more powerful GPU cards if the network connection between the GPU computer and K2 computer can support a data transfer better than 400~500MB/sec (discussed below). Note, that in our experience the higher-end computational (Tesla) cards are considerably more robust than the equivalent commodity display versions.

#### 5. Conclusions and discussion

We described here an asynchronous data acquisition procedure that is routinely being used for efficient acquisition of large numbers of dose fractionated image stacks recorded on a K2 camera connected to an FEI Tecnai microscope. This procedure enables us to collect ~600 image stacks within 10 ~ 12 hours. It can also be easily adapted for other cameras capable of recording dose fractionated image stacks. Note that the asynchronous data acquisition procedure described here was designed for improving efficiency of acquiring dosefractionated electron-counting images. While the procedure also works for charge integration cameras, the improvement of data acquisition efficiency may not be as significant as for a counting camera.

As the total number of subframes increases, the bottleneck of this asynchronous data acquisition becomes transferring data between the K2 computer and an external processing

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or storage server. Transfer rates of at least 400~500 MB/s seem to be necessary to make the asynchronous procedure smooth, requiring both high speed networking and high performance RAID storage systems. For the network, 10 Gb Ethernet is a minimal requirement, although QFSP or InfiniBand with more than 40 Gb bandwidth or the combination of multiple 10 Gb channels is preferable. To optimize the on-the-fly image processing, we configured a separate computer with a RAID0 of 10 SSDs to increase the storage bandwidth to be comparable to the high-speed network linking to the K2 computer and two nVidia Tesla K10 graphic cards for on-the-fly image processing. By sharing its storage with K2 computer, the large stack file will be directly written from K2 computer's memory in order to avoid the bandwidth and capacity bottleneck of the local storage on K2 computer.

#### **Supplementary Material**

Refer to Web version on PubMed Central for supplementary material.

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#### References

- Bai XC, Fernandez IS, McMullan G, Scheres SH. Ribosome structures to near-atomic resolution from thirty thousand cryo-EM particles. eLife. 2013; 2:e00461. [PubMed: 23427024]
- Bammes BE, Rochat RH, Jakana J, Chen DH, Chiu W. Direct electron detection yields cryo-EM reconstructions at resolutions beyond 3/4 Nyquist frequency. Journal of structural biology. 2012; 177:589–601. [PubMed: 22285189]
- Campbell MG, Cheng A, Brilot AF, Moeller A, Lyumkis D, Veesler D, Pan J, Harrison SC, Potter CS, Carragher B, et al. Movies of ice-embedded particles enhance resolution in electron cryomicroscopy. Structure. 2012; 20:1823–1828. [PubMed: 23022349]
- Crowther RA, Henderson R, Smith JM. MRC image processing programs. Journal of structural biology. 1996; 116:9–16. [PubMed: 8742717]
- Grant T, Grigorieff N. Measuring the optimal exposure for single particle cryo-EM using a 2.6 A reconstruction of rotavirus VP6. eLife. 2015; 4
- Li X, Grigorieff N, Cheng Y. GPU-enabled FREALIGN: accelerating single particle 3D reconstruction and refinement in Fourier space on graphics processors. Journal of structural biology. 2010; 172:407–412. [PubMed: 20558298]
- Li X, Mooney P, Zheng Q, Booth CR, Braunfeld MB, Gubbens S, Agard DA, Cheng Y. Electron counting and beam-induced motion correction enable near-atomic-resolution single-particle cryo-EM. Nature Methods. 2013a; 10:584–590. [PubMed: 23644547]
- Li X, Zheng SQ, Egami K, Agard DA, Cheng Y. Influence of electron dose rate on electron counting images recorded with the K2 camera. Journal of structural biology. 2013b; 184:251–260. [PubMed: 23968652]
- Liang B, Li Z, Jenni S, Rahmeh AA, Morin BM, Grant T, Grigorieff N, Harrison SC, Whelan SP. Structure of the L Protein of Vesicular Stomatitis Virus from Electron Cryomicroscopy. Cell. 2015; 162:314–327. [PubMed: 26144317]

- Liao M, Cao E, Julius D, Cheng Y. Structure of the TRPV1 ion channel determined by electron cryomicroscopy. Nature. 2013; 504:107–112. [PubMed: 24305160]
- Milazzo AC, Cheng A, Moeller A, Lyumkis D, Jacovetty E, Polukas J, Ellisman MH, Xuong NH, Carragher B, Potter CS. Initial evaluation of a direct detection device detector for single particle cryo-electron microscopy. Journal of structural biology. 2011; 176:404–408. [PubMed: 21933715]
- Paulsen CE, Armache JP, Gao Y, Cheng Y, Julius D. Structure of the TRPA1 ion channel suggests regulatory mechanisms. Nature. 2015; 520:511–517. [PubMed: 25855297]
- Scheres SH. Beam-induced motion correction for sub-megadalton cryo-EM particles. eLife. 2014; 3:e03665. [PubMed: 25122622]
- Shroff H, Galbraith CG, Galbraith JA, White H, Gillette J, Olenych S, Davidson MW, Betzig E. Dualcolor superresolution imaging of genetically expressed probes within individual adhesion complexes. Proceedings of the National Academy of Sciences of the United States of America. 2007; 104:20308–20313. [PubMed: 18077327]
- Suloway C, Pulokas J, Fellmann D, Cheng A, Guerra F, Quispe J, Stagg S, Potter CS, Carragher B. Automated molecular microscopy: the new Leginon system. Journal of structural biology. 2005; 151:41–60. [PubMed: 15890530]
- Yan C, Hang J, Wan R, Huang M, Wong CC, Shi Y. Structure of a yeast spliceosome at 3.6-angstrom resolution. Science. 2015
- Zhang X, Zhang X, Zhou ZH. Low cost, high performance GPU computing solution for atomic resolution cryoEM single-particle reconstruction. Journal of structural biology. 2010; 172:400– 406. [PubMed: 20493949]
- Zheng SQ, Keszthelyi B, Branlund E, Lyle JM, Braunfeld MB, Sedat JW, Agard DA. UCSF tomography: an integrated software suite for real-time electron microscopic tomographic data collection, alignment, and reconstruction. Journal of structural biology. 2007; 157:138–147. [PubMed: 16904341]

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#### Figure 1.

A: User interface of UCSFImage4. The left window displays live views of specimen (in Search mode) or image of specimen at a high magnification (Focus mode). In Search mode, user can move specimen by mouse pointing and clicking. The red circle is the center of the camera. Green circles mark the locations of neighboring holes. Diameter of these circles is adjusted to match the diameter of the holes shown in the Search mode. Specimen position is adjusted by moving stage following the local cross-correlation between the red circle and the targeted hole. The right window displays live FFT power spectrum from images shown in the left window (in Focus mode). After exposure mode, it displays the image recorded. The surrounding buttons and windows are used to control the data collection and configure corresponding parameters, respectively. **B**: User interface of camera server that controls K2 camera. Parameters of dose fractionation are defined in this interface. Both UCSFImage4 and CameraSever are installed in the computer controls the camera.



#### Figure 2.

Flow chart of an asynchronous three-mode low-dose cycle. The time needed for each step is shown on the top and bottom of the figure.



#### Figure 3.

Diagram of modules used for dose-fractionated data collection by the K2 camera. UCSFImage4 communicates with a FEI microscope through TEMServer (installed in the microscope computer) and with the K2 camera through a CameraServer (installed in the camera computer). Dose fractionation image acquisition parameters are defined in CameraServer. Saved image stacks are feed to MotionCorr for on-the-fly motion correction. CTFFIND module determines and display CTF information of motion corrected images.