Huygens Remote Manager
A Web Interface for High-Volume Batch Deconvolution

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Summary

Nowadays, deconvolution in cell and tissue imaging has matured into a standard restoration technique that is accessible to large fraction of the microscopy community thanks to steadily improving algorithms. Still, deconvolution is often the rate-limiting step in the analysis of the acquired data, even at today's computer performance. Here, we present the Huygens Remote Manager, an open-source, efficient, multi-user web-based interface for parallel batch deconvolutions.

Introduction

Over the past decades, live cell imaging has gone through a fundamental revolution, thanks to key innovations like the discovery of naturally fluorescent proteins [1] and the engineering of fluorescent probes, the development of an increasing number of sophisticated light microscopy techniques, the reduction of storage costs and the increase of computing performance, and the development of effective algorithms for image manipulation and analysis.

Processes at the subcellular level can today be followed in vivo, dynamically, and imaged in two or three dimensions. The choice of the microscopy technique to use for the application of interest however depends on a variety of parameters, like the resolution limit, the sensitivity of detection, the speed of acquisition, the viability and thickness of the specimen, and even the price of the microscope. As a consequence, often no single microscope system or technique will be best, and compromises will have to be made, often resulting in less-than-optimal image resolution and/or signal to noise ratio.

Deconvolution and image restoration in general [2],[3] are computer processing techniques designed to overcome the limitations of the different microscope modalities. They make use of models of the optics of the microscope (the 3D point-spread function), the noise, and to some extent also of possible aberrations. Deconvolution was initiated by the desire to remove the out-of-focus haze that characterizes the images obtained from a wide-field microscope [4] and has matured into a tool that can be applied to almost any type of microscopy modality to produce images with increased resolution, better contrast and improved signal-to-noise ratio (Figure 1). Besides the cosmetic effect, however, deconvolution is also essential for

quantitative analysis. As an example, deconvolution was shown to be crucial for colocalization analysis [5].

The Huygens Deconvolution Software by Scientific Volume Imaging (http://www.svi.nl) is the most advanced deconvolution package available today. It can process images from all current optical microscope types and can run on a large number of processors in parallel. As one of its products, SVI offers Huygens Scripting, an engine that exposes all processing functionality of the Huygens Compute Engine (the processing kernel at the core of the Huygens software) for the automated restoration of datasets through scripts written in the Tcl scripting language. This allows the processing of datasets in batch mode locally or remotely on a dedicated server. However, it requires the users to program their own scripts, which is both time-consuming and error-prone. Furthermore, this approach cannot efficiently scale to larger user bases, since it lacks a mechanism to organize the jobs into a queue and forces users to work with a first come first served policy.

To address the limitations of Huygens Scripting for a multi-user environment, we wrote the Huygens Remote Manager (HRM), a web-based interface that allows users to create jobs easily from their workstation and takes care of translating the job parameters into Tcl scripts that are then passed on to the Huygens Compute Engine via a queue manager.

In the following we present HRM in more details.

The Huygens Remote Manager

The Huygens Remote Manager is a web-based deconvolution platform primarily targeted to microscopy and imaging facilities in academic and industrial environments that must handle large user bases. HRM is a joint project of the Friedrich Miescher Institute in Basel, the BioImaging and Optics platform at the Ecole

Polytechnique Fédérale de Lausanne, Montpellier Rio Imaging, and Scientific Volume Imaging. Current development snapshots of HRM can be downloaded from http://hrm.sourceforge.net.

HRM consists of two main components, both written in PHP: a web-based interface to the Huygens Compute Engine and a queue manager. Briefly, the web interface allows users to create deconvolution jobs from remote through any reasonably recent web browser. The thus created jobs are dispatched by the queue manager to any of the dedicated servers running the Huygens software. When the job is finished, an email informs the user that the restored datasets are ready to be retrieved.

In more detail, HRM requires a web server with a database backend (to store deconvolution parameters, job descriptions and, optionally, user accounts), a file server (to temporarily store input and restored datasets), and one or more processing servers running the Huygens software. The setup is highly configurable, since (i) servers and queue manager can either be all hosted by the same machine (Figure 2 a) or be distributed onto two, three or more computers (Figure 2 b); (ii) a large number of databases are supported through the ADODB database abstraction library for PHP (http://adodb.sourceforge.net), an open-source package distributed under the BSD license: (iii) parts of HRM are optional, as is the case for the embedded user management system (see below).

Figure 3 shows the HRM welcome screen. Here existing users can login and new users can register. If the user management module is enabled, the new users can be accepted or rejected by the administrator directly through HRM. The choice of making the embedded user management module optional allows user administration at a higher level (e.g. at facility level for example by using LDAP).

After login, the user can create and launch deconvolution jobs. A job definition consists of three parts (Figure 4): (i) a set of *optical parameters* that allow the Huygens software to calculate a model of the 3D PSF for deconvolution or, alternatively, a pointer to a file containing a measured PSF; (ii) a set of *task settings*, that define the parameters for restoration; (iii) the *input files list* to be processed and the file format of the results.

Parameters and settings are stored in the database (Figure 4), therefore creating a personalized working environment for each user. This way, repeating jobs can be created with just a few clicks. Moreover, to facilitate the work of first-time users the administrator can create templates for the optical parameters and task settings, and the users can then copy and adapt them to match their needs.

In the following we briefly discuss the three parts of a job description (see Figure 4).

Optical parameters In the first step of the job definition, the user decides whether deconvolution has to be run with a theoretical PSF calculated from the user-input optical parameters, or with a measured PSF, which can be picked through a file dialog. The size and shape of the PSF is a function of the microscope type (i.e. wide-field, standard or spinning disk confocal, or two-photon), the numerical aperture of the objective, the excitation and emission wavelengths of the fluorophore, the refractive indices of the lens immersion and the sample embedding media, and of the spatial sampling. These parameters are to be set by the user and can usually be found in the metadata associated with the datasets. The PSF calculated from the optical parameters is an idealized model that will give good results if the microscope's optical path is well aligned and free of aberrations. Alternatively, a measured PSF can be

obtained by imaging sub-resolution beads with the same settings that will be used for the real experiment, and then *distilling* a PSF with the Huygens software tools.

Task settings In the next step, the user sets the parameters for image restoration: a rough estimation of the signal-to-noise ratio, a selection of the preferred background subtraction approach and the stopping criterion for the iterative restoration algorithm. As was the case for the optical parameters, again the user can select among public templates and own settings.

Input files list The last step of the job creation process is the selection of the files to be added to the job and the selection of the output file format. The default is the Image Cytometry Standard (ICS) file format (used natively by the Huygens software). In fact, the ICS file stores the result of image restoration in floating-point precision and also maintains the complete metadata information associated with the input dataset. (For compatibility reasons, also 8- and 16-bit TIFF sequences are supported for applications that cannot interpret the ICS format: unfortunately, however, metadata information is lost in standard TIFF files.) The user is presented with a list of files that are currently in his area on the file server and can add as many as he wants to the job. In the current implementation of HRM, the user is expected to copy the files to be deconvolved into a SAMBA share that HRM created on the file server during the user registration process. Other mechanisms for file upload to the file server are already partially supported. Before launching the job, the user can still review and if necessary change the selected parameters. The created job is stored into the database, from which the queue manager will pick it and dispatch it to the first free processor on the dedicated server(s). The status of the queue can be visualized at any time through HRM. At the end of the job HRM will inform the user via a summary email that the restored datasets are ready on the file server to be retrieved.

In summary, HRM allows high-volume deconvolution jobs to be created with minimal effort, performs the restoration without any additional user intervention (thus permitting the user to concentrate on other tasks), and delivers results with the renowned high quality of the Huygens software.

Outlook and conclusion

Several new features to HRM are currently being implemented that will lead to the release of the first official version of HRM, such as a better mechanism for the file transfer to and from the file server, a scheduler for the queue manager and methods to extract the optical parameters from the metadata of the datasets, among others. Better and easier installation routines will also be provided. Importantly, some changes are being introduced into the Huygens software as well, to increase the interoperability with HRM.

Handling of data and associated metadata is a rather controversial topic these days, with the imaging community trying to persuade the microscopy companies to reach an agreement on a standard file format, and all major companies sticking to their own proprietary formats (often more than one per company), thus rendering the exchange and processing of data very difficult. One of the most promising projects toward standardization is the Open Microscopy Environment (OME) from the OME consortium (http://www.openmicroscopy.org) and its OME-XML/TIFF file format. In an attempt to contribute to the standardization effort, Huygens and HRM decided to support the OME-XML format (beside several proprietary file formats).

In conclusion, we developed Huygens Remote Manager, an open-source web-based interface to Scientific Volume Imaging's Huygens Compute Engine released under the terms of the CECILL license that allows for the easy and automated generation of batch deconvolution jobs in a multi-user environment.

References

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Figure captions

Figure 1

Example of deconvolution of a wide-field dataset by the Huygens software. Primary cultures of spinal ganglion sensory neurons stained for Neurofilament (FITC, green) and alpha3 subunit of GABAA Receptor (Red, Texas Red) before (left) and after (right) deconvolution. Images were acquired using a Leica DMRA microscope, a 63X PL APO 1.32 NA oil immersion objective, a Physik Instrument Piezo stepper and a Princeton Instrument Micromax YHS Camera. The volume rendering was performed with SVI's FreeSFP. Image courtesy: Frédérique Scamps, Institute for Neurosciences of Montpellier.

Figure 2

The Huygens Remote Manager setup is highly configurable. The web (W), file (F) and processing (P) servers as well as the queue manager (Q) can be all hosted by the same machine (a) or distributed onto any number of machines (b).

Figure 3

The Huygens Remote Manager welcome screen at the Friedrich Miescher Institute.

Figure 4

A job description consists of three parts: a set of optical parameters, defining the theoretical point spread function to be used for restoration (alternatively, a

measured point spread function can be used); the task settings for the image restoration; and a list of files to be deconvolved (stored on the file server, where also the restored data will be saved).

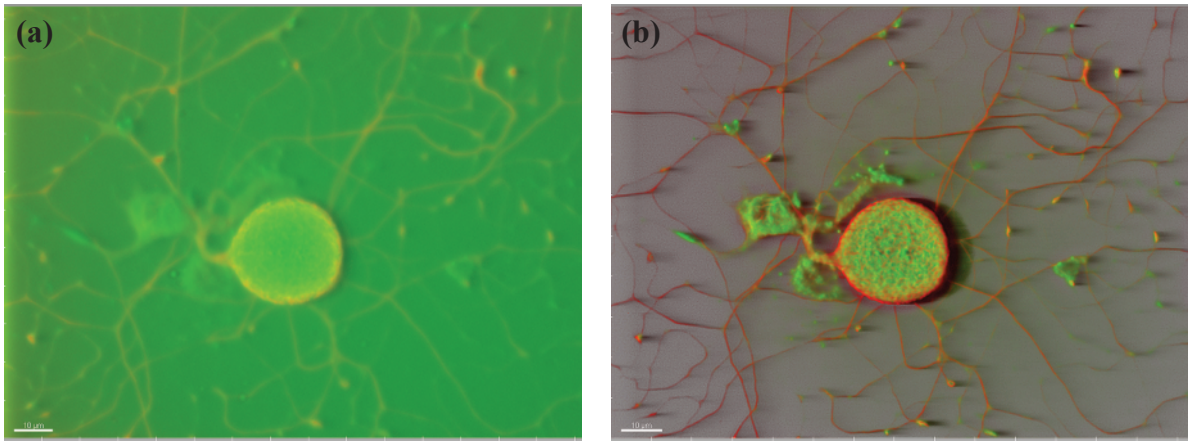

Figure 1

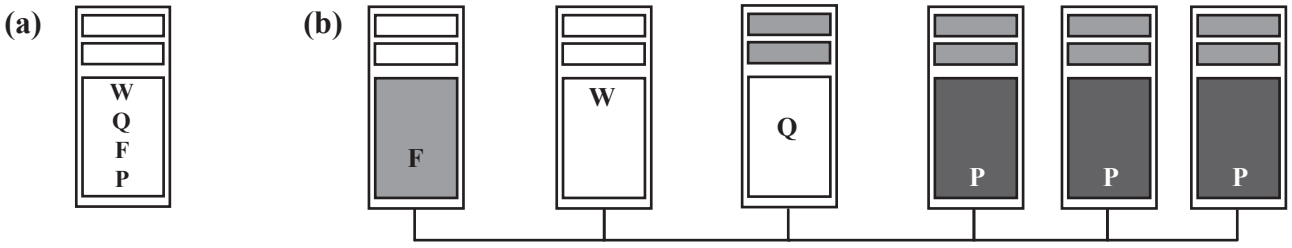

Figure 2

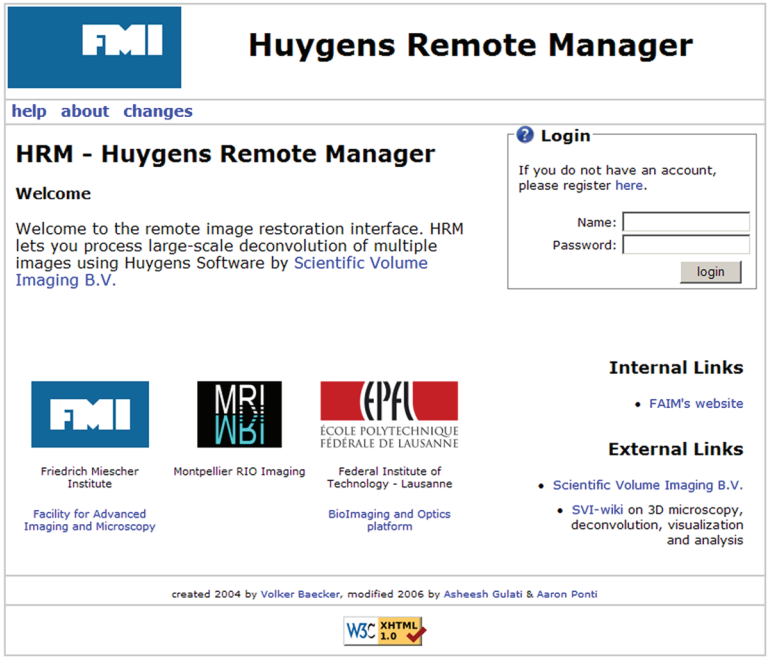
Huygens Remote Manager
help about changes
HRM - Huygens Remote Manager
Welcome
Welcome to the remote image restoration interface. HRM lets you process large-scale deconvolution of multiple images using Huygens Software by Scientific Volume Imaging B.V.
Login
If you do not have an account, please register here.
Name:
Password:
login
Friedrich Miescher Institute
Facility for Advanced Imaging and Microscopy
Montpellier RIO Imaging
Federal Institute of Technology - Lausanne
BioImaging and Optics platform
Internal Links
FAIM's website
External Links
Scientific Volume Imaging B.V.
SVI-wiki on 3D microscopy, deconvolution, visualization and analysis
created 2004 by Volker Baecker, modified 2006 by Asheesh Gulati & Aaron Ponti
XHTML 1.0

Figure 3

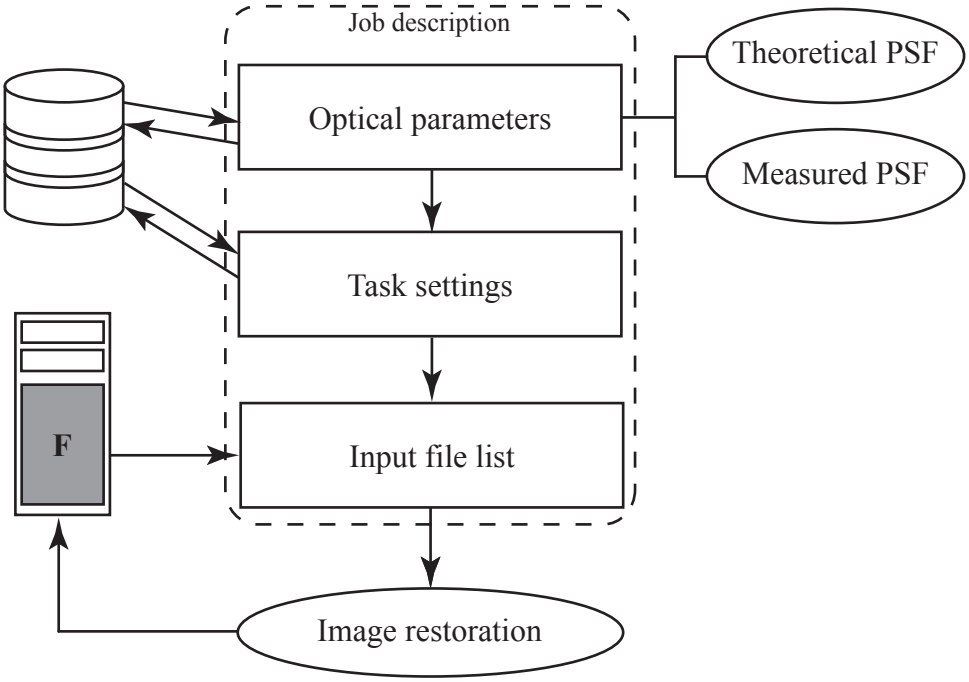
Job description
Optical parameters
Task settings
Input file list
Theoretical PSF
Measured PSF
F
Image restoration

Figure 4