Software Clearing CT Data from Effects of Instrumental Resolution

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Aims
The practical implementation and development of the EU BIO-CT-EXPLOIT project for clearing CT data from effects of instrumental resolution [2] adds a unique and specific capability to the in-house analysis GUI package “CTan” provided by SKYSCAN with its tomographic scanning equipment. Programmed in-line to sit on the “plugin” panel of the analysis package for importing tomographic image slices direct from the machine, it is a fully automated image enhancement algorithm requiring little or no expertise from the user, making it fast and easy to use in single image or indeed batch mode. The images produced use the histogram equalization technique to remove the instrumental error as documented in [1]. These may then be further processed by the main body of the SKYSCAN package according to requirement and then visualized as three-dimensional reconstructions of the computed tomography (CT) process. The incremental advances in technology in today’s market are so hard fought for that we feel confident that the unique technologies employed in this plugin concept designed for SKYSCAN will deliver a vital pre-processing step towards increasing the capability and applicability of CT scanner machines.

Method

Scientific Aspects
The presence of air inside the voids or cavities of a computed tomography (CT) sample introduces errors in the form of distributed noise in the two-dimensional output grey scale absorption image of the slice. These show up as a separate characteristic peak in the histogram of that image. According to the theory expounded in [1] the corrected image histogram is obtained by using the characteristic air error peak as the kernel in a one dimensional deconvolution operation [3] upon the original histogram. This histogram can then be mapped back to a corrected image using a variety of techniques. A very good, commonly used, method is to implement a histogram equalization (HE) [4] to derive the corrected image itself.

5 EU-FP7 project BIO-CT-EXPLOIT entitled „Innovative simulation tool for bone and bone biomaterials”, based on enhanced CT-data exploitation, information online at http://bio-ct-exploit.imws.tuwien.ac.at/
Integration into SKYSCAN software

The process chain given in Figure 1 is actually implemented in the MATLAB environment as a part of the EU BIO-CT-EXPLOIT effort. We are presently converting it into a plugin format for the SKYSCAN scanner image processing software written in Microsoft’s Visual C++ computer language. The C++ language is very fast and intricate from the programmer’s perspective, giving strong and safe control over the computer functions. The development environment provided by Microsoft and used by SKYSCAN is an established standard in such program development projects. It permits the development of software as a seamless part of the MS Windows operating system using all the graphical user elements for maximum compatibility in the target market as well as ease of use.

This implementation gives the user an option to preprocess CT image(s) in a new way as laid out in [1] to be effectively better approximations, delivering effectively a more accurate and relevant absorption map of the material. The entire chain summarized in Figure 1 has been built to run without user intervention. The underlying processes are complicated and require much knowledge of certain numerical analysis techniques to produce the treated images. Thus intervention by the user would be a time consuming process and defeat the purpose of preprocessing in this way [2]. Complete automation is fast and batch processes can also be devised which, apart from the theoretical utility of the procedure, make it practical and a step forward when implemented and distributed as a plugin.

The MATLAB implementation has a certain object model that is very useful for testing as well as an image processing toolbox. The image processing libraries have therefore been self-contained as a part of the MATLAB environment for the duration of beta development. The transformation into a C++ plugin according to the SKYSCAN requirements needs a complementary image-processing library as strong at that of MATLAB (all the functions cannot hoped to be duplicated even so, but we can custom write the missing routines to retain the original functionality). To avoid licensing issues we chose a free library available on the internet as “CIMAGE” and immediately this provided a great deal of implementation strength. There are compatibility drawbacks involved; the main one being that the library is new while the compilation of the SKYSCAN C++ software was old by almost a decade. Our first challenge has therefore been to cast a compatibility framework linking the CIMAGE library to the SKYSCAN plugin code frame. This has been now done and a transparent
process pipeline from the MATLAB routines to their C++ counterparts achieved. Images can be loaded and processed in an equivalent way without trouble.

This opens the way for custom development of the plugin to exact requirements as specified by SKYSCAN. We are therefore engaged in a two way process of duplicating the original MATLAB beta functionality in C++ for the plugin, and indeed improving upon that functionality where C++ provides a significant gateway to do so. The result will be a fast and streamlined preprocessing package for a commercial endeavor, which is extensible and useful for analysis of CT scanner images in the engineering and medical fields as was laid out in the image clearing aspect of the EU BIO-CT-EXPLOIT project specification (see Figure 2 as well as [2]).

Figure 2: An illustration of the BIO-CT-EXPLOIT “Software for clearing CT data from effects of instrumental resolution” project timeline with increase in demonstrator/deliverable platform capacity shown as the volume of the shapes at each projected stage.
Results

The MATLAB beta delivers a complete implementation of the BIOCT image-clearing pipeline. This is shown in Figure 1 in its schematic form. The complete MATLAB GUI we present in Figure 3 below.

Figure 3: An illustration of the BIO-CT-EXPLOIT project “Software for clearing CT data from effects of instrumental resolution” MATLAB beta demonstrator as implemented at month 12.

The most recent developments in the project actually come from the C++ plugin framework that is referred to in the section above. Figure 4 is a glimpse of the framework in action on a SKYSCAN raw CT image; The framework is here implemented as a plugin already mounted and running in the SKYSCAN CTan environment showing the CIMAGE library “histogram” operation on the loaded image.
Conclusion

The EU BIO-CT-EXPLOIT “Software for clearing CT data from effects of instrumental resolution” sub-specification has given rise to a unique opportunity in the image processing of CT produced two dimensional image slices for bone like materials. The coming together of the MATLAB, SKYSCAN and C++ computer technologies have proved an ideal cross platform for the integrated development of digital image processing enhancements to that connect the scientific discipline to the commercial technology distribution pipeline through SKYSCAN for example. This process has streamlined and made more efficient the path from research science to benefits realized by the public.
There are novelties associated with the image processing science behind these developments. This is particularly the case for the physical reinterpretation of so-called “image morphology” operations, which has allowed us to usefully extract porosity information hidden in the images. Further to this, the whole process is automated and can operate on batches of images in a wide variety of formats [2]. At every stage in Figure 1 a series of different sub-processes can be said to exist. These, quite apart from safeguarding automation, provide detailed information to the user about every transformation made should he or she require it. Included are the image histograms and their analytical approximations as well as the theoretical and measured final image histograms (Figure 1, stage 3). There is also the actual HE transformation curve that can be requested in the software as well as several different technical data like the Otsu background level [5] and the region of interest mask based on the porosity evaluation.

In all we feel that the integration of these technological developments into the plugin software currently being developed for SKYSCAN will provide a significant and unique advancement to the CT image preprocessing technology currently available in the market.
References:


[2] EU-FP7 project BIO-CT-EXPLOIT entitled "Innovative simulation tool for bone and bone biomaterials, based on enhanced CT-data exploitation" (coordinator: Christian Hellmich), information online at http://bio-ct-exploit.imws.tuwien.ac.at/

