
Medical Image Analysis with VTK: A Tutorial

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Abstract

This paper describes a new tutorial book titled “An Introduction to Programming for Medical Image Analysis with the Visualization Toolkit.” This book derived from a set of class handouts used in a biomedical engineering graduate seminar at Yale University. The goal for the seminar was to introduce the students to the Visualization Toolkit (VTK) and, to a lesser extent, the Insight Toolkit (ITK). A draft version of the complete book (including all the sample code) is available online at www.bioimagesuite.org/vtkbook.

Contents

1	Introduction	1
2	Motivation	2
3	Book Contents	3
4	Conclusions	4

1 Introduction

While both the Visualization Toolkit (VTK)[\[9\]](#) and the Insight Toolkit (ITK) [\[2\]](#) come with excellent online documentation, there is still a great need for introductory material to guide the beginner along the often steep learning curve required to learn using these toolkits.

This article summarizes the contents of a book in preparation[\[6\]](#), a draft version of which is available freely online in .pdf format from the BioImage Suite web-page. The goal of this book was precisely to fill that void in the availability of introductory material. This book builds on a previous similarly named tutorial [\[5\]](#) that many have found useful in the past.

This book is an edited collection of class handouts that I wrote for the graduate seminar “Programming for Medical Image Analysis” (ENAS 920a) that was taught at Yale University, Department of Biomedical Engineering, in the Fall of 2006. My goal for the class was to provide sufficient introductory material for a typical 1st year engineering graduate student with some background in programming in C and C++ to acquire the skills to leverage modern open source toolkits in medical image analysis and visualization such as the Visualization Toolkit (VTK) and, to a lesser extent, the Insight Toolkit (ITK).

One obviously has to acknowledge that there are many programming books out there that cover the material discussed in this book in more depth (and more correctly perhaps); I list many of my sources in Chapter 1. However, placed one on top of the other, these books form a pile about 1-2 feet high, which can be discouraging to a beginner. This book is meant to be an introductory guide. Many of the definitions are informal, much like one teaches math at 1st grade. As the student progresses and begins to understand the introductory material, then he/she should look at more specialized books which offer a deeper insight into what is going on. The manual pages for many of these toolkits also become useful at this point.

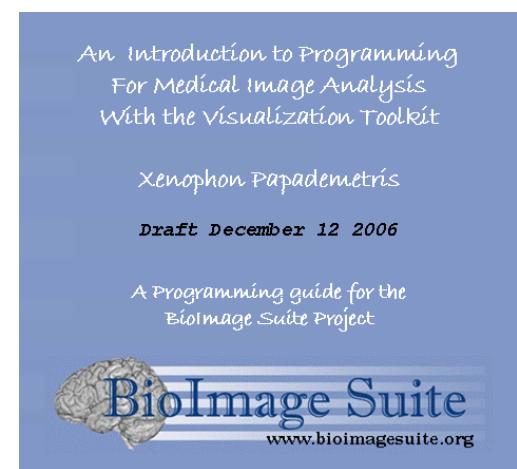


Figure 1: The Book “Cover”.

2 Motivation

Most of our graduate students – the intended audience for this book and class – while having a strong applied mathematics/signal processing background, are not expert programmers. For the most part, they would have had some programming classes at the undergraduate level and would have been, most likely, exposed to C/C++ at some point. However, with rare exceptions, a dive into the combination of object-oriented and generic programming model used in ITK, for instance, would leave such students befuddled.

Such students begin their graduate research in semester long projects called “special investigations”. This is part of the process of identifying a topic for their research as well as a lab in which they will pursue their dissertation work. In our own research in medical image analysis, the typical product of a doctoral dissertation is a mathematical framework for attacking an image analysis problem which has to be translated into computer code for testing and validation.

Most of the students, in these special investigations, prototype ideas in MATLAB[4]. While MATLAB is a wonderful prototyping tool, it leaves much to be desired in terms of the development of the programming habits needed to write a large, sustainable, and reusable body of code. Unfortunately, many students ending up in the trap of developing the best algorithms that can be implemented in MATLAB as opposed to focusing on what an optimal algorithmic strategy would be. This is especially apparent once large 3D and 4D datasets enter into the picture, and their algorithms end up taking hours and days to run.

At this point in the game, a helpful professor suggests that they should probably look to move to a more efficient language such as C++. However, one look at straight C++ without any of the additional toolkits, makes them realize that switching to C++ is easier said than done. There are very few default operations for things like linear algebra, image processing, image display etc. Then, perhaps, another helpful person suggests that they take a look at VTK and/or ITK. While now, they can see that there is a ton of functionality out there, they are often lost as to where to begin. VTK and ITK are natural tools once one is used to them but they can be imposing and “scary” to the beginner. While there are some books out there (especially the

VTK User’s Guide) which are very helpful, they are often only obliquely related to what they really need to learn how to do: implement image analysis methods, learn how to (properly) display their results, and learn how to put a graphical user interface to enable them and their potential users to interact with the methods. The goal of the course, and this book, is to precisely provide the necessary guidance for a new graduate student in order to achieve these goals.

The selection of the material, as well as its presentation, is naturally colored by the author’s own experience. I coordinate the BioImage Suite [7] project www.bioimagesuite.org, which is a large medical image analysis software package developed in a mixture of C++ and [Incr] Tcl. In part, the motivation for teaching this class and writing this book, is directly derived from the needs of the BioImage Suite project. In particular, the driving question was, how does one get a new programmer up to speed with the skills he/she will need in order to contribute? Perhaps somebody else teaching this class would have used Python instead of Tcl as the scripting language; this is as much a matter of taste (and endless discussions and sadly flame wars in this internet era) and experience with the particular language as anything else. Also, while I mention ITK towards the end , the primary toolkit used here is VTK. The template-free interface of VTK makes it easier for beginners, and I find that ITK can be downright user-hostile to the less experienced programmer.

One of my complaints with many introductory texts is that they never attempt to teach how one goes about learning how to put together decent sized applications. They focus too much on “grammar” and too little on “writing stories”. However, graduate students need to write “stories” – useful ease-to-use tools that both they and clinical and/or basic science collaborators can use and maintain. Hence, as part of the class, I have also made an attempt to introduce some software engineering tools such as Subversion and CMAKE. As any experienced developer often learns the hard way, these tools can be just as critical as the choice of programming language or toolkit.

A disclaimer: While VTK is now at version 5.0 we still focus on VTK 4.4 – this is the version in use in BioImage Suite at this point. As we migrate the software to VTK 5.x this book will be updated to reflect this.

3 Book Contents

This book consists of six main parts:

I. Introduction: This presents some introductory material including a brief overview of the Subversion revision control system. Subversion was used extensively for the class as a means to upload homework assignments and to download update notes and pdf files.

II. Programing with Tcl/Tk Here, we first introduce the Tcl [1] scripting language and the Tk graphical user interface toolkit. The [Incr] Tcl [3] object-oriented extension of Tcl is then used to introduce the concepts of object-oriented programming (OOP). While OOP could have been introduced in the context of C++, it is first deliberately discussed in a scripting language concept, deliberately, in order lower the learning curve and avoid additional complications such as compiling and linking. The final chapter of this part describes the Iwidgets object-oriented graphical user interface toolkit.

III. The Visualization Toolkit I – Using Tcl: In this part we present a guided tour of those aspects of VTK that are most relevant to medical image analysis using the Tcl language.

IV. Interfacing To BioImage Suite using Tcl Two chapters are devoted to explicitly interfacing with the BioImage Suite[8, 7] image analysis package. BioImage Suite provides a large number of additional com-

ponents, such as complex 3D viewers, that can simplify the task of developing medical image analysis applications.

V. C++ Techniques In this short part of the book, we describe first the CMake program for managing the building (i.e. compiling and linking) of software on multiple platforms.

Next, we revisit the concepts of object-oriented programming and translate the original [Incr] Tcl code to C++. Finally we also translate some of the VTK Tcl examples to C++ to demonstrate how to access VTK from C++.

VI. VTK Programming with C++ and Tcl This final part of the book is meant to guide students towards implementing their own algorithms in C++ and VTK, while using Tcl/[Incr Tcl] for graphical user interfaces.

Two large case studies, one on point based registration and one on intensity based segmentation form the heart of this part. Here we present complete examples of both algorithm implementation, user interface design and 3D viewer integration. The first case study uses vanilla VTK whereas the second makes use of BioImage Suite concepts explicitly.

The part concludes with three additional chapters. The first describes the implementation of templated image-to-image filters. The second, which was a response to common mistakes in the homeworks, describes how to properly copy data objects so as to save the results of a pipeline for later use. The final chapter briefly touches on the ITK toolkit and demonstrates how to use this in conjunction with VTK.

4 Conclusions

This book is still a work in progress. However, I thought it might be useful to many VTK/ITK users, so I decided to make it available online at this draft stage. All code from the examples in this book is also freely available. Any comments/corrections would be much appreciated.

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References

- [1] TCL Developer Exchange. <http://www.tcl.tk/>. [3](#)
- [2] L. Ibanez and W. Schroeder. *The ITK Software Guide: The Insight Segmentation and Registration Toolkit*. Kitware, Inc., Albany, NY, www.itk.org, 2003. [1](#)
- [3] [incr Tcl]. <http://incr.tcl.sourceforge.net/itcl/>. [3](#)
- [4] Matlab. <http://www.mathworks.com/products/matlab/>. [2](#)
- [5] X. Papademetris. Programming for medical image analysis using VTK, <http://noodle.med.yale.edu/papad/seminar/>. [1](#)
- [6] X. Papademetris. *An introduction to programming for medical image analysis with the visualization toolkit*. A programming guide for the BioImage Suite project (<http://www.bioimagesuite.org/vtkbook/>), December 2006. [1](#)
- [7] X. Papademetris, M. Jackowski, N. Rajeevan, R.T. Constable, and L.H Staib. BioImage Suite: An integrated medical image analysis suite, Section of Bioimaging Sciences, Dept. of Diagnostic Radiology, Yale School of Medicine, <http://www.bioimagesuite.org>. [2](#), [3](#)

- [8] X. Papademetris, M. Jackowski, N. Rajeevan, M. DiStasio, H. Okuda, R. T. Constable, and L. H. Staib. BioImage Suite: An integrated medical image analysis suite: An update. In *ISC/NA-MIC Workshop on Open Science at MICCAI 2006*, 2006. <http://hdl.handle.net/1926/209>. 3
- [9] W. Schroeder, K. Martin, and B. Lorensen. *The Visualization Toolkit: An Object-Oriented Approach to 3D Graphics*. Kitware, Inc., Albany, NY, www.vtk.org, 2003. 1

Appendix: Table Of Contents

The following is the table of contents of the current, draft, version of the book.

Preface	5
Part I: Introduction	
1. Introduction	8
2. Revision Control With Subversion	13
Part II: Programming with Tcl/Tk	
3. Introduction to Tcl	19
4. Advanced Topics in Tcl	27
5. An Introduction To Tk	35
6. Tk Part II	43
7. Object Oriented Programming with [Incr] Tcl	53
8. Iwidgets: Object Oriented GUIs	63
Part III: The Visualization Toolkit I -- Using Tcl	
9. An Introduction to the Visualization Toolkit	71
10. Curves and Surfaces in VTK	76
11. Images in VTK	86
12. Displaying Images in VTK	93
13. Transformations	105
14. Some Additional VTK Classes	114
Part IV: Interfacing To BioImage Suite using Tcl	
15. Leveraging BioImage Suite Components	122
16. Writing your own BioImage Suite Application	132
Part V: C++ Techniques	
17. Cross-Platform Compiling with CMAKE	147
18. C++ Techniques and VTK	154
Part VI: VTK Programming with C++ and Tcl	
19. Extending VTK using C++	167
20. Point-based Registration with ICP	179
21. Intensity Based Segmentation	197
22. A Templated Image to Image Filter	215
23. Copying Data Objects	222
24. The Insight Toolkit	226
Appendices	
A. Final Exam	235
B. Code License	236
References	237