Teaching Statement

C. Titus Brown

I have TAed several courses at Caltech, including an introductory course to Linear Algebra and an advanced computational course in Digital Evolution. I also contributed to the teaching of a course in Software Engineering (based on the Software Carpentry class developed by Greg Wilson at U Toronto) and am currently developing a short 10-week course in pragmatic bioinformatics scripting for biologists.

My background is sufficiently broad that I could comfortably teach classes in introductory biology, advanced development, gene regulatory networks, genomics, bioinformatics, modeling of biological systems, and systems biology, as well as introductory and advanced software engineering courses. I also have a strong background in "agile" methods of development and extensive experience in open-source software development. I have developed in C/C++, Java, Python, Perl, and Tcl, and can teach introductory or advanced courses with any of them.

At MSU, I would be interested in developing any of the following three classes.

Practical Software Development for Bioinformatics – a hands-on course in using and adapting existing tools for software development, as well as developing new tools. Most computer science departments focus on algorithms and computational theory; most biology departments have no solid introductory software course. This course will fill a gap in current curricula by introducing advanced students to the tools that are available and existing techniques. I will cover topics such as alignment algorithms, comparative sequence analysis, motif finding, RNA folding and similarity searches genome-scale data processing, and expression array analysis. Both animal and microbial genomics will be discussed.

Agile Software Development for the Web – a hands-on course in the design and implementation of database-backed Web sites. The focus of this course will be on agile development and testing techniques, including the use of one or more modern revision control systems; using online project planning tools to coordinate work; test-driven development and test-enhanced development; and the use of ACID databases. The course will be taught using several of the available scripting languages, including Python, Ruby, and Perl. The goal of the course is to expose students to technologies currently in use on the Web.

Building and Modeling Developmental Gene Regulatory Networks – a seminar course on experimental, computational, and theoretical techniques used in GRN research. GRN research is a very important and very new area of biology, and techniques are changing quickly. In addition, most students without practical research experience have only the faintest of ideas about which experiments are good at answering what questions. Understanding of relevant computational and theoretical techniques is even more lacking. The aim of this course is to give students a solid grounding in these fundamental research issues.

I will cover the embryology , molecular developmental biology, and evolutionary issues of specific organisms with GRNs (fly, worm, sea urchin, vertebrates); the experimental techniques available for studying development in each; the type, quantity and quality of genomic information available in each; the software tools used to analyze the genomic information; and the theoretical techniques that are starting to be applied in the area of modeling gene regulatory networks. The course will focus on reading and discussion of a core set of research papers, as well as "hands on" computational work in phylogeny and genomics.