Marshall Hampton* (mhampton@d.umn.edu), 1117 University Dr., UMD, Dept. Math and Stats, SCC 140, Duluth, MN 55812. Programming bioinformatics: using biopython and sage to make life easier.

For mathematicians teaching computational biology of any flavor, some sort of programming environment is essential. This presentation will introduce the free, open-source, cross-platform and extremely powerful combination of the biopython package and the SAGE project. The elegant web browser notebook interface of SAGE makes it easy for groups of students to collaborate on projects. Some examples of its use from my course Mathematical Foundations of Bioinformatics will be shown. (Received September 20, 2007)