***Modeling Microbial Growth Curves with GCAT***

Measurement of growth curves is of great utility in microbial research as a tool for characterizing strain phenotypes. Typically, a growth curve is generated by monitoring optical density of a liquid culture. Growth curves are usually sigmoid in shape. However, more complex patterns often arise as the result of various phenomena such as diauxic shifts, flocculation, and cell death.

Growth curves are modeled by fitting specialized sigmoid equations or using local regression methods. Once a growth curve has been modeled, it is possible to estimate its essential properties, such lag time, specific growth rate, and maximum growth plateau value. Modern instrumentation enables simultaneous measurement of dozens or even hundreds of growth curves in microtiter plates, with dozens or hundreds of data points in each curve. The results can be used to (1) screen microbes for desirable characteristics, such as ability to divide rapidly in certain media, (2) attempt to link phenotypes to genotypes in large strain collections, or (3) characterize effects of various growth conditions.

Our goal in developing Growth Curve Analysis Tool (GCAT) was to provide researchers with a convenient interface to analyze high-throughput, microtiter plate-based data efficiently. Although basic methodologies to analyze growth curves have long been known, instrumentation that enables their generation en masse is relatively new. Efficiently analyzing dozens or hundreds of growth curves requires automation and a convenient user interface. Plate readers and robots that are used for generating the data produce spreadsheets but lack tools for growth curve fitting. Some user-friendly tools for growth curve modeling had been available before GCAT, such as IPMP. However, they were designed for analyzing one curve at a time. Another option was R packages, such as grofit. Although these were adaptable for automation, they lacked a graphical user interface. GCAT is both highly automated and provides a graphical user interface through a web browser.

A GCAT server is publicly available at http://gcat-pub.glbrc.org/

**Reference:** **Bukhman, Yury V., Nathan W. DiPiazza, Jeff Piotrowski, Jason Shao, Adam G. W. Halstead, Minh Duc Bui, Enhai Xie, and Trey K. Sato.** 2015. “Modeling Microbial Growth Curves with GCAT.” BioEnergy Research, doi:10.1007/s12155-015-9584-3.

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