Tools for Genome Wide Fluctuation Analysis of *S. cerevisiae*

Christopher Wood, Joseph Huff, Kasthuri Kannan, and Winfried Wiegraebe
Stowers Institute for Medical Research
1000 East 50th Street, Kansas City, MO 64110, USA
E-mail: wiw@stowers-institute.org

**KEY WORDS:** Fluorescence Correlation Spectroscopy, Photon Counting Histogram, High Content Screening, Open Microscopy Environment

To understand the function of yeast proteins, we started a genome-wide investigation into their localization, concentration, diffusion properties, oligomeric state, and interactions with other partners. As measurement tools we choose Fluorescence Correlation Spectroscopy (FCS[1] and FCCS[2]), Photon Counting Histograms (PCH)[3, 4], and confocal imaging using Avalanche Photo Detectors (APD). Our instrumentation is based on a commercial confocal microscope (LSM 510 META, Carl Zeiss Jena, Germany) equipped with a fluorescence correlation spectrometer (ConfoCor 3, Carl Zeiss Jena, Germany). We developed software tools written in IDL (ITT Visual Information Solutions, Boulder, CO) to detect single yeast cells and control the data acquisition. We use a GFP (Green Fluorescence Protein) clone collection of *Saccharomyces cerevisiae* tagged open reading frames generated at UCSF[5].

We use IDL to analyze the fluctuation data and to determine the localization of the proteins based on our imaging results. To organize and query the data we use the Open Microscopy Environment [6].

---