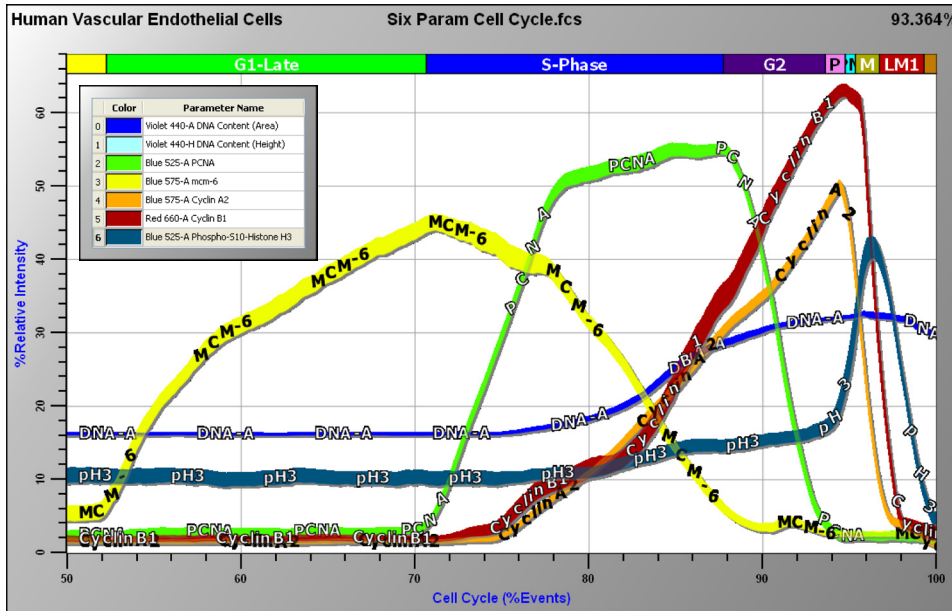


## 6-Parameter Cell Cycle Analysis in GemStone



Data kindly provided by Dr. James Jacobberger, Cleveland, OH

In the GemStone analysis shown above, progression of the cell cycle is divided into stages along the X-axis. The relative intensities of the six measured parameters are co-plotted, highlighting the intricate coordination of marker expression. DNA content is shown in the dark blue band, increasing as cells enter S-phase and leveling off in G2.

Cyclin B1 (red band) governs entry to and transition through early mitosis and affects the time spent from prophase to metaphase. Peak levels of cyclin B1 persist from late G2 through metaphase. Zone boundaries at the top of the Parametric Overlay Plot represent transition states that correspond to morphology-based mitotic stages.

Cyclin A2 (orange band) governs S, G2 and M transitions. Expression increases at the onset of S-phase and is degraded specifically by APC-Cdc20 after nuclear membrane breakdown, which coincides with the onset of prometaphase.

Aurora kinase B phosphorylates histone H3 (teal band) on S10 at the beginning of mitosis and is dephosphorylated at the end of mitosis. Chromatin-bound mcm proteins (yellow band) are helicase components and part of the DNA synthesis origin licensing mechanism. They are phosphorylated after origin firing and leave the chromatin (unbound mcm6 is not measured here).

Think of it as the MRI of cytometry.

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GemStone™ is a revolutionary new paradigm for analysis of high-dimensional, flow cytometry data. Think of it as the MRI of cytometry.

Based on the patent-pending Probability State Modeling™ system, GemStone eliminates the problems that have faced cytometry analysis for decades, providing a solution that is science-based, data-driven, scalable, and reproducible.

### Featuring:

- ▶ Novel analysis approach defines populations without gates.
- ▶ Unlike conventional analysis, GemStone's Probability State Models actually *improve* with additional parameters.
- ▶ Parametric Overlay plots present *all* parameters in a simple, correlated display that is easily understood by anyone with a basic understanding of biology.
- ▶ Advanced Panel Integration™ provides a new platform for analyzing and co-plotting all parameters for all files in a panel, revealing the true relationships of markers.
- ▶ A discovery tool - allowing scientists to understand new and previously hidden relationships of measured parameters.
- ▶ State Vector arrows and animations let you understand your data as never before. Data zooming, a batch system with a built-in database, and database parameter mapping are a few of the innovative new features.