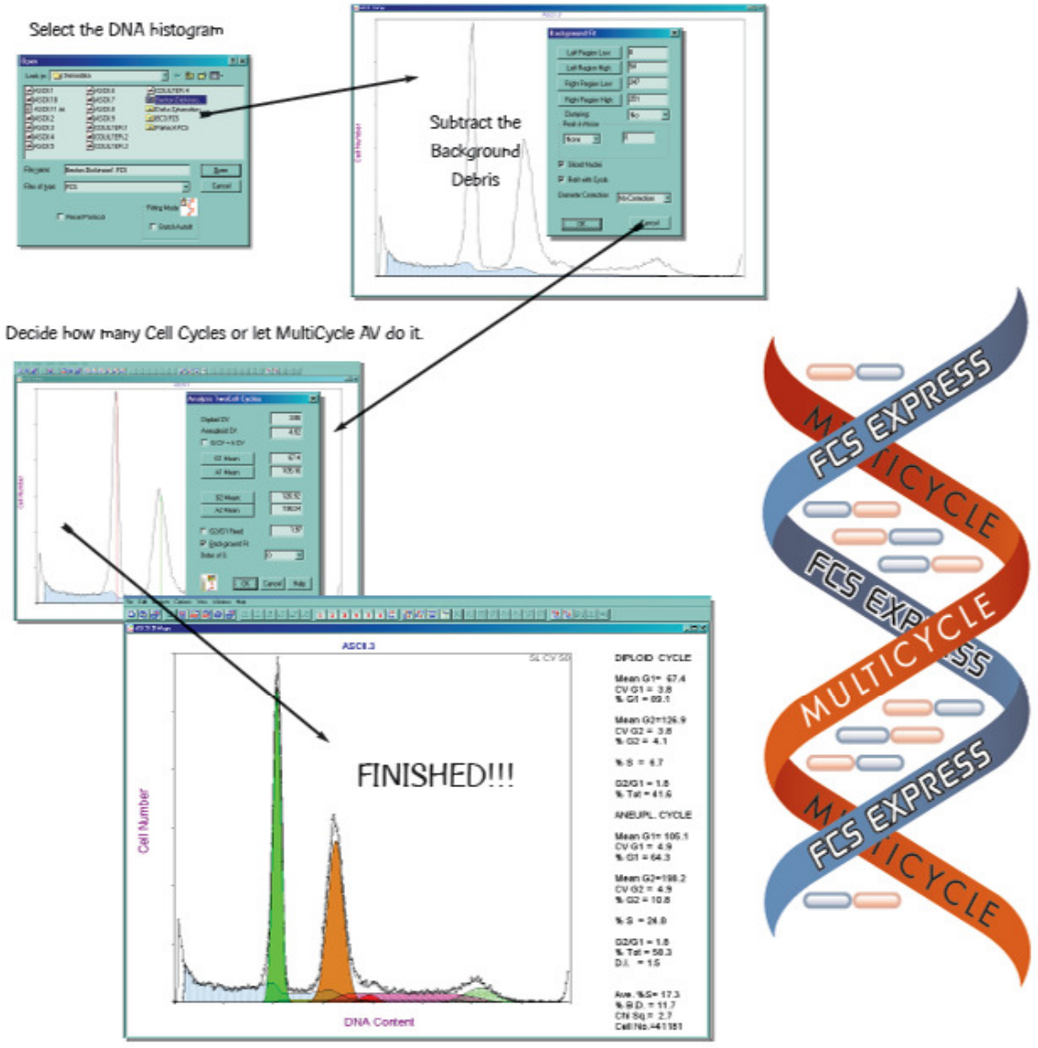
MultiCycle AV Standalone Analysis

Included with the MultiCycle AV Plug-In for FCS Express™
is a standalone copy of MultiCycle AV at no extra charge



For questions, pricing, ordering information please contact

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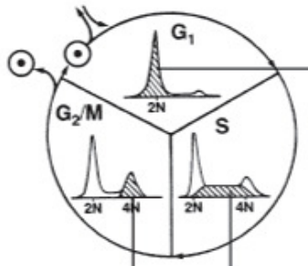
MultiCycle AV & FCS Express™

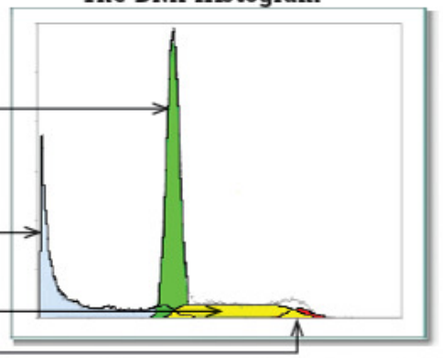
Powerful DNA Cell Cycle Analysis combined with Sophisticated List Mode Analysis

One of the earliest applications of flow cytometry was the measurement of DNA content in cells; the first technique available to characterize the non-mitotic phases of the cell cycle. This analysis is based on the ability of certain dyes to stain cellular DNA in a stoichiometric manner (the amount of stain is directly proportional to the amount of DNA within the cell).

The Biological Cell Cycle



The DNA Histogram



DNA content histograms require mathematical analysis in order to extract the underlying G1, S, and G2 phase distributions. Methods for this analysis have been developed and refined over the past two decades. The most flexible and accurate method of cell cycle analysis is based upon building a mathematical model of DNA content distribution, and then fitting this model to the data using curve-fitting methods. The most well established model, proposed by Dean and Jett (1974), is based upon the prediction that the cell cycle histogram is a result of the Gaussian broadening of the theoretically perfect distribution. The underlying distribution can be recovered or "deconvoluted" by fitting the G1 and G2 peaks as Gaussian curves and the S phase distribution as a Gaussian-broadened distribution.

Almost all cell or nuclear suspensions analyzed by DNA content flow cytometry contain some damaged or fragmented nuclei (debris) resulting in events, usually most visible to the left of the diploid G1, which are not fit by the G1, S or G2 compartments. In samples that are derived from fresh tissues or cells, most of the "debris" is visible close to the origin of the histogram and decreases rapidly farther away. In the best case, the debris signal is an insignificant proportion of the histogram in the region occupied by the cell cycle data. Unfortunately this is often not the case in archived material, stored in paraffin, and accurate debris modeling is critically important in order to subtract the effects of the underlying debris from the cell cycle fitting. DNA analysis software that does not incorporate all the features of these models may yield accurate results in the ideal scenarios, but will often return incorrect results in even mildly complex situations. Worse, it is difficult to simply look at these results and appreciate that they are invalid.

MultiCycle AV has a twenty year track record and incorporates several variations of the Dean and Jett model in order to accommodate a wide variety of experimental outcomes and cell types. In addition a "histogram dependent" exponential model or a "sliced-nuclei" model accurately removes the debris component from the true DNA histogram. More information about the justification and mathematics of these models are available at www.phoenixflow.com/cellcyclemath.pdf

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