

The choice of experts and novices alike

The choice of experts and novices alike when they need open-ended, flow cytometry modeling software. With robust applications for ploidy-based cell-cycle analysis, proliferation analysis with cell-tracking dyes, and perturbed cell-cycle modeling, it is, simply, the industry standard.

Researchers choose it for its unprecedented power and flexibility. Technicians choose it for its exceptional speed, accuracy, and ease of use. Designed by one of the industry's recognized experts, **ModFit LT™** is a proven performer with an unrivaled array of tools and exceptional support.

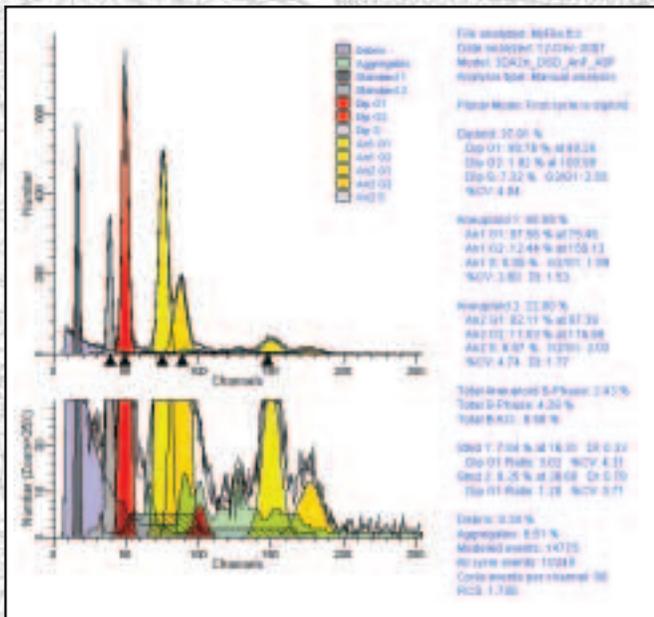
Features:

- ▶ Tools are arranged sequentially in order of use in the analysis process.
- ▶ Reporting tools add annotations and highlight key aspects of the analysis.
- ▶ Create and save analysis templates tailored to your needs.
- ▶ Automatically analyze flow cytometry DNA cell-cycle data.
- ▶ Database analysis results automatically.
- ▶ Sophisticated batch processing.
- ▶ Intuitive wizards to guide the analysis of cell-tracking studies and perturbed cell-cycle.
- ▶ Video tutorials on CD and online.
- ▶ Searchable user guide.
- ▶ Companion Rule-Based Training system offers a great way to teach proven, best practices in flow cytometry DNA analysis.

Ploidy-Based Cell-Cycle Analysis

With thousands of installations worldwide, **ModFit LT™** is the de-facto standard for automated analysis of complex DNA cell-cycle flow cytometry data.

- Automatically detects DNA ploidy and selects appropriate model.
- Exceptional accuracy.
- Reproducible analysis, person-to-person and lab-to-lab.
- Processes large batches of sample files and databases the results automatically.
- Simple report-based interface.

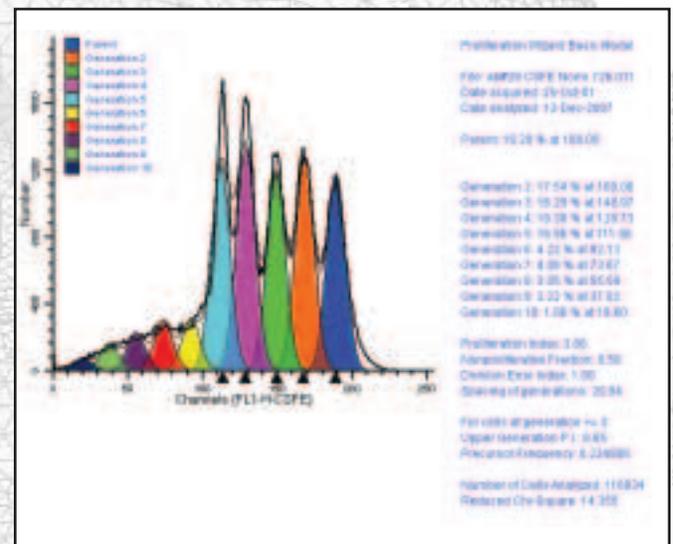


▲ Analysis of a breast cancer specimen showing two DNA Aneuploid cycles shows the power of the modeling system. The zoomed graphic reveals the complex, overlapping relationship of model components, including AutoDebris™ and AutoAggregates™. No other software package provides the capabilities of ModFit LT™ to model DNA cell cycle.

Proliferation Analysis with Cell-Tracking Dyes

When researchers want to understand how cells divide and track them over time, they turn to cell-tracking dyes. And there is only one software tool that is designed to handle every nuance in data from cell-tracking experiments: **ModFit LT™**.

- Simple-yet-flexible wizard interface allows easy identification of the parent generation, selection of daughter generation properties, and export of generation information.
- Works with data from CFSE dyes, PKH dyes, and more.
- Computes percentages, means, Proliferation Index, Non-proliferative Fraction, Upper Generation Proliferation Index, Precursor Frequency, and more.



▲ ModFit LT's Proliferation Wizard analysis of a CFSE-stained sample shows 10 generations of cell division. As cells divide, each daughter cell incorporates roughly half of the CFSE dye from its parent, allowing cell division to be tracked over time.

Support and Expertise

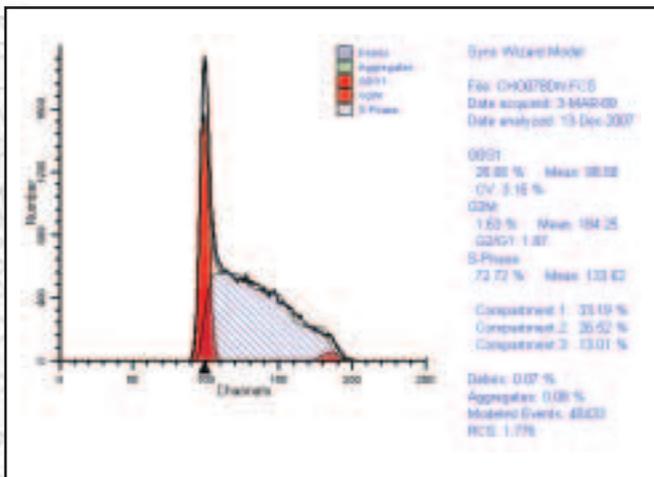
One of the end-user benefits most appreciated by **ModFit LT™** users comes from the company that built the software: Verity Software House. With decades of experience and a friendly, well-trained crew, the support team at VSH is driven by customer satisfaction. If they don't know the answer, they have unprecedented access to programmers and experts in the field.

- Exceptional tech support, no restrictions, no fees.
- Designed by C. Bruce Bagwell, MD, Ph.D., a recognized expert in DNA cell cycle modeling and analysis for over 30 years.
- With over 25 years in the industry, Verity Software House has a proven track record of excellence.

Perturbed Cell-Cycle Analysis

Investigators are often interested in understanding how a drug or treatment affects the cell cycle. For experiments where cells are blocked and then released, **ModFit LT™**'s Sync Wizard provides a robust modeling system for understanding the cell cycle.

- Flexible wizard interface provides intuitive tools for identification of G0G1 population, selection of G2-M and S-Phase characteristics, and modeling debris and aggregates.
- Alerts are triggered when peaks can not be detected to maintain well-defined modeling conditions.
- Computes percentages for sub-compartments in S-Phase to provide a clear picture of early, mid, and late S activity.

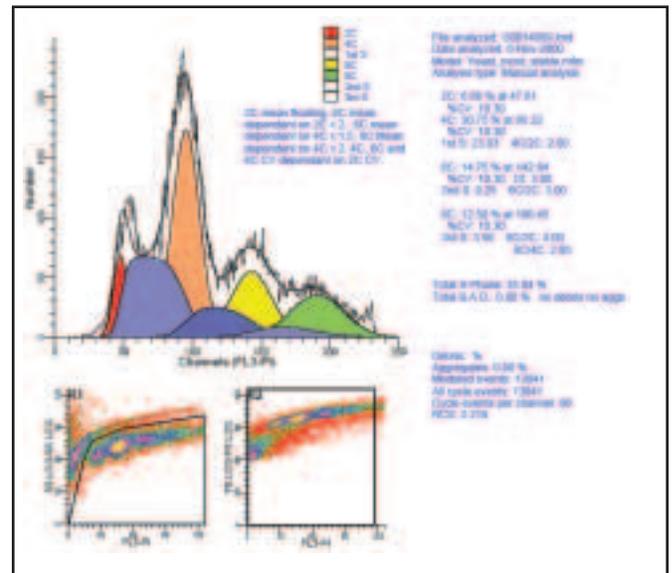


▲ Even under highly perturbed conditions, ModFit LT's Sync Wizard model provides robust fitting. In this example, the model can detect the very small G2M population even in the presence of significant S-Phase. There is no better tool for understanding blocking or treatment experiments.

Customized Least-Squares Analysis

ModFit LT™ is the only flow cytometry toolkit that allows users to build models to describe and analyze biological systems that are not yet defined in literature. Create custom models to fit the biology of a variety of cell types and organisms, providing a means to explore new and exciting areas of research.

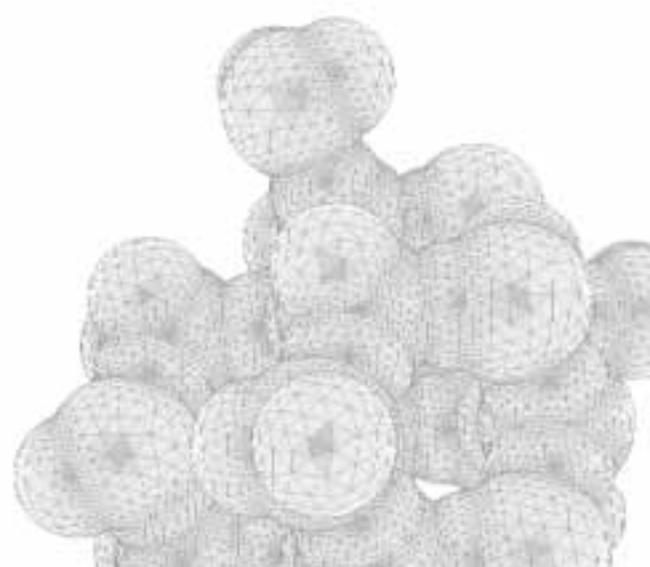
- Explore new areas of research: yeast, endo-reduplication, and more.
- Build models from a wide variety of component types: Gaussian, rectangle, trapezoid, polynomial, exponential, Weibull, AutoDebris, AutoAggregates.
- Set component dependencies, associate ranges with components, define statistic computations.
- Save models for reuse.



▲ DNA analysis of yeast samples presents researchers with interesting challenges. Investigators created a custom model in ModFit LT to analyze the cell cycle in several yeast populations simultaneously.

Cutting Edge Software.
 Total Commitment.

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Proven Performance

By far the most popular and widely distributed flow cytometry modeling software, **ModFit LT™** is the industry standard for DNA cell-cycle analysis and proliferation studies with cell-tracking dyes. Introduced in 1994 as the successor to **ModFit™**, it has maintained its position for over a decade by continuing to offer new, robust features with real benefit to its user base.

- The choice for all major studies in DNA cell-cycle analysis.
- Incorporates the 1993 DNA Consensus Conference Guidelines.
- The software used to develop the rule-based decision process described in “Optimizing Flow Cytometric DNA Ploidy and S-Phase fraction as independent prognostic markers for node-negative breast cancer specimens,” *Cytometry* 46:121-135, 2001.
- Unmatched modeling options for handling aggregates and debris in samples with **AutoDebris™** and **AutoAggregates™**.
- Capable of minimizing variations in instrument linearity, day to day, instrument to instrument, with **AutoLinearity™**.
- Rigorously tested for accuracy and consistency.
- Unparalleled automation and accuracy in analyzing complex samples based on years of R&D.



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