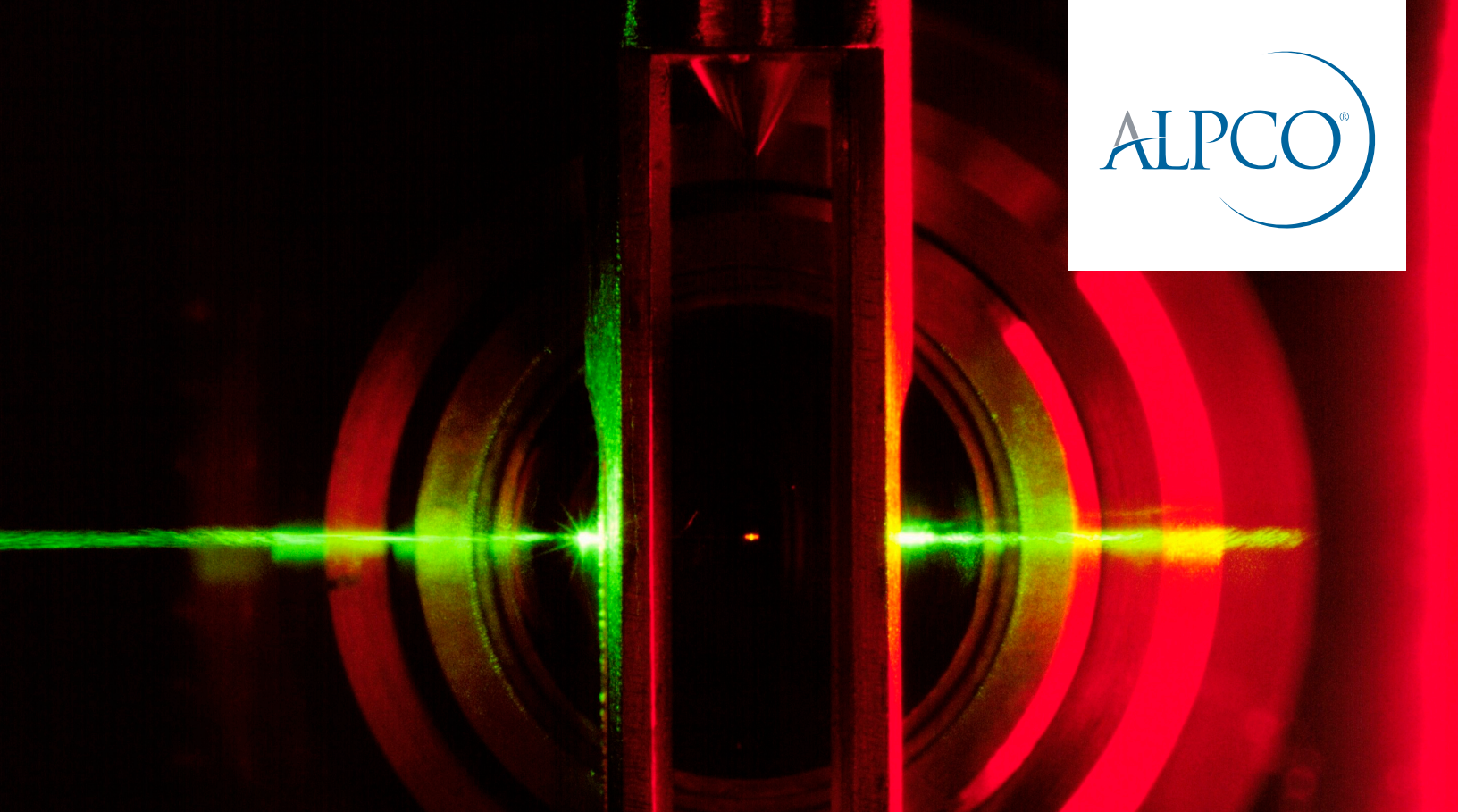


The background of the top half of the page is a close-up, artistic photograph of a flow cytometer's internal components. It shows concentric circular metal structures with a bright green laser beam passing through the center, creating a series of diffraction patterns and a strong red glow on the right side.

Infinicyt™: Flow Cytometry Data Analysis Software for Intuitive Analysis of Complex Multidimensional Data

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Challenges of Today

In the past two decades, there have been major contributions to the field of flow cytometry including new and more powerful instrumentation, development of additional reagents and updates to software analysis tools. While these advancements have all served to propel the field of cell research forward, there is still room for improvement; particularly with data analysis tools. In a 10 color staining experiment it is possible to recognize over 1,024 different cell populations, but traditional analysis using the supervised approach of sequential gating then determining the prevalence of a particular subset of cells expressing markers

Challenges of Today *continued*

of interest is a very time consuming, subjective and error-prone process. Additionally, the desire to distinguish between positive and negative expression plus the cognitive attempt to define cellular patterning all present the need for a more powerful data analysis tool. An ideal solution to these conditions would be a simple, intuitive and unsupervised analysis tool resulting in maximal data extraction with minimal variability between users.

Problem with Analytical Software Tools

Polychromatic flow cytometry is becoming increasingly popular with the advent of multi-laser cytometers having capabilities of analyzing up to 20 parameters at one time. This has resulted in the generation of highly complex data which challenges current analysis tools and urges the development of optimized programs offering unsupervised, simplified and objective data analysis with visualization strategies that do not restrict processing files having a high number of events. The Infinicyt™ software program provides an optimal solution to the increasing complexity of multidimensional flow cytometry data.

An Intuitive Solution

Infinicyt™ was developed and validated within the EuroFlow™ project as a specialized software program for addressing the needs of any basic or advanced flow cytometrist. Infinicyt™ has the ability to read files from any flow cytometer and provides an exclusive set of tools for advanced identification and description of cell populations with faster, easier and more sensitive data analysis. Key features of Infinicyt™ flow cytometry software include:

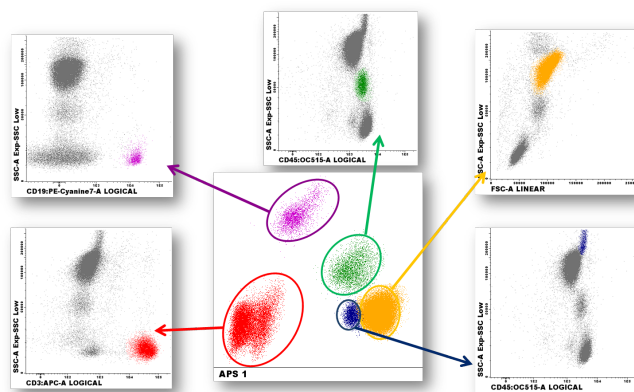
- Automated n-dimensional separation of clusters (APS)
- Analysis of multiple parameters simultaneously (File Merge)
- Comparison of new samples with previous events (Reference Image)
- Identification of similarities and difference between samples (Compass)
- Advanced evaluation of maturation patterns (Maturation Tool)
- Automated gating and analysis strategies (Batch Analysis)



Automatic Population Separator (APS)

The APS feature, based on principal component analysis, generates automatic n-dimensional separation of sample clusters for further characterization. APS analyzes all parameter combinations to display the best separation of cell clusters. It also provides information on which of these parameters are the most important for optimal separation, helping indicate if new analysis panels should be developed or improved.

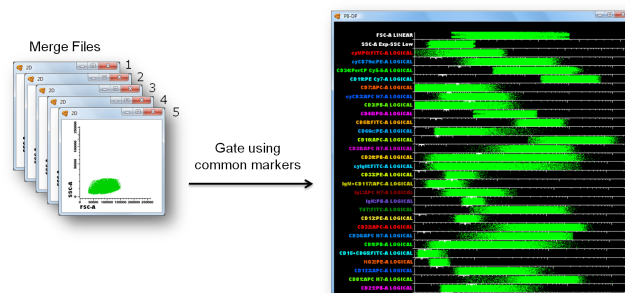
Figure 1: APS diagram displays all events separated by PCA and allows for the correct identification of different populations.



File merge

This tool allows the user to link information from different FCS files into one single file for a more complete analysis. A parameter band dot plot can be used to evaluate all of the parameters at the same time. Infinicyt™ also provides a level of quality control that confirms the selected population is equally represented in all of the files for the common parameters.

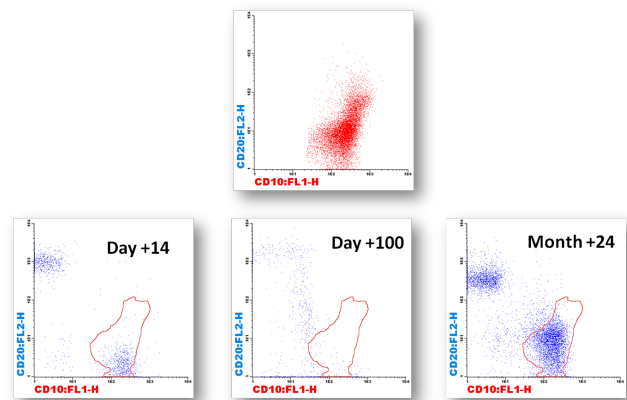
Figure 2: A parameter dot plot displays the complete results of an experiment composed of multiple single tubes.



Reference Image

Reference images can be displayed as dot plots or density lines with corresponding statistical data and allows the user to compare previously stored events with the current sample being analyzed. This tool is useful for comparing normal or abnormal marker expression, assessing maturation patterns, evaluating minimal residual disease (MRD) and comparing control samples with test samples in research laboratories. For MRD evaluations, several images can be saved at different time points for monitoring purposes.

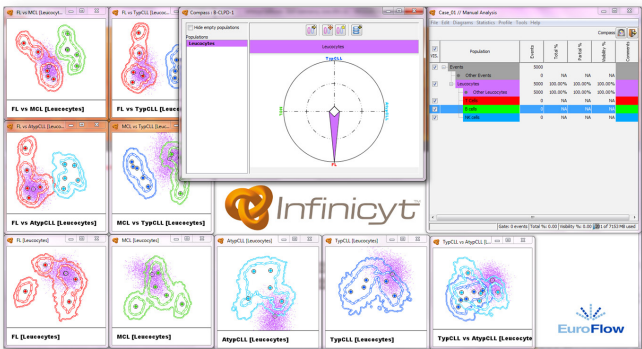
Figure 3: A reference image of an MRD sample at day 0 (red dots) compared with follow up (blue dots).



Compass Tool

The Compass function aids users in identifying similarities or differences between sample populations. Several files of reference group results can be merged into a database and used to compare against a new case study file. Databases can also be shared with other users for multi-lab comparisons as long as the same reagent panels and SOPs are used. The Compass pointer was designed to provide an instant and intuitive observation of results where a user can quickly verify whether a new case study is similar to or different from the files stored in the database.

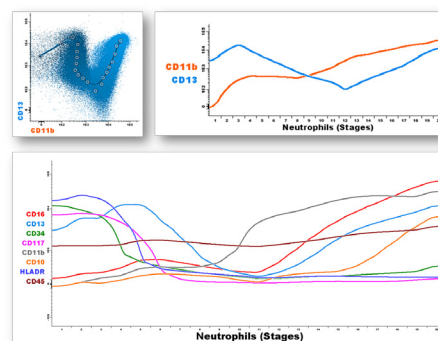
Figure 4: Compass diagram with relevant comparatives for group assigning.



Maturation Tool

The Maturation tool introduces a brand new approach for studying maturation patterns and offers an easy solution for assessing the evolution of multiple markers in a single population. It is especially useful in the study of maturation defects such as myelodysplastic syndromes (MDS). Since these syndromes comprise a heterogeneous group of clonal hematological disorders that can affect one or more bone marrow myeloid cell lineages, a tool for correctly identifying the stage and cell lineage involved is beneficial. When using a maturation database, the user can quantitatively evaluate multiple markers and how they affect the maturation blockage.

Figure 5: Maturation path of neutrophils and maturation diagram representing all sample parameters.



Calculate Data Module

The calculate data module incorporates powerful algorithms that give a precise and reliable calculation of marker expression. Information from different aliquots is integrated into the same file allowing for the parameters to be compared. It is used for cells with the same immunophenotype.

Batch Analysis

Multiple actions can be configured at the same time for high-throughput analysis of files: apply analysis strategies, export statistics, export reports, export files with a different configuration, apply compensation and compare files with a selected database using Compass.

Diagrams and Representations

Infinicyt™ offers many types of high definition diagrams that allow the user to fully customize data presentation. By choosing diagram configurations, the user can select exactly which population is to be displayed at any point of analysis.

- APS
- Dot Plots
- Histograms
- Multidimensional 3D Diagrams
- Box Plots
- Parameter Band Plots

Available Software Packages

	Infinicyt™ Basic 70-INFINICYT-P	Infinicyt™ Advanced 70-INFINICYT-ADV1
Automatic Population Separator	•	•
Manual Analysis	•	•
Batch Analysis	•	•
File Merge	•	•
File Editor	•	•
File Export	•	•
Reference Image	•	•
Analysis Strategy	•	•
Customizable Reports	•	•
Calculate Data		•
Compass Tool		•
Maturation Tool		•

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