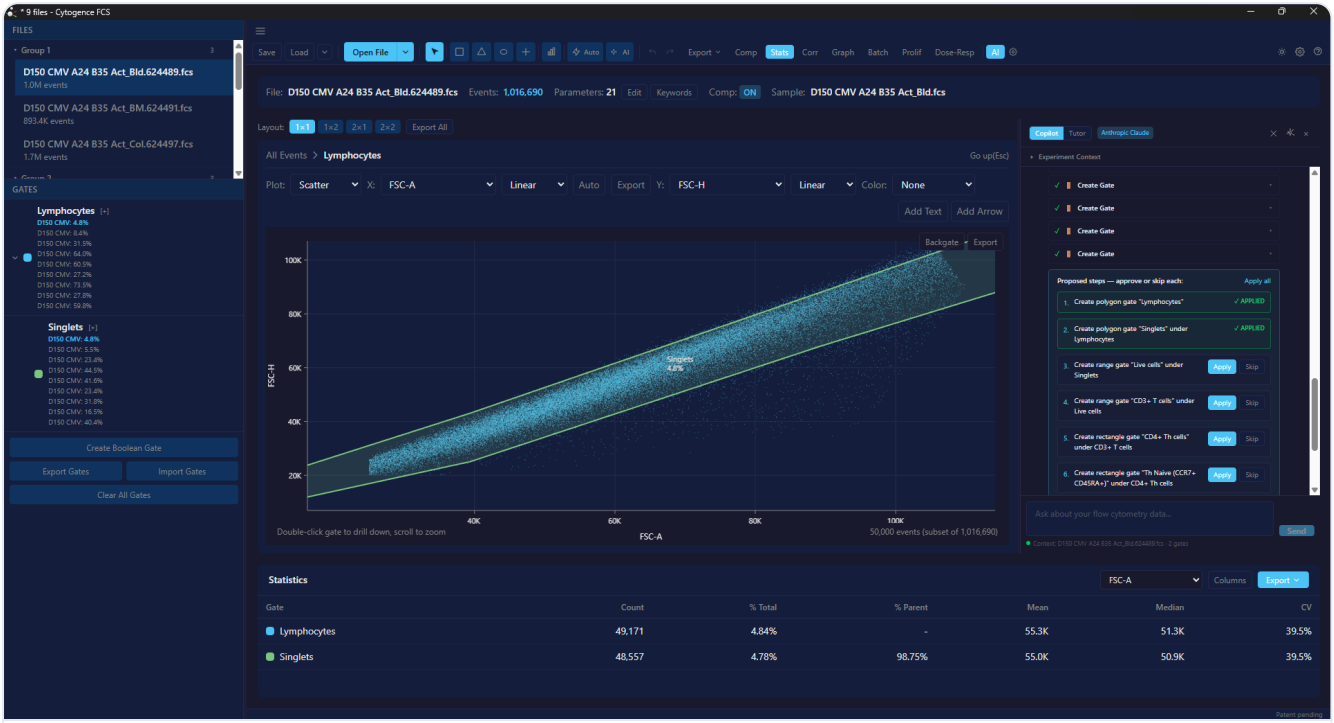
Cytogence
Be ahead. Be cytogence.

Windows · macOS · Linux | Patent pending

PRODUCT OVERVIEW

Cytogence FCS

A high-performance flow cytometry analysis platform, built from the ground up in Rust — pairing an **AI copilot** with a **flow-cytometry-trained gating model** that together propose a complete gating strategy you review and approve.



The AI copilot proposes each gate with a rationale; you approve, and the gate hierarchy and population statistics update instantly — here on a 1,000,000-event sample.

Built in Rust
Native engine built for large event files; GPU-accelerated plots.

Two AIs
A reasoning copilot plus a cytometry-trained gating model.

Privacy-first
Run the AI on-device; your data can stay on your machine.

Cross-platform
Native desktop app for Windows, macOS, and Linux.

6	16	2.0–3.1	3
Gate types + full hierarchy	Interface languages	FCS versions supported	Desktop OSes supported

> **Built on a simple principle:** the AI proposes, the analyst decides. Correctness-first engineering, transparent reasoning, and the option to keep every byte on your own machine — for labs that need to trust every gate.

Cytogence FCS covers the full workflow — from FCS loading to publication-ready figures — and backs every result with tested, standards-correct math: compensation validated against an independent reference (FlowKit), FlowJo-correct robust statistics, and hardware log-amplifier linearization at parse time.

01 Two AIs, one workflow

PATENT-PENDING AGENTIC GATING

GENERAL REASONING

AI copilot

Works through your data step by step and proposes each gate with a plain-language rationale — nothing is applied until you approve it.

- ✓ **Propose & approve** — deferred actions, committed only on your click
- ✓ **Allowlisted tool set**; a transparent, per-step log of every call and result
- ✓ **Builds Graph Builder figures** from a plain-language request and names the test it chose
- ✓ Copilot and Tutor assistant modes

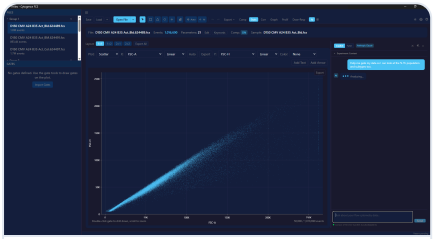
CYTOMETRY-NATIVE

AI-1 gating model

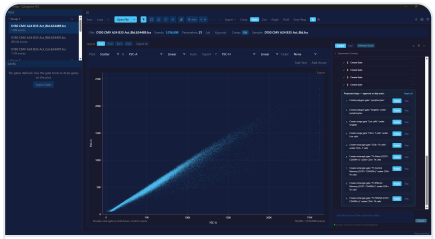
Our own model, trained specifically on flow cytometry data to identify cell populations. It runs entirely on your machine and brings domain expertise the general model doesn't have.

- ✓ **Reads markers, not fluorochromes** — an unseen panel is still interpretable
- ✓ **Knows what it knows** — per-population confidence; abstains on unfamiliar data
- ✓ Hands off to the copilot for the rest — one complete hierarchy

ASK → PROPOSE → APPROVE



1 · Ask. Describe the goal in plain language — e.g. "gate for the %Th population and subtypes."



2 · Propose. A complete, ordered strategy — each step with Apply or Skip. Nothing committed to the data.

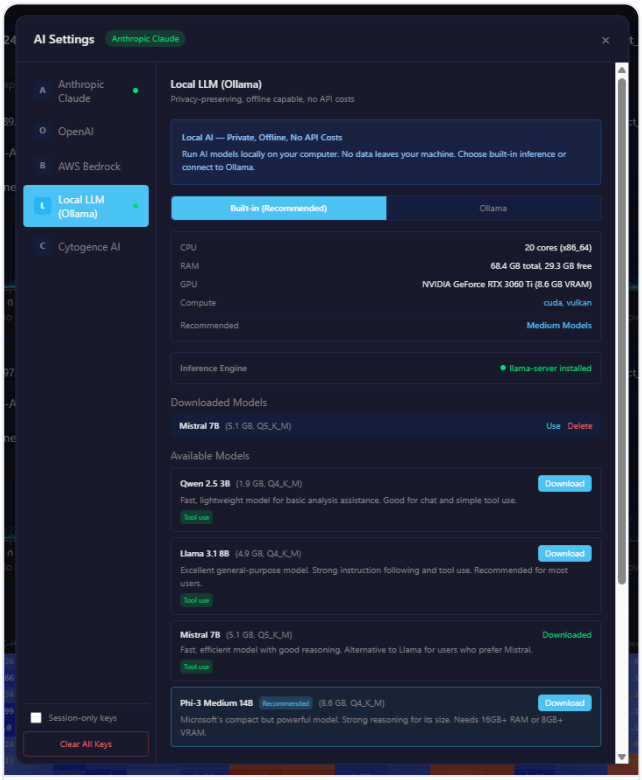
3 · Approve. Gates are applied, the hierarchy is built, and statistics compute for every population.

02 Cloud or fully local — you choose

PRIVACY BY DESIGN

Run the copilot on a frontier cloud model, or entirely on your own machine. Cytogence FCS ships built-in local inference and detects your hardware to pick a fitting model — so sensitive data can stay on-device.

- ✓ Providers: **Anthropic Claude, OpenAI, AWS Bedrock,** or a local model (built-in engine or Ollama); data leaves your machine only with a cloud provider
- ✓ **Built-in local inference**, sized to your GPU (CUDA / Vulkan) — no external API
- ✓ **Strict local mode** — no cytometry data leaves your machine
- ✓ API keys in the **OS credential store** (or session-only), zeroized on drop; SHA-256-verified model downloads



Choose a provider or run a local model; the app inventories your CPU, RAM, and GPU and offers matched, tiered models.

03 A complete analysis workspace

BEYOND GATING

Gating is only the start. Visualize, compensate, compare groups, and fit curves — then export publication-ready figures, all in one application.

Visualization & correlation. Compare samples in flexible multi-plot layouts (up to 2×2), GPU-accelerated via PixiJS, with a parameter-correlation matrix.

Group statistics & graphs. Paired and unpaired tests, ANOVA and Kruskal–Wallis with Tukey, Dunnett's, Dunn's, Holm–Šídák, Benjamini–Hochberg or Bonferroni comparisons, Shapiro–Wilk checks, significance brackets and n per group.

Auto-compensation. Compute the spillover matrix from single-stain controls with stain-index and FMO diagnostics — matrix math validated against FlowKit.

Dose-response fitting. 4-parameter logistic curves via Levenberg–Marquardt, with EC50/IC50, Hill slope, R^2, and convergence diagnostics — built in.

Gating engine

Rectangle, polygon, ellipse, range, quadrant, and boolean gates. Full hierarchy, backgating, undo/redo, real-time statistics; every gate records who made it.

Transforms

Linear, logarithmic, biexponential (logicle), arcsinh, and hyperlog, with automatic axis ticks.

ML auto-gating

K-means, DBSCAN, and Gaussian Mixture Models with BIC and elbow model selection for unsupervised populations.

Statistics

Mean, median, and geometric-mean MFI, plus FlowJo-correct robust CV and percentile metrics per population.

Proliferation

GMM-based dye-dilution modeling with generation peak fitting; division, proliferation, and expansion indices.

Export

Vector SVG and PDF with editable axes, gates, and text; print colours, title, size in points; PNG with DPI; Export All; CSV.

04 At a glance

File formats	FCS 2.0 / 3.0 / 3.1 — integer, float, double, ASCII
Core engine	Native Rust; Tauri 2 desktop
Visualization	PixiJS, GPU-accelerated (WebGPU / WebGL)
Gate types	Rectangle, polygon, ellipse, range, quadrant, boolean
Transforms	Linear, log, logicle, arcsinh, hyperlog
Compensation	Auto from single-stain controls; FlowKit-validated
Auto-gating	K-means, DBSCAN, GMM (BIC / elbow)

Statistics	MFI ×3, robust CV; t (paired / unpaired), Mann–Whitney, Wilcoxon, ANOVA, Kruskal–Wallis; Tukey, Dunnett, Dunn, Holm–Šídák, BH, Bonferroni; Shapiro–Wilk
AI providers	Anthropic Claude, OpenAI, AWS Bedrock; local via built-in engine or Ollama
Local models	GGUF, SHA-256 verified; CUDA / Vulkan
Privacy modes	Standard · Enhanced · Strict (on-device)
Exports	Vector SVG / PDF, PNG, CSV (statistics & events)
Platforms	Windows, macOS, Linux (native desktop)
Languages	16 interface languages

Engineered for correctness

Compensation validated against an independent reference (FlowKit), FlowJo-correct robust CV, and $PnE hardware-log linearization at parse time — checked by thousands of automated tests.

Private & secure

Run the AI fully on-device in strict mode — nothing leaves your machine. Keys live in the OS credential store and are zeroized on drop; session-only and clear-all-keys options.

Transparent & reproducible

Propose-and-approve keeps the analyst in control of every gate; every gate records who made it, and every suggestion, tool call, and result is shown in a per-session log. Open formats throughout — no data lock-in.

WHO IT'S FOR

Immunology & immuno-oncology

Deep immunophenotyping and functional panels — T-cell subsets, activation, exhaustion, and beyond.

Core & shared facilities

Consistent, auditable gating across operators and studies, with reproducible outputs.

Translational & biotech

Privacy-sensitive and regulated workflows that need on-device AI and traceable analysis.

Request a demo or technical session

Get in touch with the **Cytogence FCS team**. Cytogence is the bioinformatics division of KeyQ, Inc. — analysis software and computational-biology services across flow cytometry, spatial biology, and multi-omics. Patent pending.

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