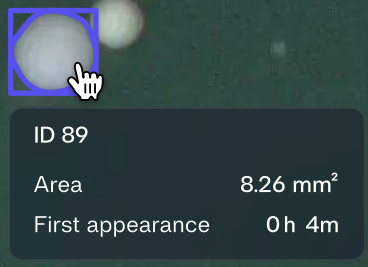
RESHAPE

APPLICATION NOTE



Automated Colony Counting & Detection

Colony Counting for R&D

APPLICATION

Comparison of Reshape and traditional manual colony counting

Why is it a critical need?

Colony counting is still one of the most common methods for estimating bioload (e.g., CFU/mL) and tracking microbial growth, but it's often performed manually—making it slow, subjective, and difficult to document consistently. In real-world R&D workflows, plates vary widely in format, media types, , densities, and plating methods (spread, pour, droplet, differential, etc.) while artifacts like condensation, bubbles, discoloration, debris, merged colonies, low-contrast growth, and edge effects increase counting difficulty and the rate of miscounts. Even with standardized operating procedures, manual counting introduces variability between individuals and across days due to fatigue and interpretation differences, reducing confidence in results. Many automated tools have failed to replace manual counting because labs don't trust them, often due to poor accuracy across diverse conditions and weak AI robustness, keeping manual counting as the default despite the inefficiency.

How does Reshape help?

Reshape solves these adoption barriers by delivering a single, end-to-end workflow that integrates controlled incubation, automated imaging, AI-based colony enumeration, and automated sample concentration calculations. The platform is designed for real lab variability, using robust AI models trained on a large foundational dataset, covering diverse organisms, media, colony morphologies, growth densities, and incubation conditions. Reshape uses the images to build task-specific models and can be rapidly retrained when new conditions or edge cases appear - enabling application optimization in days. Reshape also boosts throughput dramatically (up to ~105 plates/hour per Smart Incubator workflow, and 5× scaling with the Rack), while enabling endpoint and time-lapse imaging for deeper insight into growth kinetics. Finally, Reshape strengthens trust through in-image annotations, auditable results, structured metadata capture, barcode sample tracking, exportable datasets, and integration options (including LIMS), making colony counting faster, more consistent, and more reproducible for R&D workflows.

Introduction

The purpose of this application note is to describe the workflow and value of Reshape's automated colony counting solution for R&D microbiology teams.

Colony counting remains one of the most widely used microbiological techniques for estimating the bioload (e.g., CFU/mL) and tracking microbial growth across experiments. Despite its importance, enumeration is still frequently performed manually. This makes the process time-consuming, variable from person to person, and difficult to document and trace consistently across experiments.

While several automated tools exist, many labs have struggled to adopt them due to limitations in accuracy, weak performance across different media types and colony morphologies, and a lack of confidence in the underlying AI models. This has often reduced the perceived return on investment and kept manual counting as the default.

Reshape addresses these challenges by combining controlled incubation, automated imaging, AI-based colony counting and sample concentration calculations within a single workflow. This enables reliable colony enumeration with full traceability, reduced hands-on time, and improved reproducibility while supporting faster, more confident decision-making in R&D settings.

THE CORE CHALLENGE

Colony counting is visually complex and methodologically diverse.

Although colony counting is relatively straightforward, real-world plates are rarely clean or uniform. In routine laboratory workflows, researchers must contend with multiple media types and plate formats, each with distinct dilution and concentration calculations, alongside common visual artefacts such as bubbles in the media, condensation, discoloration, miscellaneous particles, merged colonies, faint or low-contrast growth, and edge effects.

In addition, colony counting spans a range of methodologies, from traditional spread plating to drop- and pour- plate techniques. Each introduces its own visual patterns and counting logic. Reshape's platform is designed to operate across this full spectrum, combining flexible image acquisition with AI models capable of robust performance under diverse experimental conditions.

MODES OF OPERATION

Endpoint and time-lapse workflows

Reshape supports multiple operational modes to match different R&D workflows:

Endpoint imaging

Endpoint imaging is ideal for high-throughput enumeration when incubation time is predefined. Plates are imaged at a selected time point, and colony counts are generated automatically using standardized criteria. The Reshape Smart Incubator can image a full tray of 90 mm Petri dishes in five minutes. With an additional three minutes to exchange trays and start the next imaging job in the Discovery Platform, the system can process up to 105 plates per hour. The Reshape Rack, consisting of five Smart Incubators, can scale this workflow 5x.

Time-lapse imaging integrated with incubation

Unlike standalone imaging systems, the Reshape Smart Incubator combines incubation with time-lapse imaging. This enables continuous, time-resolved monitoring of colony development under defined environmental conditions while minimizing manual handling steps. Automated imaging at consistent intervals increases data density compared to conventional enumeration approaches, which are often limited to a small number of time points (e.g., every 12–24 hours) due to manual worker availability. Higher temporal resolution supports:

- Growth kinetics characterization (e.g., time-to-appearance, growth curves)
- Earlier identification of peak growth for assay optimization
- Improved documentation of assay behavior across conditions
- Early detection of contamination events and unexpected growth patterns

How Reshape's AI models are designed

Reshape uses computer vision and machine learning to develop, train, and deploy models for accurate and reproducible colony enumeration. A key design principle is robustness to real laboratory variability: models are trained on data that reflect practical conditions across organisms, media, morphologies, and lab environments, rather than idealized or highly controlled datasets.

A foundational dataset that reflects real lab conditions

Reshape trains its models on a large and diverse image foundation dataset comprising >73 million plate images (as of January 2026). The dataset includes images collected across a wide range of experimental variables, including media types, organisms, colony morphologies, growth densities, and incubation conditions. Data generation is supported by Reshape's in-house GigaLab and selected external collaborations, and the dataset continues to expand by approximately 1 million images per week.

Rather than relying on a single general-purpose model trained across all available data, Reshape develops task- and output-specific models, each trained on curated subsets of the broader dataset. This approach supports targeted performance optimization (e.g., for specific organisms, media types, or colony phenotypes), while maintaining overall robustness.

Increased throughput and rapid iteration

The scale and diversity of the dataset also enables rapid iteration. If performance limitations are identified, for example due to a specialized organism or atypical media, relevant image data can be incorporated quickly, and updated models can be retrained and deployed directly into the user workflow. This enables onboarding and application-specific optimization on the order of days, rather than weeks or months.

In addition to consistency, the platform supports high-throughput analysis. Reshape can automatically count a tray of 15 standard 90 mm Petri dishes or 10 OmniTray plates. Using the Reshape Rack configuration (five Smart Incubator units), this scales to parallel analysis of up to 75 Petri dishes or 50 OmniTray plates.

For R&D workflows, this enables faster time-to-count and more frequent experimental decision-making. All results are captured in a structured and traceable dataset that can be reviewed, exported, and shared across teams and collaborators.

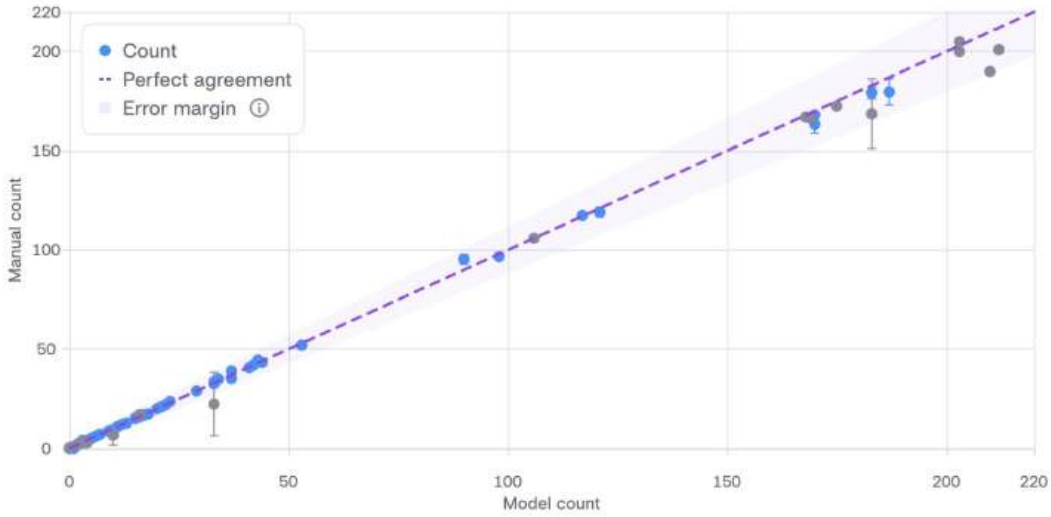
Aggregating results for rapid interpretation

In many workflows, colony counting is also used to determine the concentration of viable cells in a sample (e.g., CFU/mL). While the calculation itself is straightforward, it can become error-prone when different plating methods, dilution schemes, or inoculation volumes are used across experiments. This is particularly an issue in R&D environments where protocols are frequently adapted. Reshape supports end-to-end quantification by automatically calculating sample concentration based on the recorded plate counts and user-defined inoculation volume, improving consistency and reducing manual post-processing.

Beyond individual assays, the Reshape platform serves as a centralized tool for data management and interpretation. Results can be aggregated across multiple assays (or wells within a single multi-well assay) to enable comparison of enumeration outcomes across conditions and over time. For repeated assays on a specific organism or strain (e.g., *S. aureus*), aggregated data supports the identification of trends such as time-to-appearance at different incubation temperatures and media-dependent growth performance.

Ensuring accuracy and transparency of results

The Reshape platform is designed not only to generate counts, but also to ensure results are auditable and scientifically interpretable. Counts are supported by in-image annotations that show how colonies were detected and enumerated. This enables rapid review of model outputs and supports quality control. In time-lapse workflows, individual colonies can be tracked across time points to provide additional contextual information such as detection time and growth behavior.



- **Figure 1: Correlation between manual and model colony counts.** The purple shaded area indicates the standard error. Grey data points represent plates with sufficient disagreement between manual evaluations to warrant exclusion from statistical analysis. Data are based on 87 plate counts of *Staphylococcus aureus* on selective media, comparing Reshape's model with three independent manual evaluations.

Sample tracking, data access, and integration

Reshape supports traceable workflows through structured metadata capture and sample tracking options, including barcode-based identification (e.g., barcodes visible in the image or scanned at the start of imaging). This reduces the risk of manual transcription errors and supports reliable linkage between samples, plates, and results.

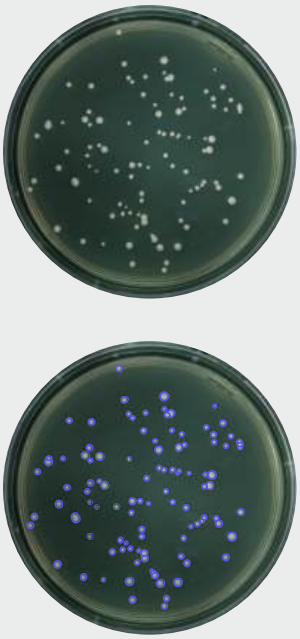
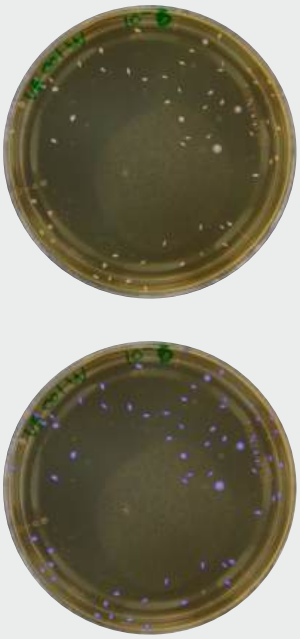
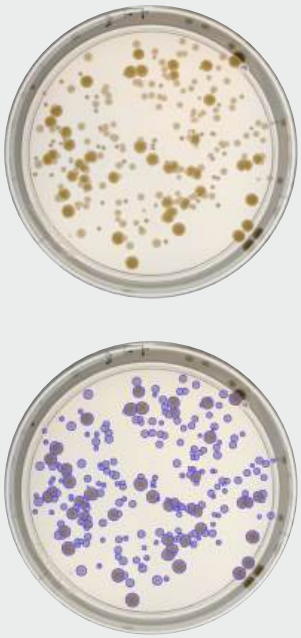
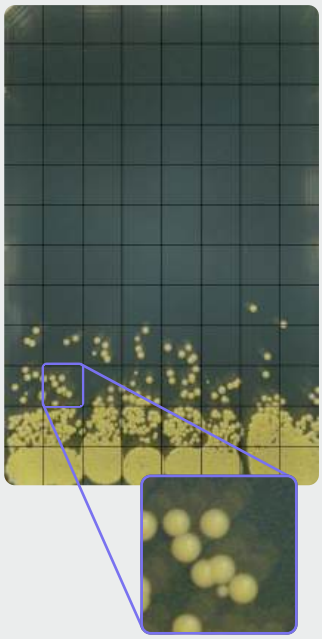
Results can be exported and shared across teams and collaborators. Access control and workspace permissions support multi-user environments, enabling secure collaboration while maintaining traceability of results and review actions. Where required, Reshape can support integration into existing digital workflows, including LIMS connectivity.

CONCLUSION

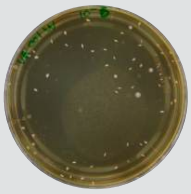
Reshape enables automated and digitized colony counting designed for real-world R&D microbiology workflows.

By integrating controlled incubation with automated imaging and AI-based analysis, the platform supports reproducible enumeration across diverse media, organisms, and plating methodologies. In addition to improved consistency and throughput, Reshape provides traceable, auditable results and centralized aggregation of colony counting outputs, enabling faster assay development, higher confidence in reported results, and more efficient experimental iteration.

Choose your method:

Spread plate	Pour plate	Differential counts	Droplet CFU
			
A known volume (commonly 100ul) of a diluted sample is pipetted onto the surface of an agar plate and spread evenly with a spreader. Colonies grow on the surface and are counted.	A diluted sample (often 1mL) is added to an empty plate, then mixed with agar and allowed to solidify. Colonies grow in the agar and on the surface.	CFUs are counted on selective/differential media that changes colour or appearance based on organism traits (e.g., fermentation, enzyme activity). Lets you count specific groups separately on the same plate.	Small droplets (e.g., 5-20uL) of several dilutions are spotted onto a single plate (multiple spots per plate). After drying/ incubation, colonies in each spot are counted.

- Choosing the best method to perform CFUs depends on the goal of your experiment and throughput needs.

	 Spread plate	 Pour plate	 Differential	 Droplet
Pros	Simple & widely used Good visibility of colonies Easy to pick colonies for downstream work	Useful for low concentration samples Colonies can form throughout agar	Can distinguish target vs non-target colonies Can estimate contamination & composition Efficient when samples has mixed organisms	Very low media/ plate usage (cheap & fast) Multiple dilutions on one plate Great for high-throughput and quick screening
Cons	Requires multiple dilutions/ plates for good count range Can be inaccurate if sample is clumpy or unevenly spread Usually limited to small volumes (often <0.1mL)	Heat from warmed agar can stress/kill sensitive organisms Colonies inside can be smaller or harder to count Not ideal for strict aerobes that prefer surface growth	Colony appearance can be ambiguous (false +ve / -ve) Selective agents may suppress stressed cells	Drops can merge/ run if technique is inconsistent Counting can be tricky if colonies overlap/are overgrown Needs careful calculations (CFU/ mL from small volume)
Best for	Routine CFU counts, microbial QC, general plating workflows	Low CFU samples (e.g. water/cleaning validation), some food micro methods	Mixed cultures, food microbiology, environmental samples, contamination tracking	Screening many samples/dilutions fast (R&D, strain work, process checks)