RESHAPE

APPLICATION NOTE

Automated Colony Differentiation

Using AI and computer vision

APPLICATION

Automated colony differentiation using AI and computer vision

Why is it a critical need?

Total plate counts are sufficient when you are only interested in overall bioburden. However, in QC, food safety, and R&D settings, plates often contain mixed cultures, background flora, or intentionally co-cultured organisms. In these cases, total counts alone can be misleading.

Examples where differentiation becomes critical:

- Food safety and environmental monitoring: You may need to distinguish yeast from mould, or target organisms from background contaminants.
- Product stability and shelf-life studies: Different colony types can have very different risk profiles.
- Strain engineering and screening: Mixed populations are common, and identifying phenotypic differences is part of the experiment.
- Challenge testing and competitive assays: Knowing how each organism performs individually is essential.

Without differentiation, analysts must manually interpret morphology, which introduces subjectivity and variability. AI-based colony differentiation models help standardize classification, reduce human bias, and generate reproducible, audit-ready data. In regulated or high-volume environments, that added assurance can be just as important as speed.

How does Reshape help?

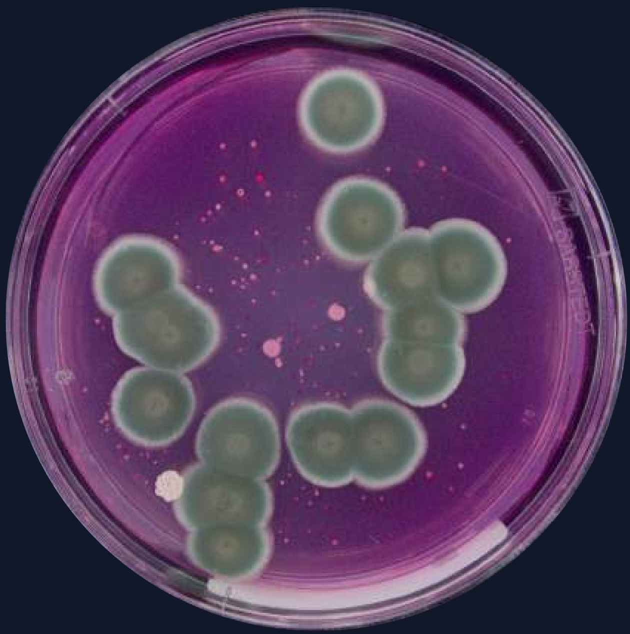
Reshape combines automated imaging with configurable colony classification models.
In practice:

- Plates are incubated and imaged automatically inside the Reshape Smart Incubator.
- High-quality images are captured at defined time points or as an end-point.
- Users define groups based on known microorganisms or phenotypic characteristics.
- The platform applies image-based analysis and AI-driven differentiation to classify and count colonies per group.
- Results are stored digitally, providing traceability and documentation.

This means users move from manual, subjective counting to standardized, reproducible colony differentiation and quantification. Instead of only knowing the total CFU on a plate, they gain structured data on each colony type, supporting better decision-making in QC, food safety, and R&D workflows.

Introduction

This application note demonstrates automated, time-resolved differential colony counting on solid media, which enables accurate discrimination and quantification of distinct colony morphologies within mixed microbial populations.



BACKGROUND

Why colony distinction matters?

Traditional colony counting provides total CFU per plate but often overlooks critical phenotypic differences between colonies. In many applications — including strain engineering, contamination screening, food safety, biocontrol development, and microbial interaction studies — distinguishing which organism is growing is just as important as how many.

Manual differentiation based on morphology (size, color, texture, opacity, edge characteristics) is:

- Time-consuming
- Subjective
- Difficult to reproduce
- Nearly impossible to scale

Automated differential colony counting enables objective, high-throughput discrimination between colony types while maintaining quantitative accuracy.

EXAMPLE I

Quantified CFU By Phenotype

Introduction

Mixed microbial populations were plated on solid agar in OmniTray format. Plates were incubated in the Reshape Smart Incubator, with high-resolution images captured at regular intervals throughout incubation.

Using automated image analysis, colonies were:

- Detected based on contrast and edge recognition
- Segmented to separate overlapping growth
- Classified using morphological features including:
  - Colony size
  - Circularity
  - Edge definition
  - Opacity
  - Color metrics (RGB/HSV)
  - Growth kinetics over time

Colonies were automatically grouped into phenotypic classes and counted individually per category. Time-resolved data enabled tracking of emergence timing, growth rate, and competitive dynamics between colony types.

Results & Discussion

The system successfully:

- Identified and separated visually distinct colony types within mixed cultures
- Quantified CFU per phenotype with high reproducibility
- Differentiated colonies with subtle morphological differences
- Tracked appearance timing of slow-growing versus fast-growing strains

Unlike endpoint manual counting, automated time-series imaging prevented underestimation of slower-growing colonies that may be obscured at later timepoints.

The approach enabled simultaneous reporting of:

- Total CFU
- CFU per colony type
- Growth curves per phenotype
- Time-to-detection per colony class

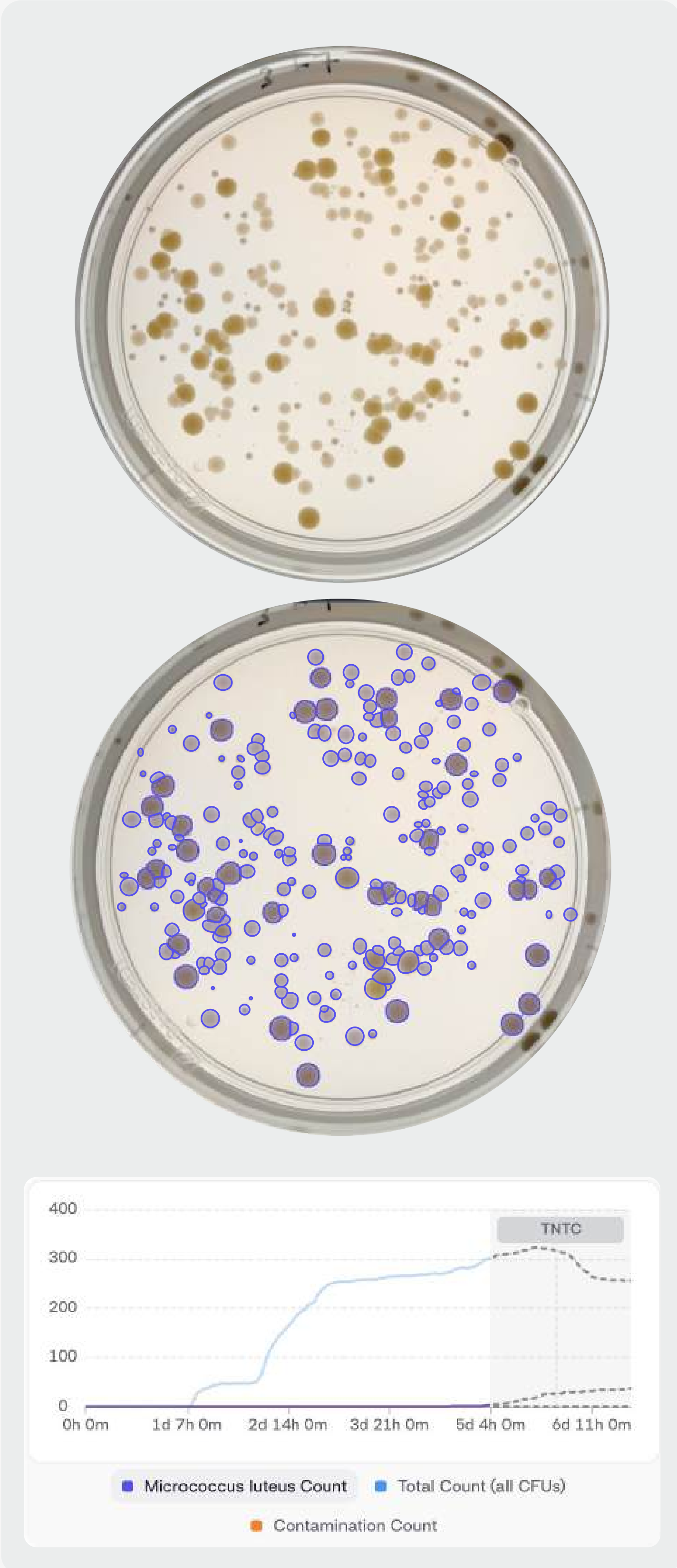


Figure 1. Filtered and differentiated counts based on colony phenotype

EXAMPLE II

When Colony Differentiation Matters In Mixed Cultures

Yeast & Mould Counting

Manually quantifying mixed colonies on a single plate, such as in yeast and mould counts, can be surprisingly challenging. Irregular shapes, spreading growth, overlapping colonies, and the presence of mixed isolates make boundaries difficult to define. Analysts must rely on visual judgment, which introduces variability and reduces consistency, particularly when clear differentiation between colony types is required.

In this example, mixed yeast and mould colonies were plated on solid DRBC agar and incubated for 72 hours in the Reshape Smart Incubator. A single end-point image was captured to characterize and quantify the colonies. Because the user knew which microorganisms were present, they defined two classification groups, one for each microbe, allowing the platform to automatically differentiate and report counts for each type.

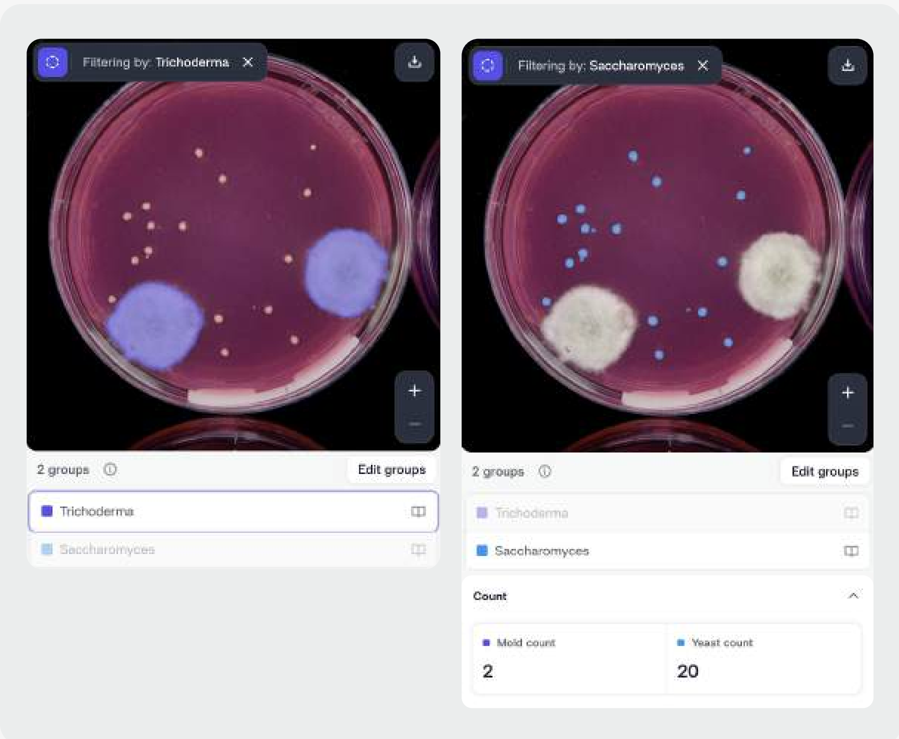


Figure 2. Automation helps standardize this process. Imaging combined with colony differentiation models enables consistent detection and classification, even on complex, mixed plates. The result is faster workflows, reduced subjectivity, and greater confidence in colony counts.