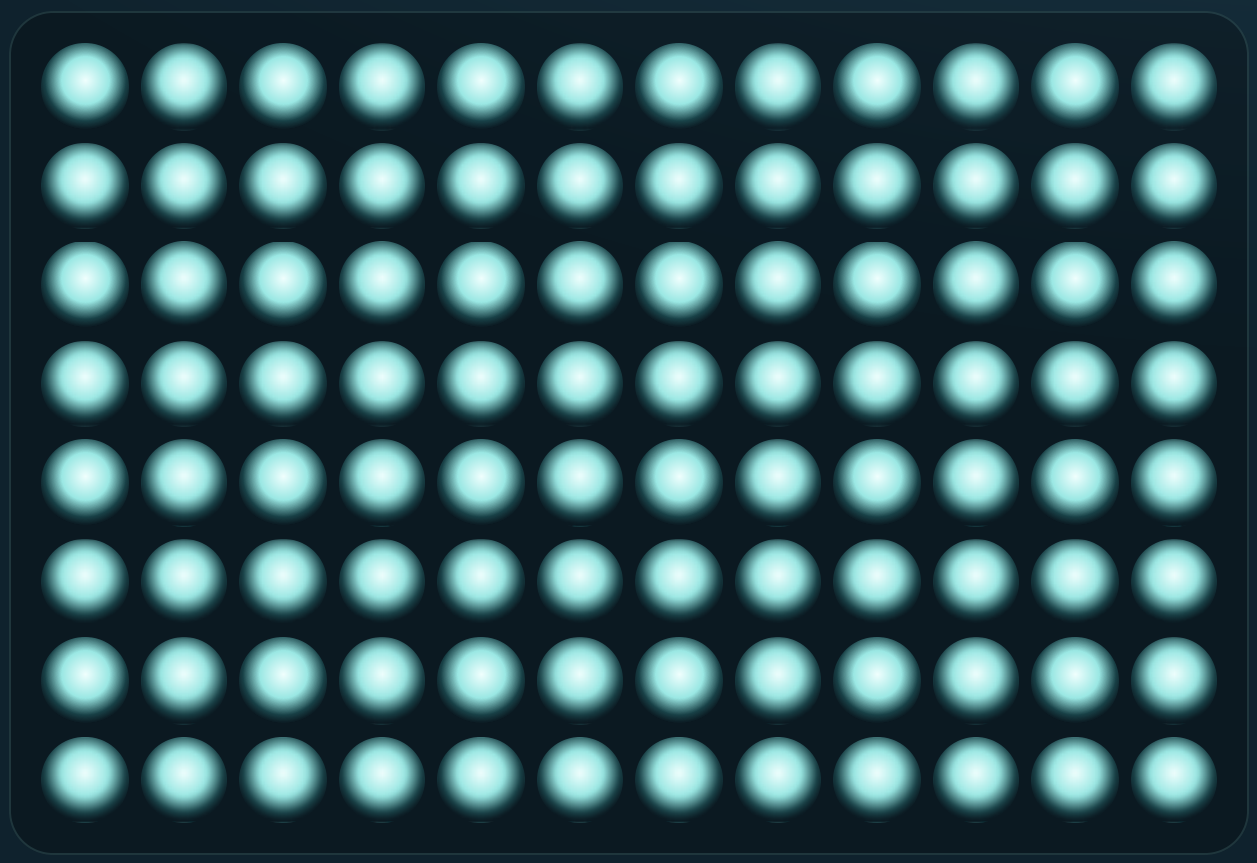
Single-cell data at scale

Where do batch effects actually come from?



Five minutes on the most manual step in the lab

The steps nobody logs

Thaw. Spin. Strain. Bead kit. Repeat for 2,000 samples.

Every one of these is a hands-on step with hands-on variance. Across a hundred-million-cell program, that variance is in the training set, and the model will learn it as biology.

Dead cells and debris become noise

Thaw, transfection, editing, dissociation: they all leave dead cells behind.

Their RNA leaks into every cell's barcode as ambient RNA. Their fragments become doublets and debris. In the Discovery Life Sciences study, the most contaminated tumor sample spent 68% of its reads on soup, not cells.

The limit of software

You can’t regress out a batch effect you can’t measure.

You cannot recover a sample that was never viable, and you cannot see the variance that entered before the first barcode. The fix has to be physical, and it has to be the same every time.

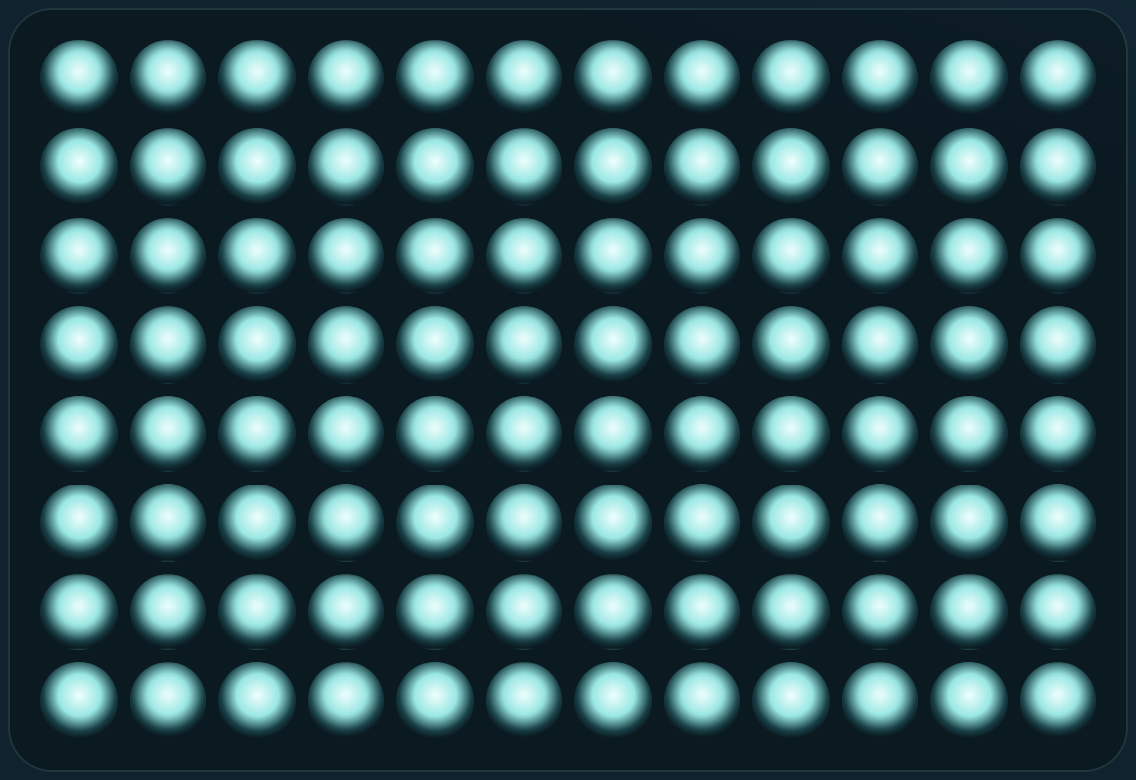
Identical, scripted, on the robot

96 samples. One array. Every step scripted.

1	Enrich: live cells levitate, dead cells and debris sink	label-free
2	Wash: buffer exchange in the well	no spins
3	Collect, pool, concentrate: ready to load	45 min total
4	Repeat, identically, plate after plate	scripted

Same script, every well, traceable.

A scripted protocol does the same thing to every well and leaves a run log behind. Pair it with viability counts before and after, and every sample in the dataset comes with a record of how it was prepared, and an answer when a cluster looks odd eighteen months later.



A prep record is part of the dataset, not a nice-to-have

What it did on 16 real samples

10×

more samples pass the 70% viability gate and produce usable results

52% → 75%

median viability after one 40-minute run

6×

fewer high-confidence doublets; 21% less ambient RNA

85/100

marker genes carry over: same biology, cleaner input

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