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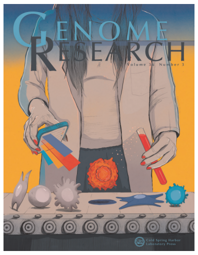

Cover In single-cell RNA sequencing studies, gene signature scores are widely used to annotate cell types and states and to quantify the activity of biological pathways. Yet, standard scoring approaches often yield biased or poorly aligned score ranges across signatures, making unsupervised cell annotation unreliable. In this issue, Adjusted Neighborhood Scoring (ANS) overcomes this limitation by selecting control genes that match the baseline expression of each signature gene, producing robust and comparable scores across tissues, samples, and experimental conditions. On the cover, a researcher oversees a "cell annotation assembly line," where incoming cells are scored and receive color-coded signature scores corresponding to specific cell types and states. Each cell is then colored with the hue matching the highest score, representing its label, and visually conveying how ANS converts noisy measurements into robust, biologically meaningful annotations. (Cover art illustrated by Marta Ruszkowska [www.martaruszkowska.pl and https://www.instagram.com/marta.ruszkowska_illustration/]. [For details, see Ciernik et al., pp. 630–644.])