Statistical power for single cell analysis

Many of us biologists are familiar with p-values, but statistical power is often less understood. In bulk analysis, we often talk about “technical replicates”, where a general rule-of-thumb is to use a minimum of three samples per group to calculate a valid p-value. However, in single cell analysis, this is often not necessary since we perform measurements on thousands of individual cells per sample.

This raises the question: **how many samples per group do we need for single cell analysis to detect differences in gene expression?**

The answer is… it depends on the **statistical power** of your experiment. Statistical power refers to the ability of your experiment to detect biological differences when they exist and is influenced by various factors. In general, larger biological differences and a higher number of samples result in greater statistical power.

As an example, we conducted simulations using single cell data from bone marrow mononuclear cells. To reliably detect a three-fold difference in gene expression with reasonable statistical power, it was found that three to four samples per group were required if >500 cells of interest are measured per sample.

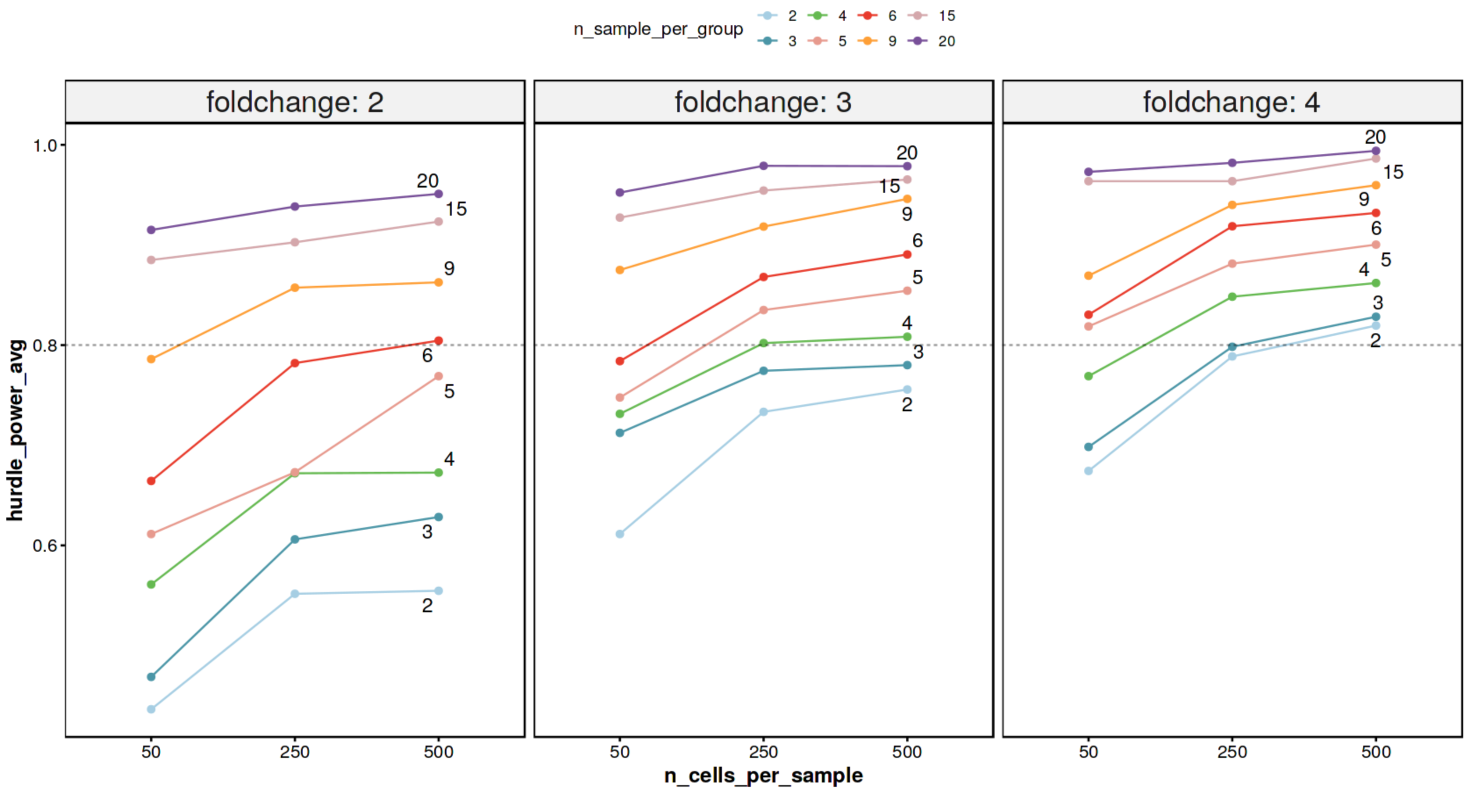

Fig. 1. Power analysis simulation. X-axis: Number of cells from the cell type of interest per sample. Y-axis: Statistical power. Horizontal line: The acceptable power threshold of 0.8. Color of datapoints indicates the number of samples per group for the two comparison groups.

With a better grasp of the sample sizes required for your single cell project, come discuss with us how to run your single cell experiments and maximize statistical power!

Contact info@singleron.bio for a free consultation

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