

## Getting more out of bulk RNA-Seq with digital cytometry



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Introduction

Bulk RNA-Seq data provide insightful look onto the overall state of transcriptome in the researched tissue. Bulk RNA-Seq is however being overshadowed by single-cell RNA sequencing, which allows for detailed identification of processes involved in damage and disease. Here, we discuss the use of deconvolution algorithm CibersortX, developed by Newman et al (2019), which estimates cell type abundancies in bulk tissue based on a singlecell reference. We have applied CibersortX to describe the dynamics of tissue composition in bulk specimen of two distinct models of acute brain injury, succesfully identifying the differences down to rare cellular subtypes.

## - Conclusions

Digital cytometry (= deconvolution) enables:

To dissect cell type composition in bulk samples, even for rare (~1%) populations

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- Identification of **unconventional** cell type markers
- To estimate the cell type-specific expression for robust markers  $\bullet$



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## Newman, A.M., Steen, C.B., Liu, C.L. et al. Determining cell type abundance and expression from bulk tissues with digital cytometry. Nat Biotechnol 37, 773–782 (2019)

Habib, N., McCabe, C., Medina, S. et al. Disease-associated astrocytes in Alzheimer's disease and aging. Nat Neurosci 23, 701–706 (2020)

