

CIBERSORTx is a new method for "*in silico* flow cytometry"

Overview

CIBERSORTx is an analytical tool developed by Newman et al. (<https://www.nature.com/articles/s41587-019-0114-2>) to impute gene expression profiles and provide an estimation of the abundances of member cell types in a mixed cell population, using gene expression data.

CIBERSORTx allows users to process gene expression data representing a bulk admixture of different cell types, along with a signature matrix file that enumerates the genes defining the expression profile for each cell type of interest. For the latter, users can either use existing/curated signature matrices for reference cell types, or can create custom signature gene files by providing the reference gene expression profiles of pure cell populations. Moreover, given the increasing use of single cell transcriptome sequencing, CIBERSORTx also provides the option to derive signature matrices from single-cell RNA sequencing data.

CIBERSORTx offers two analysis modules (see figure for overview):

1. **Cell Fractions:** This module **enumerates the proportions of distinct cell subpopulations** in bulk tissue expression profiles. Unlike its predecessor (<https://cibersort.stanford.edu>), CIBERSORTx supports deconvolution of bulk RNA-Seq data using signature genes derived from either single cell transcriptomes or sorted cell populations.
2. **Gene Expression:** This module imputes cell type specific expression profiles from bulk tissue transcriptome without physical cell sorting. It can be applied in two distinct modes:
 1. **Group-Level:** In this mode, a **representative transcriptome profile for each cell type in the signature matrix** is imputed from a group of bulk tissue transcriptomes. This mode is useful for learning context-dependent changes in a cell's expression profile (e.g., responders vs. non-responders to a therapy).
 2. **High-Resolution:** In this mode, CIBERSORTx is used to impute **sample-level gene expression variation of distinct cell types** from a collection of bulk tissue transcriptomes. Unlike Group-Level Mode, the output is an expression matrix for each cell type rather than a single transcriptome profile. This mode is useful for exploring cell type expression variation without prior knowledge of biological or functional groupings (e.g. relating cell type specific gene expression to survival).

For more detailed information about how to apply CIBERSORTx, please refer to the book chapter by Steen et al. (Methods in Molecular Biology, 2020).

Implementation Details

CIBERSORTx was developed within a web framework with its back-end based on R and PHP, minimizing inherent dependencies on specific hardware, software packages and libraries, and file-system attributes. Users are presented with a detailed guide employing several step-by-step Tutorials.

[More Information...](#)

To start using CIBERSORTx right away, press [here \(runcibersortx.php\)](#) or click [here \(tutorial.php\)](#) to start with a tutorial.

Please send questions, issues, and/or licensing requests to: cibersortx@gmail.com (<mailto://cibersortx@gmail.com>)

- The CIBERSORTx Team ([contact.php](#))

