



IO17 | Large Scale Bioinformatics for Immuno-Oncology

Deconvolution: exercise 1

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Deconvolution: Exercise 1

We have access to expression data (Illumina HumanHT-12 V4.0 expression beadchip microarrays) obtained from peripheral blood mononuclear cell (PBMC) data from 20 healthy individuals who received influenza immunization: *Mixture_Newman_PBMC.txt*

We want to estimate the cell fractions of 22 different immune sub-populations (signature: *Signature_CIBERSORT_LM22.txt*) from these samples using the web-interface of **CIBERSORT**.

PBMC data and CIBERSORT algorithm are described in:

Newman, Aaron M., et al. "Robust enumeration of cell subsets from tissue expression profiles." *Nature methods* 12.5 (2015): 453-457.

Alternative: web-based CIBERSORT

Register and sign in on CIBERSORT website: <https://cibersort.stanford.edu/>

CIBERSORT [Home](#) [About](#) [Contact](#) [Menu](#) [Register](#) Remember Me



CIBERSORT is an analytical tool developed by [Newman et al.](#) to provide an estimation of the abundances of member cell types in a mixed cell population, using gene expression data.

Absolute mode (beta) is now available.

Upload the mixture matrix (1)

Run CIBERSORT

Job Results

Upload Files

Download

Tutorial

Manual

FAQ

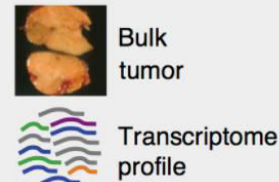
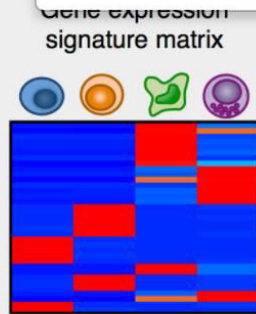
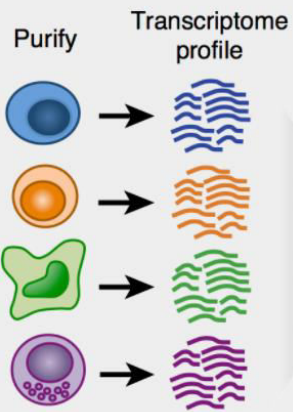
Version History

Reset Password

CIBERSORT

CIBERSORT is an analytical tool developed by Cantelmo et al. to provide an estimation of the abundances of member cell types in a mixed cell population, using gene expression data.

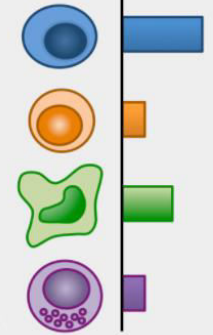
et al. to provide an estimation of the abundances of member cell types in a



CIBERSORT

Significance threshold

Relative fractions and global *P* value estimate




Run CIBERSORT »

Upload and Manage files to be analyzed with CIBERSORT

Instructions:

- Be sure all input files to be uploaded are text tab-delimited and do not contain any double quotation marks.
- Click 'Add files' or drag and drop files into the browser window.
- Enter a Title for each file, which will be used as an alias for the uploaded file. If no title is entered, the file name will be used.
- Also specify a file type for each file. This will determine which file field the file will appear in the CIBERSORT form. If no field is specified, the file will **not** appear in the form.
- Uploaded files appear below in reverse chronological order and can be individually deleted
- Note: there is a file quota of 500 MB. If your file exceeds your available quota, the file will not be saved to the server. (1 MB = 1000000 bytes)
- Please refresh the page after uploads to update quota status.

 Quota: 32.6 of 500 MB used, 467.4 MB remaining

Mixture file formatting requirements (LM22) - HUGO gene symbols in column 1; Mixture labels in row 1; Data should be in non-log space; more... ▾

➕ Add files...

🔄 Start upload

🚫 Cancel upload

🗑️ Delete

Select all

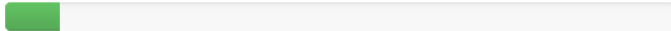
Title File Type	File name	Size	Upload Date	Actions
Title: <input type="text" value="Mixture_Newman_PBMC"/> File Type: <input type="text" value="Mixture"/>	Mixture_Newman_PBMC.txt	8.47 MB		<input type="button" value="🔄 Start"/> <input type="button" value="🚫 Cancel"/>

Upload and Manage files analyzed with CIBERSORT

Instructions:

- Be sure all input files to be uploaded are text tab-delimited.
- Click 'Add files' or drag and drop files into the browser.
- Enter a Title for each file, which will be used as an alternative name for the file.
- Also specify a file type for each file. This will determine the file format.
- Uploaded files appear below in reverse chronological order.
- Note: there is a file quota of 500 MB. If your file exceeds this quota, the file will not be saved to the server. (1 MB = 1000000 bytes)
- Please refresh the page after uploads to update quota.

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Quota: 41.1 of 500 MB used, 458.9 MB remaining

Mixture file formatting requirements (LM22) - HUGO gene symbols in column 1; Mixture labels in row 1; Data should be in non-log space; more... ▾

[+ Add files...](#) [Start upload](#) [Cancel upload](#) [Delete](#) Select all

Title	File name	Size	Upload Date	Actions
Mixture_Newman_PBMC Mixture	Mixture_Newman_PBMC.txt	8.47 MB	09/08/17 12:43:27 AM	Delete <input type="checkbox"/>



Configure Basic CIBERSORT Options

Run relative and absolute modes together (beta).

[More Information...](#) ▾

Signature gene file*

LM22 (22 immune cell types) ▾

[More Information...](#) ▾

Mixture file*

Mixture_Newman_PBMC ▾

[More Information...](#) ▾

Permutations

100 ▾

[More Information...](#) ▾

Disable quantile normalization (recommended for [RNA-Seq data](#))

[Custom Signature Genes](#) ▾

[Example Datasets](#) ▾

Run

CIBERSORT Results



Data display mode: Relative (for absolute mode, see [here](#))

Filter by max p-value: 0.01 0.05 No Filtering

Download: [TXT](#) [CSV](#) [HTML](#) [XLSX](#) [PDF](#)

Adjust contrast: low medium high default 0 0.05 0.3

Table view: [Scroll](#) [Full](#)

[Table Output Help](#)

Search:

Input Sample	B cells naive	B cells memory	Plasma cells	T cells CD8	T cells CD4 naive	T cells CD4 memory resting	T cells CD4 memory activated	T cells follicular helper	T cells regulatory (Tregs)	T cells gamma delta	NK cells resting	NK cells activated	Mo
Sample_002	0.048	0.053	0	0.241	0	0	0.046	0	0.019	0	0.11	0.018	0
Sample_006	0.06	0	0	0.363	0	0.107	0.029	0.024	0.114	0	0	0.043	0
Sample_019	0.111	0.027	0	0.218	0.02	0.073	0	0	0.003	0.01	0.256	0.034	0
Sample_023	0.066	0.046	0	0.061	0	0.298	0	0.013	0.022	0	0.024	0.044	0
Sample_026	0.036	0.045	0	0.26	0	0.054	0.015	0.013	0.032	0	0.023	0.016	0
Sample_027	0.066	0.019	0	0.23	0.081	0	0.008	0	0.026	0.058	0.02	0.057	0
Sample_030	0.024	0.044	0	0.178	0	0.071	0.008	0.012	0.024	0.069	0.052	0.086	0
Sample_034	0.069	0	0	0.138	0.069	0.119	0.036	0	0	0	0.055	0.063	0
Sample_040	0.142	0	0	0.12	0.006	0	0.094	0.027	0.029	0.014	0.031	0.068	0
Sample_041	0.046	0	0	0.149	0.198	0.051	0.084	0	0.019	0.004	0.049	0.088	0
Sample_042	0.02	0.002	0	0.071	0	0.068	0.076	0.023	0	0.014	0.051	0.057	0