

DeMixT (v 1.20.1)

DeMixT is a frequentist-based method and fast in yielding accurate estimates of cell proportions and compartment-specific expression profiles for two- and three-component deconvolution from heterogeneous tumor samples.

Updates

(06/23/2024) Script `DeMixT_preprocessing.R` is included in the package for input data preprocessing. The DeMixT tutorial at <https://wwylab.github.io/DeMixT/> is updated.

(06/18/2022) Fixed a bug in `R/DeMixT_GS.R:130`: changed `return(class(try(solve(m), silent = T)) == "matrix")` to `return(class(try(solve(m), silent = T))[1] == "matrix")` to make it work properly under both `R 3.x` and `R 4.x`; since under `R 4.x`, `class(matrix object)` returns `"matrix"`, `"array"`, instead only `"matrix"` under `R 3.x`. Please be aware of this bug for those who installed `DeMixT` (v1.10.0) from Bioconductor.

Installation

The DeMixT package is compatible with Windows, Linux and MacOS. Specifically, for Linux and MacOS, the user can install the latest `DeMixT` (v 1.20.1) from GitHub:

```
if (!require("devtools", quietly = TRUE))
  install.packages('devtools')

devtools::install_github("wwylab/DeMixT")
```

For Windows, we recommend the user to install DeMixT (v 1.20.0) from `Bioconductor`:

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install("DeMixT")
```

Please note, Linux and MacOS users can also install DeMixT from `Bioconductor`.

Check if `DeMixT` is installed successfully:

```
# load package
library(DeMixT)
```

We highly recommend the user to use DeMixT on Linux or Windows machines.

Issues of DeMixT on MacOS

1. DeMixT relies on OpenMP for parallel computing. Starting from R 4.00, R no longer supports OpenMP on MacOS, meaning the user can only run DeMixT with one core on MacOS.
2. We noticed there may be installation/running errors for DeMixT on MacOS machines with M1 chips. We are trying to fix it.

Use DeMixT

A tutorial is available at <https://wwylab.github.io/DeMixT/>.

Cite DeMixT

[1] Ahn, J. et al. DeMix: Deconvolution for mixed cancer transcriptomes using raw measured data. *Bioinformatics* 29, 1865–1871 (2013).

[2] Wang, Z. et al. Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. *iScience* 9, 451–460 (2018).