

# DeMixT Log

Cell type-specific deconvolution of heterogeneous tumor samples with two or three components using expression data from RNAseq or microarray platforms.

## Update from version 1.4.0 to 1.6.0

Gene expression data of normal tissues (Lung, Prostate and Thyroid) from the GTEx study are included.  
Rename DeMixT\_S1 function to DeMixT\_DE.

## Update from version 1.2.5 to 1.4.0

Disabled OpenMP under R 4.0.0 for Mac OS platform.

## Update from version 1.2.4 to 1.2.5

Error appears if the number of genes is not multiplied by 10.

```
ngene.Profile.selected<-min(1500, 0.3*nrow(data.Y))
```

```
ngene.Profile.selected<-min(1500, round(0.3*nrow(data.Y)))
```

## Update from version 1.2.3 to 1.2.4

The step for computing MuN mis-specify the groupid, since MuN corresponds to groupid == 1.

```
mun.obs<-rowMeans(log2(inputdata2[, groupid == 3]+0.001))
```

```
mun.obs<-rowMeans(log2(inputdata2[, groupid == 1]+0.001))
```

## Update from version 1.2.1 to 1.2.3

### Major Changes

1. Added pi01 and pi02 as input values for users to initialize the proportion estimation.
2. Added nspikein as an input value in the DeMixT, DeMixT\_S1 and DeMixT\_GS functions to specify how many spike-in normal reference samples need to be generated; Setting nspikein at null as a default value, the number of spike-in normal reference samples equal the  $\min(200, 0.3 \times My)$ , where  $My$  is the number of mixed samples; By setting nspikein equals 0, no spike-in normal reference will be generated; If the input value of data.N2 is not null, nspikein will be forced to be 0.
3. Added DeMixT\_GS function, new proposed gene selection method which applies profile likelihood, for proportion estimation.
4. Added simulate\_2comp function for users to simulate test data for 2-component de-convolution.
5. Added simulate\_3comp function for users to simulate test data for 3-component de-convolution.
6. Added row names and column names for all output values.
7. Added gene.selection.method as an input value for DeMixT function. The default is 'GS'.

8. Added `ngene.Profile.selected` as an input value for `DeMixT` function. The default is `NA`.

## Bug fix

The filter step failed to set the value into `inputdata` in the previous version, and it has been resolved in the 1.3.0 version.

```
## filter out genes with constant value across all samples
inputdata <- ifelse(is.null(data.comp2),
  inputdata[apply(data.comp1, 1, function(x) length(unique(x)) > 1), ],
  inputdata[apply(data.comp1, 1, function(x) length(unique(x)) > 1) &
    apply(data.comp2, 1, function(x) length(unique(x)) > 1), ]])

## filter out genes with constant value across all samples
if (is.null(data.comp2)) {
  if (dim(inputdata)[1] == 1) {
    inputdata <- t(as.matrix(inputdata[apply(data.comp1,
      1, function(x) length(unique(x)) > 1), ]]))
  }
  else {
    inputdata <- inputdata[apply(data.comp1, 1, function(x) length(unique(x)) >
      1), ]
  }
}
else {
  if (dim(inputdata)[1] == 1) {
    inputdata <- t(as.matrix(inputdata[apply(data.comp1,
      1, function(x) length(unique(x)) > 1) & apply(data.comp2,
      1, function(x) length(unique(x)) > 1), ]]))
  }
  else {
    inputdata <- inputdata[apply(data.comp1, 1, function(x) length(unique(x)) >
      1) & apply(data.comp2, 1, function(x) length(unique(x)) >
      1), ]
  }
}
```