

# R documentation

## of ‘digitalDLSorter.Rd’

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digitalDLSorter

*digitalDLSorter: R package for deconvolution of bulk RNA-Seq samples based on Deep Learning.*

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### Description

*digitalDLSorter* is an R package that implements a Deep Learning based method to enumerate and quantify the cell type composition of bulk RNA-Seq samples. Our method makes use of Deep Neural Network (DNN) models to adjust any cell type composition starting from single-cell RNA-Seq (scRNA-Seq) data.

### Details

The rationale of the method consists in a process that starts from scRNA-Seq data and, after a few steps, a Deep Neural Network (DNN) model is trained with simulated bulk RNA-seq samples whose cell composition is known. The trained model is able to deconvolve any bulk RNA-seq sample by determining the proportion of the different cell types present in it. The main advantage of this method is the possibility of building deconvolution models trained with real data which comes from certain biological environments. For example, for quantifying the proportion of tumor infiltrated lymphocytes (TILs) in breast cancer, by following this protocol you can obtain a specific model for this type of samples. This fact overcomes the limitation of other methods, since stromal and immune cells change significantly their profiles depending on the tissue and disease context.

The package can be used in two ways: for deconvolving bulk RNA-seq samples using a pre-trained model provided by us or for building your own models trained from your own scRNA-seq samples. These new models may be published in order to make them available for other users that work with similar data (e.g. neural environment, prostate cancer environment, etc.). For the moment, the available models allows the deconvolution of TILs from breast cancer classified by our team.

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