

# R documentation

## of 'breast.chung.generic.Rd'

September 3, 2020

---

```
breast.chung.generic
```

*Pre-trained DigitalDLSorter DNN model for deconvolution of TILs present in breast cancer environment (generic version).*

---

### Description

DigitalDLSorter DNN model built and trained with single-cell data from Chung et al., 2017 (GSE75688). This model allows the enumeration and quantification of immune infiltrated cell types in breast cancer environment. This data set consists in single-cell profiles from 11 patients from different tumor etiology and stages (see Torroja and Sanchez-Cabo, 2019 for more details). The analysis and characterization of the cells was carried out by the authors of digitalDLSorter package.

### Usage

```
breast.chung.generic
```

### Format

A DigitalDLSorterDNN object with the following slots:

**model** Trained DNN model.

**training.history** Evolution of metrics and loss function during training.

**eval.stats** Metrics and loss results on test data.

**predict.results** Predictions of cell types on test data.

**cell.types** Cell types considered by DNN model.

**features** Features (genes) considered by model.

### Details

The cell types considered in this model are 7. They are the generic groups from cell types considered in specific version: B cells, T CD4+ cells, T CD8+ cells, monocytes, dendritic cells, stromal cells and tumor cells.

The genes considered are 23.260 in SYMBOL notation.

The model consists in 2 hidden layers with 200 neurons per layer trained with 'kullback\_leibler\_divergence' loss function batch size equal to 128 and a number of epochs equal to 25.

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE75688>

**References**

Chung, W., Eum, H. H., Lee, H. O., Lee, K. M., Lee, H. B., Kim, K. T., et al. (2017). Single-cell RNA-seq enables comprehensive tumour and immune cell profiling in primary breast cancer. Nat. Commun. 8 (1), 15081. doi: [10.1038/ncomms15081](https://doi.org/10.1038/ncomms15081).

Torroja, C. y Sánchez-Cabo, F. (2019). digitalDLSorter: A Deep Learning algorithm to quantify immune cell populations based on scRNA-Seq data. Frontiers in Genetics 10, 978. doi: [10.3389/fgene.2019.00978](https://doi.org/10.3389/fgene.2019.00978)

# Index

## \*Topic **datasets**

`breast.chung.generic`, [1](#)

`breast.chung.generic`, [1](#)