

R documentation

of 'breast.chung.specific.Rd'

September 3, 2020

`breast.chung.specific`

Pre-trained DigitalDLSorter DNN model for deconvolution of TILs present in breast cancer environment (specific 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 cells was carried out by the authors of `digitalDLSorter` package.

Usage

`breast.chung.specific`

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 13, four of them being the intrinsic molecular subtypes of breast cancer: ER+, HER2+, ER+/HER2+, TNBC, Stromal, Monocyte, TCD4mem (memory CD4+ T cells), BGC (germinal center B cells), Bmem (memory B cells), DC (dendritic cells), Macrophage, TCD8 (CD8+ T cells) and TCD4reg (regulatory CD4+ T 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.specific, [1](#)

breast.chung.specific, [1](#)