Package 'easierData'

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Title easier internal data and exemplary dataset from IMvigor210CoreBiologies package

Version 1.18.0

Description Access to internal data required for the functional performance of easier package and exemplary bladder cancer dataset with both processed RNA-seq data and information on response to ICB therapy generated by Mariathasan et al. ``TGF-B attenuates tumour response to PD-L1 blockade by contributing to exclusion of T cells", published in Nature, 2018 [doi:10.1038/nature25501](https://doi.org/10.1038/nature25501). The data is made available via [`IMvigor210CoreBiologies`](http://research-pub.gene.com/IMvigor210CoreBiologies/) package under the CC-BY license.

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Depends R (>= 4.1.0)

Imports ExperimentHub, AnnotationHub, utils, SummarizedExperiment

Suggests knitr, rmarkdown, BiocStyle, testthat (>= 3.0.0)

biocViews RNASeqData, ExperimentHub, ReproducibleResearch, ImmunoOncologyData, CancerData, ExperimentData

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`easierData-pkg` *easierData: easier data package*

Description

This experiment data package provides access to an exemplary bladder cancer dataset with both processed RNA-seq data and information on response to ICB therapy publicly available via IMvigor210CoreBiologies package, and to internal data indispensable for the functional performance of easier package.

References

Óscar Lapuente-Santana, Maisa van Genderen, Peter A. J. Hilbers, Francesca Finotello, and Federica Eduati. 2021. Interpretable Systems Biomarkers Predict Response to Immune-Checkpoint Inhibitors. Patterns, 100293. https://doi.org/10.1016/j.patter.2021.100293.

get_cor_scores_genes *Get the list of genes used to define correlated scores of immune response*

Description

Obtain the list of genes used to define each of the correlated scores of immune response. These scores were found to be highly correlated across all 18 cancer types.

Usage

```
get_cor_scores_genes()
```

Value

A character vector with gene names.

References

Óscar Lapuente-Santana, Maisa van Genderen, Peter A. J. Hilbers, Francesca Finotello, and Federica Eduati. 2021. Interpretable Systems Biomarkers Predict Response to Immune-Checkpoint Inhibitors. Patterns, 100293. https://doi.org/10.1016/j.patter.2021.100293.

Mariathasan, S., Turley, S., Nickles, D. et al. TGFB attenuates tumour response to PD-L1 blockade by contributing to exclusion of T cells. Nature 554, 544–548 (2018). https://doi.org/10.1038/nature25501.

Examples

```
if (interactive()) {
    cor_scores_genes <- get_cor_scores_genes()
}
```

get_group_lrpairs *Get the groups of ligand-receptor pairs*

Description

Obtain the information to group ligand-receptor pairs because of sharing the same gene, either as ligand or receptor.

Usage

```
get_group_lrpairs()
```

Value

A list containing grouping information for 56 groups of l igand-receptor pairs.

Examples

```
if (interactive()) {
    group_lrpairs <- get_group_lrpairs()
}
```

`get_HGNC_annotation` *Get the gene symbols approved annotations*

Description

Get the gene symbols approved annotations

Usage

```
get_HGNC_annotation()
```

Value

A data.frame with gene symbols information.

Source

https://www.genenames.org/tools/multi-symbol-checker/

References

Tweedie S, Braschi B, Gray KA, Jones TEM, Seal RL, Yates B, Bruford EA. Genenames.org: the HGNC and VGNC resources in 2021. Nucleic Acids Res. PMID: 33152070 PMCID: PMC7779007 DOI: 10.1093/nar/gkaa980

Examples

```
if (interactive()) {
    HGNC <- get_HGNC_annotation()
}
```

get_intercell_networks

Get the cancer-specific intercellular networks, including a pan-cancer network

Description

Obtain the cancer-specific intercellular networks based on literature supported pairs from the Ramilowski database (Ramilowski et al., Nat.Commun., 2015), filtering for 24 cell types acknowledged to be present in the TME. Additionally, a pan-cancer cell type is included using data from the CCLE (Barretina et al., Nature, 2012) by computing the median expression of each gene across cell lines related to the selected cancer types. A pan-cancer network is also available and this is based on the union of all ligand-receptor pairs present across the cancer-specific networks.

Usage

```
get_intercell_networks()
```

Value

A list containing for each cancer type, a data.frame with cell-cell ligands and receptors information.

References

Ramilowski, Jordan A., Tatyana Goldberg, Jayson Harshbarger, Edda Kloppmann, Marina Lizio, Venkata P. Satagopam, Masayoshi Itoh, et al. 2015. "A Draft Network of Ligand–Receptor-Mediated Multicellular Signalling in Human." Nature Communications 6 (1): 7866. https://doi.org/10.1038/ncomms8866.

Barretina, J., Caponigro, G., Stransky, N. et al. The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature 483, 603–607 (2012). https://doi.org/10.1038/nature11003

Examples

```
if (interactive()) {
    intercell_networks <- get_intercell_networks()
}
```

get_lr_frequency_TCGA

Get the frequency of each ligand-receptor pair feature across the whole TCGA database

Description

Obtain the frequency of each ligand-receptor pair feature across the whole TCGA database. Only ligand-receptor pairs with frequency different from zero are kept. Each cell-cell pair feature score is calculated as the sum of the inverse of the frequency of all the active ligand-receptor pairs.

Usage

```
get_lr_frequency_TCGA()
```

Value

A numeric vector with the frequency of each ligand-receptor pair feature.

References

The Cancer Genome Atlas Research Network., Weinstein, J., Collisson, E. et al. The Cancer Genome Atlas Pan-Cancer analysis project. Nat Genet 45, 1113–1120 (2013). https://doi.org/10.1038/ng.2764

Examples

```
if (interactive()) {
    lr_frequency <- get_lr_frequency_TCGA()
}
```

---

get_Mariathasan2018_PDL1_treatment

Get the Mariathasan2018 PD-L1 treatment data

Description

Obtain the gene expression data (count and tpm values) and the sample metadata from Mariathasan et al. (2018).

Usage

```
get_Mariathasan2018_PDL1_treatment()
```

Details

The `SummarizedExperiment` object returned contains:

- two assays: `counts` and `tpm`.
- additional sample metadata in the `colData` slot, including pat_id (the id of the patient in the original study), BOR to PD-L1 treatment, and TMB (Tumor Mutational Burden).

Value

A SummarizedExperiment object with counts and TPM quantifications.

Source

IMvigor210CoreBiologies package under the CC-BY license. http://research-pub.gene.com/IMvigor210CoreBiologies/

References

Óscar Lapuente-Santana, Maisa van Genderen, Peter A. J. Hilbers, Francesca Finotello, and Federica Eduati. 2021. Interpretable Systems Biomarkers Predict Response to Immune-Checkpoint Inhibitors. Patterns, 100293. https://doi.org/10.1016/j.patter.2021.100293.

Mariathasan, S., Turley, S., Nickles, D. et al. TGFB attenuates tumour response to PD-L1 blockade by contributing to exclusion of T cells. Nature 554, 544–548 (2018). https://doi.org/10.1038/nature25501.

Examples

```
if (interactive()) {
    se_mariathasan <- get_Mariathasan2018_PDL1_treatment()
}
```

`get_opt_models` *Get the cancer-specific model feature parameters*

Description

Obtain the cancer-specific model feature parameters learned in Lapuente-Santana et al. (2021). For each quantitative descriptor, models were trained using multi-task learning with randomized cross-validation repeated 100 times. For each quantitative descriptor, 1000 models are available (100 per task).

Usage

```
get_opt_models()
```

Value

A list containing for each cancer type and quantitative descriptor, a matrix of feature coefficient values across different tasks. The cancer types, for which a cancer-specific model is available, are: "BLCA", "BRCA", "CESC", "CRC", "GBM", "HNSC", "KIRC", "KIRP", "LIHC", "LUAD", "LUSC", "NSCLC", "OV", "PAAD", "PRAD", "SKCM", "STAD", "THCA" and "UCEC".

References

Óscar Lapuente-Santana, Maisa van Genderen, Peter A. J. Hilbers, Francesca Finotello, and Federica Eduati. 2021. Interpretable Systems Biomarkers Predict Response to Immune-Checkpoint Inhibitors. Patterns, 100293. https://doi.org/10.1016/j.patter.2021.100293.

Examples

```
if (interactive()) {
    opt_models <- get_opt_models()
}
```

get_opt_xtrain_stats *Get training set cancer-specific features mean and standard deviation*

Description

Obtain the cancer-specific features mean and standard deviation (sd) of the training set used in Lapuente-Santana et al. (2021) for model training by using randomized cross-validation repeated 100 times. It is required for normalization of the test set.

Usage

```
get_opt_xtrain_stats()
```

Value

A list containing for each cancer type and quantitative descriptor, a matrix with feature mean and sd values across the 100 cross-validation runs. The cancer types, for which cancer-specific features mean and sd is available, are: "BLCA", "BRCA", "CESC", "CRC", "GBM", "HNSC", "KIRC", "KIRP", "LIHC", "LUAD", "LUSC", "NSCLC", "OV", "PAAD", "PRAD", "SKCM", "STAD", "THCA" and "UCEC".

References

Óscar Lapuente-Santana, Maisa van Genderen, Peter A. J. Hilbers, Francesca Finotello, and Federica Eduati. 2021. Interpretable Systems Biomarkers Predict Response to Immune-Checkpoint Inhibitors. Patterns, 100293. https://doi.org/10.1016/j.patter.2021.100293.

Examples

```
if (interactive()) {
    opt_xtrain_stats <- get_opt_xtrain_stats()
}
```

get_scores_signature_genes *Get the gene signatures for each score of immune response*

Description

Obtain the gene signatures for each score of immune response: CYT, TLS, IFNy, Ayers_expIS, Tcell_inflamed, Roh_IS, Davoli_IS, chemokines, IMPRES, MSI and RIR.

Usage

```
get_scores_signature_genes()
```

Value

A list with the gene signature of each score of immune response.

References

Rooney, Michael S., Sachet A. Shukla, Catherine J. Wu, Gad Getz, and Nir Hacohen. 2015. "Molecular and Genetic Properties of Tumors Associated with Local Immune Cytolytic Activity." Cell 160 (1): 48–61. https://doi.org/10.1016/j.cell.2014.12.033.

Cabrita, Rita, Martin Lauss, Adriana Sanna, Marco Donia, Mathilde Skaarup Larsen, Shamik Mitra, Iva Johansson, et al. 2020. "Tertiary Lymphoid Structures Improve Immunotherapy and Survival in Melanoma." Nature 577 (7791):561–65. https://doi.org/10.1038/s41586-019-1914-8.

McClanahan, Mark Ayers AND Jared Lunceford AND Michael Nebozhyn AND Erin Murphy AND Andrey Loboda AND David R. Kaufman AND Andrew Albright AND Jonathan D. Cheng AND S. Peter Kang AND Veena Shankaran AND Sarina A. Piha-Paul AND Jennifer Yearley AND Tanguy Y. Seiwert AND Antoni Ribas AND Terrill K. 2017. "IFN-y–Related mRNA Profile Predicts Clinical Response to PD-1 Blockade." The Journal of Clinical Investigation 127 (8): 2930–40. https://doi.org/10.1172/JCI91190.

Roh, Whijae, Pei-Ling Chen, Alexandre Reuben, Christine N. Spencer, Peter A. Prieto, John P. Miller, Vancheswaran Gopalakrishnan, et al. 2017. "Integrated Molecular Analysis of Tumor Biopsies on Sequential CTLA-4 and PD-1 Blockade Reveals Markers of Response and Resistance." Science Translational Medicine 9 (379). https://doi.org/10.1126/scitranslmed.aah3560.

Davoli, Teresa, Hajime Uno, Eric C. Wooten, and Stephen J. Elledge. 2017. "Tumor Aneuploidy Correlates with Markers of Immune Evasion and with Reduced Response to Immunotherapy." Science 355 (6322). https://doi.org/10.1126/science.aaf8399.

Messina, Jane L., David A. Fenstermacher, Steven Eschrich, Xiaotao Qu, Anders E. Berglund, Mark C. Lloyd, Michael J. Schell, Vernon K. Sondak, Jeffrey S. Weber, and James J. Mulé. 2012. "12-Chemokine Gene Signature Identifies Lymph Node-Like Structures in Melanoma: Potential for Patient Selection for Immunotherapy?" Scientific Reports 2 (1): 765. https://doi.org/10.1038/srep00765.

Auslander, Noam, Gao Zhang, Joo Sang Lee, Dennie T. Frederick, Benchun Miao, Tabea Moll, Tian Tian, et al. 2018. "Robust Prediction of Response to Immune Checkpoint Blockade Therapy in Metastatic Melanoma." Nature Medicine 24(10): 1545–49. https://doi.org/10.1038/s41591-018-0157-9.

Fu, Yelin, Lishuang Qi, Wenbing Guo, Liangliang Jin, Kai Song, Tianyi You, Shuobo Zhang, Yunyan Gu, Wenyuan Zha, and Zheng Guo. 2019. "A Qualitative Transcriptional Signature for Predicting Microsatellite Instability Status of Right-Sided Colon Cancer." BMC Genomics 20 (1): 769. https://doi.org/10.1186/s12864-019-6129-8.

Jerby-Arnon, Livnat, Parin Shah, Michael S. Cuoco, Christopher Rodman, Mei-Ju Su, Johannes C. Melms, Rachel Leeso, et al. 2018. "A Cancer Cell Program Promotes t Cell Exclusion and Resistance to Checkpoint Blockade." Cell 175 (4): 984–997.e24. https://doi.org/10.1016/j.cell.2018.09.006.

Óscar Lapuente-Santana, Maisa van Genderen, Peter A. J. Hilbers, Francesca Finotello, and Federica Eduati. 2021. Interpretable Systems Biomarkers Predict Response to Immune-Checkpoint Inhibitors. Patterns, 100293. https://doi.org/10.1016/j.patter.2021.100293.

Examples

```
if (interactive()) {
```

```
    easier_sigs <- get_scores_signature_genes()
}
```

`get_TCGA_mean_pancancer` *Get the mean of the TPM expression of each gene across all TCGA cancer types*

Description

Obtain the mean of the TPM expression of each gene across all TCGA cancer types. It is required for normalization of input TPM gene expression data.

Usage

```
get_TCGA_mean_pancancer()
```

Value

A numeric vector with gene TPM mean values.

References

The Cancer Genome Atlas Research Network., Weinstein, J., Collisson, E. et al. The Cancer Genome Atlas Pan-Cancer analysis project. Nat Genet 45, 1113–1120 (2013). https://doi.org/10.1038/ng.2764

Examples

```
if (interactive()) {
    TCGA_mean_pancancer <- get_TCGA_mean_pancancer()
}
```

`get_TCGA_sd_pancancer` *Get the standard deviation of the TPM expression of each gene across all TCGA cancer types*

Description

Obtain the standard deviation (sd) of the TPM expression of each gene across all TCGA cancer types. It is required for normalization of input TPM gene expression data.

Usage

```
get_TCGA_sd_pancancer()
```

Value

A numeric vector with gene TPM sd values.

References

The Cancer Genome Atlas Research Network., Weinstein, J., Collisson, E. et al. The Cancer Genome Atlas Pan-Cancer analysis project. Nat Genet 45, 1113–1120 (2013). https://doi.org/10.1038/ng.2764

Examples

```
if (interactive()) {
    TCGA_sd_pancancer <- get_TCGA_sd_pancancer()
}
```

---

list_easierData *List the datasets*

Description

List the datasets contained in the easierData package.

Usage

```
list_easierData()
```

Value

A data.frame for a compact visualization.

Examples

```
df <- list_easierData()
df
```

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