

Anatomy of an R package

Content

Location

Content

Location

Code

R/

Content	Location
Code	R/

Metadata

DESCRIPTION

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API docs

man/

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Metadata	DESCRIPTION
API docs	man/

User guide

vignettes/

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Testing

tests/

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Namespaces

NAMESPACE

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Data

data/

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Compiled code

src/

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Installed files

inst/

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Case study: Monocle 3

R/

File	Functions
RcppExports.R	Needed for C++ integration
alignment.R	Data set alignment & batch effect correction
cell_data_set.R	Core classes (e.g. cell_data_set)
cluster_cells.R	Clustering cells in PCA, t-SNE, or UMAP space (e.g. louvain)
cluster_genes.R	Finding modules of co-regulated genes
expr_models.R	Regression modeling of gene expression data
find_markers.R	Finding biomarkers for cell types and clusters
generics.R	Implementations of standard BioC interfaces
graph_test.R	Tests for gene expression autocorrelation across cells
learn_graph.R	Inferring geometry of cell trajectories
load_cellranger_data.R	Importing 10X data
methods-cell_data_set.R	Core methods for cell_data_set objects
order_cells.R	Ordering cells in pseudotime
plotting.R	Many visualization functions
preprocess_cds.R	PCA, LSI
reduce_dimensions.R	Nonlinear embedding with t-SNE and UMAP
select_cells.R	Methods for selecting subsets of cells interactively
utils.R	Miscellaneous useful functions