

Package ‘spatialDmelxsim’

January 2, 2025

Title Spatial allelic expression counts for fly cross embryo

Version 1.13.0

Description Spatial allelic expression counts from Combs & Fraser (2018), compiled into a SummarizedExperiment object. This package contains data of allelic expression counts of spatial slices of a fly embryo, a *Drosophila melanogaster* x *Drosophila simulans* cross. See the CITATION file for the data source, and the associated script for how the object was constructed from publicly available data.

Imports utils

Depends R (>= 4.1), ExperimentHub, SummarizedExperiment

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

URL <https://github.com/mikelove/spatialDmelxsim>

BugReports <https://github.com/mikelove/spatialDmelxsim/issues>

Suggests knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

biocViews ExperimentHub, SequencingData, RNASeqData, ExpressionData, *Drosophila_melanogaster_Data*, GEO

git_url <https://git.bioconductor.org/packages/spatialDmelxsim>

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Description

Allelic expression counts of spatial slices of a fly embryo from Combs & Fraser (2018), a *D melanogaster* x *D simulans* reciprocal cross

References

Combs PA, Fraser HB (2018) Spatially varying cis-regulatory divergence in *Drosophila* embryos elucidates cis-regulatory logic. *PLOS Genetics* 14(11): e1007631.

Examples

```
suppressPackageStartupMessages(library(SummarizedExperiment))
se <- spatialDmelxsim()
se
```

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