

Package ‘Cytangle’

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Title Analyzing Single Cell Mass Cytometry Data

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Description Defines classes and methods to analyze how relationships between protein markers vary in single cell mass cytometry data.

Depends R (>= 3.5.0)

Imports methods, graphics, Biobase, flowCore, plotrix, igraph, colorspace, fields

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URL <http://oompa.r-forge.r-project.org/>

NeedsCompilation no

R topics documented: