

R documentation

of ‘corrExpPredPlot.Rd’

September 3, 2020

<code>corrExpPredPlot</code>	<i>Generate correlation plot between predicted and expected cell type proportions from test samples.</i>
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Description

Generate correlation plot between predicted and expected cell type proportions from test samples. The correlation plots can be displayed all mixed or split based on cell type (`CellType`) or the number of cell types present in the sample (`nMix`). See `facet.by` argument and examples for more information. Moreover, a correlation value selected by user is displayed as annotation on the plots. See `corr` argument for details.

Usage

```
corrExpPredPlot(  
  object,  
  colors,  
  facet.by = NULL,  
  color.by = "CellType",  
  corr = "both",  
  filter.sc = TRUE,  
  pos.x.label = 0.01,  
  pos.y.label = 0.95,  
  sep.labels = 0.15,  
  size.point = 0.1,  
  alpha.point = 1,  
  ncol = NULL,  
  nrow = NULL,  
  title = NULL,  
  theme = theme_grey(),  
  ...  
)
```

Arguments

<code>object</code>	DigitalDLSorter object with <code>trained.model</code> slot containing metrics in <code>eval.stats.samples</code> slot.
<code>colors</code>	Vector of colors to use. Only vectors with a number of colors equal to or greater than the levels of <code>color.by</code> will be accepted. By default it is used a list of custom colors provided by the package.
<code>facet.by</code>	Variable used to display data in different panels. If it is <code>NULL</code> , the plot is not separated into different panels. The options are <code>nMix</code> (by number of different cell types) and <code>CellType</code> (by cell type).
<code>color.by</code>	Variable used to color data. The options are <code>nMix</code> and <code>CellType</code> .
<code>corr</code>	Correlation value displayed as annotation. The available metrics are Pearson's correlation coefficient (<code>'pearson'</code>) and concordance correlation coefficient (<code>'ccc'</code>). The argument can be equal to <code>'pearson'</code> , <code>'ccc'</code> or <code>'both'</code> (by default).
<code>filter.sc</code>	Boolean indicating if filter single-cell profiles and only display correlations of results associated with bulk samples (<code>TRUE</code> by default).
<code>pos.x.label</code>	Position on the X axis of the errors annotations. 0.95 by default.
<code>pos.y.label</code>	Position on the Y axis of the errors annotations. 0.1 by default.
<code>sep.labels</code>	Space separating annotations if <code>corr</code> is equal to <code>'both'</code> . 0.15 by default.
<code>size.point</code>	Size of points (0.1 by default).
<code>alpha.point</code>	Alpha of points (0.1 by default).
<code>ncol</code>	Number of columns if <code>facet.by</code> is different than <code>NULL</code> .
<code>nrow</code>	Number of rows if <code>facet.by</code> is different than <code>NULL</code> .
<code>title</code>	Title of the plot.
<code>theme</code>	ggplot theme.
<code>...</code>	Additional argument for <code>facet_wrap</code> ggplot function if <code>facet.by</code> is not equal to <code>NULL</code> .
<code>error.labels</code>	Boolean indicating if show average error as annotation.

See Also

[calculateEvalMetrics](#) [distErrorPlot](#) [blandAltmanLehPlot](#) [barErrorPlot](#)

Examples

```
## correlations by cell type
corrExpPredPlot(
  object = DDLSchung,
  facet.by = "CellType",
  color.by = "CellType",
  corr = "both"
)
## correlations of all samples mixed
corrExpPredPlot(
  DDLSchung,
  facet.by = NULL,
  color.by = "CellType",
  corr = "ccc",
  pos.x.label = 0.2,
  alpha.point = 0.3
)
```

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